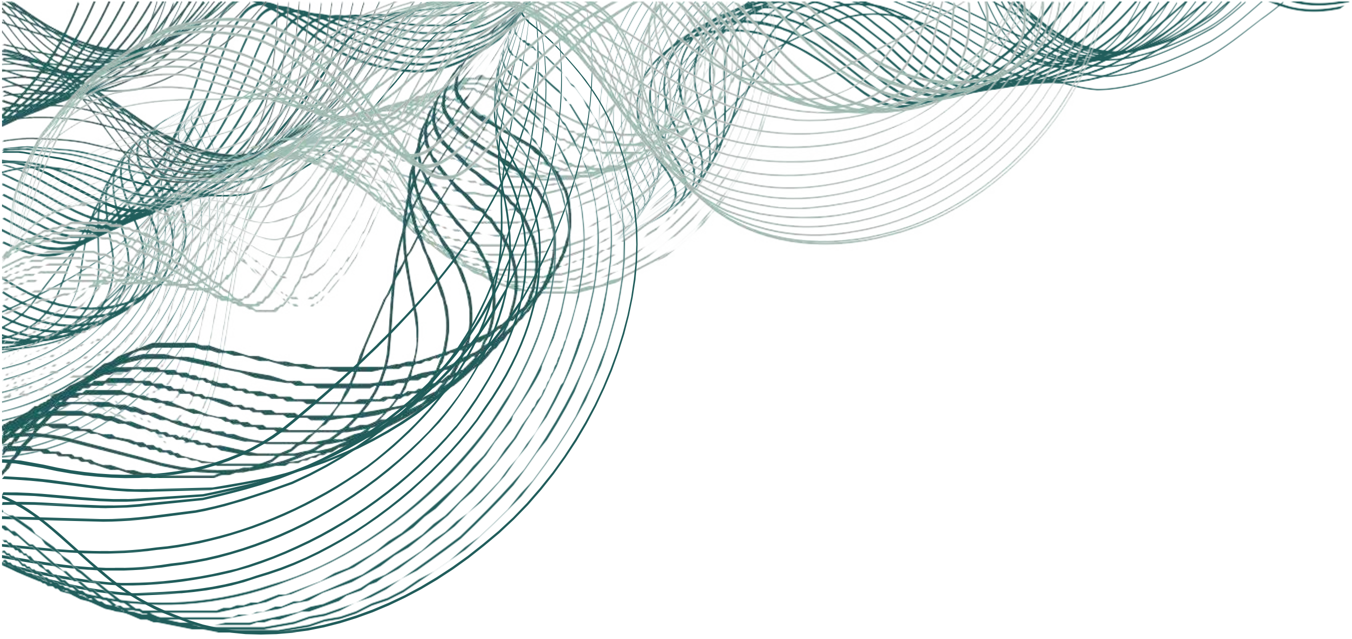
Proceedings Paper:

Burton, Simon, McDermid, John Alexander orcid.org/0000-0003-4745-4272, Garnett, Philip orcid.org/0000-0001-6651-0220 et al. (1 more author) (2020) An Initial Framework Assessing the Safety of Complex Systems. In: CCS2020 - Conference on Complex System 2020. Zenodo , p. 69.

https://doi.org/10.5281/zenodo.4419177

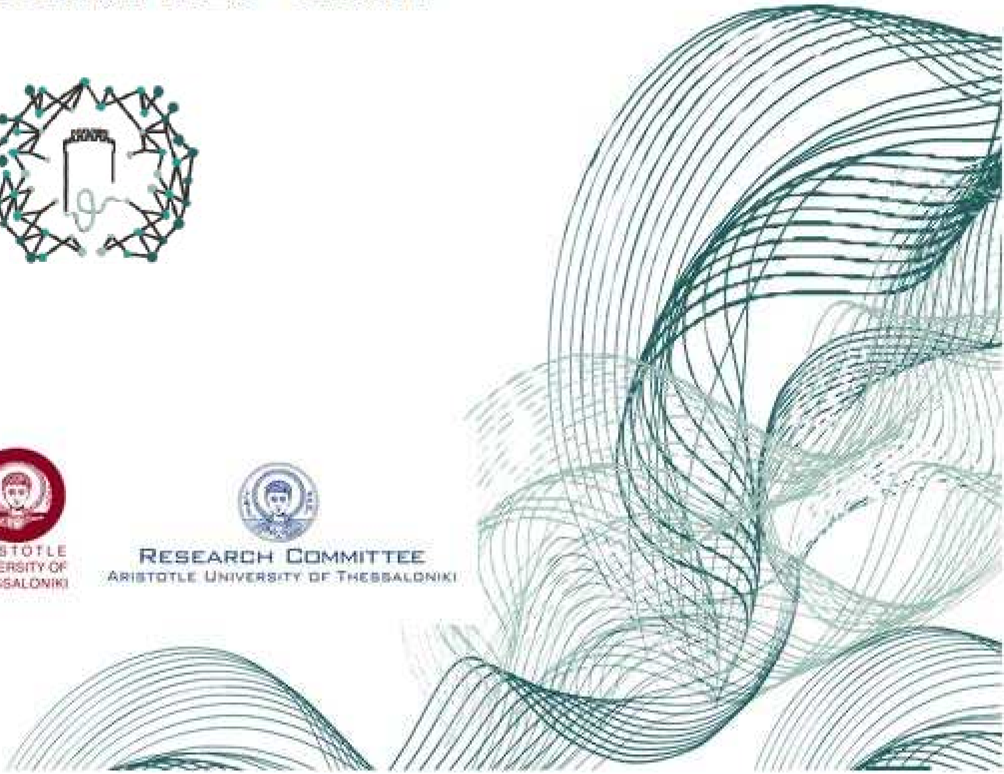


CCS2020

BOOK OF ABSTRACTS

CONFERENCE on COMPLEX SYSTEMS

7 - 11 December 2020 - ONLINE



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Preface

During this year 2020, and for the first time in the history of the series of Conferences sponsored by the Complex Systems Society, the CCS series, the annual meeting was organized virtually in the period December 7-11, 2020 and the young researchers CCS2020 Warm Up sessions on December 4, 2020. This Conference is in line with the series of meetings previously held in Singapore (2019), Thessaloniki, Greece (2018), Cancun, Mexico (2017), Amsterdam, Netherlands (2016), Tempe, Arizona, USA (2015), Lucca, Italy (2014), and more meetings in previous years. All these past meetings have delivered the highest quality of presentations, the most up-to-date findings, have been attended by the pioneers in the field of Complex Systems, as well by young aspiring students, numbering an attendance of close to one thousand. Our purpose is to deliver a well-tailored and focused event of the highest scientific and organizational standards, and for the first time in this online mode. We all for sure missed the warmth and cordiality that has been the tradition of past CCS meetings, but in view of the current world situation we were forced to this unprecedented step of meeting online. We all hope that next year we will return to the classical physical meetings that we all know.

This year’s meeting was organized by the Aristotle University of Thessaloniki in Greece. It was attended by ~600 scientists from ~60 different countries spanning ~18 different time zones. It comprised of four (4) full days of 17 plenary and invited presentations, and ~350 contributed oral, ignite, and poster presentations. Additionally, there was one (1) day of 16 satellite meetings, with over ~100 presentations. Here in this volume are given the abstracts of these presentations in the four regular days.

Furthermore, during this annual meeting we had some exciting special sessions that attracted interest. These included a presentation of journals from the European Physical Society and other publishers that specialize in Complexity topics. A session was given on funding opportunities by the European Commission. A round-table discussion took place with the subject of Covid-19 and Complexity. Finally, the annual presentation of awards took place, to honor members of our community who have given outstanding contributions to our field. Due to the online mode of presentations all events were recorded and are available to all participants.

On behalf of the Organizing Committee

Panos Argyrakis, Chairman of CCS2020

CCS2020

Plenary and Invited Talks

Spatial Organization and Survival of Biological Populations

C. Anteneodo, *PUC-Rio, Rio de Janeiro, Brazil,* *celia.fis@puc-rio.br*

The collective organization of living organisms in heterogeneous environments is a central issue in population dynamics. In particular, it is relevant to know how fragmented structures arise and, mainly, if in the long term the population will survive or become extinct. We address these problems from the perspective of single species populations. The FKPP equation provides a fundamental mathematical description of the spatial distribution at the mesoscopic level, governed by elementary processes (growth, competition for limited resources and random dispersion), and can be generalized in several realistic directions by including for instance: density-dependencies in growth and diffusion rates, selective spatial spreading, nonlocality, and fluctuations, under appropriate boundary conditions. We will discuss mainly the role of noise and boundary conditions on the survival of the population, as well as on the emergence of spatial structures (Fig. 1).

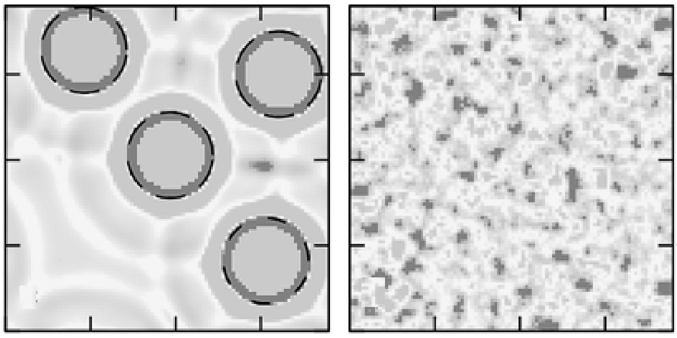

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Figure 1: Examples of patterns emerging from the interplay between spatial dynamics and environment heterogeneity [2]

Acknowledgements

We acknowledge partial support from CAPES, CNPq and FAPERJ.

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From Social Behavior to Network Structure for Animal Disease Transmission

Sweta Bansal

Department of Biology, Georgetown University, Washington DC 20057, USA

Past studies examining the disease costs of sociality have generally explored hypotheses that link larger group size to higher rates of infection transmission. However, beyond a simple dependence on group size, infection spread is largely influenced by the organization of infection-spreading interactions between individuals. In this talk, I will consider how we can use tools from network analysis with a meta-analytic approach to broadly understand the disease consequences of sociality from the individual level to the population scale, and the role of transmission mode in predicting network structure.

Understanding the COVID-19 pandemic - complexity, networks, dynamics and taking a nations temperature

Dirk Brockmann
Humboldt University, and Robert Koch Institute, Berlin, Germany

I will give a summary of scientific activities we designed and are still engaged in to unterstand the dynamics of the ongoing covid-19-pandemic. These activities include i) the application of computational models that we used to predict the global dissemination of the virus during the early phase of the pandemic, ii) the discovery of universal subexponential growth regimes in the first epidemic wave in China and other countries and a theoretical model that explains these observations by accounting for systematic behavioural changes in the population, iii) a nationwide high-resolution mobility monitor that we developed in Germany, that quantifies how much and in what way mobility was affected during lockdown periods and iv) a participatory experiment that we launched in March 2020 that involves >500,000 participants that donate resting heart rate, physical activity and sleep data by means of their smartwatches and based on which we designed and implemented a national fever thermometer to detect and predict the time course of confirmed cases of covid-19 in Germany and that is now used as an important surveillance data stream for the federal covid-19 situation.

Dynamical Motifs in Temporal Networks

Siew Ann Cheong

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Complexity Institute, Nanyang Technological University

Abstract

Recently, complexity scientists have suggested understanding complex systems from an information processing perspective [1–4], and the natural way to do so is to think of information processing pathways as functions transforming inputs to outputs. By combining a small number of building blocks in different ways, very many functions can be obtained [5]. In this talk, I will explain the connection between information processing by complex systems and recurrent activity sequences in their dynamics, and argue that an understanding of information processing pathways in terms of these dynamical motifs is important for designing effective interventions. I then describe two recently completed studies, where recurrent activity sequences (or *dynamical motifs*) were identified and tested for statistical significance. In the first study [6], we video recorded 37 shared book reading (SBR) sessions, and thereafter annotated each of these sessions for 26 activities (reading the book, comments and questions, management talk by the teacher, and responses from the children). For all SBR sessions, the annotations consisted of sequences of one activity followed by another (transitions). We tested the empirical data against a null model where activities occur randomly, to identify 34 transitions that occur more frequently than by chance, and visualize these transitions in the form of a static network. We then chose six significant transitions, and tested their extensions against the same null model to identify statistically significant length-3 sequences. We repeated this extension procedure to obtain length-4, length-5, and longer sequences until no further statistically significant extensions can be found. Finally, we organized the longest significant sequences into five families of dynamical motifs, and discuss their implications on the effectiveness of SBR. In the second study [7], we manually annotated 184 recorded lectures from the Nanyang Technological University for 17 activities, before visualizing the transitions between these activities in the form of a static network. With a modification in our statistical procedure, we tested sequences of lengths up to 8 for significance, to explore the phenomenon of adaptation in the dynamical motifs.

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Cascading Failures and Recovery in Complex Interdependent Networks

Shlomo Havlin, *Department of Physics, Bar-Ilan University, Ramat Gan,*

A framework for studying the vulnerability and the recovery of networks and interdependent networks will be presented. In interdependent networks, such as infrastructures, when nodes in one network fail, they cause dependent nodes in other networks to also fail. This may happen recursively and can lead to a cascade of failures and to a sudden fragmentation of the system. I will present analytical solutions based on percolation theory, for the critical thresholds and the giant component of a network of n interdependent networks. I will show, that the general theory has many novel features that are not present in the classical network theory. When recovery of components is possible, global spontaneous failure and recovery of the networks, as well as hysteresis phenomena, occur. The theory suggests an optimal repair strategy for a system of systems.

I will also show that interdependent networks embedded in space are significantly more vulnerable compared to non-embedded networks. In particular, small localized attacks of zero fraction but above a critical size may lead to cascading failures that dynamically propagate and yield catastrophic consequences.

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Self-Organization and Developments of Super-Individuals in Large Scale Systems: HoneyBees, Tetrahymena, Web data, Boids ,,,

Takashi Ikegami *Department of General Systems Studies, the Graduate School of Arts and Sci, University of Tokyo, 3-8-1 Komaba, Meguroku, Tokyo , Japan, ikeg@sacral.c.u-tokyo.ac.jp*

Using powerful algorithms, we propose a new theory of collective intelligence by studying the dynamics of living and non-living populations and their collective phenomena. In particular, I will discuss two perspectives.

First, we analyze a large amount of individual tracking data obtained from actual biological experiments (such as honeybees, Tetrahymena,,) to develop a new theory of emergent phenomena in collective motion, especially the macroscopic emergence phenomenon called the super-individual. A super-individual is a collective state created from (replicating) individuals that behave as if they were individuals.

The second is to build a theory of collective intelligence by analyzing the collective motion of populations at scales of tens of millions of individuals through large scale computer experiments (e.g. Boids model). Collective intelligence here is the “vital” intelligence as a behavior of a group of individuals, and we explore the possibility in a large swarming dynamics.

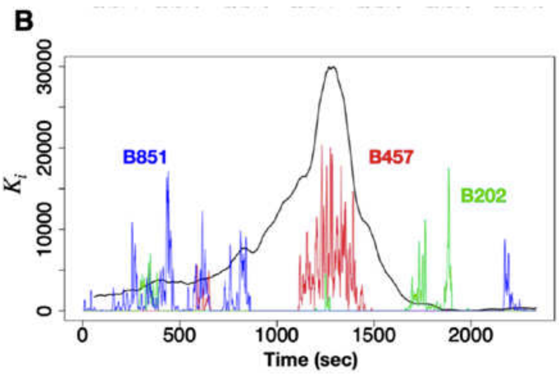

Figure 1: An example of $\square_{g}(\square)$ and $\square_{i}(\square)$ (the kinetic energy of bees) in an endogenous bursting region. The black curve describes $\square_{g}(\square)$, and the colored curves describe $\square_{i}(\square)$ (for individuals with the bCodes: B457, B202 and B851). [2]

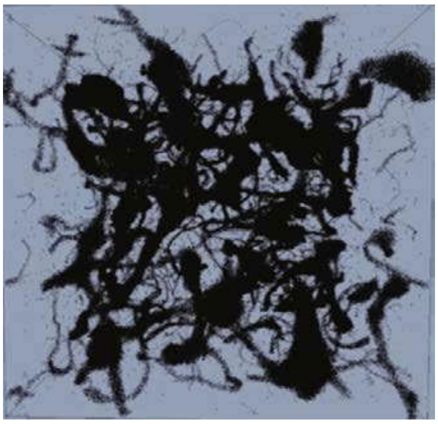

Figure 2: Snapshots of simulated swarming behavior of Boids model. The total number of boids is 524288. [1]

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Informal Networks and Formal Markets

Matthew O. Jackson[1,2]. *(1) Stanford University, USA, jacksonm@stanford.edu. (2) Santa Fe Institute, USA*

I discuss the interaction between social networks and economic institutions: how information flows through a network to help people learn about the availability of a formal market in the form of microfinance [1,2], as well as how the availability of that microfinance changes the structure of social networks [3,4]. The presence of the network is instrumental to gaining participation in the market, and the presence of that market erodes social networks – not just borrowing and lending networks but advice sharing and other networks.

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On Coordination

J.A Scott Kelso[1,2] (1) Center for Complex Systems & Brain Sciences, Florida Atlantic University, Boca Raton, USA, jkelso@fau.edu.
(2) Intelligent Systems Research Centre, Derry~Londonderry, N. Ireland

Key concepts of complexity science, such as nonlinearity, emergence and self-organization all follow from the old adage that the whole is greater than (or different from) the sum of the parts [1]. The fact that we use the word 'parts' (and like words such as components, elements, and even 'agents') implies that nature may be broken into separate pieces, basic 'building blocks' that somehow are brought together to produce coordinated behavior. Yet we know that even in the simplest complex system of just two components interacting nonlinearly, this is a complicated business. Inspired originally by physical theories of self-organization in open, nonequilibrium systems [2] the science of coordination (Coordination Dynamics) seeks to understand how coordinated patterns of behavior form and change at many scales and for multiple functions in living things [3]. In Coordination Dynamics a "part" is actually a softly assembled collective called a *synergy*. The synergy is a minimally complex system: perturbing it in one place often has remote effects somewhere else, in such a way as to preserve function. A conceptual and practical benefit of the synergy is that it can be defined in terms of *collective variables* and their dynamics. As I will show in this talk, using both experiment and theory, the basic coordination dynamics accommodates synergies of just a few elements and synergies composed of many (heterogeneous) elements [4] A dominant feature of the dynamics is *metastability* in which, strictly speaking, there are no coordinated states, only opposing tendencies, e.g. segregation ~ integration, competition ~ cooperation, individual ~ collective etc. Such complementary pairs fall directly out of the coordination dynamics [5]. Finally, new work--still preliminary [6]--suggests that synergies become functional when the organism (here a human baby) realizes it is an *agent* and can make things happen in the world [7]. Initially spontaneous self-organized coordination thus becomes directed.

Acknowledgements

Work supported by NIMH Grant MH080838 and FAU Foundation

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Collective motion, collective decision-making, and collective action

Simon A. Levin *(Princeton University, USA)*

There exists a rich history of research on the mathematical modeling of animal populations. The classical literature, however, is inadequate to explain observed spatial patterning, or foraging and anti-predator behavior, because animals actively aggregate. This lecture will begin from models of animal aggregation, the role of leadership in collective motion and the evolution of collective behavior, and move from there to implications for decision-making in human societies. Ecological and economic systems are alike in that individual agents compete for limited resources, evolve their behaviors in response to interactions with others, and form exploitative as well as cooperative interactions as a result. In these complex-adaptive systems, macroscopic properties like the flow patterns of resources like nutrients and capital emerge from large numbers of microscopic interactions, and feedback to affect individual behaviors. I will explore common features of these systems, especially as they involve the evolution of cooperation in dealing with public goods, common pool resources and collective movement across systems; Examples and lessons will range from bacteria and slime molds to groups to insurance arrangements in human societies and international agreements on environmental issues.

How easy is it to be a hub? What the dynamical complexity can reveal about the network structure.

I. ***Leyva***[1,2], *A. Tlaie*[3], *I. Sendiña-Nadal*[1,2], *L. M. Ballesteros-Esteban*[1,2] *(1) Complex Systems Group & GISC, Universidad Rey Juan Carlos, Madrid, Spain,* inmaculada.leyva@urjc.es*. (2) Center for Biomedical Technology, Universidad Politécnica de Madrid, Spain (3) Italian Institute of Technology, Naples, Italy.*

Since the beginning of the research on the dynamics of complex networks, the deep relationship between topology and dynamics has been thoroughly explored with regard the synchronization between the nodes' dynamics, and the knowledge gathered so far has driven the advance in crucial applications.

However, there are cases in which the system performs its activity in a partial or weakly synchronization regime to preserve the balance between functional integration and segregation, whereas full synchronization is pathological. But even in this far from synchronized state, each coupled unit is encoding in its own dynamics the signature of its structural role. We explore how this prominent feature could be used to extract information about the network, without having the need to make any reference to pairwise correlations, even in those situations where the structure is unknown. The effect of the coupling strength against the dynamical complexity of the nodes is found to be a function of their topological roles, with nodes of higher degree displaying lower levels of complexity (Fig. 1). We provide several examples of theoretical models of chaotic oscillators, pulse-coupled neurons, and experimental networks of nonlinear electronic circuits evidencing such a hierarchical behavior. Importantly, our results imply that it is possible to infer the degree distribution of a network only from individual dynamical measurements [1].

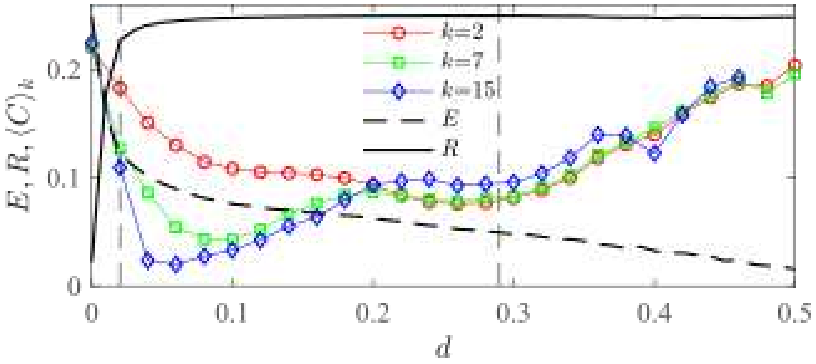

Figure 1: Averaged k-class complexity C_k as a function of coupling in scale-free networks.

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Reliability & Resilience in urban traffic

Daqing Li *(1) School of Reliability and Systems Engineering, Beihang University, No. 37 Xueyuan Road, Beijing, China, daqingl@buaa.edu.cn.*

Given Holling's definition of resilience in ecology, resilience studies in engineering fields have recently begun to focus on the system's ability to absorb, adapt, and recover. While traditional system reliability engineering has focused on the design of a system to avoid operational collapse, the more recent study of system resilience has shifted the viewpoint for system reliability and safety from "safe - fail" to "fail - safe", suggesting a systematic management paradigm to recover from unexpected disturbances. It is found that many natural systems can become stabilized at different levels under the influence of random events, which suggests the existence of different domains of attraction in these systems. In this sense, resilience suggests multiple metastable states in ecology, climate, and biology systems. Meanwhile, for engineering systems including critical infrastructures, it is usually assumed that the system has only one single equilibrium state and will return to this original state after perturbations. Identification of multiple network states suggests the necessity of paradigm shift for the corresponding complex system management. In this talk, I will introduce our recent findings about Reliability & Resilience in urban traffic.

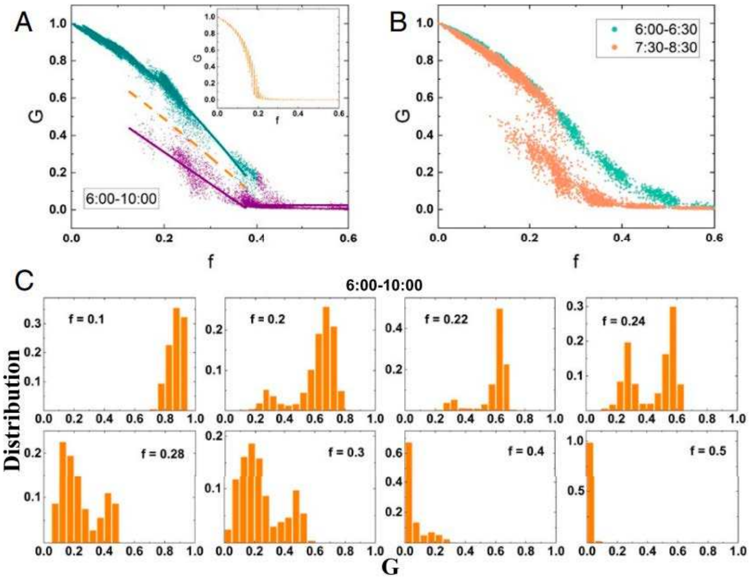

Figure 1: Multiple states in real-time traffic percolation.

Guanwen Zeng, Jianxi Gao, Louis Shekhtman, Shengmin Guo, Weifeng Lv, Jianjun Wu, Hao Liu, Orr Levy, **Daqing Li***, Ziyou Gao*, H. Eugene Stanley*, Shlomo Havlin. (2020). "Multiple metastable network states in urban traffic". *Proceedings of the National Academy of Sciences* 117(30), 17528--17534.

Combining complex network analysis and machine learning for image classification and outlier detection

Cristina Masoller, *Departament de Física, Universitat Politècnica de Catalunya, Rambla St. Nebridi 22, Terrassa 08222, Barcelona, Spain, cristina.masoller@upc.edu*

Today, unprecedented advances in machine learning applied to biomedicine have led to a variety of unsupervised techniques for remote image analysis, enabling cost-effective early detection of diseases. In this talk I will present various methods for ophthalmic image analysis, which take advantage of network theory and non-linear data analysis tools. First, I will present an unsupervised machine learning algorithm for optical coherence tomography (OCT) image analysis, which extracts features that discriminate between healthy and unhealthy subjects [1]. Then, I will show how the analysis of the tree-like structure of the network of vessels in the retina allows to extract features that discriminate between healthy subjects and those with glaucoma or diabetic retinopathy [2]. Finally, I will discuss how the network percolation transition can be exploited for outlier mining in different types of data sets, including ophthalmic images [3].

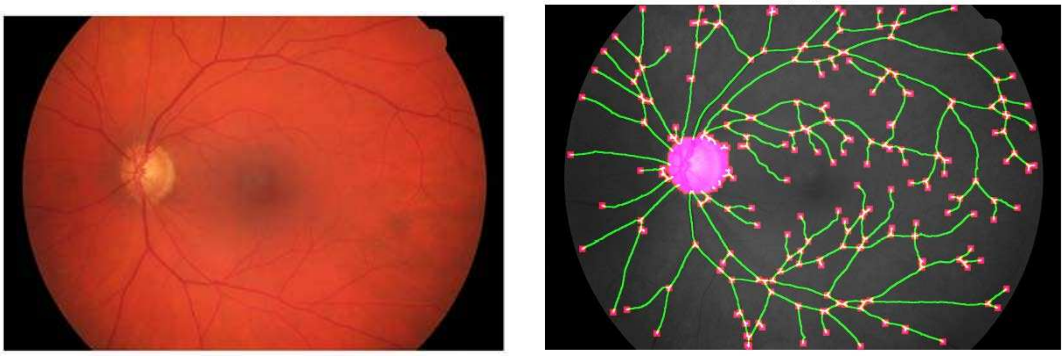

Figure 1: Example of a retinal fundus image and the extracted network.

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Diversity in humans and pathogens: implications for the dynamics of epidemics and the impact of interventions

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In the last decades, new network theories and epidemiological evidences have substantially advanced our knowledge about how acute respiratory infections spread in the human population. Temporal and multi-layer networks provide a paradigmatic example. These frameworks allow for clearly describing the heterogeneous connectivity features driving transmission, e.g. different connectivity by settings (household, workplace, school, etc.), and occasional vs. recurrent encounters. However, intrinsic properties of individuals and pathogens, besides individuals' connectivity are central in shaping the dynamics of transmission. For instance, individuals may be heterogeneous in their susceptibility and their probability to develop a severe form of infection. On the other hand, heterogeneous pathogens and pathogen strains alter the dynamics and burden of an epidemic and are among the drivers of pathogen emergence events. These levels of complexity mutually affect each other which makes it difficult to disentangle their relative role on the epidemic unfolding and the effect of interventions. During the talk I will tackle this issue, presenting recent theoretical and applied works. I will review some studies on the COVID-19 pandemic and discuss the implications of multi-strain/multi-pathogen interaction for the emergence of new pathogens and their co-existence.

Uncertainty and institutional governance in climate change dilemmas

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When attempting to avoid global warming, individuals often face a social dilemma in which, besides securing uncertain future benefits, it is also necessary to reduce the chances of future losses. In this talk, I will resort to mathematical modeling and lab experiments to offer an analysis of this type of dilemmas. I will start by discussing how *timing uncertainty* — related to when collective targets need to be reached — changes individuals' behavior [1]. Our analysis shows that this type of uncertainty reduces collective success, and increase polarized behaviors and inequality. This outcome also suggests the inclusion of new incentives handling these societal issues. Inspired by the design principles proposed by the late Nobel Prize Elinor Ostrom [2], we study the evolution and impact of a new form of institutional sanctioning, where punishment is graduated, growing with the incidence of free-riding [3]. We develop an analytical model capable of identifying the conditions under which this design principle is conducive to the self-organization of stable institutions and cooperation, and in which conditions rewards may perform better than sanctions [4]. In particular, we show that rewards are essential to initiate cooperation in this class of non-linear dilemmas. On the other hand, we find that sanctions are instrumental in maintaining cooperation. Altogether, our results are gratifying, given the a-priori limitations of effectively implementing strict forms of sanctioning in international agreements.

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A History of Possible Futures: What history tells us about our Age of Discord

Peter Turchin
Complexity Science Hub Vienna and *University of Connecticut*

Social and political turbulence in the United States and a number of European countries has been rising in recent years. My research, which combines analysis of historical data with the tools of complexity science, has identified the deep structural forces that work to undermine societal stability and resilience to internal and external shocks. Here I look beneath the surface of day-to-day contentious politics and social unrest, and focus on the negative social and economic trends that explain our current “Age of Discord.” I also discuss the current research by my group aiming to translate these insights from historical analysis into a computational model that would allow us to construct a series of probabilistic scenarios of social breakdown and recovery.

Prediction in immune repertoires

***Aleksandra M. Walczak**. (1) CNRS, LPENS, 24 rue Lhomond, 75005 Paris, France*

Living systems often attempt to calculate and predict the future state of the environment. Given the stochastic nature of many biological systems how is that possible? Since the functioning of the repertoire relies on statistical properties, statistical analysis is needed to identify responding clones. Using such methods I will describe the repertoire level response to the SARS-CoV-2. I will also show that even a system as complicated as the immune system has reproducible outcomes. Yet predicting the future state of a complex environment requires weighing the trust in new observations against prior experiences. In this light, I will present a view of the adaptive immune system as a dynamic Bayesian machinery that updates its memory repertoire by balancing evidence from new pathogen encounters against past experience of infection to predict and prepare for future threats.

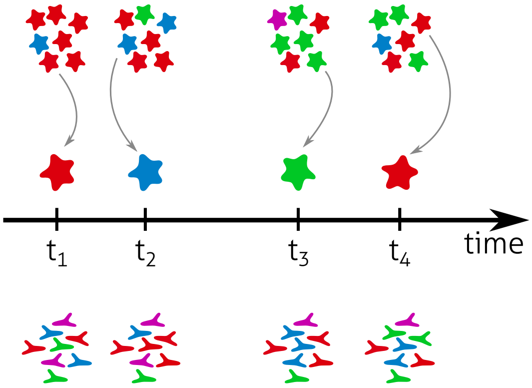

Figure 1: Predicting the future state of the immune system.

Acknowledgements (optional)

This work was supported by the ERC Consolidator Grant 724208.

Economic Inequality from a Statistical Physics Point of View

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Inequality is an important and seemingly inevitable aspect of the human society. Various manifestations of inequality can be derived from the concept of entropy in statistical physics. In a stylized model of monetary economy, with a constrained money supply implicitly reflecting constrained resources, the probability distribution of money among the agents converges to the exponential Boltzmann-Gibbs law due to entropy maximization. Our empirical data analysis shows that income distributions in the USA, European Union, and other countries exhibit a well-defined two-class structure. The majority of the population (about 97%) belongs to the lower class characterized by the exponential ("thermal") distribution, which we recently observed in the data for 67 countries around the world. In contrast, the upper class (about 3% of the population) is characterized by the Pareto power-law ("superthermal") distribution, and its share of the total income expands and contracts dramatically during booms and busts in financial markets. Globally, energy consumption (and CO_2 emissions) per capita around the world shows decreasing inequality in the last 30 years and convergence toward the exponential probability distribution, as expected from the maximal entropy principle. All papers are available at http://physics.umd.edu/~yakovenk/econophysics/.

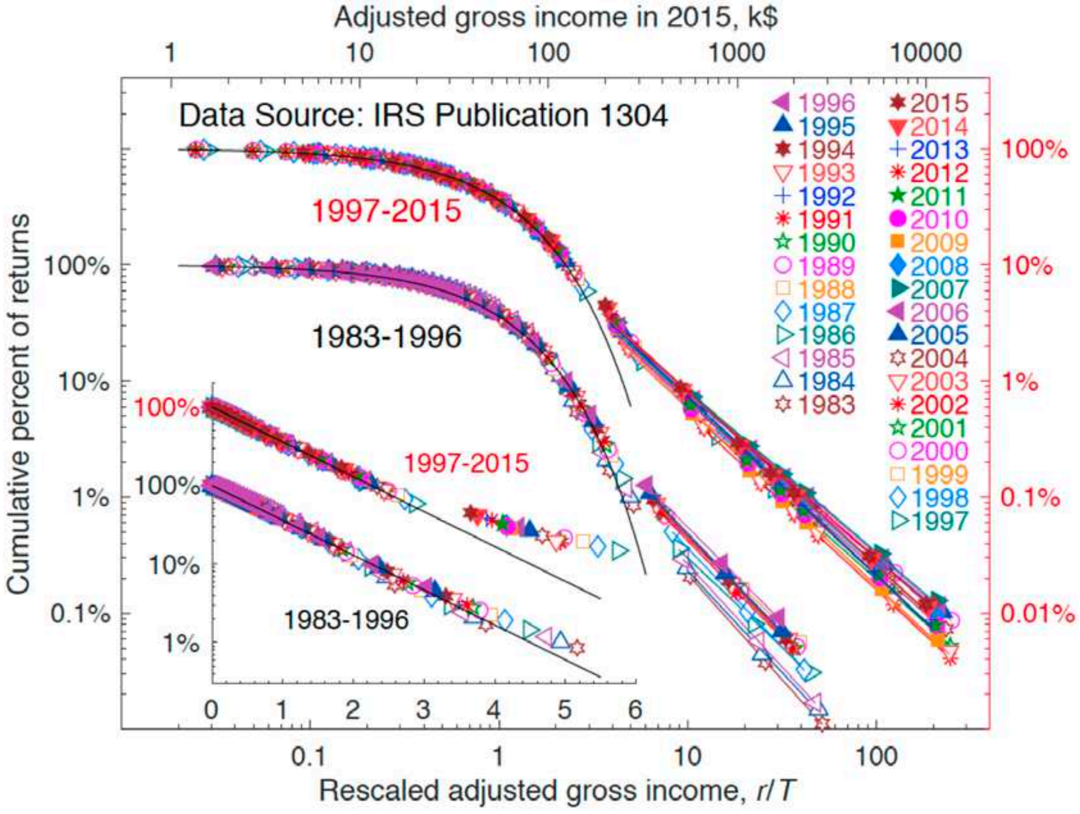

Figure 1: Normalized income distribution in USA 1983-2015 in log-log and log-linear scales.

CCS2020

Contributed Presentations

COVID-19 Reproduction Number Estimation: Spatial and Temporal in Convex Optimization to Promote Piecewise Smoothness

P. Abry[1], *N. Pustelnik*[1], *S. Roux*[1], *P. Jensen*[1], *P. Flandrin*[1], *R. Gribonval*[2], *C.-G. Lucas*[1], *E. Guichard*[3], *P. Borgnat*[1], *N. Garnier*[1]. *(1) Université de Lyon, ENS de Lyon, CNRS, Laboratoire de Physique, France, patrice.abry@ens-lyon.fr (2) Université de Lyon, ENS de Lyon, UCB Lyon 1, Inria, LIP, France (3) Université de Lyon, ENS de Lyon, CNRS, Lab. Triangle, France*

Among the different indicators that quantify the spread of an epidemic such as the on-going COVID-19, stands first the reproduction number which measures how many people can be contaminated by an infected person. In order to permit the monitoring of the evolution of this number, a new estimation procedure is proposed here, assuming a well-accepted model for current incidence data, based on past observations [1]. The novelty of the proposed approach [2] is twofold: 1) the estimation of the reproduction number is achieved by convex optimization within a proximal-based inverse problem formulation, with constraints aimed at promoting piecewise smoothness; 2) the approach is developed in a multivariate setting, allowing for the simultaneous handling of multiple time series attached to different geographical regions, together with a spatial (graph-based) regularization of their evolutions in time. The effectiveness of the approach is first supported by simulations, and two main applications to real COVID-19 data are then discussed. The first one refers to the comparative evolution of the reproduction number for a number of countries, while the second one focuses on French departments and their joint analysis, leading to dynamic maps revealing the temporal co-evolution of their reproduction numbers. Additionally, we will report new work showing how to deal, in this framework, with outliers coming from errors in data reporting or other events.

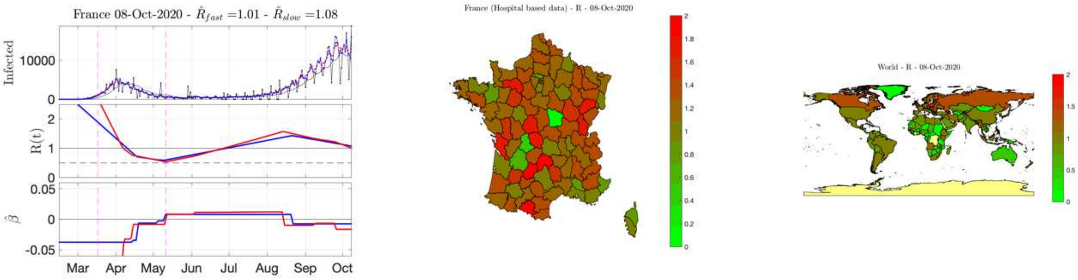

Figure 1: Current estimate of the Reproduction number in France (left), at the level of departments in France using the graph-based regularization (center) and for the world (right). Maps update daily at https://perso.ens-lyon.fr/patrice.abry/, and interactive maps: http://barthes.enssib.fr/coronavirus/cartes/R-Covid-19-today-World.svg

Acknowledgements

The authors participate to IXXI, the Complex Systems Institute in Lyon.

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Roughness of Vicinal Surface: Crossover from Berezinskii-Kosterlitz-Thouless-Rough to Kardar-Parisi-Zhang-Rough Surfaces

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Roughness of vicinal surface is studied by calculating surface width using the Monte Carlo Method in the non-equilibrium steady state [1] in order to clarify discrepancies between theoretical results and experiments. The adopted model is a restricted solid-on-solid (RSOS) model with a discrete Hamiltonian,

$$\mathscr{H} = \sum_{\{m,n\}} \{\varepsilon[|h(m+1,n)-h(m,n)| + |h(m,n+1)-h(m,n)|] - \Delta\mu\, h(m,n)\} + \mathscr{N} E_{\mathrm{surf}},$$

where $h(m,n)$ is the surface-height at a site (m,n), ε is the microscopic ledge energy, N is the total number of unit cells on the (001) surface, Δμ is the driving force for growth, and E_{surf} is the surface energy per unit cell. Here, “restricted” means that the surface-height difference between nearest-neighbor sites is restricted to 0, and ±1. The temperature T, driving force for growth Δμ, system size L, and surface slope dependences of the surface width $g^{1/2}W$ are calculated for vicinal surfaces tilted between the (001) and (111) surfaces [2]. Initial 2×10^8 Monte Carlo step/site (MCS/site) are discarded. Surface width is averaged over following 2×10^8 MCS/site. We found a crossover from a Berezinskii–Kosterlitz–Thouless (BKT) rough surface to a Kardar–Parisi–Zhang (KPZ) rough surface (figure 1). We also found that the crossover point from a BKT (logarithmic) rough surface to a KPZ (algebraic) rough surface is different from the kinetic roughening point for the (001) surface. Ad-atoms, ad-holes, islands, and negative-islands on the surface are found to block surface fluctuations, which contributes to making a BKT-rough surface.

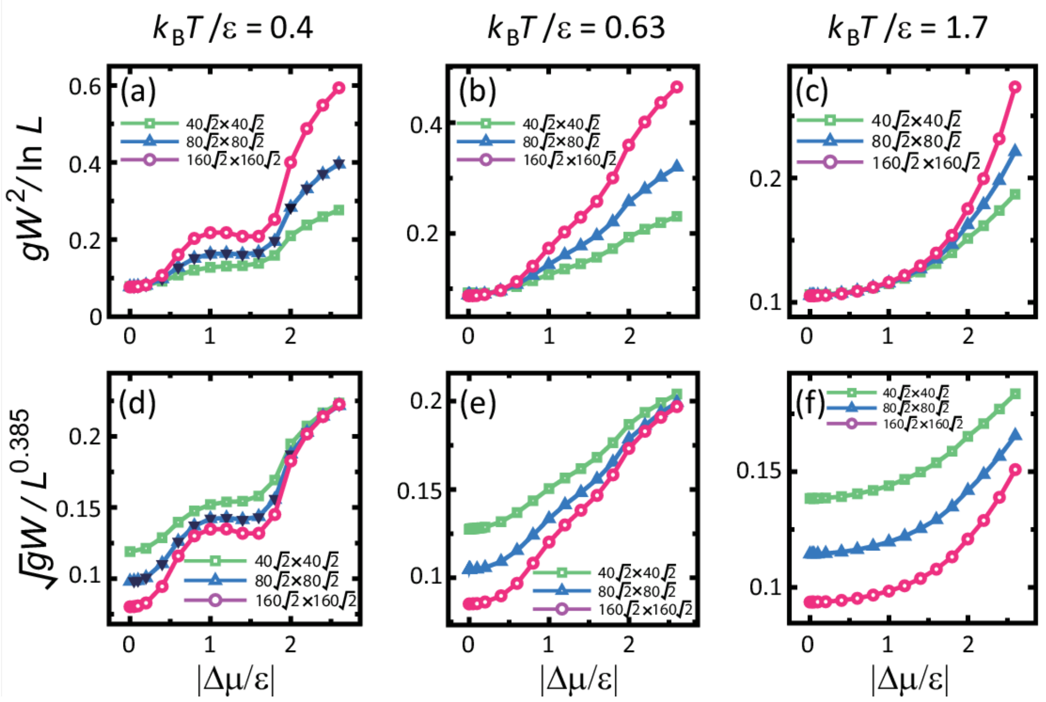

Figure 1: Scaled surface width.

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Studying The Effect of Population Size on The Cooperation in Healthcare System

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In this research, we investigate the evolution of cooperation in a complex system, namely the healthcare system in England, which is made up of populations consisting of different healthcare providers interacting with patients. Our investigation examines individual agents' behaviors as viewed by an external policymaker, in this case, the Health Department. Generally, policies are initiated and managed by the Health Department, which allocates a specific budget to interfere. To this end, our analysis here is carried out based on a baseline model we developed in [1]. This previous work focuses on numerical analysis of the proposed healthcare model, studying evolutionary dynamics of three well-mixed finite populations. The analytical approach we adopted therein relied on the assumptions of rare behavioral mutation by the agents, and that all populations having an equal size. Our finding shows that agents from all three populations tend to not cooperate (i.e. defect) [1]. While these simplified assumptions allowed us, as a very first step, to provide clear mathematical analysis, they prevented us from analyzing some important factors. Namely, mutation or behavioral exploration, where agents can freely experiment with new behaviors, has been shown to play an important role in enabling cooperation in the context of social dilemmas [2]. Overall our finding shows cooperation tends to increase with N_S when b_R is sufficiently large, while it tends to decrease with N_S when b_R is small. That is, trying to meet patients' demand only has a positive effect on cooperation outcomes if providers' benefit is secured, regardless of high patients' benefit (i.e $b_R = 3$).

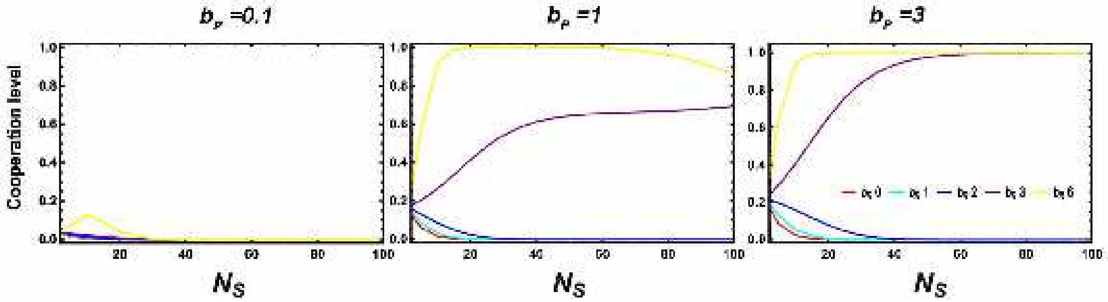

Figure 1: The frequency that cooperation is adopted by all three populations (i.e. frequency of CCC) for increasing providers' capacity to meet patients' demand (i.e. for increasing of providers' population size). We assume $N_1 = N_2 = N_S$, while fixing $N_3 = 100$. Results are obtained using Small Mutation Limit for different values of $b_R = 0, 1, 2, 3$ and 6, and $b_P = 0{:}1$; 1 and 3. We observe that when b_P and b_R are sufficiently large, cooperation is abundant. For sufficiently large b_P (1 and 3), cooperation tends to increase with N_S when b_R is sufficiently large while decrease otherwise. Other parameters are: c_I ; c_T ; $c_M = 1$; $\varepsilon = 0.2$ and $\beta = 0.1$.

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Data-driven contact structures: from homogeneous mixing to multilayer networks

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The modeling of the spreading of communicable diseases has experienced significant advances in the last decades. This has been possible due to the proliferation of data and the development of new methods to gather, mine and analyze it. A key role has also been played by the latest advances in new disciplines like network science. Nonetheless, current models still lack a faithful representation of many possible heterogeneities and features that can be extracted from data. Here, we bridge a current gap in the mathematical modeling of infectious diseases and develop a framework that allows to account simultaneously for both the connectivity of individuals and the age-structure of the population. We compare different scenarios, namely, i) the homogeneous mixing setting, ii) one in which only the social mixing is taken into account, iii) a setting that considers the connectivity of individuals alone, and finally, iv) a multilayer representation in which both the social mixing and the number of contacts are included in the model. We analytically show that the thresholds obtained for these four scenarios are different. In addition, we conduct extensive numerical simulations and conclude that heterogeneities in the contact network are important for a proper determination of the epidemic threshold, whereas the age-structure plays a bigger role beyond the onset of the outbreak. Altogether, when it comes to evaluate interventions such as vaccination, both sources of individual heterogeneity are important and should be concurrently considered. Our results also provide an indication of the errors incurred in situations in which one cannot access all needed information in terms of connectivity and age of the population.

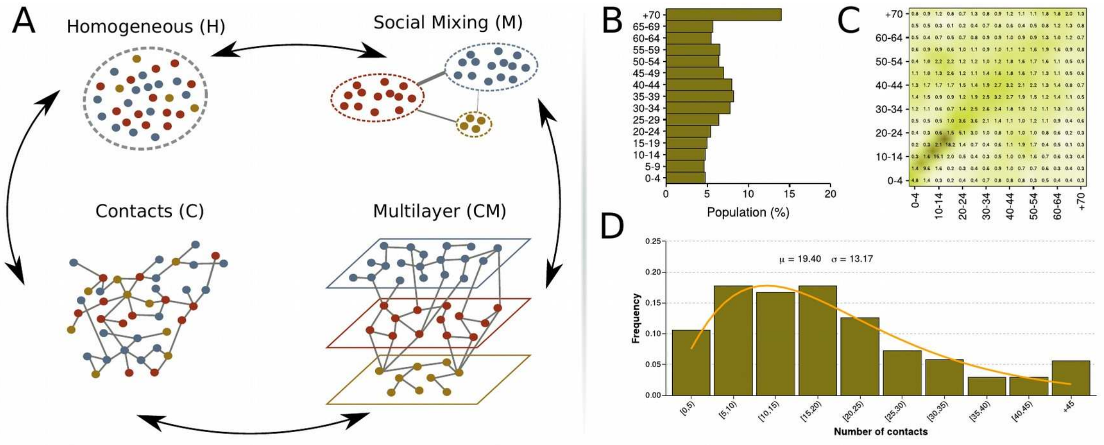

Figure 1: Modeling the contact patterns of the population. The most basic approach, homogeneous mixing (A:H), has low data requirements. For more heterogeneous models such as multilayer networks (A:CM), a large amount of data is required (B: age distribution, C: age-mixing patterns, D: contact distribution).

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A Study of the Network of Military Treaties

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Since the conclusion of World War II in 1945, international military conflicts have largely been between nations of great power and “underdog” nations. This paper studies the network of military treaties between states in the international system. Examining this network leads to important conclusions about how state actors are prone to respond if an international or regional conflict were to arise. One influential such scenario was the launch of World War I, when great power nations got dragged into conflict due to their binding military treaties with weaker auxiliary states. The network below is highly connected with all small countries connected to “hubs” representing global powers. Main centrality measures and network analytics are performed on the data and differences between binding and non-binding treaties are highlighted. All data are taken from [1].

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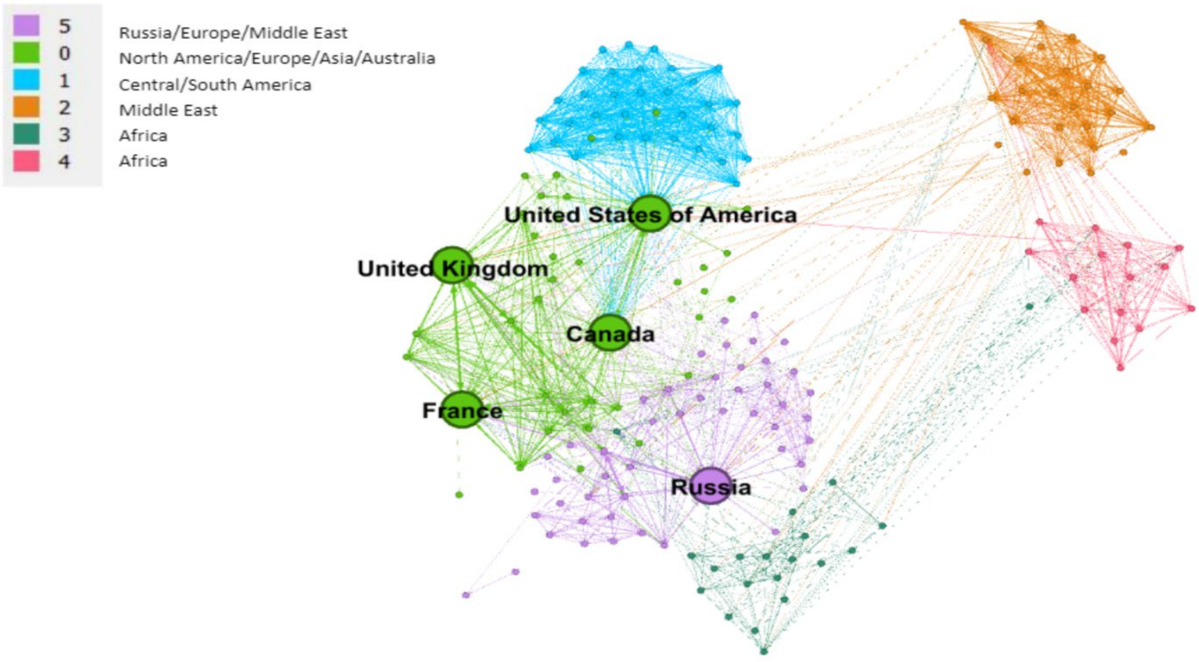

Figure 1 Network overview partitioned by modularity class.

Agent Based Models and Simulation in Social Sciences: A bibliometric review

Emiliano Alvarez [*] Gabriel Brida[†] Silvia London[‡]

Abstract

Since the first agent-based models (ABM), the scientific community has been interested in making not only the results of computational models understandable but also the modeling description, to facilitate their replication. The form that has been adopted to a greater extent has been the ODD (Overview, Design concepts, and Details) protocol, which provides a generic structure for its documentation. This protocol provides a way to clearly explain the procedures and interactions of the complex systems to be analyzed, with applications that have spread across different disciplines. This work will show a bibliometric review of the articles that emerged from the first publication of this protocol in 2006, analyzing the development that ABMs have had in the social sciences. A description will be made of the lines of research with the greatest activity and the links between them will be analyzed; while summarizing the countries, universities, and journals with the highest contributions.

Keywords: Social Simulation; Complex Systems; ODD protocol; Bibliometric Analysis

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[1] "...computer programs offer the possibility of creating 'artificial' societies in which individuals and collective actors such as organisations could be directly represented and the effect of their interactions observed." (Gilbert, 2004)

Symmetries Uncover the Minimal Regulatory Network for Logical Computations in Bacteria

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The use of symmetries to reduce a complex system to its underlying components and interactions is a widely known useful tool. Recently we have shown that relevant symmetries of biological network systems allow for a systematic reduction of the networks that preserves information flow. Symmetry fibrations, which consists of grouping nodes that share an isomorphic input tree into equivalence relations called fibers, allows for the collapse of the network while preserving information flow. Further reducing by the k-core decomposition of the collapsed network gives the minimal network driving the dynamics of the entire network. In gene transcriptional regulatory networks (TRN) of model bacteria *E. coli*, where fibers consist of genes that are synchronized for being co-expressed, this process gives the minimal transcriptional regulatory network. This minimal structure is understood as a combination of genetic circuits which perform core logical computations from outside inputs and the current state of the bacteria. We found symmetry breaking circuits and synthetically constructed circuits from synthetic biology at the computational core of the network controlled by outside inputs which function as the controllers of the circuits. Hence, symmetry principles unveil the minimal TRN that corresponds to the core computational machinery of bacteria.

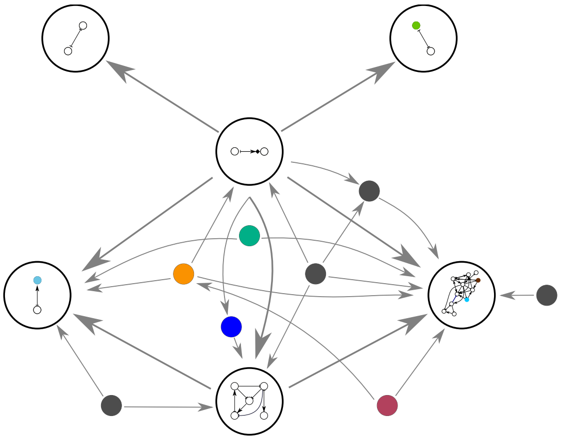

Figure 1: Minimal Transcriptional Regulatory Network of *E. coli*

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An Agent Based Model Of Economic Growth With Adaptive Agents

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This paper presents an agent-based model of economic growth featuring adaptive agents. It aims at modeling the emergence and evolution of complexity, here understood as the (neg) entropy of the methods of production used by firms and final goods sold on a market to households.

Economic growth is a process of growth of knowledge: and moreover, that process may be combinatorial and recombinant in nature [1], as firms and entrepreneurs learn how to combine goods to satisfy, and indeed create, demand. This process of discovery and creation is at the heart of business cycles, as agents go about inventing new products, new means of productions, and replacing methods and preferences. New goods and services borne out of entrepreneurial activity displace old ones; similarly [2] state that the generation and resolution of economic diversity are the main engines of growth. This process is continuous [3] and at the heart of the gales of “creative destruction” characterizing Schumpeterian growth. In the ethos of evolutionary economics, this process is akin to a biological one. In this view, more than a mechanism for the spreading of information through prices, the market is a testbed for new ideas - it is the selection environment that places a fitness on entrepreneurial decisions, in which the resulting ideas thrive or die. Moreover, markets for goods emerge endogenously as combinations of knowledge, ambition, new technologies and consumer needs in a Variation-Selection- retention environment fed by a population of rules.

The agent based model proposed here is built on a metaphor of biological evolution, it features gales of Schumpeterian “creative destruction” in both production methods used and final goods sold as an emergent process, and is adaptive in that firms learn about household preferences and these adapt to labour search by firms. It features both a labour market and a final goods market where firms interact with households. Households have a labour capacity they can supply every period. Firms hold a population of blueprints that consist in an instruction set for combining intermediate goods along with the labour supply of households to produce a final good.

The observed results of simulations are the time series of GDP, Investment, entropy of the distribution of the populations of final goods and blueprints, and diffusion of technological standards, along with suggestions for further work.

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Higher-Order Structures Surrounding Functional Hubs in Human Connectomes

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We consider whole-brain networks that we have generated at the Budapest connectome server based on the brain imaging data from Human Connectome Project [1]. It is mapped from the diffusion tensor imaging data available from the human Connectome Project. The network nodes are identifed as the grey-matter anatomical brain regions, while the edges consist of the white-matter fibres between them. Beyond the pairwise connections between the nodes, we have shown that the human connectomes have a rich structure of simplicial complexes which are defined as aggregates of simplices (cliques) of different sizes [2,3]. With this structure at hand, we have identified the leading hubs, which appear to be the central brain regions, see Fig., through which multiple neural pathways go. We identified the core subgraph, consisting of the hubs and all simplexes attached to them. Simplicial complex is created from underlying mathematical graph using Bron-Kerbouch algorithm which identifies cliques and shared faces together forming simplicial complex. By analysis of the architecture of these simplicial complexes, we have determined the structure through which the hubs perform their function by transferring the neural signals between different parts of the brain. Analysis of structure of simplicial complex, provided us with information about local and global (sub)sctructure of high-order connectivity, i.e. structure vectors, face vector [4], topological entropy which describes occupation of every layer of simplicial complex [5]. Moreover, our analysis of higher-order structures in these core graphs reveals some differences between female and male connectomes. This analysis enabled us to identify brain regions participating in simplexes of different orders that are attached to hubs as well as their hierarchical organisation, which manifests in sharing common weighted subgraphs. In this context, we have also provided new evidence for (dis)similarity between female and male core graphs.

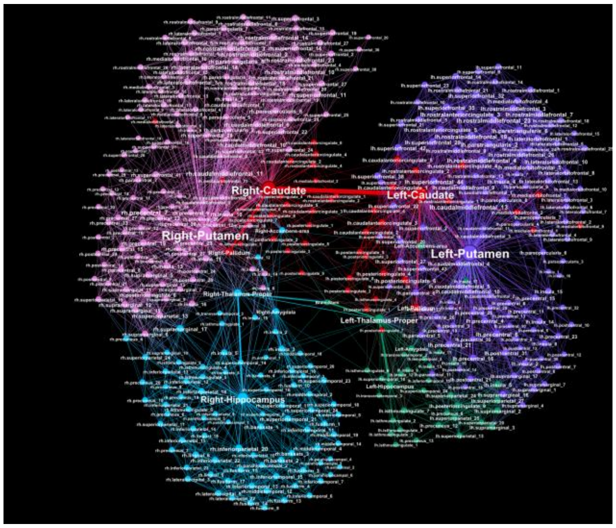

Figure: Male connectome: Core network with labeled nodes (brain areas) and communities

Acknowledgements

Supported by The Research Agency of the Republic of Slovenia Program P1-0044 and The Ministry of Education, Science and Technological Developments of the Republic of Serbia.

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Are triangular scientific collaborations preferable or not?

K. Angelou[1], *M. Maragakis*[,12], *K. Kosmidis*[1], *P. Argyrakis*[1]. *(1) Department of Physics, University of Thessaloniki, Thessaloniki, Greece, kaggelou@physics.auth.gr (2) Department of Physics, International Hellenic University, Kavala, Greece*

In the current study, we examine a multiplex collaboration network to find out if there is a preference in forming extended, triangularly shaped, collaborations or just regular links. The first layer corresponds to the collaborations that have accomplished for the creation of patents, while the second one to the collaborations between scientists that took part in Framework Programme projects. The nodes of the multiplex are the NUTS2 geographic regions of the inventors-scientists, while a link between two such regions exists when scientists from different regions collaborate. In our analysis we use the notion of triangles, which is a fully connected network between any three nodes. Initially, we split the data into 28 networks, each one having a span of 6 years. At the end of each network we calculate the number of triangles on the patent and the FP layer, as well as their common network. In order to identify whether the observed behavior is the anticipated one, we shuffle the data, repeat the analysis, and compare the two results using z-score. We also repeat the procedure, this time by calculating clustering coefficient, which is the number of triangles over the number of possible triangles. Both metrics show that the FP collaborations tend to be extended, while on the patent and the common layer, they tend to be more isolated. Finally, we rank the NUTS2 regions according to their clustering coefficient over time and produce a map with these values for all regions, figure 1. The current analysis could prove useful for policy makers in order to understand the spatial dimension of research and innovation collaboration networks.

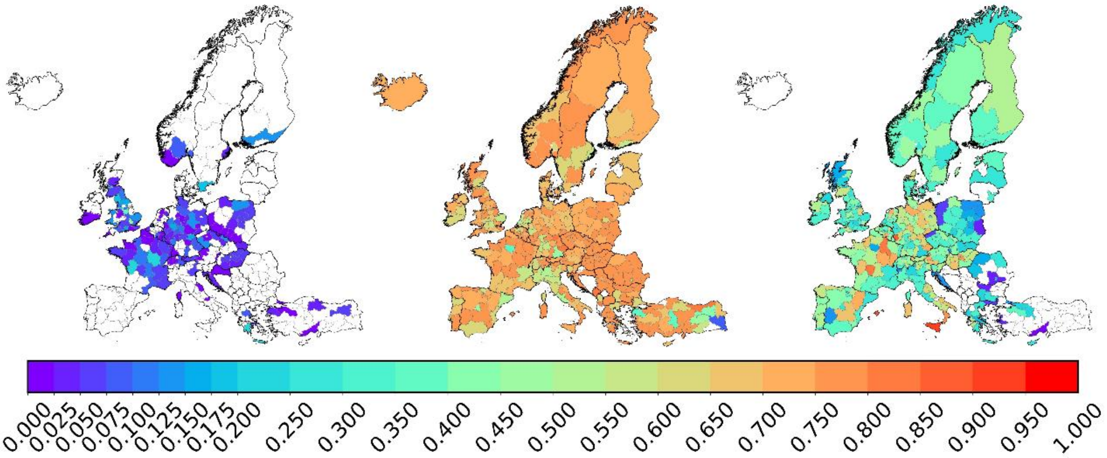

Figure 1 Average clustering coefficient of the 28 networks for each NUTS2 region for a) patents, b) FP, and c) the common layer. The colors correspond to various average clustering coefficient values as indicated by the colorbar. White color indicates regions with zero clustering coefficient in the specific layer.

Acknowledgements

Results presented in this work have been produced using the Aristotle University of Thessaloniki (AUTh) High Performance Computing Infrastructure and Resources.

Signatures for Acute and Chronic Insomnia from Locomotor Time Series Data

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Sleep is an important part of human existence. During sleep the body functions restore and recharge. The sleep process is a complex multi-dimensional cycle that reflects the developmental changes in mental and physical health, along with the day-to-day state fluctuations. However, sleep disturbances, and insomnia in particular, affect a large part of the human population and their quality of life, work productivity and individual's performance. Insomnia is characterised by the inability to fall asleep or stay asleep and/or waking too early and being unable to fall back asleep. It is a sleep disorder that remains under-diagnosed. Insomnia is strongly influenced by the brain activities, chronic conditions, physiological and cognitive health. Here, it is investigated as part of the brain activities, cardio and respiratory systems, blood flow and other physiological functions, namely in the context of network physiology [1] and as part of the neuronal, cardiorespiratory and blood networks.

We propose two new data driven and model free algorithms for investigation and classification of nocturnal awakenings in acute [2] and chronic [3] insomnia and normal sleep from nocturnal actigraphy collected from pre-medicated individuals with insomnia and normal sleep controls. The tri-axial accelerometer build in the Philips ActiWatch collects wrist movements (locomotor motion) data at epochs of 1 minute. Our algorithms are based on signals obtained from the ActiWatch capturing the locomotor activities. They do not require sleep diaries or any other subjective information from the individuals. They can be used as pre-screening tools for assessing insomnia at home. We derive the dynamical fingertips which form the signature of acute or chronic insomnia derived from actigraphy data and distinguish them from the normal sleep. We use spectral [4] and fractal [5] analysis, and obtain statistical, dynamical and sleep parameters (features) from the actigraphy time series data [1,2,3,4]. These features are then combined in machine learning models to classify individuals with acute or chronic insomnia from healthy sleepers [2,3]. The algorithms include classifiers and optimization that incorporate the predicted quality of each night of sleep for an individual to classify into acute or chronic insomnia or healthy group. The developed algorithms provide signatures for acute and chronic insomnia and healthy sleep and are very promising pre-screening tools for early detection of insomnia at home.

Acknowledgements

The authors acknowledge partial support from the Newton Advanced Fellowship, Academy of Medical Sciences, UK.

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A warning tool for financial time-series based on time dependent Generalized Hurst exponents

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The study of scaling in financial systems has been a field of investigation for many years now. Previous studies have shown that financial series, especially from stock-markets, display multiscaling, which is nowadays widely accepted as an empirical stylized fact of financial time series. However, scaling in a financial time series has also been shown to vary with time. For example, there have been studies trying to link this variation with dynamical elements in the underlying title such as, for example, with the development of stock-market bubbles, and predictability of an index raising the question whether scaling analysis can be used as a signaling tool for financial markets. In this work, we attempt to contribute towards this question by applying a visual methodology to algorithmically detect critical changes in the scaling of the underlying complex time-series based on the Generalized Hurst Exponent (GHE) method. The methodology involves the degree of multiscaling at a particular time instance, the multiscaling trend evaluated by the Change Point Analysis method and a rigorous evaluation of the statistical significance of the results. Applying this methodology to a number of stock market indices we have identified particular patterns in the temporal co-evolution of the different GHE time-series, $H(q)$, for various values of the parameter q (figure 1). These GHE patterns, distinguish in a statistically robust way, not only between time periods of uniscaling and multiscaling, but also among different types of multiscaling: symmetric multiscaling (M) and asymmetric multiscaling (A). Transitions from uniscaling to multiscaling behavior occur before critical market events, such as stock market bubbles. Moreover, particular asymmetric multiscaling patterns appear during critical stock market eras and provide useful information about market conditions suggesting that the method could be used as a signaling tool for future critical market events.

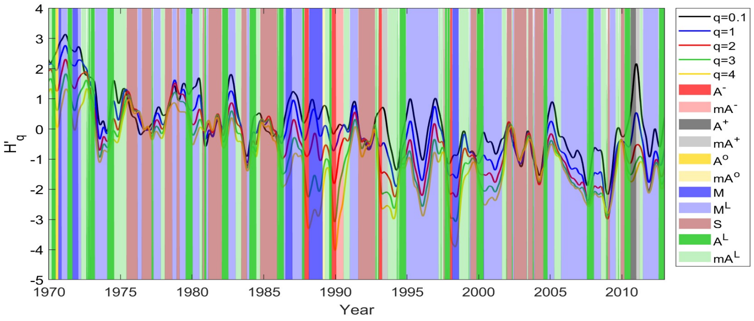

Figure 1: Application of the visual algorithm on the GHE time-series for S&P 500 index. Colors show the various identified scaling patterns. $H(q)$ series are shown for q=0.1,1,2,3,4

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Emergence of synchronised and amplified oscillations in neuromorphic networks with long-range interactions

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Neuromorphic networks can be described in terms of coarse-grained variables, where emergent sustained behaviours spontaneously arise if stochasticity is properly taken in account. For example it has been recently found[1] that a directed linear chain of connected patch of neurons amplifies an input signal, also tuning its characteristic frequency. We study a generalization of such a simple model, introducing heterogeneity and variability in the parameter space and long-range interactions [2], breaking, in turn, the preferential direction of information transmission of a directed chain (see figure). On one hand, enlarging the region of parameters leads to a more complex state space that we analytically characterise; moreover, we explicitly link the strength distribution of the non-local interactions with the frequency distribution of the network oscillations. On the other hand, we found that adding long range interactions can cause the onset of novel phenomena, as coherent and synchronous oscillations among all the interacting units, which can also coexist with the amplification of the signal.

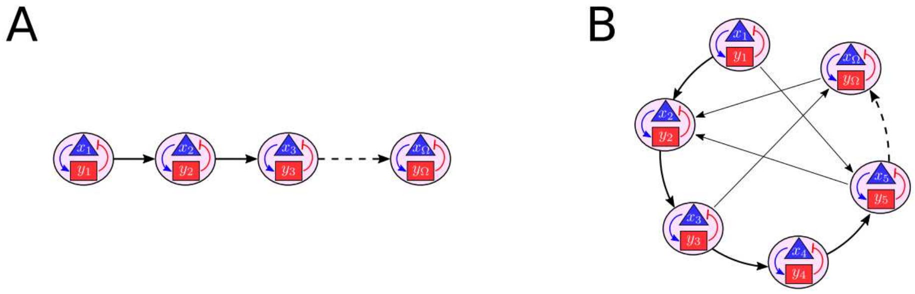

Figure 1: Schematic representation of a neuromorphic network with **Ω** nodes, constituted by excitatory (blue triangles) and inhibitory (red squares) populations, like in Wilson-Cowan model for neuronal networks. The two topologies studied here are shown. The simplest topology is the directed linear chain (Panel A). A more complex structure, with the addition of long-range links to the directed linear chain, is shown in Panel B.

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Complexity of micro- and nanostructured surfaces

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The aim of this work is the elaboration of a methodology for the quantitative characterization of the complexity of nanostructured surfaces in order to provide novel means to link nanostructure morphology to surface properties and functionalities. The key point is the distinction of complexity from randomness contrary to the usual approaches in nanometrology. The inspiration is based on the work of R. Alamino [1] where the notion of the average symmetry is proposed to put on the same footing full order and full randomness. According to this approach, the complexity is defined with an entropy-based metric quantifying the "distance" of a system morphology from average symmetry. Here, we propose and apply an alternative of this measure properly adapted to the specific characteristics of nanorough surfaces.

Firstly, the method is tested to synthesized nanostructured surfaces with controlled mixture of randomness and order to validate its results. Three series of synthesized surfaces are used. In the first case, the full order is represented by a homogeneous flat surface and noise is added by gradually and randomly replacing the surfaces points. In the second case, the full order is represented by an almost homogeneous surface with very large correlation length and the randomness is introduced through a reduction of correlations (smaller correlation length) resulting in the random morphology of almost zero correlation length. In the last case, we generate mounded periodic surfaces which are ordered. Randomness is induced by affecting positions, widths and heights of the surface peaks. The gradual increase of noise amplitude in these dimensions degrades periodicity and leads to fully randomization of surfaces.

In all cases, the proposed metric of complexity exhibits a bell-like curve with a maximum in between full order and randomness at the point where the morphological heterogeneity of surfaces seems to maximize. Besides the applications in synthesized surfaces, the complexity measure has been calculated in real surfaces of polymer materials after their treatment in plasma reactors measured with Atomic Force Microscope. The polymer morphology presents an increased complexity in the course of etching time which cannot be described with the conventional math tools. Also, we applied our methodology in surfaces of Aluminium which are etched with a solution of $FeCl_3$ or $CuCl_2$ and then with boiling water to create micro- and nanostructuring respectively. The surfaces are depicted with top-down SEM images which are analyzed to calculate the complexity of their morphologies. The proposed complexity metric seems to capture our intuition and quantify the change of complexity with etchant ($FeCl_3$ or $CuCl_2$) in accordance with the variation of the surface heat transfer.

Acknowledgements

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Analyzing clusterability in signed networks of political collaboration using graph optimization models

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A graph with positive and negative signs on the edges is called a *signed graph*. A signed graph (network) is *balanced* if its set of vertices can be partitioned into two subsets such that each negative (positive) edge joins vertices belonging to different subsets (same subset) [1]. If a signed network satisfies the same condition when partitioned into k subsets, it is *clusterable* (k-balanced) [2].

Signed networks representing real data often do not satisfy these conditions [3]. This motivates analyzing them based on their distance to balance and clusterability. Among different methods for measuring such distance is the minimum number of edges whose removal makes a network balanced (*frustration index* $L(G)$ [4]), k-balanced for the given value k (*k-clusterability index* $C_k(G)$ [5]) or clusterable (*clusterability index* $C(G)$ [6]). These measures are complementary, giving different perspectives on balance as a multi-faceted property of signed networks.

Fig. 1(A) shows an example signed graph in which the dotted (solid) lines represent negative (positive) edges. Balance can be evaluated using 3-cycles (B), bi-partitioning (C), or k-partitioning (D). The first approach, (Fig. 1B), involves identifying triangle 1-4-5 as unbalanced and triangle 1-3-4 as balanced and only provides limited insight into the overall structure. The second approach, (Fig. 1C), involves finding a bi-partitioning of vertices $\{\{1, 2, 3\}, \{4, 5\}\}$ (shown by green and purple colors in Fig. 1C) which minimizes the total number of intra-group negative and inter-group positive edges to 1 ($L(G) = 1$). The last approach, (Fig. 1D), involves finding an optimal k-partitioning for the vertices $\{\{1, 2, 3\}, \{4\}, \{5\}\}$ which satisfies the conditions of generalized balance ($C(G) = 0, k^* = 3$).

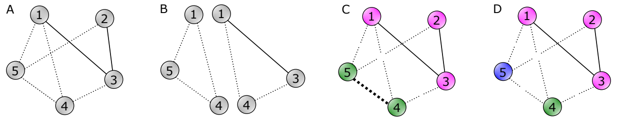

Fig. 1. An example signed network(A), evaluating balance using 3-cycles(B), bi-partitioning(C), and k-partitioning(D)

Using the above definitions and concepts, we analyze signed networks of US Congress legislators [7, 8] in the Senate and House of Representatives based on their clusterability for different number of subsets. These signed networks are statistically inferred from co-sponsorship data such that having too many collaborations is recorded as a positive tie and having too few collaborations is recorded as a negative edge [8]. Substantively, this analysis allows examining the US Congress similar to a parliamentary body, where coalitions form to achieve a majority voting bloc. Previous studies show that signed networks of US Congress are close to being balanced according to cycle-based measures [8, 3] and optimal bi-partitionings of the networks [9]. We use more general mathematical models for (1) specific predefined values of k [6] and (2) general value of k^* which provide a nuanced view on the structure of political collaborations in the US Congress.

Our numerical results show that the clusterability indices of US Congress signed networks initially decrease for $k > 2$ which suggest that the signed ties between legislators in the US Congress are more consistent with a parliamentary-style set of coalitions than with a more conventional two-group categorization. We also obtain the globally minimum number of groups, k^*, which minimize the clusterability index of each network by grouping legislators into a number of clusters which is observed to be always more than two $k^* > 2$. Our results demonstrate that signed network of US Congress can be partitioned into coalitions exhibiting substantial closeness to generalized balance and that the coalitions are not strictly related to party membership. The initial decline of k-clusterability index when k is gradually increased shows that the networks are more consistent with generalized balance than classic balance theory. However, k-clusterability index increases if the number of pre-defined groups is set to a value larger than k^* which seems to suggest that political collaborations prevents legislators from forming too many opposing sides.

Our observations show that legislators in US Congress seem to act more like a parliamentary body with more than two coalitions, but that these coalitions still mirror broad liberal-conservative tendencies. In this presentation, we provide our results on clusterability of US Congress network and the dynamics of its major coalitions over 1979-2018.

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Multilevel Structural Evaluation of Signed Directed Social Networks

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A *signed network* is a network with positive and negative signs on the edges. Balance theory [1] explains the forces behind the structure of social systems commonly modeled as static undirected signed networks. A signed graph (network) is *balanced* if its set of vertices can be partitioned into two subsets such that each negative edge joins vertices belonging to different subsets and each positive edge joins vertices belonging to the same subset [1]. This definition is more often expressed in terms of network triads; which considers triads with an even number of negative edges to be balanced [1].

We expand this modeling to incorporate directionality of the edges, and consider three levels of analysis: micro- (triads), meso- (subgroups), and macro-level (whole network). For micro-level balance, we utilize semicycles of length 3 that satisfy the condition of transitivity and sign consistency. For meso-level balance, we derive measures of cohesiveness (internal solidarity) and divisiveness (external antagonism) to capture balance in subgroups using the most fitting partition of nodes into two groups [2, 3]. For macro-level balance, we use the normalized line index [4, 5], which relies on the proportion of edges whose position suits balance.

Figure 1 shows the signed network of 16 tribes in the Papua New Guinea [6] and our proposed approach to evaluating balance at the micro-, meso-, and macro-level. Through extensive computational analysis of 11 social networks, we document frequently repeated patterns of social structure in triads, subgroups, and the whole network across a range of social settings; from college students and Wikipedia users to philosophers and Bitcoin traders.

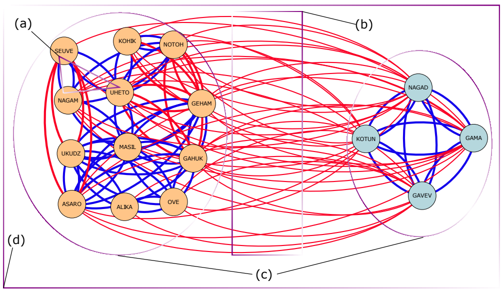

Fig. 1. Signed network of alliance (blue) and antagonism (red) between 16 highland tribes [6]. (a) We measure micro-level balance by evaluating all transitive semicycles of length 3 in a network. (b) We quantify divisiveness by looking at the signs of the external edges between two subgroups. (c) We quantify cohesiveness by looking at the signs of internal edges in subgroups. (d) We measure macro-level balance by partitioning the network into two subgroups (node colors) with minimum intra-group negative and inter-group positive edges.

In most cases, we observe relatively high values of balance across the three levels considered despite the differences in social setting and types of signed ties. This is yet another confirmation [5] for balance theory, with which the networks show a partial yet considerable consistency. Our quantitative results show that values of balance at the micro-, meso-, and macro-level may match up to some extent. In the absence of other network dynamics, which we have not tested, this suggests that the underlying mechanisms of avoiding tension may be reflected in micro-level patterns of balanced transitive semicycles. At a higher level, such patterns form a meso-level of internally cohesive and externally divisive subgroups. This eventually gives rise to a macro-level polarization where only a relatively few edges are positioned inconsistently with respect to the premise of balance theory. We then apply our multilevel framework to examine balance in temporal and multilayer networks, which demonstrates the generalizability of our approach and leads to new observations on how balance at different levels may change over time and across types of relationships. In the temporal networks, we document two patterns on the temporal dynamics of balance [3]: (1) networks which move towards higher polarization over time, and (2) networks without a monotone trend, oscillating over time within a short range of balance values. Our results for the multilayer network shows that the co-existence of multiple types of signed ties may impact balance of a multilayer network in a more profound manner compared to the individual impact of each type of relation in its respective single-layer network.

Our complementary findings on a variety of social networks highlight the need to evaluate balance at different levels for which we propose a comprehensive yet parsimonious approach. The code and data used in this study [7] are made publicly available.

Full text: nature.com/articles/s41598-020-71838-6

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Percolation on feature-enriched interconnected systems

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Percolation is an emblematic model used to understand the robustness of interconnected systems, in which the nodes of a network are removed and different topological properties of the resulting topological structure are analyzed. Despite being a model broadly studied in statistical physics and mathematics -- with insightful applications ranging from biological and neural systems to large-scale communication and transportation networks --, from a theoretical perspective this process is usually investigated in relatively simple scenarios, such as the removal of the system's units in random order -- simulating unpredictable site failures -- or sequentially ordered -- simulating targeted attacks -- by specific topological descriptors, the simplest one being the number of node connections. However, in the vast majority of empirical applications, it is required to dismantle the network following more sophisticated protocols than the aforementioned ones, such as based on more convoluted topological properties or even non-topological node metadata obtained from the application domain.

In this work we propose a novel mathematical framework to fill this gap: a network is enriched with features and its nodes are then removed according to their importance in the feature space. Percolation analysis is performed, theoretically and numerically, as a function of the feature distribution. We are able to provide an excellent match between the analytical results and the simulations when the network is intervened following feature-based protocols. Several examples are given to show the applicability of the theory. In particular, we apply our framework to degree-feature relations of different nature. We start from *ad hoc* degree-feature distributions that capture the main characteristics of correlations observed in empirical systems, moving to features that arise naturally in the process of network creation and ending with the case in which features are coupled to dynamical processes running on top of the network, such as epidemics or biochemical dynamics, among others. Both synthetic and real-world networks of different nature are considered in the analysis. Moreover, we show the potential of our model by employing state-of-the-art Bayesian probability techniques that are able to give the most plausible closed-form expression for the degree-feature distribution when it cannot be computed analytically. By feeding these most plausible expressions into the equations of our model, we can study feature-based percolation in systems for which it is only known the feature and the degree of the individual nodes, instead of the entire degree-feature joint probability distribution (see Fig.). This considerably broadens the applicability of the theory and bridges our theory, grounded on statistical physics, with Bayesian machine learning techniques suitable for knowledge discovery. The article is currently under review.

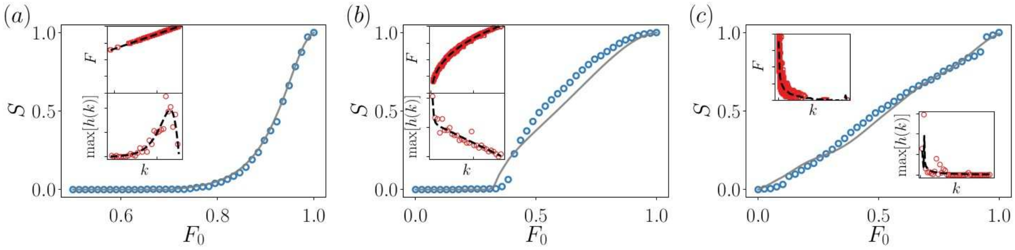

Figure: Percolation for *(a)* mutualistic dynamics in symbiotic ecosystems, *(b)* population dynamics and *(c)* mass-action kinetics in biochemistry. *F0* is a parameter of the feature distribution, *S* is the size of the largest connected component. The insets are different variables fitted using machine-learning techniques that are necessary to compute *S*.

Abrupt transition due to non-local cascade propagation in multiplex systems

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The overall function of networked systems is known to be closely related to their structural properties. This structure, i.e., the nodes and the links, might undergo random failures or suffer targeted attacks. Depending on how and where these events occur, the global properties of the network can be severely affected or remain almost unaltered. This roughly defines the concept of network robustness or resilience. In this work we focus our analysis on cascade-based attacks, i.e., those attacks that, by removing a single node, cause disproportionate damage to a large part of the system. Moreover, they evolve nonlocally, which means that the next removed node need not to be in contact with an already removed one. This contrasts, for example, with the typical propagation observed in disease spreading models such as the SIS or SIR. Classical models of cascade propagation assume that each node is assigned a load and a capacity: the former is the total number of shortest path crossing the nodes, used as a proxy for energy or information exchange, and the latter is the maximum load that each node can handle. Inspired by these models, we study for first time the the cascade propagation on multilayer networks. In particular, we address the question of the network robustness in function of several multilayer properties. By means of extensive numerical simulations, we find that this dynamics induces a discontinuous transition in the size of the largest connected component (LCC) (Fig. (a)) and we characterize it. We also compare the cascade propagation on multilayers and on their aggregated counterpart, reporting the similarities and differences among them. We observe that the aggregation process leads to a more robust network. Counter-intuitively to this result, however, we find that the number of layers composing the network plays an important role on the resilience of the global network: by adding more and more layers, the system turns out to be more robust (Fig. (b)). We are able to find an explanation to this phenomenon in terms of the topological quantities, such as the average path length of the resulting networks. Finally, we validate our findings in a real multilayer networks, the European Air Transport Network. The results of this work can be found in [1].

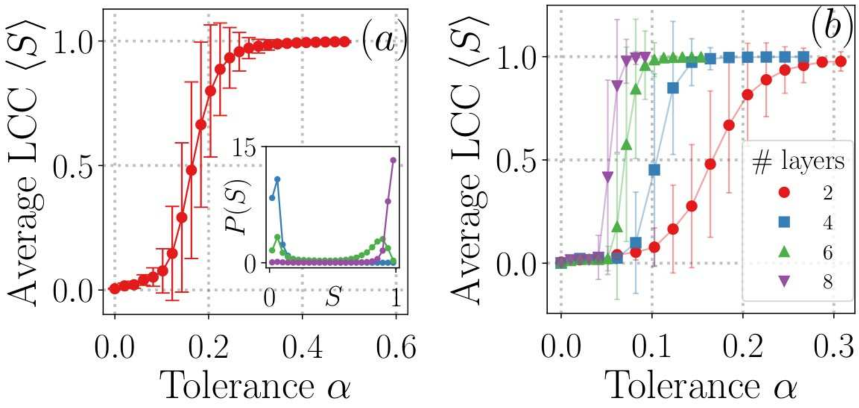

Figure: (a), average of the (normalized) size of the LCC as a function of the tolerance parameter α, taken as the proportional factor that defines the capacity of node *i*: *C_i = (1 + α)L_0^i* , being *L_0^i* the initial load. In the inset, probability of finding a cascade of size *S* for different values of α. In (b), we show that as we add more layers to the network, the transition becomes more abrupt but the robustness increases.

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Effectiveness of dismantling strategies on moderated vs. unmoderated online social platforms

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Social networking services have become an important piece of our lives and, as such, human behavior in online social networks have been a central topic in the research agenda of several scientific disciplines. Nevertheless, understanding the propagation of undesired content across these systems, such as fake news or hateful speech, and how this couples with the guarantee of the right freedom of speech is still largely debated. We tackle this challenge by identifying two suitable large-scale online social laboratories, Twitter and Gab, the former being a moderated microblogging platform and the latter being an unmoderated one. From millions of messages where users directly interact (mentions and replies), we address i) the structural properties of active relationships of users in the platforms; ii) the impact of banning the most socially prominent users (degree); and iii) effective banning strategies that combine topological properties and intensity of inflammatory content (user sentiment). Hence, by banning users we are assessing the possible pathways information can take to reach a global audience. We accompany our analyses with a discussion about the role played by the moderated or unmoderated nature of the social networks.

Our analyses show that the moderated or unmoderated nature of the online social network does not induce clear robustness patterns when facing both the degree-based and sentiment-based attacks. The degree-based dismantling strategy, is a very effective one, when compared to the sentiment-based one (see 1st and 2nd panel in Fig.). To understand the different responses to degree attacks, we resort to higher-order topological correlations: the degree assortativity and a novel concept, the inter-*k*-shell correlation, which is designed to give an idea of how the different centrality hierarchies in the network are connected among them (see 3rd and 4th panels in Fig.). Moreover, our results unravel the fact that the strategy of banning the users who create and spread the most inflammatory content is not effective because those users, typically, are not very socially prominent. For a faster network dismantling that still targets based on content, we propose viable strategies that combine topological and sentimental information, which turn to be much more effective. If removal is carried out by targeting the more inflammatory users above a minimal degree.

All the details and further results can be found in the recently published article [1].

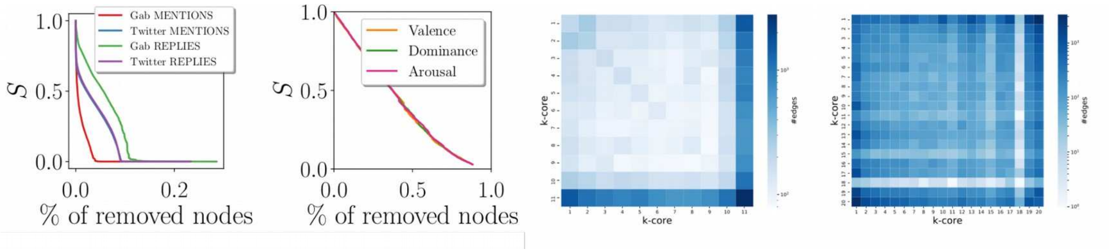

Figure. Left: Sizes of the largest connected component as a function of the fraction of removed nodes, for degree-based attacks, and for sentiment-based attacks. **Right:** Different inter-*k*-shell correlation patterns in the analyzed networks.

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Dynamics impose limits to detectability of network structure [1]

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Networks constitute a paradigm of complexity in real life systems by assembling the structure of the interactions of their elementary constituents [2, 3]. They are found at every level of biological organisation, from genes inside the cells to the trophic relations between species in large ecosystems [3]. Nowadays, with the enormous development of data science, there is a huge interest related to the network inference, namely detecting the interacting structure from external measurements or observations. For example, reconstructing the structure of brain networks from the activity of neuronal patches has been a major goal in computational neuroscience. The dynamics that takes place on networked systems can, in some cases, strongly influence the perception that we have regarding local topological features such as the degree [4] or global ones such as network non-normality [5]. In this work, we focus specifically on the problem of measuring network centralities from the dynamical point of view. We show that the inference of networks' structural properties depends heavily on the competition between the node-based dynamics on one hand and the interactions between the nodes on the other. In particular, we illustrate such a phenomenon based on the communicability centrality, considered as a reliable measure for dynamical inference. We show that when the local intra-nodes dynamics is slower than the inter-nodes one then the ranking of the nodes according to the standard definition of the communicability, becomes inadequate. Such ranking can be enhanced if further information regarding the nature of the dynamics occurring on the network is available. As an example, we show that for networks with different time-scale structures such as strong modularity, the existence of fast global dynamics can imply that precise inference of the community structure is impossible (see Fig. 1).

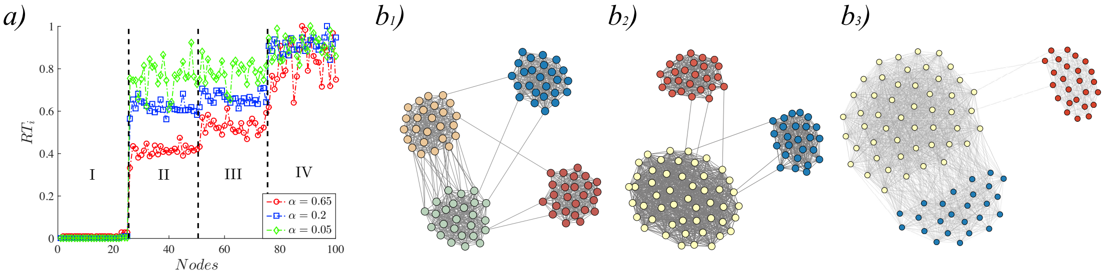

Figure 1. *a) We plot the observable associated with each node (the normalised reaching time* RT_i*) of the four modules showing that for decreasing values of the local intra-nodes dynamics parameter* α*, the ranges of the dynamical variables for different modules overlap. b) A representative visualisation of the networks reconstruction where it is shown the gradual deformation perceived in the network modularity from* b_1 *(*$\alpha = 0.65$*) the original 4 modules topology,* b_2 *(*$\alpha = 0.2$*) modules II and III have merged, and* b_3 *(*$\alpha = 0.05$*) module IV is merging with the union of the modules* $II - III$*. The network has 100 nodes with total link density* $p = 0.2$ *and probability 0.01 for an inter-module link.*

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A universal route to pattern formation in multicellular systems [1]

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A general framework for the generation of long wavelength patterns in multi-cellular (discrete) systems is proposed, which extends beyond conventional reaction-diffusion (continuum) paradigms [2]. The standard partial differential equations of reaction-diffusion framework can be considered as a mean-field like ansatz which corresponds, in the biological setting, to sending to zero the size (or volume) of each individual cell. By relaxing this approximation and, provided a directionality in the flux is allowed for, we demonstrate here that instability leading to spatial pattern formation can always develop if the (discrete) system is large enough, namely, composed of sufficiently many cells, the units of spatial patchiness. The macroscopic patterns that follow the onset of the instability are robust and show oscillatory or steady state behavior.

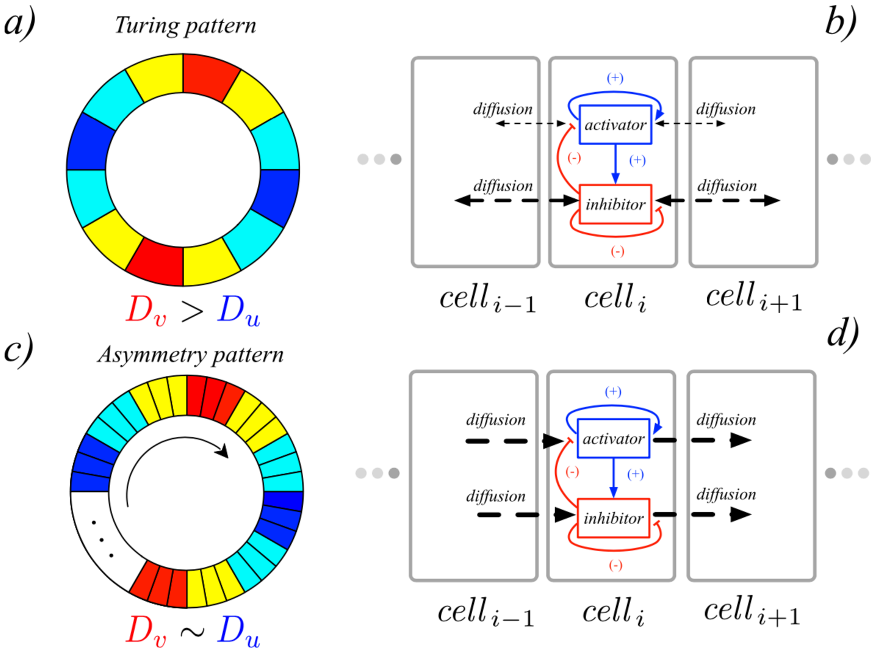

Figure 1. *Conventional Turing instability vs. the asymmetry-driven model: a schematic representation. (a) In Turing's original model, the onset of pattern formation is studied for a model of two species reacting and diffusing on a collection of cells, arranged so as to form a 1D ring. (b) Turing instability requires breaking the symmetry among the species. In particular, feedback loops (positive for the activators and negative for the inhibitors) are proposed. Further, the inhibitor should relocate in space faster than the activator,* $D_V > D_U$*. The diffusion between neighboring cells is assumed symmetric. (c) In the asymmetry-induced instability instead the system is made up of a larger number of cells and the diffusion is asymmetric, as schematised by the clockwise arrow. (d) The instability is triggered by increasing the number of cells, for virtually any ratio of the diffusion constants, provided the latter take sufficiently large values.*

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Statistical mechanics of semantic evolution

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Semantic evolution, the change in meaning of meaningful linguistic units, is driven by a variety of distinct factors, including linguistic, social, and technological ones. Disentangling these factors to set up a predictive and explanatory theory of semantic evolution is notoriously difficult. Here we ask an alternative question: is it possible to reliably identify statistical regularities of semantic change from large corpora in an automated fashion? If yes, what are those statistical patterns? In this paper, we show that if an 'enseble of trajectories' perspective is taken, there is one law that holds universally across languages: that semantic evolution is subdiffusive. Using a pipeline of diachronic distributional semantic embeddings that controls for underlying symmetries, we show that words follow a stochastic trajectories with average Hurst exponent $H\approx 0.2$, in contrast with diffusing particles that follow $H=0.5$. Randomization methods indicate that part of this deviation comes from non-independent directions, part of it comes from non-independent velocities at subsequent times. Yet neither observed jump size distributions, nor memory in single trajectories indicate subdiffusion, which is therefore a more complicated, ensemble-level phenomenon. Discovering statistical laws of semantic change might point at mechanisms underlying our collective cumulative cultural evolution, the very feature that distinguishes us humans from the rest of the animal world.

Space-Independent Modular Structure of Brain Functional Networks

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The brain's intrinsic organization into functional networks has been assessed using imaging techniques, such as functional magnetic resonance imaging (fMRI). In several recent studies, the dynamic functional connectivity (dFC) of these networks was analyzed using a graph theory approach to extract features that characterize their topology over time. The question arises whether the features captured can be explained by the spatial constraints determined by the brain's underlying structure[1], or if functional coactivation is to some extent responsible for the patterns found. We address this by investigating modular configuration in resting-state fMRI (rs-fMRI) data through community detection using a spatially informed null model.

A previously described rs-fMRI dataset acquired from 9 healthy subjects at 7T was used[2]. We started by identifying the graph's nodes through parcellation of the data into 68 brain regions using the Desikan atlas. The edges were then obtained for each time point (TR=1s) and subject, by computing dFC between pairs of brain regions using phase coherence[3], and then by thresholding, while keeping the giant component structure and the main topological characteristics of the network. To analyze the community structure, we applied the Louvain algorithm to the time points for which the topology deviated significantly from the random case, using a rewiring null model. We obtained 6-7 communities with an average modularity $Q_{\text{original}} = 0.693$, which was significantly greater than $Q_{\text{rewiring}} = 0.297$ for this null model, indicating there is a community structure for these networks. To investigate whether this modular configuration can be explained solely by the network's spatial constraints, we then used a degree-constrained spatial null model[4], for which the modularity was slightly lower than for the networks being analyzed ($Q_{\text{spatial}} = 0.625$). However, since the difference between these two was still statistically significant for most time points, we applied a modified Louvain algorithm[4] that regresses out spatial restrictions. This resulted in an average of 6 communities with modularity $Q_{\text{modified}} = 0.071$, for these selected time points. In conclusion, although the topology and community structure of the rs-fMRI dFC networks is mainly explained by the spatial embedding, some significant and non-negligible degree of functional specialization of the community structure can still be detected, which is space-independent.

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Ab-Initio Investigation of the Nature of α-Keratin EPR Signals

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Using fingernail as a biodosimeter compiling with the electron paramagnetic resonance (EPR) technique has been dedicated to several experimental studies. However, the most challenging factor to consider when using fingernail EPR dosimetry is additional types of signals that will mask the radiation-induced signals (RIS). Using ORCA package, we provided a qualitative analysis of the RIS radicals and their spectra to develop better methods for removing unwanted interference from the spectra of irradiated nails and improving the accuracy of the measurements. In this way, three categories of cysteine, tyrosine, and cystine radicals, were considered, which might be produced in α-keratin sequence via reduction-oxidation processes. We have shown that different sequences will not yield new peaks, which is limited to a small broadening. Molecular dynamics and on-the-fly magnetic parameter calculations were employed using GROMACS to obtain the broadening ratio of the EPR signals due to the system's dynamics. We benchmarked our calculations with respect to an experimental spectrum obtained in another study. At a dose of 10 Gy, only one feature of the RIS stood out, a singlet at 2.0059 with a peak-peak width of 10 G. Other peaks in this range of dose were interpreted as MIS signal, which would fade away by chemical treatment, heating, etc. Comparing the signal positions of experimental and computational curves, we found that the best conformity is tyrosine radical category. In comparison to other studies, our results were in proper consistency with both the experimental and computational results of Tipikin et al. [1] and Black and Swarts15 [2]. Moreover, for doses above 500 Gy, a broad signal at 2.056, 2.026, and 1.996 was reported as a prominent signal, which was not in the vicinity of the g-tensors calculated in this work. In another study done by Trompier et al. [3], a g-tensor had been reported for high dose irradiation, [2.003, 2.008, 2.025], which was in agreement with the calculated g-tensor for one of the cysteine radicals in this work.

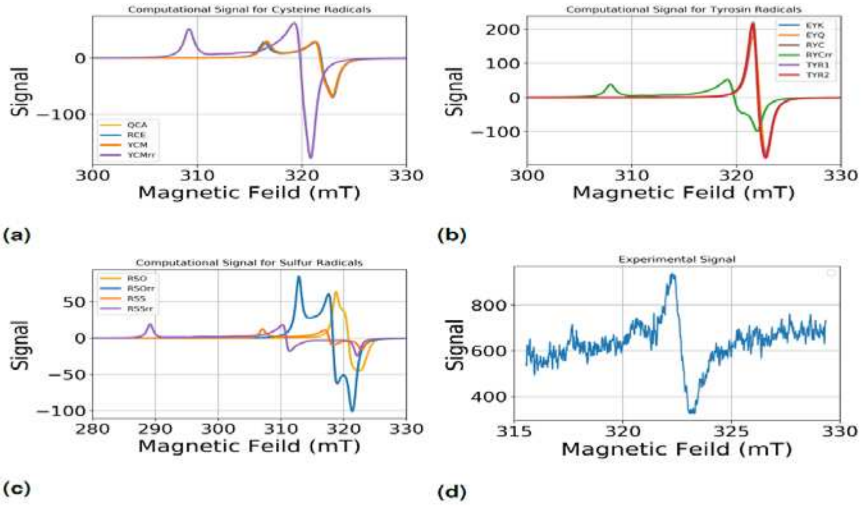

Figure 1: Calculated EPR signals for different configurations of (a) cysteine's radicals (b) tyrosine's radicals, and (c) cystine's radicals; (d) Experimental EPR signal

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Co-sponsorship analysis of party politics in the 20th National Assembly of Republic of Korea

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We investigate co-sponsorship among lawmakers by applying the principal-component analysis to the bills introduced in the 20th National Assembly of Korea. The most relevant factor for co-sponsorship is their party membership, and we clearly observe a signal of a third-party system in action. To identify other factors than the party influence, we analyze how lawmakers are clustered inside each party, and the result shows significant similarity between their committee membership and co-sponsorship in case of the ruling party. In addition, by monitoring each lawmaker's similarity to the average behavior of his or her party, we have found that it begins to decrease approximately one month before the lawmaker actually changes the party membership.

Acknowledgements

We are grateful to Woncheol Jang for his careful reading and helpful comments. S.K.B. was supported by Pukyong National University Research Fund in 2019. B.J.K. was supported by the National Research Foundation of Korea (NRF) grant funded by the Korea government (MSIT) Grant No. 2019R1A2C2089463.

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Generalized entropies, density of states, and non-extensivity

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The concept of entropy connects the number of possible configurations with the number of variables in large stochastic systems. Independent or weakly interacting variables render the number of configurations scale exponentially with the number of variables, making the Boltzmann–Gibbs–Shannon entropy extensive. In systems with strongly interacting variables, or with variables driven by history-dependent dynamics, this is no longer true. Here we show that contrary to the generally held belief, not only strong correlations or history-dependence, but skewed-enough distribution of visiting probabilities, that is, first-order statistics, also play a role in determining the relation between configuration space size and system size, or, equivalently, the extensive form of generalized entropy. We present a macroscopic formalism describing this interplay between first-order statistics, higher-order statistics, and configuration space growth. We demonstrate that knowing any two strongly restricts the possibilities of the third. We believe that this unified macroscopic picture of emergent degrees of freedom constraining mechanisms provides a step towards finding order in the zoo of strongly interacting complex systems.

Modeling Economic Cascades due to a Pandemic Shock

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We propose a dynamic cascade model to examine the systemic risk posed by sector level industries within the U.S. inter-industry network. We then apply this model to the case of COVID-19 and estimate its impact on the U.S. economy. The network is constructed as a weighted digraph $G = (V, E, W)$ using the industry-by-industry total requirements table for the year 2018, provided by the Bureau of Economic Analysis. In this graph, the nodes V_i represent sector level industries, edges E_{ij} represent commodity flows from industry i to industry j, and weights W_{ij} capture the value of each commodity. Each node in the network follows a modified Cobb-Douglas production function, in which the out-degree of each node is a function of its in-degree, productivity, and labor supply. We impose an initial shock that disrupts the production capacity of one or more nodes, which negatively impacts downstream industries. Additionally, the industries in the network are assigned a common resilience r that determines their ability to absorb input losses, such that if the rate of input loss exceeds the resilience r, the industry fails and its outputs go to zero. We observe a critical resilience r_c, such that below this critical value the network experiences a catastrophic cascade resulting in total network collapse. The dependence of the critical resilience on the shock magnitude (β) and Cobb-Douglas exponents is also investigated.

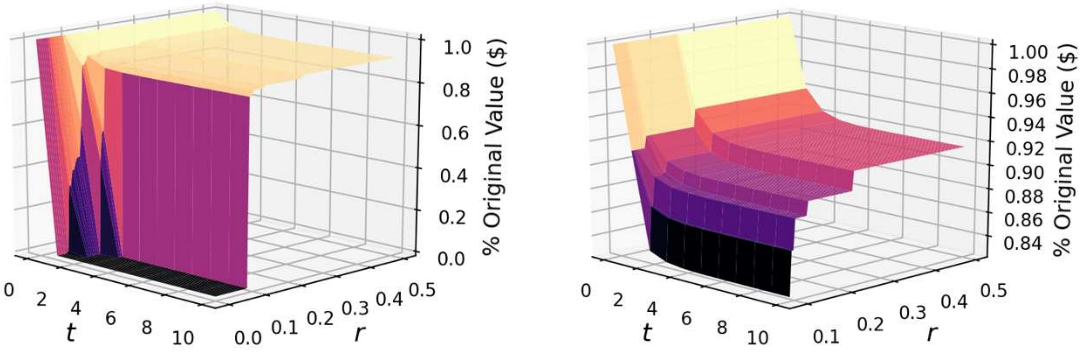

Figure 1: Response of the network to the COVID-19 shock applied at time $t = 0$. (left) The z-axis gives the percent original value in the network as a function of time $t \in [0,10]$, and resilience $r \in [0,0.5]$. (right) Percent original value over time for simulations that do not result in network collapse ($r > r_c$). The critical resilience due to this shock is found to be $r_c = 0.088$.

For the case of COVID-19, the initial shock is modeled on the loss of employment between March and April 2020 as reported by the Bureau of Labor Statistics.

Physics-informed machine learning for the COVID-19 pandemic: Adherence to social distancing and short-term predictions for eight countries

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Abstract

The spread of COVID-19 during the initial phase of the first half of 2020 was curtailed to a larger or lesser extent through measures of social distancing imposed by most countries. In this work, we link directly, through machine learning techniques, infection data at a country level to a single number that signifies social distancing effectiveness. We assume that the standard SIR model gives a reasonable description of the dynamics of spreading, and thus the social distancing aspect can be modeled through time-dependent infection rates that are imposed externally. We use an exponential ansatz to analyze the SIR model, find an exact solution for the time-independent infection rate, and derive a simple first-order differential equation for the time-dependent infection rate as a function of the infected population. Using infected number data from the “first wave" of the infection from eight countries, and through physics-informed machine learning, we extract the degree of linear dependence in social distancing that led to the specific infections. We find that in the two extremes are Greece, with the highest decay slope on one side, and the US on the other with a practically flat “decay". The hierarchy of slopes is compatible with the effectiveness of the pandemic containment in each country. Finally, we train our network with data after the end of the analyzed period, and we make week-long predictions for the current phase of the infection that appear to be very close to the actual infection values.

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Effect of manual and digital contact tracing on COVID-19 outbreaks: a study on empirical contact data

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In the fight against the COVID-19 pandemic, lockdowns have succeeded in limiting contagions in many countries, at however heavy societal costs: more targeted non-pharmaceutical interventions are desirable to contain or mitigate resurgences. Contact tracing, by identifying and quarantining people who have been in prolonged contact with an infectious individual, has the potential to stop the spread where and when it occurs, with thus limited impact. The limitations of manual contact tracing (MCT), due to delays and imperfect recall of contacts, might be compensated by digital contact tracing (DCT) based on smartphone apps, whose impact however depends on the app adoption. To assess the efficiency of such interventions in realistic settings, we use datasets describing contacts between individuals in several contexts, namely a university campus, offices, and a highschool, with high spatial and temporal resolution, to feed numerical simulations of a realistic compartmental model for COVID-19. This model includes contagious presymptomatics and a distinction between asymptomatics and symptomatics with mild or severe symptoms. We implement standard measures of detection and isolation of severe cases, with a tunable probability of detection of mild cases, and simulate in addition MCT and DCT, taking into account their respective limitations (limited app adoption, limited efficiency and delays of MCT, limited compliance) and considering various thresholds to define at-risk contacts. We find that the obtained reduction of epidemic size has a robust behavior as a function of the MCT and DCT efficiencies, independently of datasets and parameters: this benefit is linear in the fraction of contacts recalled during MCT, and quadratic in the app adoption, with no threshold effect. The combination of tracing strategies can yield important benefits, and the cost (number of quarantines) vs. benefit curve has a typical parabolic shape, independent on the type of tracing, with a high benefit and low cost if app adoption and MCT efficiency are high enough. Our numerical results are qualitatively confirmed by analytical results on simplified models.

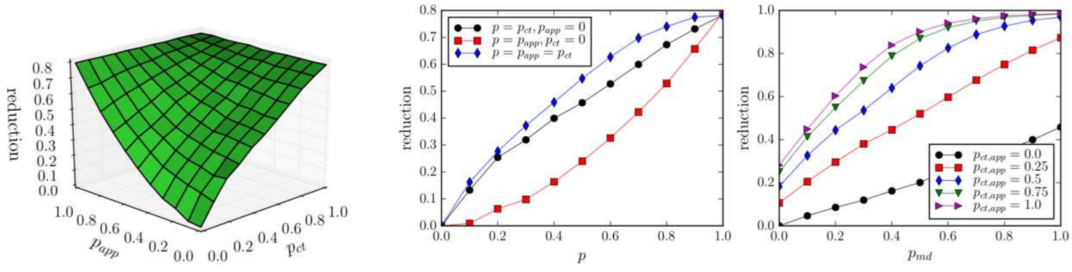

Figure: impact of contact tracing on the epidemic size. Left: Relative reduction in the average epidemic size as a function of manual contact tracing probability p_{ct} and app adoption rate p_{app}. Here contacts longer than 15 minutes are considered at risk. Here the probability to detect mildly symptomatics is $p_{md} = 0.5$. Middle: Same, for three slices: along the p_{ct} axis with $p_{app} = 0$, along the p_{app} axis with $p_{ct} = 0$, and along the diagonal with $p_{ct} = p_{app}$. Right: Relative reduction as a function of the testing and diagnosis rate of mildly symptomatic p_{md} for various values of $p_{ct} = p_{app}$

Reference: medRxiv 2020.07.24.20159947v1

A new representation framework for social temporal networks

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Networks are well-established tools to represent social systems, and, thanks to the increased availability of temporally resolved data, temporal networks are now widely used to model their dynamics. Temporal network data are usually presented as a succession of point events (if the data is in continuous time), or as a series of static snapshots networks aggregated on successive time windows. In the latter case, the time window length is arbitrary and does not necessarily correspond to any intrinsic timescale. Short time windows contain little information on the underlying system at each time, while long time windows provide a blurred image of the dynamics. An interesting alternative consists then in transforming the temporal network data into a continuously evolving representation that gives at any time a sensible image of the social system under study. Here we introduce such a representation that maps temporal network data of discretized dyadic interactions into an evolving weighted network in which the weights of the links between individuals are updated at every event of the temporal network. The starting point of this representation is the assumption that each individual has a limited capital of "attention" or available time: as a result, if individual i has an interaction with a peer j, the weight of the tie between i and j strengthens while the weight of the ties between i and other peers decreases. The rate of increase or decrease of weights depends on a parameter α that determines the sensitivity of this representation to changes in the underlying interaction dynamics. To show the interest of our framework, we consider several temporal data sets describing interactions (i) in a group of baboons (ii) among humans, and we simulate a change in the group's social structure by switching the identity of 2 individuals in the data at a time t0. We then consider the capacity of three representations of the data to automatically detect the perturbation: (i) a time aggregation from the initial time to t (ii) a time-aggregation at a daily scale (iii) our framework. We show that the procedure of comparing the representations at all pairs of times (t, t') and hierarchically clustering times allows us to recover t0 in all cases, but with a better performance (as measured by the quality factor of the hierarchical clustering) on a broad range of values of α for the proposed representation. This shows that our representation is well suited to the detection of significant events in the network evolution.

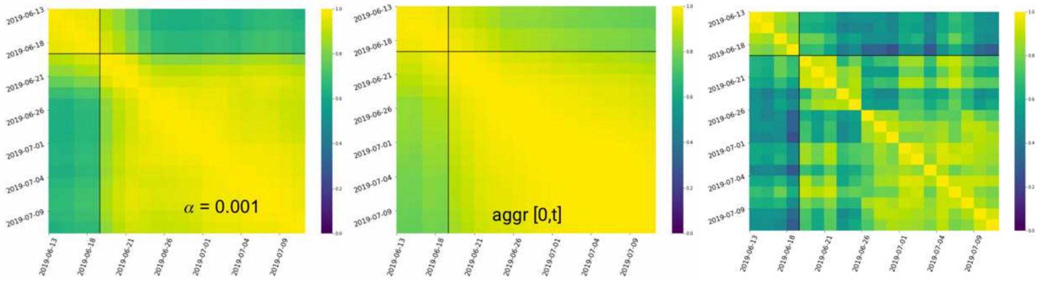

Figure 1: Comparison between various representations of the temporal social network of a group of baboons in response to a simulated perturbation (i.e., exchange of two nodes' id in the network on the 4th day of data, t0=2019-06-19): Matrices of cosine similarity values between representations at different times for all possible couples of days, computed (left) with our framework with α=0.001, (middle) aggregating the data on [0,t], (right) aggregating the data daily. Black lines correspond to the time t0 of the perturbation. The matrices show qualitatively that t0 is better detected by our framework than by the aggregated networks.

“Labyrinth Chaos & Labyrinth Walks:
Elegant Chaos & Chaotic Walks without Attractors”

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Abstract

Labyrinth chaos was discovered by Otto Rossler and Rene Thomas in their endeavour to identify the necessary mathematical conditions for the appearance of chaotic and hyperchaotic motion in continuous flows.

This is a generic and minimal model of a dynamical system which turned out that, even though it is simple, it is full of surprising properties. Simple and elegant as it is, it still holds great promise for elucidating aspects of chaotic dynamics that are not evident in other systems.

Our work highlights the incredible riches of this system in its disconcerting simplicity and importance in the context of dynamical systems and in other fields.

As an example, we consider an array of coupled labyrinth chaos systems found to exhibit complex chaotic behaviour reminiscent of chimera-like states. We discuss a peculiar synchronization phenomenon due to the properties of the labyrinth walks as well as their ability of to exhibit chimera-like states due to the unique properties of their space-filling, chaotic trajectories.

Finally, we discuss further implications in relation to the labyrinth walks system by showing that even though it is volume-preserving, it is not force-conservative. ._

Dynamic segregation and the disproportionate incidence of COVID-19 in African American communities

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(Dated: October 12, 2020)

One of the most concerning aspects of the ongoing COVID-19 pandemics is that it disproportionately affects people from Black and African American backgrounds, creating a so-called "COVID-19 infection gap", i.e., a marked difference between the percentage of African Americans citizens in a community and the percentage of African Americans infected by (or died of) COVID-19. The abnormal impact of COVID-19 on these ethnic groups seem to be almost uncorrelated with other risk factors, including co-morbidity, poverty, level of education, access to healthcare and response to cures. Here we introduce the concept of dynamic segregation, that is the extent to which a given group of people is internally clustered or exposed to other groups, as a result of mobility and commuting habits [1]. By analysing census and mobility data on major US cities, we found that the weekly excess COVID-19 incidence and mortality in African American communities is significantly associated with their dynamic segregation. The results confirm that knowing where people commute to, rather than where they live, is much more relevant for disease containment.

We quantify the dynamic segregation of a certain group in a urban area by means of the typical time needed by individuals of that group to get in touch with individuals of other groups when they move around the city. In our model, a city is represented by a graph $\mathcal{G}$ where nodes are census tracts and each edge indicates a relation between two areas, namely either physical adjacency or the existence of commuting flows between them. Each node is assigned to a class, according to the ethnicity distribution in the corresponding area. Then, we consider a random walk on the graph $\mathcal{G}$, and we look at the statistics of Class Mean First Passage Times (CMFPT) and Class Coverage Times (CCT). The former is the expected number of steps needed to a walker starting on a node of a certain class α to end up for the first time on a node of class β, while the latter is related to the time needed to a random walk to visit a certain fraction of all the classes present in the system. The underlying idea is that a random walk through the graph preserves most of the information about correlations and heterogeneity of node classes [2]. Consequently, if a system is dynamically segregated, the statistics of CMFPT and CCT will be substantially different from those observed on a null-model graph having exactly the same set of nodes and edges, but where a node is assigned a class at random from the underlying ethnicity distribution. Starting from the statistics of CMFPT and CCT at the level of each city, we defined three indices of dynamic segregation, namely dynamic clustering (C), dynamic exposure (E), and dynamic isolation (I), and we associated to each state in the US the weighted average of each of those indices across the largest metropolitan areas of the state

In Fig. 1**A-C** we show the correlation between the infection gap and our segregation measures as the pandemic progresses. Indeed, there exists a quite strong correlation between dynamic segregation and the disproportionate number of infected in African American communities. In particular, the dynamic clustering of African Americans in a state correlates positively and quite strongly with the infection gap observed in that state in the first weeks of the data set, both on the adjacency and commuting networks. The dynamic segregation also provides significantly higher correlations than other state-of-the-art indicators. Interestingly, the combination of dynamic segregation and use of public transport seems to explain the persistence of infection gap throughout the early phases of the pandemic (Fig. 1**D-F**).

Our results suggest that before lock-downs are put in place, the commuting patterns of African Americans increase their exposure to the virus. After lock-downs are enforced, instead, they are more likely to pass the virus over to other African Americans, as a result of the high levels of clustering and isolation of these communities, as measured in the adjacency graphs of census tracts. In general, the states where African Americans are more exposed due to long-distance trips are also those where they are more clustered due to short-range mobility. The existence of such positive correlations provides an interesting hint for policy makers: by mitigating the clustering of dynamically segregated ethnicities one would be able to also reduce their disproportionate exposure to the spread of diseases.

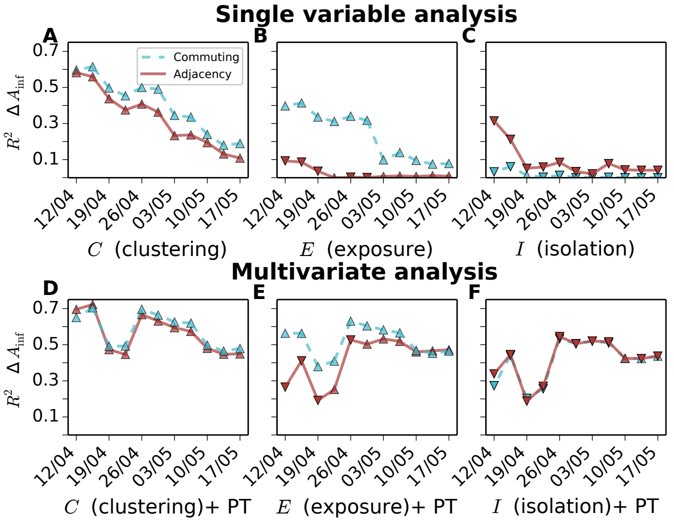

FIG. 1. Evolution of the Pearson correlation (R^2) between African American incidence gap and (**A**) dynamic clustering, (**B**) dynamic exposure and (**C**) dynamic isolation, respectively on the adjacency (solid red lines) and commuting graphs (dashed blue lines). Multivariate analysis of the same indices and usage of public transportation by African Americans for (**D**) dynamic clustering, (**E**) dynamic exposure and (**F**) dynamic isolation. The type of marker indicates the sign of the correlation (triangles pointing up for positive correlations, and down for negative correlation).

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Exploring the interplay between brain and mind in Alzheimer's disease

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The mechanisms behind the interplay between brain structure, function and cognition are, fundamentally, still unknown. On one hand, there is evidence that damages to brain structure affect its function and, as a consequence, cognitive processes. On the other hand, there is also convincing evidence that altered cognitive processes can influence the structure of the human brain. In most clinical cases, this lack of knowledge makes it difficult to characterize in time an ongoing disease or to identify early warning signals of neurodegenerative diseases and psychiatric disorders in healthy subjects, with obvious limitations to prevention and treatment. Interestingly, there is increasing evidence for speech disorder and language alteration in humans affected by neurodegenerative diseases and psychiatric disorders. The tight relationship between brain and mind is further strengthened by recent studies which proved the existence of semantic maps tiling the human cerebral cortex [1]. Organization of language and exploration of concepts in human mind are usually represented by cognitive units, namely the concepts, linked together by associative relationships which form semantic networks or clusters. However, understanding how humans navigate such networks remains elusive, because the underlying topology of concepts can not be observed directly and only functional representations are accessible.

Here, we overcome those limitations and show that the hypothesis of an underlying, latent, geometry characterizing the human mind is plausible. We characterize this geometry by means of adequate descriptors for exploring and navigating dynamics, demonstrating that they are able to capture the differences between healthy subjects and patients at different stages of dementia, namely mild cognitive impairment and Alzheimer's disease. We present preliminary results from a joint collaboration with the Department of Mental Health of health services agency of the Trento Province (APSS), that aims at integrating the neuro-psychological analysis of individuals affected by Alzheimer's disease to enrich the clinical assessment with information provided by mental pathways - sequential associations of concepts - and their altered navigation. Given the complex nature of the system in question, after investigating the potential latent geometry of semantic space, we propose to explore the mental navigation strategies and the emerging pathways by leveraging the network approach. We assume that concepts in the human mind are cognitive units (nodes) connected with each other by semantic links, as suggested by Collins and Quillian almost fifty years ago, and that the navigation of the corresponding cognitive network can be used to gain insight about the disease dynamics. Our work capitalizes on recent studies relating, for instance, abnormal priming in Alzheimer's patients to the degradation of their cognitive network [2]. To this aim, we use existing word embeddings [3] made for the Italian language [4] and patient clinical data collected at APSS. Our results provide a new unifying conceptual and computational framework, that can also be used to assess neurodegenerative diseases from language and semantic memory retrieval tasks resulting in a more complete, mathematical and data-driven output.

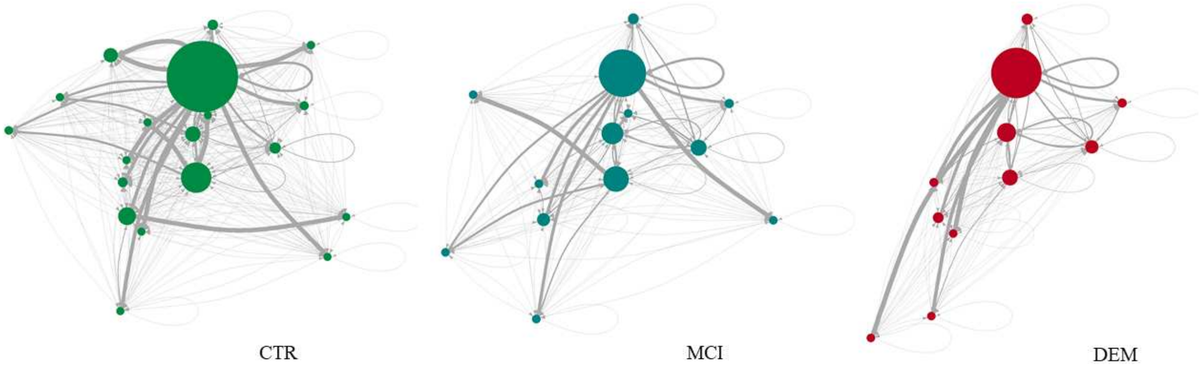

Figure 1: **Mapping mental pathways emerging from the navigation of concepts in healty controls (CTR), mild cognitive impairment subjects (MCI) and patients with dementia (DEM).** Networks of concepts as reconstructed from neuropsychological tests. Colored nodes encode clusters of concepts reported by patients while performing a neuropsychological test where they are asked to report similar words according to a specific semantic category. The size of nodes is proportional to the nodes' strenght, while the thickness of the edges is proportional to their weight.

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Privacy and Contact Tracing

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During the early months of the COVID-19 pandemic, many nations around the world developed smartphone-based solutions to mitigate the disease. Among these solutions have been contact tracing technologies. These smartphone based contact tracing systems use data about phone proximity, such as Bluetooth connectivity data, to track when smartphone users have been in contact for a significant duration. This data is used to signal to users when they may have been exposed to a person who has tested positive for COVID-19.

Smartphone based contact tracing has raised many policy and technical design questions. Unlike contact tracing programs executed mainly by public health personnel, smartphone based contact tracing systems depend on the population's smartphone ownership and willingness to install a dedicated application. In practice, these systems depend on hardware and software produced by commercial providers like Apple and Google. Early on, researchers raised flags about the potential misuses of data collected by these systems, as well as how the public's privacy concerns could pose a barrier to adoption.

Our research draws on network modeling techniques to develop the theoretical foundations of how privacy concerns interact with mobile-based contact tracing programs. Drawing on the Contextual Integrity theory (Nissenbaum, 2009), we define privacy as *appropriate information flow*, according to contextually situated norms. Hence, the privacy concerns of the public are multifaceted, including potentially everything from distrust of industrial or state institutions to concerns about contact information leaking to community or family members.

Through analytical modeling and simulation of infection and contact tracing on a complex network, we chart the tradeoffs between privacy and contact tracing effectiveness. Our preliminary finding is that the efficacy of smartphone-based contact tracing is more sensitive to institutional privacy than interpersonal privacy.

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A Behavioral Perspective to Community Resilience During the Covid-19 Pandemic: the Case of Paraisópolis in São Paulo, Brazil.

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Government's policies in response to the Covid-19 crises have varied from highly restrictive social distancing measures closing most public spaces to rather flexible ones. However, from the complex systems perspective, it is also important to consider the decentralized emergence of community's practices in response to the pandemic. The present article discusses the emergence and dynamics of community resilience by empirically investigating the case of the favela of Paraisópolis in São Paulo, Brazil. We observe the emergence of innovative practices that initially contributed to significant lower infection and mortality rates than the city average. We then consider possible factor associated with increase in infection rates in the community after six months. Our analytical framework combines two conceptual perspectives in the study of complex systems. First, resilience in socio-ecological systems highlights adaptation processes characterized by an interplay of previous experience and emerging new knowledge (1). Second, the cultural milieu (2) represents the set of different stimulus functions that embed the acquisition and continuity of interlocking behavioral contingencies. We aim at contributing to the understanding of community resilience by identifying geographic, psychological and ecological factors (contextual variables) that facilitate responses to the pandemic. The elements of the descriptive analysis and an exploratory basic qualitative study are employed to understand how the community may have self-organized in this period. We analyze publicly available information through previous publication, research reports and media material to descriptively present objects and stimulus functions associated to three environments and thereby presenting an overview of cultural milieu at Paraisópolis. Second, we present qualitative accounts of emerging practices through interviews with community members, analysis of reports and media news. Findings demonstrate how previous experience with social problems facilitated self-organization and the emergence of innovative practices in the context of uncoordinated state policies in Brazil. The identification of cultural milieu factors may inform public health measures that facilitate and sustain self-organization at the community level.

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What adaptive neuronal networks teach us about power grids

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Power grid networks, as well as neuronal networks with synaptic plasticity, describe real-world systems of tremendous importance for our daily life. We provide insight into the fundamental relation between these two types of networks by proving that phase oscillator models with inertia can be viewed as a particular class of adaptive networks. As an immediate consequence of the unification, we find a novel type of multicluster state for phase oscillators with inertia and the emergence of solitary nodes (see also Figure 1). Moreover, the phenomenon of cascading line failures in power grids is translated into a neuronal model of adaptively coupled phase oscillators.

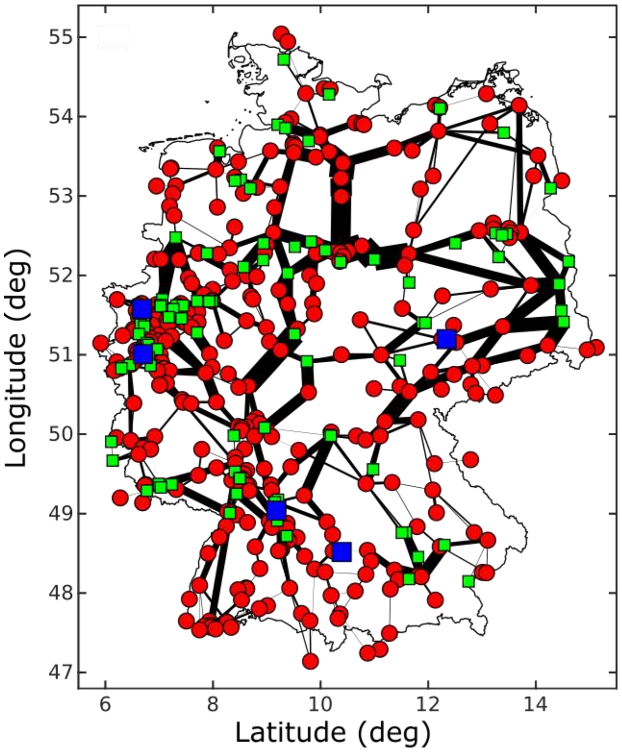

Figure 1: Average power flow of each line in the German ultra-high voltage power grid in the presence of solitary nodes (blue nodes).

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Diffusion Geometry of Multiplex and Interdependent Systems.

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Random walks (RWs) represent a powerful tool for the exploration of complex systems. Different dynamics, from random search to information exchange, can be modelled or approximated by RWs and, once they take place *on* networks, they provide both, new insights about their structure and function, and a geometric tool for their analysis [1,2]. In [3] we generalise the framework of diffusion geometry [1] to multilayer networks, which enable not only the representation of different types of interactions between pairs of units (through layers), but also of the interdependencies of these interactions (inter-layer connections). This richer structure should be taken into account when studying the functional shape of the system, as shown in Fig.1. Given the synthetic network represented in (a), in (b) we first aggregate the layers and then compute diffusion distances, while in (c) distances are evaluated on the multiplex and are then aggregated (by parallel sum). Although both matrices display two main blocks, in (c) we can more clearly detect the functional modules: nodes 20-30 are weakly connected to the main module in layer 1, while they belong to the largest component (LCC) of layer 2; nodes 1-10 (except for 8) do not belong to the LCC in layer 2, but are in the main module in 1, they hence form a sub-group in the second cluster. Finally, we extend the family of diffusion distances to different RW dynamics. In Fig.1(d), together with the supra-distance matrix w.r.t. the classical random walk (CRW), we have those corresponding to the diffusive (DRW) characterised by transition probabilities depending on the maximum node strength and the physical random walk with relaxation, *r*, (PrRW), describing a process where a particle can jump to one of its neighbours in the same layer or in other layers, with probability *1-r* and *r*, respectively. The shape of the network varies in the induced geometries.

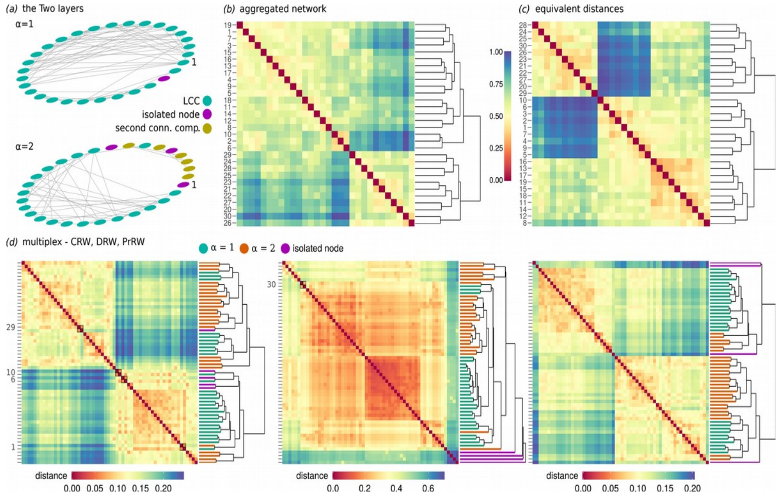

Figure 1: Distance matrices (b)-(c) and supra-matrices (d) corresponding to different RW dynamics on the synthetic two-layer network depicted in (a).

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Quantifying the Efficiency of Network Flows

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The apparently naive representation of a complex system as a collection of binary relations between indistinguishable units has since long proved to be a powerful tool for understanding dynamical systems. An important feature of interconnected systems is their ability to exchange information efficiently [1]. Assuming that the efficiency of a communication decreases as the distance between sender and receiver increases, one can easily quantify the communication efficiency of a networked system by the harmonic average of shortest-path distances $E(G)=\frac{1}{N}\sum_{i\neq j}\frac{1}{d_{ij}}$. While in the topological case this descriptor is normalised in [0,1] by definition, in the weighted case it needs to divided by the efficiency of an ideal network. In this work [2] we define a physically-grounded procedure to build the idealised version of a given network G, whose edge weights encode the intensities of the interactions. This procedure can be seen as adding to G shortcuts between connected but non-adjacent nodes, delivering the total flow (sum of weights) along their weighted shortest (or least resistance) path. The applications to real networks show that reducing the weight heterogeneity (by removing heavy links or re-distributing large flows) may lead to a more efficient communication.

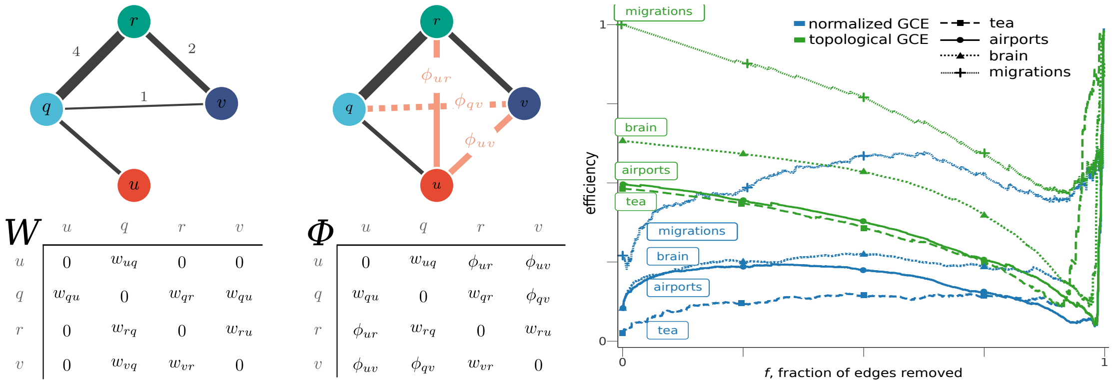

Figure 1: Global communication efficiency (GCE). (a) Right: a simple graph G and its weighted adjacency matrix W. Left: The total flows among nodes in G encoded in the matrix Φ. G_{ideal} is given by the average among real (W) and ideal (Φ) flows. (b) Topological and weighted GCEs for four real complex networks, during a targeted attack of heaviest links. The topological descriptor over-estimates their efficiency. The systems have different scales, e.g. the internal migrations network in Vietnam is a full network with 63 nodes. The efficiency of the tea trade network is the smallest, while the migration network is the most efficient, but also the most expensive being it a full network. The human brain network is topologically more efficient than the airports network, while they behave similarly as weighted systems.

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The Influence of Confidence and Social Networks on an Agent-Based Model of Stock Exchange

Abstract: The aim of this paper is to investigate the influence of investors' confidence in their portfolio holding with respect to their social group and of various social network topologies on the dynamics of an artificial stock exchange. An investor's confidence depends on the growth rate of her wealth relative to her social group average wealth. If the investor's confidence is low, the agent will change her asset allocation, otherwise she will maintain it. We consider three types of social networks: Barabási, small-world, and random.

It is noteworthy that the behavioral (confidence) variable plays a crucial role within the model, as it determines that the investor - whether fundamentalist, chartist or random – decides to change or not her investment strategy, once confidence changes according to the her wealth growth rate in comparison with the investor's average wealth growth rate in her social network. The confidence is not very volatile, and enjoys a large interval of stability and, in addition, the investor only changes her strategy when her confidence value reaches below C_n, a neutral confidence index. In other words, the fundamentalist, chartist or random investor will change her strategy to a more profitable one whenever she has little confidence in her current investment strategy.

Many statistical properties of the real stock exchange data are recovered in our model: high excess kurtosis, skewness, volatility clustering, random walk prices, and stationary return rates. The incorporation of networks in conjunction with the behavioral variable sheds light on several properties that are little explored in this literature. For instance, the small-world network has the highest degree of homophily. As the investors can switch to more profitable strategies, we found that the fundamentalist strategy is prevalent only in the random network. In the other networks (Barabási and small-world), the best approach to make profitable investments is the chartist one, which is a surprising outcome, since the network models are compatible with the random walk hypothesis. We also investigated the cumulative distribution function of the absolute value of normalized returns. The exponent of the power law distribution is found close to 3, in agreement with empirical stylized facts. Also, the largest spread of social contagion occurs in the small-world network, an expected result since this network topology has the highest clustering. Finally, more unequal wealth distribution and a greater relative gain were found in the Barabási network, followed by the random network.

Risk Sensitivity Emergence in a Prey-Predators Agent-based Model

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Risk sensibility is a phenomenon that appears in different field like psychology, economics and biology. Although diverse in several features, all these disciplines assume that risk-sensible individuals take decision characterized by different level of caution under conditions of uncertainty. This feature could emerge from an evolutionary process in certain circumstances. Nevertheless, there is a lack of studies about the effect of the environmental characteristics on the evolutionary emergence of risk-sensible behavior in a population.

To address this issue, we developed an evolutionary prey-predator agent-based model. In this model, a prey dies when a predator reaches it or when it runs out of energy. The longer a prey stays alive, the higher is its expected number of offsprings. Preys have limited information available; they can detect energy sources and predators only in the vicinity. When a prey perceives an energy source and a predator, it decides where to head computing a utility function whose parameters are its genotype, made of two genes: one gene aims at estimating the magnitude of the risk, the other the magnitude of the benefit. The difference between the values of the two genes defines the risk sensibility of the individual. The model is evolutionary because preys reproduce sexually and transfer the genotype to their offsprings. In this process, mutations can occur.

The analysis of the simulation results shows that the evolutionary process changes the distribution of genes in the population and can generate a risk-sensitive population. Moreover, it highlights that specific environmental factors influence the size and direction of the emergence of risk-sensitivity. A Bayesian network (Figure 1) helps us to understand the relationships between environmental features and the emergence of risk sensitivity.

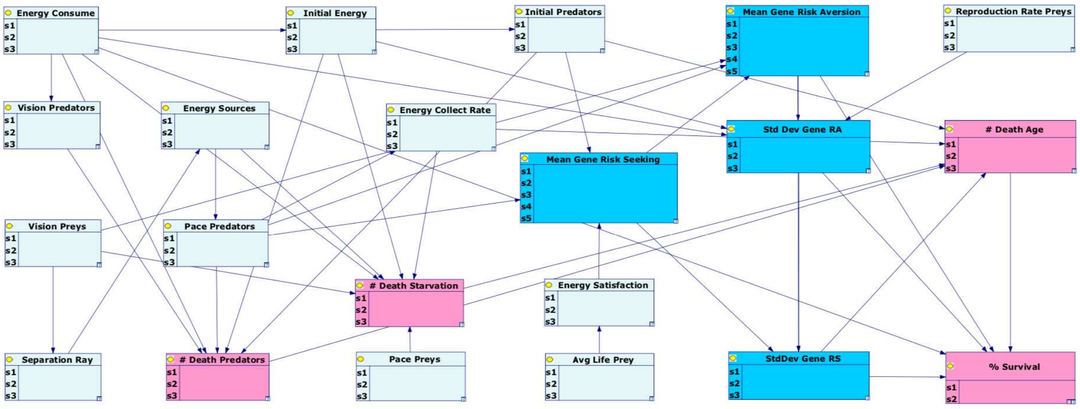

Figure 1: Bayesian network of the simulation meta-data

We find out that the riskiness of the environment has a non-monotonic influence on the risk sensitivity of the preys' population. For low levels of riskiness, it is risk-averse, and the risk sensitivity grows with the riskiness. For high levels of riskiness, risk sensitivity decreases until the population becomes risk-seeking. Furthermore, we find observable relationships between the emergence of risk aversion in preys' population and information process capacity, energy management, coordination ability and escaping strategy of preys' individuals. Further extensions to this work could include explorations of risk aversion emergence in a coevolution prey-predator environment with more complex coordination strategies.

Geometric Analysis of a Phantom Bursting Model

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The phantom bursting model was introduced to describe the episodic bursting of the pancreatic beta-cells, where active phases are interspersed by silent ones. The model is characterised by two slow and two fast variables with the two slow variables having very different time scales [1]. Considering the different time scales of the four variables of ordinary differential equations, Mixed-Mode Bursting Oscillations (MMBOs) solutions can be found. MMBOs are characterized by both small-amplitude oscillations (SAOs) and bursts consisting of one or multiple large-amplitude oscillations (LAOs) [2].

Here we focus our attention on the mechanism that generate the MMBOs due to both canards and delayed-Hopf-bifurcation [3]. Canards are central to the dynamics of MMBOs and we study them starting from the folded singularities, that are equilibria of the desingularized system of the phantom burster model. The canard phenomenon explains the very fast transition upon variation of a parameter from a small amplitude limit cycle via canard cycles to a large amplitude relaxation cycle. Furthermore the presence of the subcritical Hopf bifurcation via fast/slow analysis of the fast subsystem is found. A detailed geometric explanation of MMBOs is done using numerical simulations and the attracting slow manifold is obtained using numerical continuation technics.

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A Message-Passing Approach to Epidemic Tracing and Mitigation with Apps

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With the hit of new pandemic threats, scientific frameworks are needed to understand the unfolding of the epidemic. The use of mobile apps that are able to trace contacts is of utmost importance in order to control new infected cases and contain further propagation.

Here we present a theoretical approach [1] that uses both percolation and message--passing techniques to quantify the role of automated contact tracing in mitigating an epidemic wave.

Our approach captures the steady state of the SIR epidemic spreading with contact-tracing and test policies based on the mapping of the process to link percolation. Each individual is assigned a variable indicating the adoption or not of the app. Assuming perfect efficiency of the app, the model is based on the fact that only individuals with the app infected by individuals with the app are not able to spread the disease further if infected (see Figure 1).

Our study goes beyond previous attempts to study the effect of the app by fully capturing the non-linear effects of the dynamics and the phase diagram of the process. Moreover, we show that the adoption of the app by a large fraction of the population increases the value of epidemic threshold, and the best strategy in order to maximally delay the percolation transition is given by targeting the hubs. We use both percolation and message-passing techniques to study the role of contact tracing in mitigating an epidemic wave and we predict analytically the phase diagram of the model in random networks with given degree sequence. The analytical results are compared with extensive Monte Carlo simulations showing good agreement for homogeneous, heterogeneous networks models and for real data.

In conclusion, the proposed theoretical framework is able to assess the expected impact of contact-tracing apps in the course of an epidemic capturing the non-linear effect of the spreading dynamics. These results are important to quantify the level of adoption needed for contact-tracing apps to be effective in mitigating an epidemic.

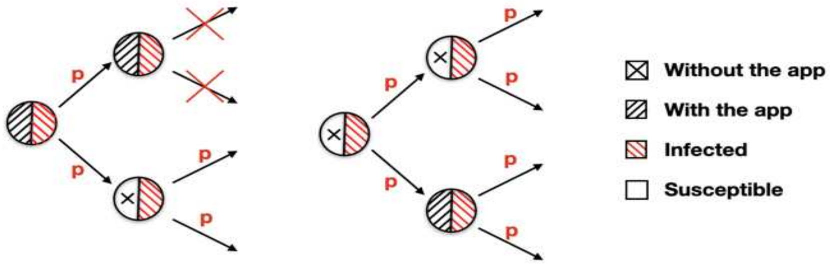

Figure 1: Sketch of the infection pathways that leads to the epidemic spreading in a population in which there are individuals that have adopted the app and individual that have not adopted the app.

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Complex Task Solving in Groups of Autonomous and Collaborative Agents: Effects of Individual and Collective Adaptation

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We model a system of autonomous and collaborative decision-making agents who self-organize themselves in groups in order to solve complex tasks. Previous literature argues that such groups should be static, in terms of not periodically adapting to the environment by replacing its members, since it is detrimental to the groups' performances [1]. In contrast, other lines of research suggest that static group structures do not necessarily bring a better performance than dynamic group structures [2]. As these findings look contradictory, our objective is to better understand the effects that static and dynamic group structures have on group performance.

In order to do so we incorporate the idea of adaptation [3] into the autonomous formation of groups. We set up an agent-based model and base the task environment on the *NK*-framework [4], which we adapt for complex task solving in groups (see also [5]). Dynamic (and static) features of groups are studied at two levels: First, we consider various degrees of *individual adaptation* to the task environment by endowing agents with capabilities to learn new partial solutions to the complex decision-making problem. Second, by allowing for the autonomous reorganization of group structures using an auction-based mechanism, we consider different extents of *collective adaptation* at the level of the group.

The results of our simulation study suggest that there are complex trade-offs between individual and collective adaptation and task performance. For scenarios with low task complexity, we find that a high level of individual adaptation improves performance significantly, whereas collective adaptation has only marginal effects. For highly complex tasks, however, we can observe that whether a high frequency of collective adaptation is desirable or not depends on the extent of individual adaptation. If individual adaptation is low, collective adaptation results in better group performance. Collective adaptation, however, can be detrimental to the performance of groups formed by agents who are already endowed with well-performing learning mechanisms. Based on our results, we provide advice for the efficient design of systems composed of autonomous and collaborative agents.

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Hurst Space Analysis, data clustering technique for long-range correlated time series

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Preference: regular talk

It was shown for variables across different complex systems that their fluctuation functions calculated with detrending methods of scaling analysis are rarely, as in theory, ideal linear functions on log-log graphs of scale dependence. Instead, they frequently exhibit existence of transient crossovers in behavior, signs of trends that arise as effects of periodic or aperiodic cycles (Hu et al., 2001). The use of global and local wavelet transform spectral analysis (WTS) and their detrended fluctuation analysis (DFA) variants provides a possibility to detect these cyclic trends and to investigate their timing, nature and effects on the analyzed time series.

We recently developed a technique to cluster or differentiate records from an arbitrary complex system dataset based on the presence and influence of these cycles in data (Stratimirović et al., 2018), which we dubbed the Hurst Space Analysis (HSA). We defined a space of p-vectors h^{ts} that represent record ts in the dataset, which we called the Hurts space. Vectors h^{ts} are populated by scaling exponents α calculated on subsets of time scale windows of time series ts that bound cyclic peaks in WTS, by way of use of time dependent detrended moving average analysis (tdDMA; Carbone, Castelli and Stanley, 2004). The length p of h^{ts} depends on the number of WTS peaks in that complex system. This number is, as was shown across complex systems, universal. In order to be able to quantify any time series ts with a single number, we projected its relative Hurst space unit vectors $s^{ts} = \frac{h^{ts}-m}{\sqrt{\sum_{i=1}^{n}\left(h_i^{ts}-m_i\right)^2}}$ (with $m_i = \frac{1}{n}\sum_{ts=1}^{n} h_i^{ts}$) onto a unit vector e of an assigned preferred direction in the Hurst space. The definition of the 'preferred' direction depends on the characteristic behavior one wants to investigate with HSA - projection of unit vectors s^{ts} of any record ts with a 'preferred' behavior onto the unit vector e will then always be positive.

The HSA procedure can serve to examine and differentiate records within datasets of randomly selected time series of any complex variable. We used HSA to differentiate complex time series of stock market data, based on the preferred characteristic of marked development, and to cluster datasets of observed temperature records from land stations from different climatically and topologically homogeneous regions, based on the 'belonging to a continent' preference.

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Positive algorithmic bias cannot stop fragmentation in homophilic networks

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Echo chambers or filter bubbles have been a concern since the early years of the commercial Internet, despite lacking a clear-cut definition. Sunstein [1] warned that too much personalization may lead to 'online segregation', where individuals would surround themselves with people of ostensibly similar characteristics or ideologies.

Here we ask

RQ1: Is fragmentation in (online) social networks inevitable, given presence of homophily and the high-pace dynamic of the structure of the network?

Algorithmically biased recommender systems have often been blamed for fostering these segregative tendencies. Thus, if part of the problem is algorithmic so should be its remedy. Therefore, we formulate our second research question as

RQ2: Can algorithmic bias counteract homophilic fragmentation of social networks? If so, what is the minimal algorithmic bias needed for fragmentation not to occur?

We show how, under the assumption of homophily, echo chambers and fragmentation are system-immanent phenomena of highly flexible social networks, even under ideal conditions for heterogeneity [2]. We achieve this by finding an analytical, network-based solution to the Schelling model and by proving that weak ties do not hinder the process. Furthermore, we derive that no level of positive algorithmic bias in the form of rewiring is capable of preventing fragmentation and its effect on reducing the fragmentation speed is negligible.

Future work could be conducted in testing the fundamental assumption of the model, namely homophily in opinion networks. That is, are dynamics in opinion networks on social media mainly driven by homophily, due to psychological phenomena like confirmation bias, or are they sufficiently malleable by neighboring nodes?

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Phase diagrams of the a generic model of exponential random networks with different soft constraints

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Complex networks have attracted a huge attention in the last twenty years, due to their wide range of applications in physics, biology, sociology, and information science. Models of random graphs are used to describe network structures and understand the patterns of connections among the elements of a network. An important feature of random graph models is that they undergo structural phase transitions, such as the percolation and condensation transitions, which are characterized by changes in the structural properties of a network as a function of the model parameters. In this context, models of exponential random graphs play a very important role, as they allow to study such transitions in a detailed way. In this work we study a generic model of exponential random networks with sparse and bounded degrees. The model is formulated in such a way that a variety of soft constraints can be simultaneously implemented, such as the average number of two-stars, the average number of edges, and the average correlations between the degrees of adjacent nodes. We solve the model exactly and obtain the free energy, from which we analyze the stability and the structural properties of different graph configurations. We construct the full phase diagram of the two-star model and of a model including degree correlations. We observe that both models display a region of metastability and undergo a first-order phase transition to a condensed state. The critical lines marking the phase transitions are exactly determined by means of the free-energy, while the nature of the different phases is characterized by the degree distribution. Finally, we establish the formal link between exponential random graph models and the large deviation theory of Erdös-Rényi random graphs, from which we present explicit results for the rate functions describing the large deviations of certain structural features characterizing Erdös-Rényi graphs. We point out that our formalism and results are valid in the *sparse* regime.

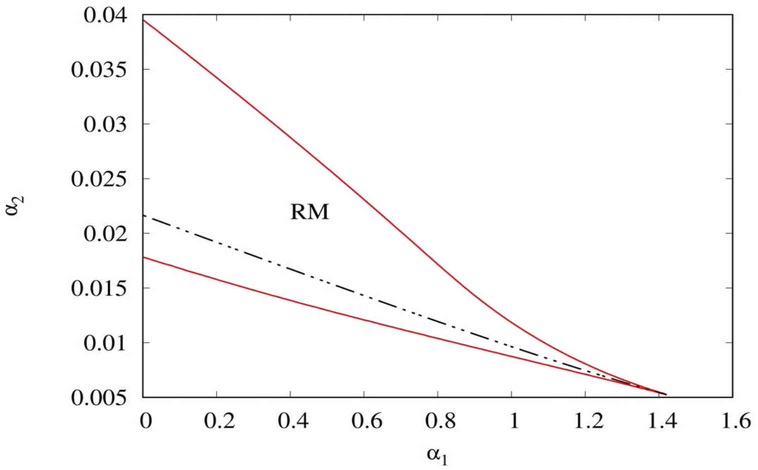

Figure 1: Phase diagram of the two-star model in the plane (α_2, α_1). The solid red lines delimit the metastability region (RM), while the dashed-dotted black line marks a first-order phase transition.

Heterogeneity in social and epidemiological factors determine the risk of measles infectious outbreaks

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Political and environmental factors – e.g., regional conflicts and global warming – increase large-scale migrations, posing extraordinary societal challenges to policy makers of destination countries. A common concern is that such a massive arrival of people – often from a country with a disrupted healthcare system – can increase the risk of vaccine-preventable diseases outbreaks like measles. We analyze human flows of 3.5M Syrian refugees in Turkey inferred from massive mobile phone data to verify this concern. We use multilayer modeling of interdependent social and epidemic dynamics to demonstrate that the risk of disease re-emergence in Turkey, the main host country, can be dramatically reduced by 75–90% when the mixing of Turkish and Syrian populations is high. Our results suggest that maximizing the dispersal of refugees in the recipient population contribute to impede the spread of sustained measles epidemics, rather than favoring it. Targeted vaccination campaigns and policies enhancing social integration of refugees are the most effective strategies to reduce epidemic risks for all citizens [1].

Transmission model. To model measles transmission in Turkey and the mobility of Turkish and Syrian refugees, we assume two populations of individuals, namely population T of size $N^{(T)}$ and population R of size $N^{(R)}$, living in a territory consisting of L distinct geographically patches (i.e. Turkish prefectures) accounting for $N_k^{(T)}$ and $N_k^{(R)}$ individuals, $k = 1, ..., L$ with $\sum_{k=1}^{L} N_k^{(T)} = N^{(T)}$ and $\sum_{k=1}^{L} N_k^{(R)} = N^{(R)}$.

The formulation of the force of infection for the two populations encodes how the interplay between the level of mixing of refugees with local populations and their mobility patterns shapes the spatial spread of simulated epidemics. Let us indicate by $c_{ki}^{(p)}$ $(p \in T, R)$ the elements of a matrix $\mathbf{C}^{(p)}$ encoding the number of people belonging to population p travelling from patch k to patch i, and with α the fraction of Syrian contacts with Turkish citizens. The force of infection for each population in the i–th patch depends on the contribution of all patches in the country:

$$\lambda_i^{(T)}(\alpha, \mathbf{C}^{(T)}, \mathbf{C}^{(R)}) = \beta_T \sum_{k=1}^{L} \left[\underbrace{c_{ki}^{(T)} \frac{I_k^{(T)}}{N_k^{(T)}}}_{\text{Endogenous}} + \underbrace{\alpha c_{ki}^{(R)} \frac{I_k^{(R)}}{N_k^{(R)}}}_{\text{Exogenous}} \right], \qquad \lambda_i^{(R)}(\alpha, \mathbf{C}^{(T)}, \mathbf{C}^{(R)}) = \beta_R \sum_{k=1}^{L} \left[\underbrace{\alpha c_{ki}^{(T)} \frac{I_k^{(T)}}{N_k^{(T)}}}_{\text{Exogenous}} + \underbrace{c_{ki}^{(R)} \frac{I_k^{(R)}}{N_k^{(R)}}}_{\text{Endogenous}} \right],$$

where $\beta_p = \beta / P_i^{(p)}(\alpha, c)$ is the transmission rate for population p and $P_i^{(p)}(\alpha, c)$ is an appropriate normalization factor (such that all individuals have the same number of contacts, regardless of geography and citizenship, see *SI Appendix* for further details). Each contribution consists of an endogenous term, accounting for the infectivity due to individuals from the same population, and an exogenous term, accounting for the infectivity due to the other population. The levels of mixing between refugees and Turkish citizens are modelled by considering a tunable parameter (i.e. α).

The absolute number of individuals moving between patches is inferred from available Call Detail Records (CDRs) as in Refs. [2, 3] and rescaled to adequately represent the volumes corresponding to 80M Turkish individuals and 3.5M Syrian refugees.

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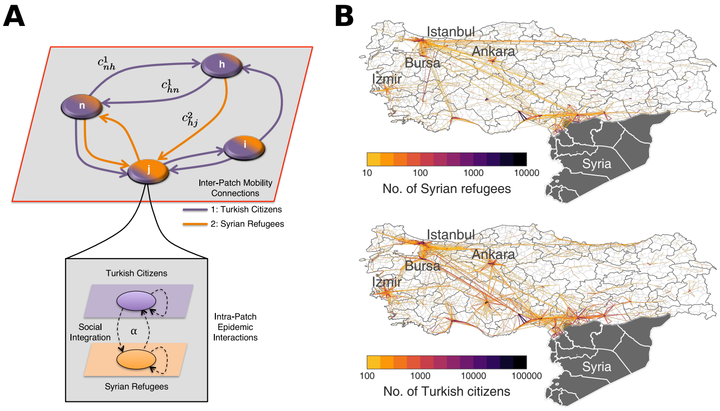

Figure 1: **Model structure and human mobility. A** Schematic illustration of the model considered in this work. Each prefecture of Turkey is considered as a node of a meta–population network of geographic patches. Two populations, namely Turkish and Syrians, are encoded by different colors and move between patches following the inferred inter-patch mobility pathways. Turkish and Syrian populations encode two different layers of a multilayer system [4, 5] where social dynamics and epidemics spreading happen simultaneously. **B** Mobility of Syrian refugees (Top) and Turkish citizens (Bottom) between the prefectures of Turkey as inferred from Call Detail Records. Different colors are used to indicate the number of individuals moving from a prefecture to another.

In search of art: rapid estimates of gallery and museum visits using Google Trends

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The number of visitors to museums is a key indicator of the performance of cultural institutions. Being able to have early estimates of visits is of crucial importance for cultural policy makers who need to allocate resources and funding, or to evaluate the impact of cultural policies.

Traditional data gathering and processing methods result in delayed estimates on the number of visitors to free museums. Here, we show how our information gathering process using the online search engine Google could help policy makers have early and accurate estimates of the number of people visiting a museum or gallery. We use time series methods, as well as artificial neural networks, to combine historical visits data with data on museums search volume on Google to generate rapid and accurate estimates of the number of visitors to a range of UK-based museums and galleries. We also provide an extensive validation of our analysis to reduce the risk of our findings being the result of a spurious correlation.

Our results provide further evidence that publicly available data sets detailing our online behaviour can be used to better understand the current state of society.

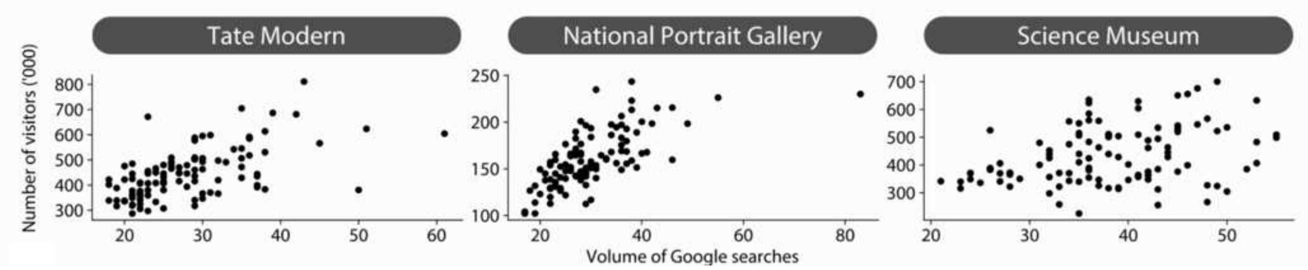

Figure 1: Rapid estimates of museum and gallery visitor numbers using *Google* search data. We investigate whether we can generate rapid estimates of visitor numbers for a range of museums and galleries in the UK using data on how frequently a museum has been searched for on *Google*. Here, we illustrate the data using three example museums: the *Tate Modern*, the *National Portrait Gallery* and the *Science Museum* group. We compare visitor numbers provided by the *Department for Digital, Culture, Media, and Sport*, and data on the volume of searches for each museum on *Google* between January 2010 and December 2018.

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Thermodynamic Machine Learning through Maximum Work Production

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Adaptive thermodynamic systems —such as a biological organism attempting to gain survival advantage, an autonomous robot performing a functional task, or a motor protein transporting intracellular nutrients— can improve their performance by effectively modeling the regularities and stochasticity in their environments. Analogously, but in a purely computational realm, machine learning algorithms seek to estimate models that capture predictable structure and identify irrelevant noise in training data by optimizing performance measures, such as a model's log-likelihood of having generated the data. Is there a sense in which these computational models are physically preferred? For adaptive physical systems we introduce the organizing principle that thermodynamic work is the most relevant performance measure of advantageously modeling an environment. Specifically, a physical agent's model determines how much useful work it can harvest from an environment. We show that when such agents maximize work production they also maximize their environmental model's log-likelihood, establishing an equivalence between thermodynamics and learning. In this way, work maximization appears as an organizing principle that underlies learning in adaptive thermodynamic systems.

Acknowledgements

The authors thank the Telluride Science Research Center for hospitality during visits and the participants of the Information Engines Workshops there. JPC acknowledges the kind hospitality of the Santa Fe Institute, Institute for Advanced Study at the University of Amsterdam, and California Institute of Technology for their hospitality during visits. This material is based upon work supported by, or in part by, Grant No. FQXi-RFP-IPW-1902 and FQXi-RFP-1809 from the Foundational Questions Institute and Fetzer Franklin Fund (a donor-advised fund of Silicon Valley Community Foundation), the Templeton World Charity Foundation Power of In-formation fellowship TWCF0337, the National Research Foundation, Singapore, under its NRFF Fellow program (Award No. NRF-NRFF2016-02), Singapore Ministry of Education Tier 1 Grants No. MOE2017-T1-002-043, and U.S. Army Research Laboratory and the U.S. Army Research Office under contracts W911NF-13-1-0390 andW911NF-18-1-0028. Any opinions, findings and conclusions or recommendations expressed in this material are those of the authors and do not reflect the views of Na-tional Research Foundation, Singapore.

During submission we became aware of related work: L. Touzo, M. Marsili, N. Merhav, and E. Roldan. Optimal work extraction and the minimum description lengthprinciple.arXiv:2006.04544.

An Initial Framework Assessing the Safety of Complex Systems

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There is no doubt that our lives are dependant on a diverse range of critical systems and infrastructure that are becoming increasingly *complex*. This raises difficult questions around how do we ensure the safety of these complex *engineered* systems (where by engineered we mean that they are at least partly deliberately designed), when they exhibit many if not all of the characteristics of complex systems [1, 2]? These properties include emergence, self-organisation, non-linearity and so on. Thus, we are not able to predict all the behaviours of a system from knowledge about its parts and their interactions alone, due to systems having emergent properties, something that has long been understood by the complex systems field.

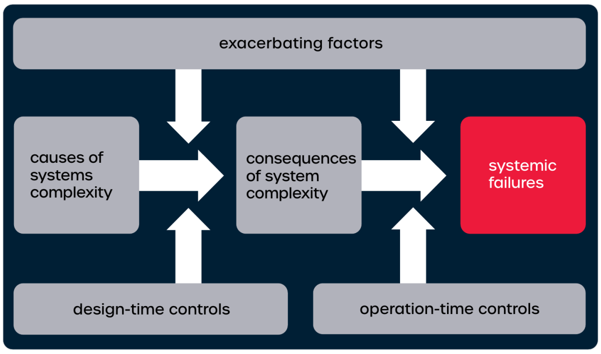

Fig. 1. Framework Overview - arrows indicate where different parts of a process can contribute to the overall complexity, not a linear path through the framework.

The paper presents an evolving framework that seeks to raise awareness of the potential consequences of the characteristics of complex systems in those who are involved in their design, implementation, management, and governance. We break the framework down into three layers, **task and technical**, **management**, and **governance**. The framework, which is supported by a series of diagrams (see figure 1 for an overview), seeks to identify the “causal chain” that can result in undesirable impacts and systemic failures. The framework highlights where steps might need to be taken – both at design-time and in operation – to acknowledge and potentially mitigate those impacts. Examples of systems included in the initial study and report are (semi-)autonomous vehicles, modern aircraft, health technologies, healthcare, diagnostic systems, and complex supply chain networks.

The framework diagrams are intended to be populated with specifics (at potentially varying levels of detail) relevant to a domain of interest, figure 1 provides an overview of the whole framework. The users of the framework are encouraged to document:

- Exacerbating factors that are important to the context in which the system is being used/deployed, e.g. production pressures;
- Causes of system complexity inherent to the system of interest, e.g. stakeholder diversity;
- Consequences of system complexity, e.g. competing objectives;
- Systemic failures, e.g. unanticipated risks;
- Design-time controls, e.g. redundant systems;
- Operation-time controls, e.g. incident and accident analysis.

The intention therefore is that, through engagement with the framework, the complexity of systems is accounted for through a systematic process that will support the documentation and analysis of that system. The desire is not to *engineer* complexity out of the system. Nor is it intended to, for example, identify and mitigate every possible emergent property of a system. Rather the framework should support a process where by the characteristics of complex systems, and their potential impacts, can be considered as an ever present part of system development and operation with a view to increasing the safety of complex systems in the engineering process.

Acknowledgements

This project was supported by the Royal Academy of Engineering and the Lloyd’s Register Foundation. The authors would like to thank all those who contributed to the project.

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A multifractal neural coding scheme reproducing foraging trajectories

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The movement of many animals follows Lévy patterns. The possible endogenous neuronal dynamics that generates this behaviour is unknown. In this work, we show the novel discovery of multifractality in winnerless competition systems and how it reveals an encoding mechanism able to generate two dimensional superdiffusive Lévy movements from a Lotka-Volterra map, experimental data for Long-Evans rats during chasing tasks, mice motor cortex neurons and the Grasshopper auditory receptor cell. The endogenous origin of the superdiffusive movement in animals has been established recently [2].

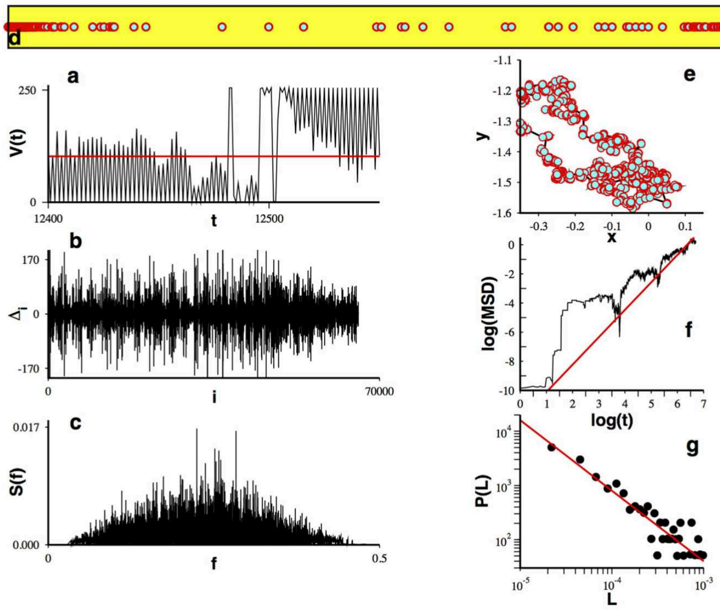

Figure 1: A superdiffusive Lévy random walk can be decoded from data of Long-Evans rats during a searching task.

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An analytical structure for turbulent cascades from a 2D discrete map

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In turbulent flows energy cascades from larger to smaller scales following the Kolmogorov -5/3 power law. An analytical picture of the process underlying cascades in fluids or in other systems is not known. Based on a well-known discrete map we show a procedure that generates an analytical structure that produces a cascade from which the energy scaling law for isotropic homogeneous turbulence can be calculated. It is done by finding a function that unveils a non-self-similar (possibly) multifractal ruling the cascade. The backbone underlying the cascade is formed by deterministic nested polynomials. These results show that turbulent cascade behaviour can be found in low dimensional nonlinear dynamics. Consequently, turbulent cascades are not only exclusive for fluids but may also be present in many other systems, such as neurological information processing and epidemic dynamics.

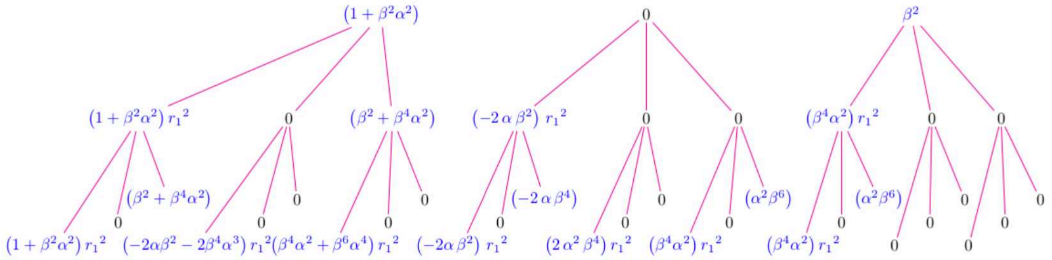

Figure 1: An example of the analytical generation of cascades.

Transient Dynamics in Dynamical Systems Subjected to Parameter Drift

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In nature, there is a vast variety of systems that cannot be modeled by the same set of equations and parameters as time passes. This may be caused either by the contact with its environment or due to internal factors. In this talk, we present the study of dynamical systems subjected to parameter drift and its implications in their evolution. For that purpose, we show the analysis of two multi-stable systems with chaotic attractors: the Lorenz system and the time-delayed Duffing oscillator. In the first case, the drift is contained in the Rayleigh number. In the case of the Duffing oscillator, it is the time delay itself which suffers the drift. For small but non-negligible parameter change rates, we show that when a parameter crosses a bifurcation point at p_{bif} , the non-autonomous system suffers a regime shift which appears for $p_{cr} > p_{bif}$. This fact can be seen for the Duffing oscillator in Fig. 1. The chaotic attractor loses stability for $\tau = 3.6$ for the frozen-in case. However, trajectories continue to behave chaotically for further values before jumping to (a) the fixed point or (b) the limit cycle. From an experimental point of view, one would observe a transient regime before the parameter crossing and a steady state afterwards. We have uncovered the scaling laws relating the transient lifetime and the parameter value for the transition with the parameter change rate. Surprisingly, we find a gamma distribution of lifetimes in the case of the time-delayed oscillator, instead of a normal distribution as previously reported for non-delayed systems. Finally, for the Lorenz system we also explore the possibility of recovering the transient state by reversing the parameter to its original value. We obtain the relationship between the parameter change rate and the number of trajectories that tip back to the initial attractor.

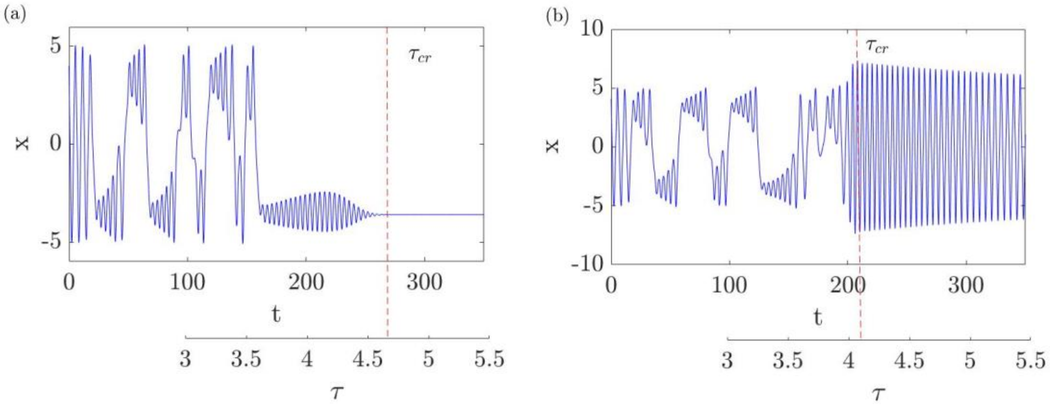

Figure 1: Time series for the time-delayed Duffing oscillator with $\tau(t)$. The transition to the steady state starts at a value of τ past the bifurcation value for the frozen-in system. Afterwards, trajectories end in (a) the fixed point or (b) the limit cycle.

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Random walks on hypergraphs

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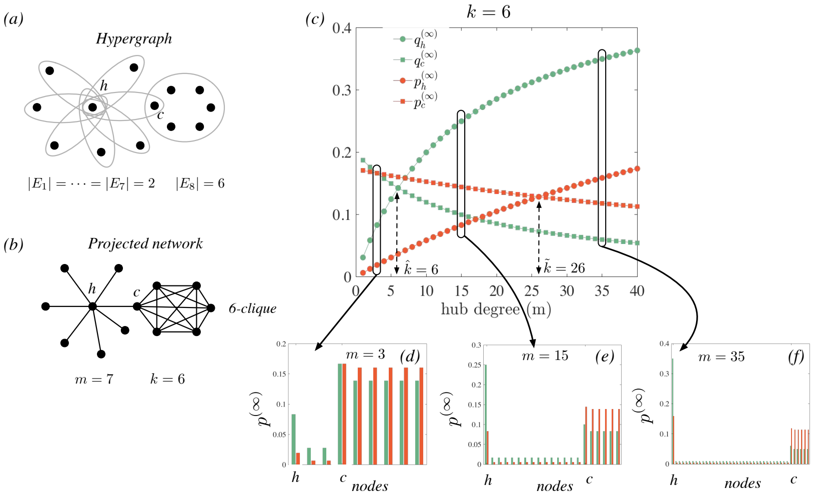
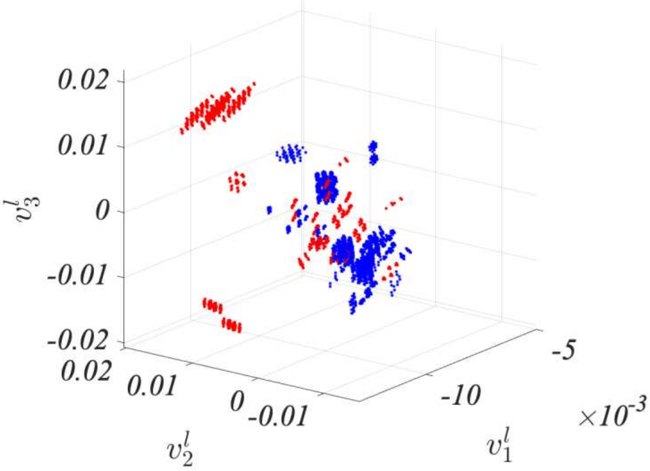
In the last twenty years network science has proven its strength in modelling many real-world interacting systems as generic agents, the nodes, connected by pairwise edges. Yet, in many relevant cases, interactions are not pairwise but involve larger sets of nodes, at a time. These systems are thus better described in the framework of *hypergraphs*, whose *hyperedges* effectively account for multi-body interactions. We hereby propose and study a new class of random walks defined on such higher-order structures, and grounded on a microscopic physical model where multi-body proximity is associated to highly probable exchanges among agents belonging to the same hyperedge. We provide an analytical characterisation of the process whose behaviour is ruled out by a *generalised random walk Laplace* operator that reduces to the standard random walk Laplacian when all the hyperedges have size 2 and are thus meant to describe pairwise couplings. We illustrate our results on synthetic models for which we have a full control of the high-order structures, and real-world networks where higher-order interactions are at play. As a first application of the method, we compare the behaviour of random walkers on hypergraphs to that of traditional random walkers on the corresponding projected networks, drawing interesting conclusions on *node rankings in collaboration networks* (left panel in the Figure). As a second application, we show how information derived from the random walk on hypergraphs can be successfully used for *classification* tasks involving objects with several features, each one represented by a hyperedge (right panel in the Figure). Taken together, our work contributes to unveiling the effect of higher-order interactions on diffusive processes in higher-order networks, shading light on mechanisms at the hearth of biased information spreading in complex networked systems.



The (m, k)-star-clique network. (a): hypergraph made by m + k = 13 nodes, divided into m = 7 hyperedges of size 2 and one large hyperedge of size k = 6. The node h belongs to all 2-hyperedges, while the node c belongs to one 2-hyperedge and to the 6-hyperedge. (b): the projected network (hyperedges mapped into cliques). (c): we show the dependence on m of the asymptotic probability of finding the walker on the node h (circle) or on the node c (square), in the projected network (green symbols) and in the hypergraph (orange symbols). (d), (e) and (f): we report the asymptotic probabilities $q_i^{(\infty)}$ and $p_i^{(\infty)}$ for three values of m: $m = 3 < \hat{k}$, $\hat{k} < m = 15 < \tilde{k}$ and $\tilde{k} < m = 35$, where $\hat{k} = 6$ and $\tilde{k} = 26$.



Classification of the mushrooms according to their features. We report a 3D embedding of the mushroom data set taken from UCI Machine Learning Depository, using the first three hypergraph Laplace eigenvectors. Each combination colour refers to a known class, red for poisonous and blue for edible.

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Sound – Complexity – Incompleteness

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Is sound predictable, or computable? What distinguishes an organized or "complex" sound? Although the literature on complex systems is vast, research on the application of complexity measures to sound is notably scarce. Sound certainly has the potential to a "complex approach", particularly for its double nature as acoustic entity (as studied by physics) and as conscious experience (as studied by cognitive science), which might suggest a "multilevel hypernetwork". One of the few attempts to measure the "complexity" of sound [1] is based on spectral flatness (which indicates whether the energy distribution is smooth or spiky), defined as the ratio between the geometric and the arithmetic means: $\frac{\sqrt{\prod_{n=0}^{N-1} x\,(n)}}{\frac{\sum_{n=0}^{N-1} x\,(n)}{N}}$. In this straightforward model, the rate of change of spectral dynamics is the only variable in consideration for the classification of sounds as "simple" or "complex". Although evidently too simplistic, this model has some practical advantages. It is presumably difficult to measure, for instance, the logical depth or the Kolmogorov complexity of a Beethoven recording, or of any sound produced by a system evolving under Natural Selection for billions of years (not to mention cultural evolution). It is hard enough to produce realistic acoustic simulations using physical modelling synthesis, digital waveguides or other solutions to the wave equation. But it is even harder to imagine an algorithm that would produce the number sequence required to digitally encode a symphony other than a copy of the sound samples of the original recording, which amounts to a string as long as its source. In information theory, Shannon's entropy is a common starting point to investigate "complexity": $H(X) \coloneqq -\sum_{i=1}^{n} p\,(x_i)\log_b(p\,(x_i))$. To compare sounds of different durations, we require a measure of entropy that is independent of the sequence length: $-\frac{\sum_{i=1}^{n} p\,(x_i)\log_b(p\,(x_i))}{\log_b(\text{length}\,(p\,(x_i)))}$. While entropy tends to increase in a closed system, complexity intuitively increases only at first, decreasing when approaching equilibrium. To investigate this behavior and expand on the model [1], this paper explores "sonic complexity" through an analysis of large numbers of properties related to timbre, such as entropy, flatness, mfcc, roughness and irregularity at different orthogonal representations (time domain, spectral domain, cepstral domain and wavelets). Presently, there are two leading paradigms to digitally codify sound: 1) an ordered set of natural or real numbers representing variations in pressure 2) an ordered set of complex numbers representing the amplitudes and phases of complex exponentials at different frequencies. Each representation can be derived from the other using the Fourier Transform. From the short-time Fourier transform it is possible to obtain not only the Cepstrum (the Fourier transform of a log Fourier Transform), on a frame-by-frame basis, but also the 'spectral fluctuation', by taking a second spectrum estimation of each spectral band, while simultaneously accounting for masking effects. We argue that a multilevel approach combining advanced methods of music information retrieval, machine learning and cluster analysis can reveal new insights towards measuring the complexity of sound.

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Junk News Bubbles: Modelling the Rise and Fall of Attention in OnlineArenas

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Despite the ever growing availability of traces produced by digital media, so far no large-scale empirical research has been devoted to online attention cycles, with few remarkable exceptions. To encourage such research, we propose a toy model inspired by one of the most influential accounts of attention dynamics: the “public arenas model” introduced in 1988 by Stephen Hilgartner and Charles Bosk (H&B) [4]. Despite its clarity and insightfulness, H&B’s framework has never been mathematically formalized because of its complexity and lack of formal description. We streamline H&B’s model focusing on the rise and fall of attention matters and proposing a ready-to-test version that we hope will encourage further investigation with empirical data. The main consideration of H&B work that we included in our formalization can be summarized as follows:

1. a population of **“matters of attention”**(or “social problems”, as in H&B original formulation) defined self-referentially as the entities that compete to capture public attention in a media arena;
2. a **fixed attention capacity** (or “carrying capacity”, in H&B terms) by each debate arena, justified by the limited attention of media audiences;
3. a competition mechanism that primes **trendiness**. Each attention matter see its visibility promoted or demoted according to its previous variation multiplied by a parameter that amplifies or dampens this dynamics.

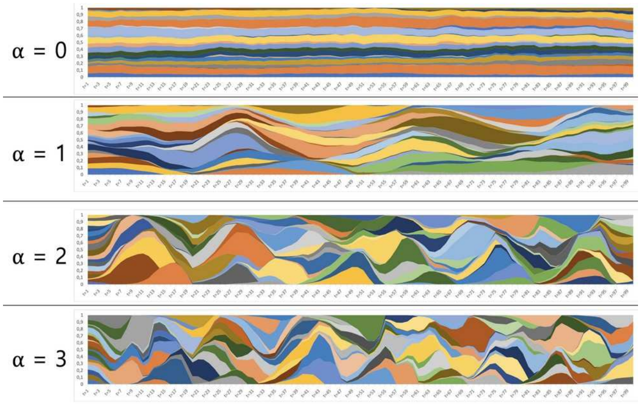

Figura 1: *Arena partition among attention matters alongtime with different trendiness weights*

Figure 1 simulates how attention is partitioned between attention matters in arenas where a different weight α is given to trendiness. Each color represents a different attention matter and the horizontal axis represents time. The comparison between the graphs in Figure 1 suggests that trendiness boost the steepness in the rise-and-fall of attention matters and affects both dimensions of the media cycle: the life time of an attention matter, and the diversity of the public debate. On the one hand, the stronger is trendiness boost, the shorter is the lifecycle of attention matters, allowing a higher number of matters to enter and exit the arena. On the other hand, a higher trendiness boost increases the maximum visibility reached by attention matters and, most importantly, amplifies the difference between successful and unsuccessful attention matters, creating a situation in which most of the available attention is captured by a minority of over-visible items. We claim that debate arenas that reward to trendiness excessively end up displaying a syncopated rhythm of attention that is at the same time increasingly dispersed and increasingly concentrated. We call such phenomenons *junk news bubbles*: speculative weaves that destroy rather than create richness in public debate.

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The Rhythms of the Night: increase in online night activity andemotional resilience during the Covid-19 lockdown

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The lockdown established in France from March 17th to May 11th as a response to the Covid-19 pandemic has created a sudden and severe transformation of daily routines. This disruption represents a textbook case of exogenous shock on human behaviors, which can,by comparison reveal features of normal social life. This work carries out this comparative analysis, focusing on online behaviors and leveraging a unique YouTube dataset. A few weeks before the lockdown, we had started following a corpus of more than one thousand French political YouTube channels with an exceptional temporal granularity – recording hour by hour the number of views of all of their videos. This provided us with a unique dataset to study how the lockdown transformed the circadian rhythms of online activities. To make sure our findings are not platform specific, we compare the results obtained on YouTube with a Twitter dataset of 33 million tweets in French. Our analysis shows, for both platforms, a substantial albeit not surprising increase of online activities as a consequence of the decrease of real-life interactions (Figure 3). Moreover, the growth in online participation and content consumption is not uniform across the 24 hours but is more salient during night. Besides this variation in volume, we register changes in the kind of content shared from an emotional and thematic point of view. In both platforms, the lockdown is marked by a decrease in emotional contents, positive and negative, and a thematic shift from topics like ”money, work and social life” to ”safety and death”. Against these lockdown-induced changes, some constants of YouTube and Twitter stand out. Despite its quantitative change, the shape of the daily cycle of different emotions (i.e. their prevalence by hour) is not impacted by the lockdown: this finding confirms the results of previous studies that showed a stability of emotional rhythms trough seasons and cultures [1]. The resilience of these patterns, despite the disruption of the lockdown, supports the biological origin of the emotional expression, which seems to be more strongly influenced by the biological clock than by exogenous factors.

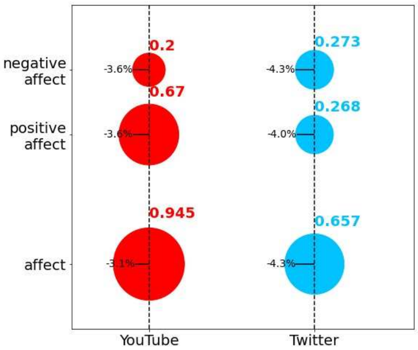

Figure 1: Emotion changes before and after lockdowns: fraction of videos/Tweets with positive and negative emotions and relative change with lockdown

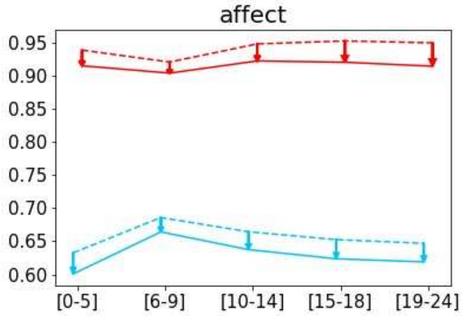

Figure 2: Resilience of emotional patterns: fraction of videos/Tweets with emotional content by hour.

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The Hypothesis of Quantum Coherent Brain Dynamics and Human Behavior

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The hypothesis of "quantum coherent brain dynamics" was introduced by Ricciardi and Umezawa in the late sixties [1]. In the following years, the hypothesis was further advanced to decipher behavior and memory effects [2,3]. According to the proposition, the coherent quantum functionality of the brain is founded on the interaction between a large number of 50 μm spatially distributed coherent quantum states, known as "tunneling photons" and the vector potential of the electromagnetic field. Because a tunneling photon system behaves as a superconducting functional system, an extensive number of data processing requires not only minimum energy consumption but also brain memory and instantaneous and coordinated functionalities of different brain areas emerge as the natural outcome of brain tunneling photon interactions. Furthermore, brain functionality and human behavior is adequately described on account of transitions (oscillations) between three quantum coherent states; one pure ground state (logic-L), one pure excited state (paranoiac-P) and a metastable (M) symmetric (a superposition of the previous L and P quantum states).Transitions between pure quantum states and metastable antisymmetric states are forbidden, in agreement with the classical metastable brain theory [4].

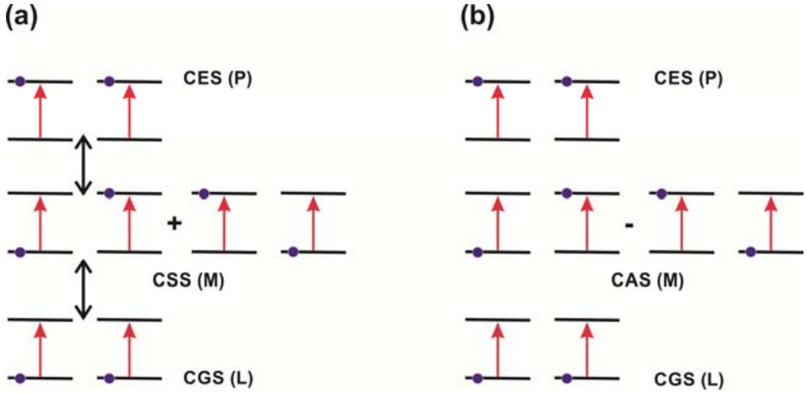

Figure1. Quantum coherent brain dynamics and functionality. **(a)** A reversible brain transition between logic (L) and paranoiac states (P) via metastable coherent symmetric states. **(b)** A metastable (M) antisymmetric state implies a permanent brain state, either logic or paranoiac. CGS: Coherent ground state. CAS: Coherent antisymmetric state. CSS: Coherent symmetric state. CES: Coherent excited state.

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How to Measure the Goodness of Fit of Bibliometric Models?

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Scientometrics deals with the quantitative characteristics of science and scientific research. We find many approaches to the modeling of citation vectors of individual authors: the so-called Lotka's informetrics [1], the discrete generalized beta distribution (DGBD) [2], or an the agent-based model by Ionescu and Chopard [3], to name a few. In our recent paper "Three Dimensions of Scientific Impact" [4] which has recently been published in PNAS, we proposed a model which, in addition to the preferential attachment rule, also employs an "accidental" component.

In this presentation we will address the question of how to assess the fitness of such models and whether it is possible to indicate the best performing tool in the case of the DBLP v12 [5] database of computer science papers.

Acknowledgements

The project was funded by POB Research Centre Cybersecurity and Data Science of Warsaw University of Technology within the Excellence Initiative Program - Research University (ID-UB).

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The Origin of the Extreme Wealth Inequality in the Talent vs Luck Model

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While wealth distribution in the world is highly skewed and heavy-tailed, human talent as the majority of individual features is normally distributed. In a recent computational study by Pluchino et al. [1], it has been shown that the combined effects of both random external factors (lucky and unlucky events) and multiplicative dynamics in capital accumulation are able to clarify this apparent contradiction. We discuss a simplified version (STvL) of the original Talent versus Luck (TvL) model, where only lucky events are present, and verify that its dynamical rules lead to the same very large wealth inequality [2]. We also derive some analytical approximations aimed to capture the mechanism responsible for the creation of such wealth inequality from a Gaussian-distributed talent. Under these approximations, our analysis is able to reproduce quite well the results of the numerical simulations of the simplified model in special cases. On the other hand, it also shows that the complexity of the model lies in the fact that lucky events are transformed into an increase of capital with heterogeneous rates, which yields a nontrivial generalization of the role of multiplicative processes in generating wealth inequality, whose fully generic case is still not amenable to analytical computations.

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An Integrated Semantic Schematic Model of the Energy Sector with Hypernetworks

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Keywords: energy, complex systems, computational models, ontology, multiadic relations, mutlilevel systems, hypergraphs, simplicial complexes, hypernetworks, industrial applications

Abstract

Data is being collected and generated at a rate never seen before in human history and this is no different in the energy sector. Despite the frightening volume of data, it can quite often be difficult to find what you need or to find the connectives in the data sources that form representative structures of the domain.

To combat this, considerable effort has been placed into various technologies, such as, Big Data, machine learning and search engines that will attempt to discover the relations amongst data elements in the system from the data itself, to form networks and graphs; or in web-ontologies and linked-data that have languages that will describe each individual relation.

However, the data in many of the sources in the energy domain show that much of it is described through levels of abstraction. Where parts go to make up wholes, which in turn may form parts of other wholes, and where more than two elements are needed to form a semantic relation, capturing the thing being described. For example, a substation is made up of transformers, in-feeders, lines and many other parts, but the substation itself forms a part of the distribution or other power network. The diadic relations of networks provide a powerful way of representing this structure. However the relations that make up many of them are multiadic (n-ary rather than binary) and require a generalisation of network theory. Hypergraphs and simplicial complexes pave the way towards this generalisation which is provided by hypernetworks. The essential first step is the definition of a hypersimplex as an ordered list of parts (simplex) with an assembly relation that gives the information needed to assemble the parts into a whole at a higher level in a multilevel representation of the system. This algebraic structure is required to support the bottom-up top down dynamics of the system which is often but not always modelled by numbers representing local and global system states and transformations. In complex systems in general and energy systems in particular a part is not constrained to a single multi-level structure: a part can belong to many such structures forming an overlap where interaction amongst systems and subsystems can occur. For example the Air-source Heat Pump exists in both the power and heat networks as well as, it could be argued, the weather system.

Looking at the technologies often used to describe such systems, such as, XML, JSON, RDF, UML and others, all have been used to describe parts of the system, but on closer consideration, they all naturally form multilevel and n-ary relations; relations that do not form from raw data.

In an attempt to bring together these structures in a way that will facilitate mass connectivity and discovery in the energy sector, Hypernetwork Theory (HT) has been adopted as the modelling language of choice to create a single semantic schema. A set of software tools, including the HnC (Hypernetwork Compiler) have been developed to support the creation and manipulation of Hypernetworks. These enable a simple description of the system to be turned into a hypernetwork (Hn), or to merge them to create larger models or to facilitate different views to be created out of the model.

Not only does HT allow for the description of complex systems and facilitate the interplay amongst them through overlapping and other meronymic and taxonomic techniques, it also enables ontologies and other structures to be both ingested into the model and to be generated easily. HT makes modelling much simpler. Although web-ontologies with RDF, OWL and Description Logics create good models, they can be very difficult to develop and maintain, as each individual relation has to be individually defined, and even then the true semantics can be lost as the model does not capture the n-ary relation that actually forms the meaning. HT simplifies this by grouping the elements into a single n-ary relation where required, but still allows other relations amongst them if desired.

HT is flexible and adaptable, and given the tools available different models can be merged dynamically at runtime, and new ones created that can form new and important relations from the models, even allowing for models to be combined across domains.

Identification of super-spreaders and super-susceptibles locations from directed and weighted human movement networks for disease control and prevention

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Human movement is key to the spread of infectious diseases, including COVID-19. Hence, it is also key to the control and containment of the disease itself [1]. The flow of people from places to places is not uniform across all links in a city. Some links—edges of the human flow network connecting two nodes corresponding to two locales—exhibit particularly high flows, while others are experience less intense flows despite the fact that they may connect two busy places. This leads to some heterogeneity in both the spreadability and vulnerability of the disease. Indeed, certain places, like some people, can be "super-spreaders." Here, we aim at extending the concept of 'super-spreader' from complex network analysis to understand the spatial distribution of **spatial super-spreaders**, and **spatial super-susceptibles**, i.e. respectively, places most likely to contribute to disease spread or to people contracting it [2]. In this framework, we seek to uncover these specific locales using the daily-aggregated ridership data of public transport in Singapore. Specifically, we developed a systematic way to identify super-spreader and super-susceptible locations based on the integration of human flow intensity with two neighborhood diversity metrics. Our results show that most spatial super-spreaders are also spatial super-susceptibles. Counterintuitively, busy peripheral bus interchanges are riskier places than crowded central train stations. This framework is useful for the post-outbreak reopening and future disease control preparedness.

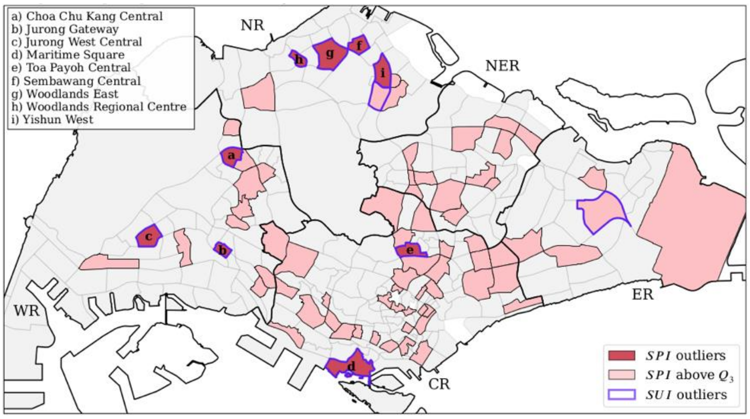

Figure 1: Spatial super-spreaders on weekdays for the Republic of Singapore. *SPI*: Spreader index, *SUI*: Susceptible index.

Acknowledgements

This research was supported by an SUTD grant (Cities Sector: PIE-SGP-CTRS-1803).

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Market competition and government interventionism: a Monte Carlo approach

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In this work, we present a Monte Carlo simulational model of technological growth and innovation diffusion under the influence of government intervention. Our goal is to show how company markets behave under varying intensity and effectiveness of state intervention. We also aim to specify conditions in which government intervention increases economic growth. Using the Monte Carlo method, we performed vast simulations of interacting and competing companies in a market, under a varying degree of outside intervention. Our model's predictions about the average level of market technology were compared to empirical data for several countries. We found that there is no one-size-fits-all intervention policy. Our model also suggests that often the quality of the intervention is much more important than its quantity. However, a policy that maximizes economic growth must be tailored for each country, depending on its market's susceptibility to technological backwardness. Our model allowed us to find conditions for which an intervention policy can positively impact economic growth. Finding an intervention policy that will rapidly increase economic growth can be of profound practical importance, especially in the current pandemic situation. One of the most significant advantages of the model is its flexibility. It is easy to incorporate further extensions to the model that will make it more realistic in the future, such as specifying the state's budget constraints and sources of funding for intervention.

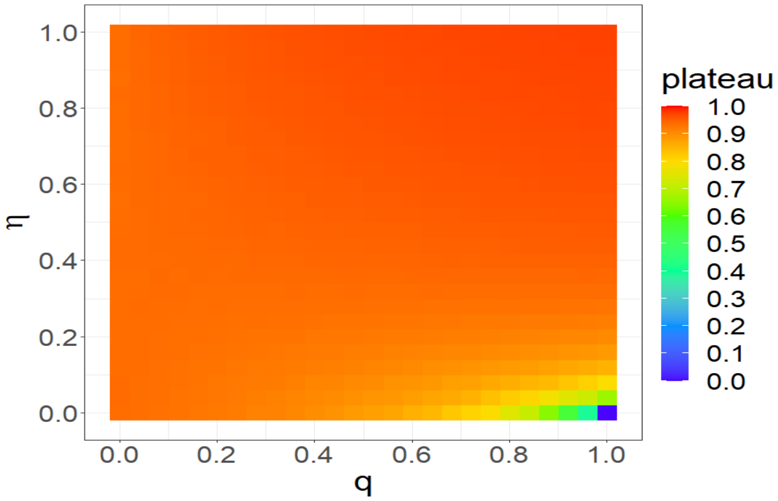

Figure 1: Heatmap showing a market average technology to the World Frontier ratio in the long run. The horizontal axis is the probability of intervention. The vertical axis is the efficiency of the intervention. Low efficiency and high probability lead to market destruction, while high efficiency for some *q* can improve the average technology in the long run.

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Promoting Fairness in the Spatial Ultimatum Game

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Institutions and investors alike have often been confronted with the question of which individuals are most eligible for the distribution of endowments. Here [1], we consider the Ultimatum game in a spatial setting and propose a hierarchy of interference mechanisms based upon the amount of information available to an external decision-maker and desired standards of fairness. Starting from previous findings on the spatial Prisoner's Dilemma [2], we explore the differences arising from targeting different roles, but also the effects of mutation and stochasticity. Our key findings show that macroscopic monitoring of the population requires thorough information-gathering and that local observations can mediate this requirement. Moreover, we discuss the circumstances in which fair behaviour should be fostered in order to reduce unnecessary spending. Finally, we present our suggestions for promoting fairness as an external decision-maker when asymmetric roles in interactions can be targeted.

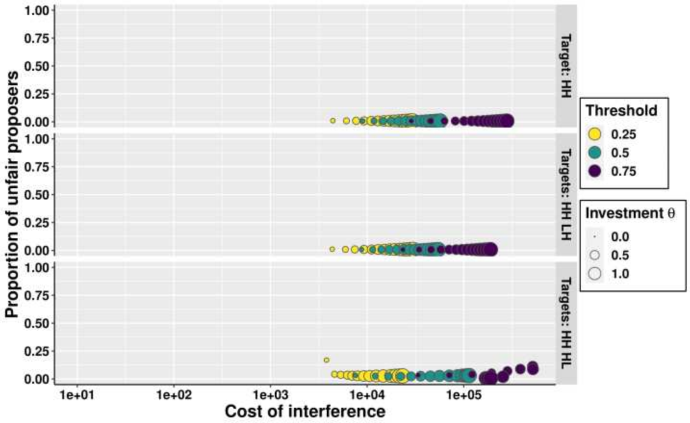

Figure 1: Proportion of unfair proposers as a function of the average cost of interference for different local targeting schemes. Optimal cases are on the bottom left. For all schemes, investors should only invest if there is at most one fair agent in the neighbourhood.

Acknowledgements

This work was supported by the Future of Life Institute (grant RFP2-154).

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Shapes of Road-Bounded Blocks as Indicators of Degree of Urbanization

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Over 55% of the world's population live in cities, and the figure is expected to grow to 68% by the year 2050 [1]. Not all cities are created equal, though; several factors such as the geography, age, and economic factors, among others, affect the degree of exploration and densification over these urban areas [2]. Here, we attempt to capture the visual differences in the degrees of urbanization of Philippine (PH) cities through image processing techniques. We track the statistical distributions of the circularities $\sigma_b = 4\pi A_b/P_b^2$, a normalized measure of the shape of all the road-bounded blocks b with areas A_b and perimeters P_b found within the city boundaries [3,4].

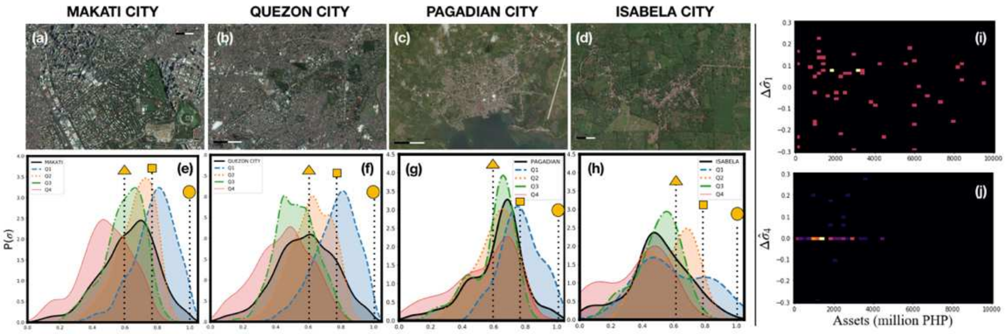

Figure 1: Representative Philippine cities under different legal classes (a-b) Makati and Quezon City (c-d) Pagadian and Isabela City (CC) with their corresponding conditional probability block circularity distributions (e)-(h) [values of σ corresponding to the regular triangle, square, and circle are marked for reference] and lastly (i)-(j) modal differences between the total and the large (Q_4) and small (Q_1) block statistics, respectively.

Cities in PH are created by legislation, and are grouped based on socio-political standing. Highly urbanized cities (HUC's) are cities with population of over 200,000 and a net asset of atleast P50-M; independent component cities (ICC's) are separated from the jurisdiction of the province where it is geographically located; and component cities (CC's) do not meet the aforementioned criteria, i.e. having considerably lower population, lower net assets, and within the provincial jurisdiction. We take the image of all PH city road networks at a scale of 1:25000 and a resolution of 300dpi and compute the circularities of all road-bounded blocks. The values are then sorted into area quartiles: Q_1 $[0 < A_b \leq 1179 \text{ m}^2]$; Q_2 $[1179 \text{ m}^2 < A_b \leq 3011 \text{ m}^2]$; Q_3 $[3011 \text{ m}^2 < A_b \leq 6957 \text{ m}^2]$; and Q_4 $[6957 \text{ m}^2 < A_b \leq 39\,138\,120 \text{ m}^2]$.

The conditional statistics of these subsets are shown for representative cities in Figure 1, where the values of σ for the regular triangle, square, and circle are shown for reference. One readily notices that the separation of the modes of these subsets are different for each representative city class. Makati [**(a)**, **(e)**] and Quezon City [**(b)**, **(f)**] are the highest-income HUCs, and Pagadian [**(c)**, **(g)**] and Isabela [**(d)**, **(h)**] are CCs with the lowest net assets. The Q_1 (smallest) areas peak around the value σ_{square}, indicating regular blocks; as such, the HUCs generally have more proportions of these shapes than CCs; in fact, there are CCs that do not have small blocks due to their space being yet undivided into small, regular blocks. Conversely, CCs tend to have more proportion of Q_4 (largest) areas; in fact, in **(j)**, the difference in the modes of the Q_4 and the total distribution or lower-income cities tend to be zero, a fact that is not observed for the same difference with Q_1 in **(i)**. In general, highly- [least-] developed cities are therefore more characterized by planned [undifferentiated], smaller [bigger], and regularly- [irregularly-] shaped blocks.

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Crisis contagion in the world trade network

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The Google matrix analysis of the world trade network (WTN) allows to probe the direct and indirect trade exchange dependencies between countries (see e.g. [1]). Unlike the simple accounting view obtained from the usual import-export balance, relying on the total volumes of exchanged commodities between countries, the PageRank-CheiRank trade balance (PCTB) allows to take account of the long range inter-dependencies between world economies. We present a WTN crisis contagion model [2, 3] built upon the iterative measure of the PCTB for each country.[1] Once a country have a PCTB below a threshold κ, it is declared in a bankruptcy state in which it can no more import commodities excepting some vital one for the industry, eg, petroleum and gas. This state corresponds either to the fact that a country with a very negative trade balance have not enough liquidity to import non essential commodities, or to the decision of a supranational economic authority trying to contain a crisis by placing an unhealthy national economy in bankruptcy. The bankruptcies of economies with PCTB less than κ induce a rewiring of the world trade network which possibly weaken other economies. In the phase corresponding to a bankruptcy threshold $\kappa < \kappa_c$, the crisis contagion is rapid and contained since it affects only less than 10% of the world countries and induces a total cost of less than 5% of the total USD volume exchanged in the WTN. This total cost of the crisis drops exponentially with the decrease of κ. In the phase corresponding to a bankruptcy threshold $\kappa > \kappa_c$, the cascade of bankruptcies can not be contained and the crisis is global, affecting about 90% of the world countries. In the global crisis phase ($\kappa > \kappa_c$), at the first stage of the contagion, myriads of countries with low exchanged volume (ie, low import and export volumes) go to bankruptcy. These countries belong mainly to Sub Saharan Africa, Central and South America, Middle East, and Eastern Europe. In the next stage of the crisis contagion, the conjugated effect of the bankruptcies of these countries contribute to the fall of big exporters, such as the US or Western European countries. As an example, for 2004, 2012, and 2016 WTNs, the bankruptcy of France is solely due to the failure of many low exchanged volume countries, which, here, individually import from France a volume of commodities less than 10 billions USD. Otherwise stated, France failure is caused by the failure of many small importers. Great Britain is a similar case for the 2004, 2008, and 2016 WTNs. Among the big exporters (ie, with a exchanged volume greater than 10 billions USD), European and American countries are the sources of the crisis contagion. The gates from which crisis enters Asia are Japan, Korea, and Singapore. Generally, Asian countries go to bankruptcy at the end of the crisis contagion, with China, India, Indonesia, Malaysia and Thailand, being, with Australia, usually the last economies to fall. We also observe that failures of the four BRIC occur during the last stages of the crisis contagion.

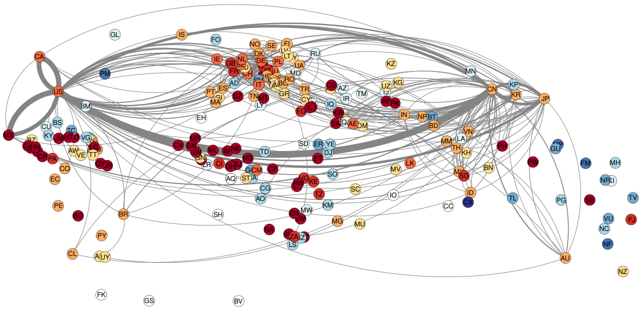

Fig. 1. World trade network in 2016. Two countries A and B are related by a directed link, the direction of which is given by its curvature. If A points to B following the bent path in the clockwise direction ($A \frown B$) then A exports to B, otherwise, i.e. ($A \smile B$), B exports to A. The width of the link is proportional to the exportation volume in the WTN from the source country to the target country. The colors of country nodes range from red (blue) for a country going to bankruptcy at stage $\tau = 0$ ($\tau = \tau_\infty$) in the case of a bankruptcy threshold $\kappa = -0.1$. Only transactions above 10^{10}USD are shown. Raw data from UN Comtrade [4].

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Putting a Spin on Language: A Quantum Interpretation of Ambiguous Sentence Readings

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One of the biggest challenges in Artificial Intelligence (AI) is to understand and formulate coherent and meaningful discourse in natural language. Words are traditionally represented as vectors, agnostic to their syntactical role, and used in specific tasks such as word similarity. Once we wish to represent the meanings of well-formed larger fragments, we have to deal with the complexity of sentence structure.

On a sentence, words can be seen as having a function-argument relationship. Basic words, like nouns, are arguments of complex words, like verbs and adjectives, taken as functions. Such a grammar, formalized by Lambek [1], is mirrored in vector space representations of meaning, originally introduced by Coecke et al. [2]. Basic words are still described as vectors, but complex words are now interpreted as higher order linear maps. By mapping the first to quantum states and the latter to quantum operators, we can describe the meaning of a grammatical string of words as a quantum process.

The complexity of this process is further increased by the many ambiguities that arise at different levels. Words can be ambiguous in their meanings ("bank", financial or of a river) or their grammatical roles ("bite" as a noun or a verb), forming conflicting interpretations of sentences ("I saw a boy by the bank", "Man helps dog bite victim"). Lastly, different words taken as argument of the same complex word give rise to different readings of the same sentence ("I shot an elephant in my pajamas" is ambiguous about who wears the pajamas; in Dutch, "Man die de hond bijt" can either mean "man that bites the dog" or "man that the dog bites").

In our work, we raise the building blocks of meaning to density matrices, leveraging their treatment of meaning ambiguity and including the directionality the information in the function-argument structure of the original Lambek grammar [3]. We deal with higher-level ambiguous readings by extending this grammar with unary operators, which trace structural and syntactic variations. We interpret them by attaching an extra spin state to each word, encoding multiple readings on a parallel quantum process [4]. Our method contributes to a growing field of complexity research at the intersection of AI, Linguistics and Quantum Computation.

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Unveiling the Infodemic Mindset Linked to the Climate Emergency

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Despite the climate emergency, climate disinformation actors keep broadcasting infodemic content to millions of people. Here we use semantic patterns to unveil emotionally distorted content linked to polarization. Mindset reconstruction with *forma mentis* networks exposes the emotional backbone of language, and such exposure highlights the attitudes towards “climate change” fueling the climate divide. Greta Thunberg’s speeches, combining anger (towards inaction), fear (of an approaching threat) and trust (in solving this crisis), perceive “climate change” as an indispensable “call-to-action” fight. This makes climate activism’s mindset entwined to revolutionary emotions. In comparison, the emotional profile adopted by climate disinformation actors shows conceptual associations and emotions indicating that climate disinformation promotes hypercritical skepticism, hiding under a generally trustful promotion of (climate) change and including: (i) discussing numbers in terms of imbalanced exaggerations, (ii) referring to scientists in a stereotypical way, i.e. isolated individuals that attempt to provide abstract, theoretical evidence to climate disinformation, (iii) displaying negative emotions against children, and (iv) showing fear against public policy interventions. Through this hidden cognitive dissimulation, climate disinformation can greatly inhibit social activism and, consequently, policy making addressing climate change. Cognitive tools exposing distorted emotional content should be adopted to foster pro-active climate debates.

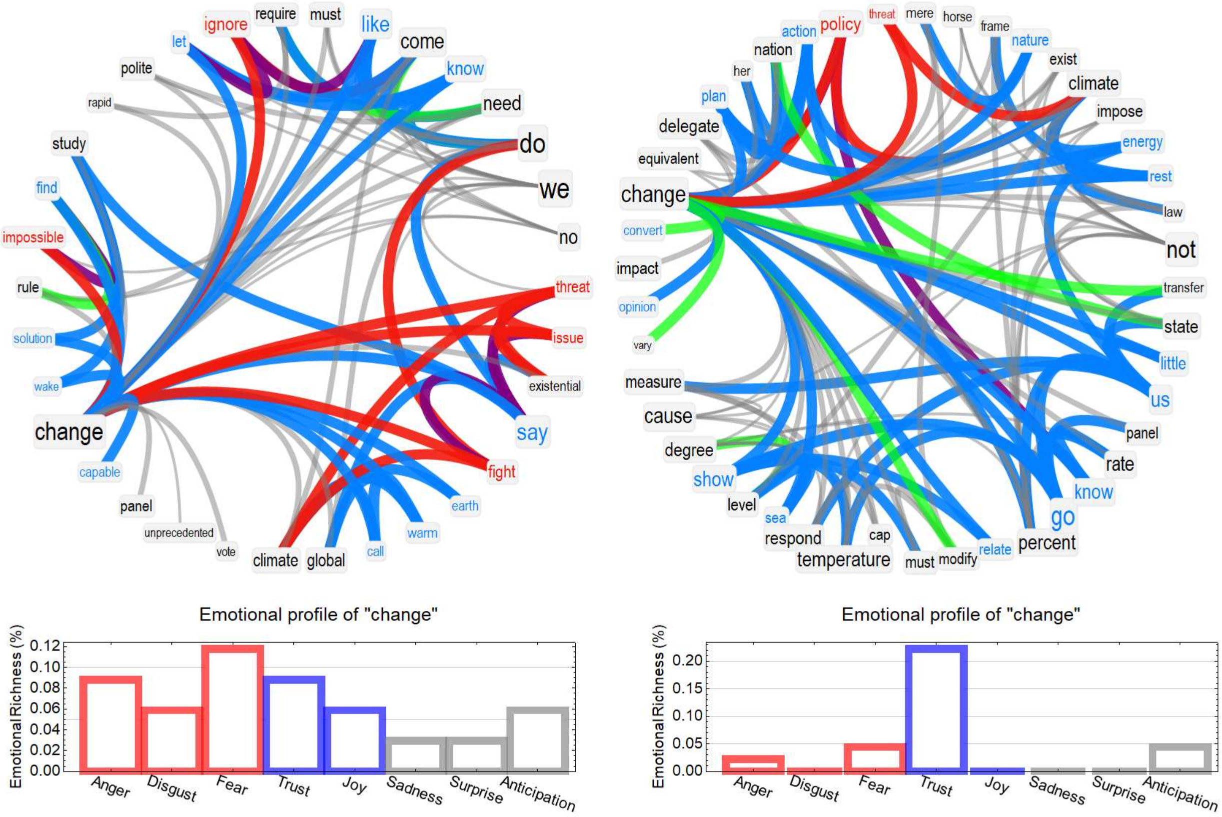

Figure 1: Speakers’ mindset reconstruction in *forma mentis* networks around “change” in the speeches of Greta Thunberg (left) and Christopher Monckton (right). Grey/blue/red (green) links indicate syntactic relationships (synonyms) between words in speeches. Blue (red, black) indicates words perceived as positive (negative, neutral) in language.

From metaphor to computation: Constructing the potential landscape for the dynamics of panic disorder

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In recent years, formal models are gaining momentum in the field of psychology, aimed to address the theory crisis and provide a quantitative foundation for theoretical inferences. These formal models are often used to study psychological states, for example, a healthy state and a psychopathological state. The relative stability of these psychological states is an important avenue for research to better understand individual differences and (clinical) change processes. The potential landscape is often used as a metaphor to conceptually illustrate stability. But recently the corresponding numerical method has been developed, which provides a novel approach to gain quantitative insights into the stability of various states in psychological systems.

In this project, we use Wang's method to quantitatively compute the landscape function for a formal dynamic model of panic disorder. Besides developing a general method, we also aim to examine the stable states of the model based on the landscape function. First results show one stable state – the healthy state – and one quasi-stable state – the panic state. We speculate that the quasi-stable panic state is due to the excitability of the considered model system, which shows longer residence time but not a metastable state. We further found that the stability of the panic state increases as the arousal schema becomes more sensitive. These results are in line with previous clinical findings, providing evidence for the validity of the model. In addition, we also investigated how other model variables and parameter settings influence the relative stability of different psychological states.

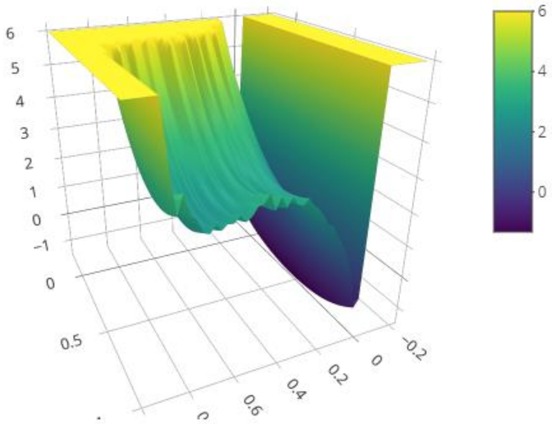

Figure 1: The potential landscape for the variables *fear* and *arousal schema*.

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Attention Dynamics on the Chinese Social Media Sina Weibo during the COVID-19 Pandemic

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COVID-19 was first detected in China's Hubei province and has had a severe impact on the life in the country since then. We investigate how this epidemic has influenced attention dynamics on the biggest Chinese microblogging website Sina Weibo in the period December 16, 2019 - April 17, 2020. We focus on the real-time Hot Search List (HSL), which provides the ranking of the most popular 50 hashtags based on the amount of Sina Weibo searches. We show, how the specific events, measures and developments during the epidemic affected the emergence of new hashtags and the ranking on the HSL. A significant increase of COVID-19 related hashtags started to occur on HSL around January 20, 2020, when the transmission of the disease between humans was announced. Then very rapidly a situation was reached where the COVID-related hashtags occupied 30-70% of the HSL, however, with changing content. We give an analysis of how the hashtag topics changed during the investigated time span and conclude that there are three periods separated by February 12 and March 12. In period 1, we see strong topical correlations and clustering of hashtags; in period 2, the correlations are weakened, without clustering pattern; in period 3, we see potential of clustering while not as strong as in period 1. To quantify the dynamics of HSL we measured the lifetimes of hashtags on the list and the rank diversity at given ranks. Our observations indicate attention diversification since the COVID-19 outbreak in Mainland China and a higher rank diversity in the top 15 ranks on HSL due to the COVID-19 related hashtags, a drastic attention decay shortly after the outburst and a slower decay for a longer period.

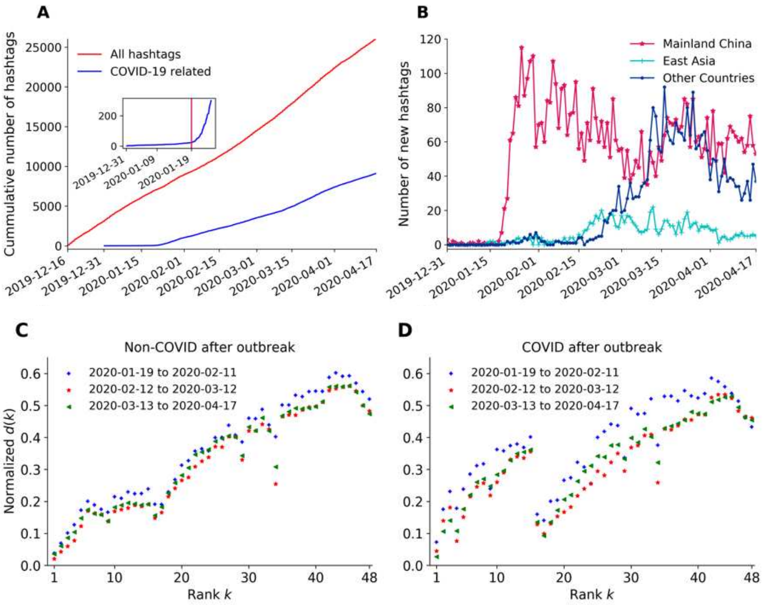

Figure 1: Overview of COVID-hashtags on Weibo re-ranked Hot Search List (HSL) throughout the pandemic. (A) Cumulative number of all hashtags and all COVID-hashtags with time. The inset indicates rapid increase in COVID-related hashtags starting from January 19 marked by a vertical red line. (B) Daily new COVID-hashtags on Mainland China, East Asia outside of Mainland China and Other Countries outside of East Asia. (C) Rank diversity of the 48 ranks on the HSL taking all non-COVID hashtags in the three periods after the outbreak. (D) Rank diversity taking all COVID-hashtags in the three periods after the outbreak. A large gap occurs after the top 15th rank. The result in period 1 is higher than period 2 and period 3, revealing a more dynamic change of the hashtags appeared on the HSL.

Statistical learning by replicator systems

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The Bayesian framework offers a flexible language for consistent modular assembly of statistical models used by both minds and machines. Another algorithmic domain capable of adaptation in potentially high-dimensional and stochastic environments is Darwinian evolution. The equivalence of their fundamental dynamical equations, replicator dynamics and Bayesian update, hints at a deeper algorithmic analogy. Here we show, based on a unified mathematical discussion of evolutionary dynamics and statistical learning in terms of Bayesian graphical models, that this is indeed the case. Building blocks of Bayesian computations, such as inference in hierarchical models, filtering in hidden Markov models, gradient likelihood optimization, and expectation-maximization dynamics of mixture models, map naturally to fundamental concepts of evolution: multilevel selection, quasispecies dynamics, phenotypic adaptation and ecological competition, respectively. These correspondences point towards a unified computational understanding of mechanisms Nature invented to adapt to high-dimensional and uncertain environments.

Epidemic proximity and imitation dynamics drive infodemic waves during the COVID-19 pandemic.

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The spreading of COVID-19 pandemic is accompanied an by an infodemic, defined as an overabundance of misinformation and disinformation. Infodemic is an emergent phenomenon due to information dissemination with unintended consequences of the complex dynamics of human behavior.

Modeling infodemic waves which spread through online social media during an ongoing epidemic is a challenging problem. To tackle this challenge, we collected more than 180 millions Twitter messages posted across 40 countries worldwide, with the aim to analyze the infodemic dynamics and its causal relationships with epidemic outbreaks. We considered three different modeling setups, namely, a compartmental model inspired by epidemic processes (SIS), an evolutionary game theoretic model driven by imitation dynamics (DI), and a bounded rationality model that assumes not pure rational individual behaviours (BR). These three models are statistically compared among them in order to evaluate which one better explains the infodemic modulation around the beginning of local epidemic.

We found that the most effective model in both the reproduction of local infodemic waves and for out-of-sample predictions is an evolutionary model of population dynamics, driven by epidemic incidence as an exogenous signal. Our model advances our current understanding of the epidemic-infodemic interplay and their co-evolution dynamics, demonstrating that the emergence of infodemic in the digital sphere cannot be easily understood in terms of epidemic-like spreading.

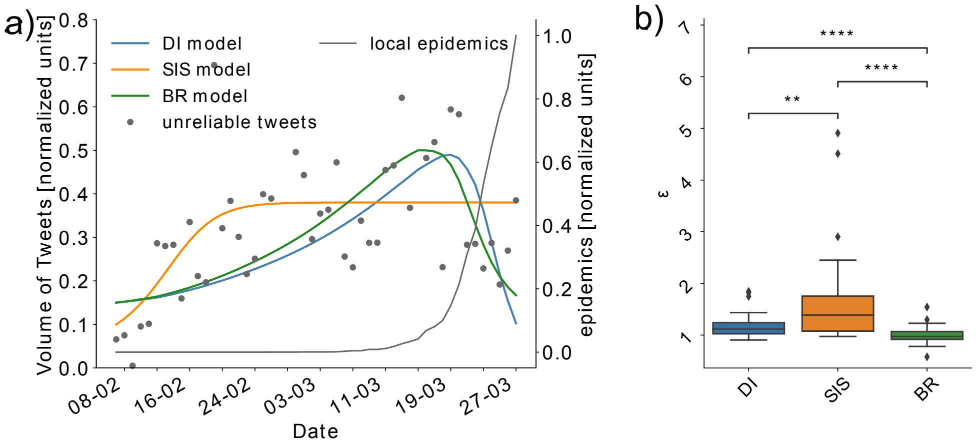

Figure 1: (a) Modeling dynamics in an example country: Double Infection (DI), SIS and Bounded Rationality (BR) dynamics are plotted as, respectively, blue, orange and green lines. Local epidemic is grey line. The empirical fraction of unreliable tweets is represented grey dots. (b) Distributions of normalized root mean square errors (RMSE) for leave-one-out validation (Mann-Whitney with multiple comparisons test), **:p <0.01, ****:p <10−4). Blue, orange and green bars refer respectively to DI, SIS and BR models. Results show that BR model has the lowest normalized RMSE when it is applied to out-of-sample prediction, whereas SIS model shows errors significantly higher than DI.

Different collaboration patterns and impact of prominent researchers in Europe and North America

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Science is a social endeavor that progresses through the concerted effort of many individuals. With the surge in the complexity of the most pressing open problems in science and society, the role of collaboration networks among researchers is becoming more and more relevant.

Despite the importance of the structure of such networks, we still do not have a comprehensive picture of the most relevant factors affecting it. Here, we suggest that the research environment (for example, institutional arrangements or culture) may leave measurable structural fingerprints in collaboration networks. We assess this hypothesis by comparing the structure of collaboration networks between prominent researchers in North America and Europe, and we find systematic differences that are robust across research fields. We find that prominent researchers in North America and Europe fulfill different structural roles in field-specific collaboration networks, with Europeans establishing much denser collaboration networks with each other, and North Americans establishing more decentralized networks. We also observe collaboration-dependent differences in the impact of the publications of each community. Specifically, prominent researchers in North America are significantly more impactful than those in Europe when they do not collaborate with other prominent researchers. When prominent researchers collaborate with each other, which Europeans do more often, impact differences between North America and Europe often disappear. Our results suggest that funding schemes and other science-related policies may have long-term, systemic impacts on how researchers establish collaborations, and therefore on how they develop new ideas and share them with others.

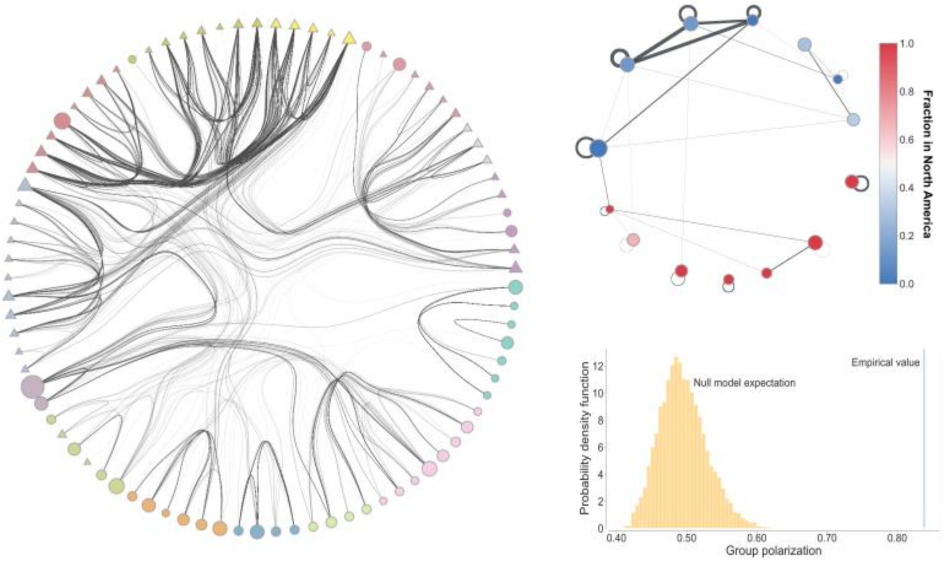

Figure 1: Collaborative patterns for the field Inequalities in health

Impact of Cryptocurrency Tweet Sentiments on Crypto Prices

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Cryptocurrencies have become an important dual entity (asset and currency) of the global financial system. Investing in cryptocurrencies as well as using them as a payment method is exponentially expanding. Prediction of cryptocurrency prices is a challenging task mainly because they represent a relatively new phenomenon, exhibiting high volatility. To better understand cryptocurrency trends and to improve price predictability, we propose to use sentiments of cryptocurrency-related news and micro-blogs.

Using bitcoin-related tweets and Bitcoin prices between 2016 and 2020, we propose a transfer learning methodology [1] for Bitcoin price prediction based on sentiment analysis of finance micro-blogs. We use deep learning-based natural language processing (NLP) transformers like RoBERTa [2], which currently outperforms most of the methods used in NLP related tasks.

We fine-tune the pre-trained RoBERTa model by using a labeled dataset of general financial tweets. Next, we leverage the fine-tuned model to evaluate the sentiment of the bitcoin-related tweets, which we use as an input dataset. As output, we use the "softmax" function in order to obtain probabilities for the positive or negative sentiment of the observed sample of tweets. Afterward, we compose two temporal numeric streams for the positiveness and negativeness of the news related to crypto assets. We use both streams as input for recurrent and convolutional networks used for Bitcoin price prediction. We align temporally the sentiment and price vectors of Bitcoin with related tweets' time of publishing. We evaluate different model architectures in order to identify the model that best fits the empirical data. The evaluation of the models is performed by using F1 and Matthews Correlation Coefficient (MCC) scores.

The initial results show that the RoBERTa model shows accuracy of F1=0.908 and MCC=0.765 for the Bitcoin sentiment classification task. Additionally, we find that the Pearson correlation between the volume of published tweets and the price of the Bitcoin is 0.68. The future direction of this research is to evaluate networks of tweets related to different cryptocurrencies to study their comovements and establish communities of cryptoassets.

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Abstract

Understanding motivation in large public organisations is essential to managing them successfully. Phil Davies is a senior officer in Greater Manchester Police and is investigating motivation in Police Community Support Officers (PCSOs). PCSOs undertake many tasks that enable warranted police officers to focus on tasks that require their higher levels of training and capabilities. The tasks for PCSOs include patrolling urban streets and shopping centres, visiting victims of crime, and dealing with antisocial behaviour. Davies has undertaken a major study of PCSO motivation by methods including interviews and focus groups. From these data some of the main demotivating factors have been abstracted. These include patrolling areas where there is a risk to their safety, and being required to undertake tasks outside their core role or outside their normal patrol area. Motivating factors include patrolling with another PCSO but this is not normal. Feedback from colleagues, superiors, and the public is also motivating or demotivating. Sometimes the sergeant supervising PCSOs is absent or called away, and PCSOs can find this demotivating. We are using these data in a computer simulation of individual and group motivation over short and long periods. This simulation uses hypernetworks to represent relational structure between combinations of motivating factors. Hypernetworks are also used to represent management structures between many agents. In this paper we present the main conclusions from Davies' empirical study, show how this is used in our simulation program, explain the use of hypernetworks to model the PCSO systems, and present the results of our experiments to date. We will discuss how such simulations could provide operational support for the management of staff at all levels in the police and other public services.

Keywords

Police
Police Community Support Officers
PCSO
Motivation
Management
Hypernetworks
Computer Simulation

Facing COVID-19 in Mexico City: from network epidemiology to modular economic reactivation.

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The COVID-19 pandemic has had a terrible toll in cities across the world, including Mexico City. The main transmission route of SARS-CoV-2 requires close physical contacts between people; reducing these contacts has been the basis of mitigation strategies worldwide. The mexican government instituted a federally mandated soft (voluntary) lockdown (Jornada Nacional de Sana Distancia), reducing general mobility among the population to about 25% of its original levels for the months of April and May. With economic activities gradually and slowly reopening, the question of how many people can return to the public space without an increase of the epidemic activity remains open.

In this work, we used network epidemiology models to identify the effects of economic reactivation on the epidemic dynamics [https://arxiv.org/abs/2008.12688]. We used an contact network empirically reconstructed from mobile device localization data for Mexico City [https://arxiv.org/abs/2007.14596]. We modelled the lockdown as a removal of a 75% of links in this network. We then modelled economic reactivation as the reconnection of a fraction of nodes, representing people returning to the public space. We compared the epidemic dynamics for different fractions of randomly reactivated nodes, ranging from 0% (ie. continuing the lockdown) up to 100% (a full economic reactivation). We observe that the downward behaviour of epidemic curves is lost if more than 5% of the population returns to the public space; furthermore, a reactivation of 50% of the population leads to an epidemic dynamic indistinguishable from a full economic reactivation.

As an alternative, we analyzed the epidemic behaviour if the economic reactivation is done by reactivating nodes belonging to the same module or community within the network. We observe that by reactivating whole modules instead of randomly dispersed people, a larger fraction of the population can return to the public space without risking a new spike in the epidemic dynamics. Furthermore, by spreading the reactivated population throughout small, non-adjacent modules, a large fraction (~50%) of the population can return to economic activities without negative effects in the epidemic curve. We consider that such reactivation can be achieved in practice through a combination of public policy measures to manage the economic and health damages caused by the pandemic.

References:

https://arxiv.org/abs/2008.12688
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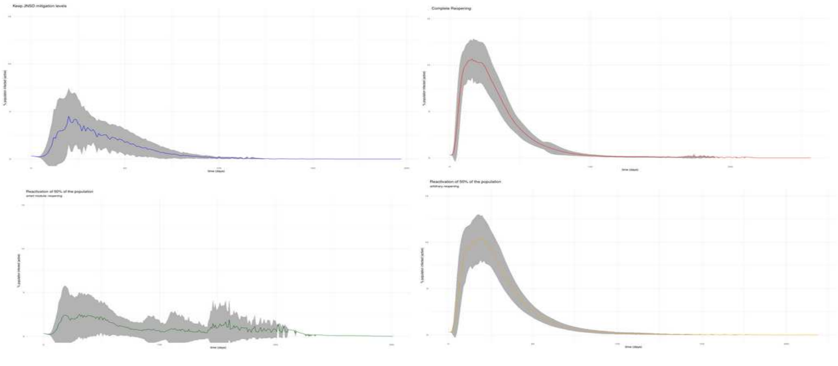

Figure 1: Active cases curves considering different levels of economic reactivation in Mexico City.

The contact network of Mexico City.

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Physical contacts are at the core of most human interactions. These contacts form large networks of physical interactions that are guided by social, economic, and urban factors, and through which complex dynamics, from product exchange to disease spread, can occur. The characterization of these contact networks for large settings, such as a metropolitan area, is unfeasible without the use of technological approaches.

In this work, we characterised the contact network for Mexico City, using mobile device position data. For the day of 2020-02-18, we analysed 10 minute time windows to identify the position of devices within a fine-grained (<0.9m2) hexagonal tesselation of the city. For each time window, we represented this positions as a bipartite device-position network, which we projected to identify co-localization events. We joined all these co-localization networks to generate a single network capturing all close contacts of device owners. The resulting network was characterized in terms of its topology. We identified that this network has a heavy-tailed degree distribution, and a well defined modular structure. We used device position data to infer the residence of each mobile device. We used this information to characterize the spatial and socioeconomic patterns that are captured by the network. The majority of contacts occur between devices that are resident of the same neighborhoods; with intra-neighborhood contacts being more common in less affluent neighborhoods. Nevertheless, contacts between residents of geographically distant neighborhoods are also observed; even contacts with residents of nearby cities. We further characterized whether these contacts are more frequent between residents of geographically distant neighborhoods with similar socioeconomic indicators, identifying specific patterns of connectivity.

This work has been used in the context of the current COVID-19 emergency to advise and orient public policy decision makers with regards of the social dynamics observed within Mexico City.

References:

https://arxiv.org/abs/2007.14596

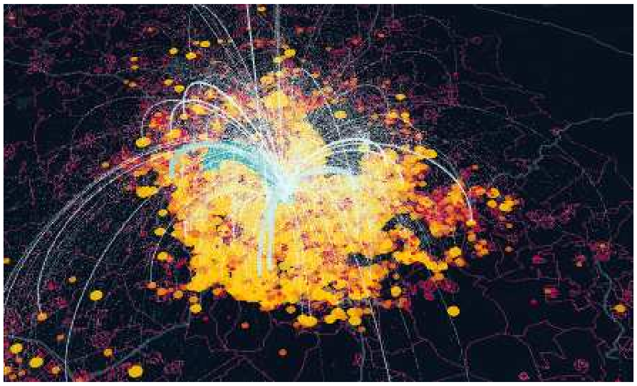

Figure 1: Visualization of the contact network of Mexico City.

Multiscale analysis of complex networks: from micro- to macro- with spectral entropy

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Many empirical complex systems, from biochemical to social ones, exhibit a network structure with heterogeneous connectivity patterns, their topology being characterized by mesoscale and/or hierarchical organization. However, such systems are identified not only by their structure but also from the dynamical processes on its top: the interplay between topology and dynamics often leads to a rich spectrum of phenomena, from localization to phase transitions and collective behavior.

Recently, we have introduced a novel framework for the analysis of complex networks in terms of a macroscopic description which accounts, simultaneously, for the full microscopic knowledge of the system – i.e., its adjacency matrix $\mathbf{W}$ – and its interplay with diffusive dynamics – such as continuous diffusion and random walks [1]. There are two main novelties coming from this framework, which is based on a new fundamental operator – i.e., the density matrix $\boldsymbol{\rho}_\beta$ – which encodes the network state in terms of a Gibbsian operator $\boldsymbol{\rho}_\beta = e^{-\beta \mathbf{H}(\mathbf{W})}/Z$ – where $\mathbf{H}(\cdot)$ is a function encoding dynamics, e.g. $\mathbf{H} = \mathbf{L}$ is the combinatorial Laplacian governing continuous diffusion, and Z is the partition function. Remarkably, this framework i) allows to calculate macroscopic descriptors such as information entropy without limiting one's focus to a specific subset of network features (e.g., degree distribution, which provide only partial information about the structure); ii) by using dynamical processes, their evolution across time is used to probe the system at different *temporal scales* which, in turn, provide multiscale information about distinct *topological scales*. In this talk we will briefly introduce the theoretical foundations of this framework while pointing to the broad range of its successful applications to practical problems: the dimensionality reduction of multilayer biological and transportation networks [2], the functional reducibility of multilayer social and transportation systems to enhance their transport properties [3], the quantification of the unit-system entanglement and its effect on the disintegration of social and biological networks [4], the multiscale analysis of virus-host interactions with a special focus on the SARS-CoV2–human interactome [5].

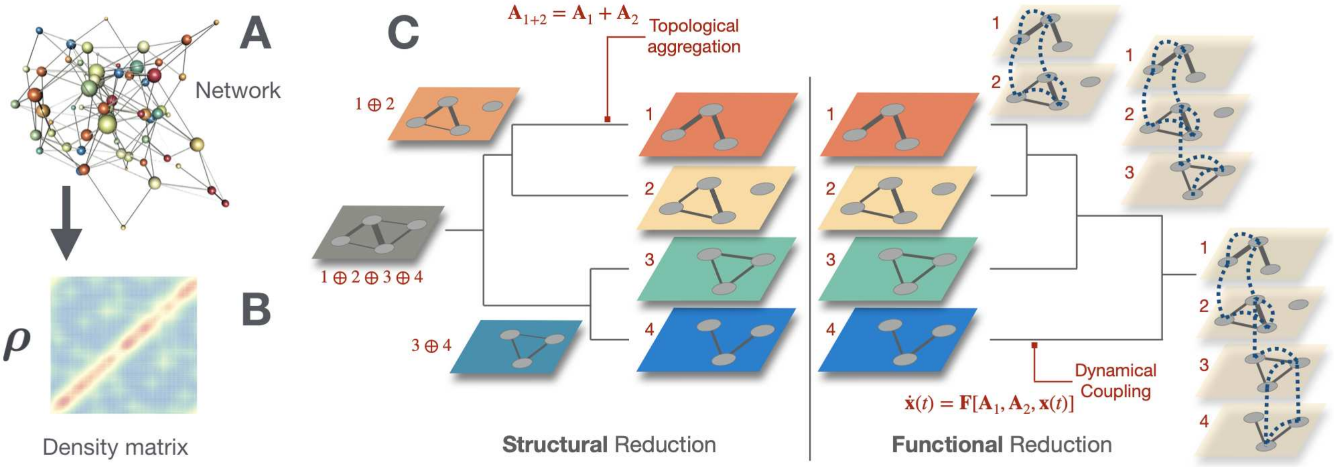

Figure 1: **(A)** Schematic illustration of a complex network, whose mathematical representation is usually given by its adjacency matrix $\mathbf{W}$ and **(B)** our mapping to a new representation of the network state, the density matrix $\boldsymbol{\rho}_\beta = \frac{e^{-\beta \mathbf{H}}}{Z}$. Here, for the choice $\mathbf{H} = \mathbf{L}$, i.e. the combinatorial Laplacian matrix, and interpreting the hyperparameter β as a time, the density operator become proportional to the propagator of diffusion dynamics on the top of the network [1]. The partition function $Z = \mathrm{Tr}[e^{-\beta \mathbf{H}}]$ encodes a feature known as *dynamical trapping*, quantifying the ability of the network to hinder or facilitate information flow exchange among system's units [3]. **(C)** Schematic illustration of structural [2] and functional [3] reducibility of multilayer systems, a procedure allowing to coarse-grain the multilayer structure in polynomial time – rather than super-exponential time – in the number of layers.

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The Emergence of Typical Characteristics of Complex Systems

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Complex systems can be modelled with all sorts of computer models such as cellular automata, random Boolean networks, artificial neural networks, and agent-based models. The models themselves are thereby as complex as the systems they are supposed to model. Like concrete complex systems, complex models exhibit the same typical characteristics such as network structures of a vast number of individual elements, non-linear and time-varying interactions, feedback loops, distributed control, adaptation, self-organisation, hierarchical organisation, and emergence [1]. Once these concepts appear, a complex system is present. The critical question however is how these characteristics appear in the first place: e.g., how exactly does hierarchical organisation emerge in a system? So far, these concepts are described only *a posteriori* and this question has until now been mostly neglected.

To tackle this problem, we have developed a so-called allagmatic method [2] that allows to follow creations of computer models from very abstract building blocks such as structure, operation, system, entity and so on to more concrete models such as cellular automata and artificial neural networks. The abstract building blocks have been defined on the basis of the philosophy of individuation of Gilbert Simondon and the philosophy of organism of Alfred North Whitehead and already proved to be useful for automatic programming. The allagmatic method consists of three different regimes – called virtual, metastable, and actual – reaching from the abstract to the concrete. The virtual regime is a template of model building blocks whereas in the metastable regime parameters such as number of entities, update function, and initial conditions are defined. In the actual regime then the concrete model is run.

The model building blocks are implemented in such a way that they pass through these regimes aligning program code and abstract philosophical concepts. Generic programming and object-oriented programming allow the abstract generic definition of building blocks *entity* and *system model* in the virtual regime which do not have a type or size yet. The type is defined with the creation of a system model object in the metastable regime followed by concretisation with parameters such as number of entities and a specific update function. Once the system model object is fully concretised, it is executed in the actual regime.

In this paper we would like to present our allagmatic method and show how the emergence of typical characteristics of complex systems is possible to describe by following the concretisation of models. Concepts such as adaptation and hierarchical organisation are then not described *a posteriori* but as the models emerge themselves. In other words: as a metamodel, the allagmatic method allows to give philosophical definitions of every single concept and its relation to all other concepts in the model. In this sense, perpetual interpretation is possible while the allagmatic method is operating and thus understanding of processes. The emergence of characteristics is not veiled but laid open and made accessible for understanding.

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Adapting the Kuramoto model to group drumming

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Rhythm affords the ability to coordinate and synchronize, for which there are numerous examples in humans. One such example, group drumming, allows us to examine the dynamics of rhythmic coordination and synchrony in human groups. When investigating four individuals drumming to an isochronous rhythm individually, in a duet, and in a quartet, results showed that variability among the individual drummers was *higher* in the quartet condition than it was as individuals [1].

When presented with this experimental research paradigm, we sought to use nonlinear dynamics to model the phenomenon found during group drumming. To do so, we utilized the Kuramoto model of nonlinearly coupled oscillators, in which synchronous behavior emerges from a population of oscillators with a distribution of natural frequencies [2]. For the purpose of this research, we consider each oscillator in the model to be one drummer, and each drum hit occurs when the oscillation reaches a phase of zero. However, during group drumming, each individual is not continuously coupled as the original model suggests, which required us to modify the model to allow for pulse coupling (i.e., oscillators synchronizing at discrete points in time).

We were able to modify the Kuramoto model by replacing the continuous coupling function with a pulse function to mimic the sound of a drum hit. A gamma function is used to simulate a drum hit's acoustic envelope to which the individual drummers synchronize (Figure 1C). This adapted model is capable of simulating previous data (Figure 1A) [1], as shown in Figure 1B. Ongoing and future research will utilize a larger group size during drumming to better adjust the model to predict synchronous behavior among more performers and more data types.

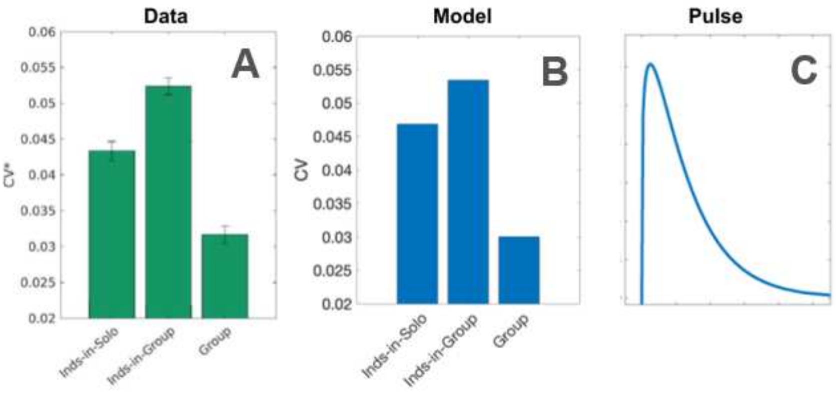

Figure 1

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1 Abstract

We devise a simple but powerful method based on physiochemical properties to analyze the evolution, interactions, and correlations between the amino acids in a protein family. The method converts the protein sequences into a vector in three-dimensional physiochemical property space, from which residue positions controlling protein function can be extracted. A new graphical method to represent protein sequences using physiochemical properties is devised which gives a fast, easy and informative way of comparing the evolutionary distances between protein sequences. In this space, the evolutionary conservation of a position is specified by the conservation in the physiochemical property values. We observe that the favorable substitutions at a position are the ones which preserve the property crucial for functioning of that site which is quantified by the entropy and Kullback-Leibler divergence. The entropic measures shows that during the evolutionary history of the protein family, it is the certain physiochemical properties that are conserved rather than the type of amino acids. For each property the correlation matrix is created, and the noise reduction and information filtering is done using random matrix theory (RMT) involving an ensemble of Wishart matrices. The spectral properties of correlation matrices are calculated and compared with the analytical results for the Wishart matrices. The analysis of the eigenvalue statistics of the correlation matrix for the betalactamase family shows the universal features as observed in the Gaussian orthogonal ensemble (GOE) capturing the short as well as the long range correlation (approximately following GOE) between the eigenvalues. When compared with the previous approach (treating amino acids as characters) gives the usual short range correlations while the long range correlations are the same as that of an uncorrelated series. The distribution of the eigenvector components for the eigenvalues outside the bulk (RMT bound) deviates significantly from RMT observations and contains important information about the system. The information content of each eigenvector of the correlation matrix is quantified by introducing an entropic estimate which shows that for the betalactamase family the smallest eigenvectors (low eigenmodes) are highly localized as well as informative. These small eigenvectors when processed gives clusters involving positions that have well defined biological and structural importance matching with experiments. The proposed method not only identifies the dominant properties within the family but also evaluate each site based on physiochemical property to identify properties crucial for a position to function. We use the correlation and interaction information to create an interaction network between the position in the sequence for each property. The network analysis offers an understanding of how the positions within the sectors are interacting but also allows recognition of the structural motifs in the β-lactamase family (an enzyme released by bacteria to counter beta-lactam antibiotics like penicillin). The method selectively identifies the key nodes/edges of the amino acid networks for targets to deactivate (activate) the enzymatic actions.

Bayesian Network Analysis of the Course of Type 2 Diabetes Mellitus

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Diabetes Mellitus is one of the most common chronic diseases in the world. This disease can lead to a lot of different complications, associated with heart, kidneys, liver, nervous system, limbs, and disability[1], [2]. Therefore, the task of research this disease is very important. In this study, we propose a method for analyzing the dynamics of this disease using the Bayesian Networks and graph theory tools. Research is based on 8100 cases of T2DM diseases. Each of these cases was presented as a graph - pathways. This approach proposes in article [3]. This oriented graph includes the consequence of tuples. These tuples include all events that important in the terms of the treatment process and include patient age when this event was diagnosed. Then, we create a graph to include all 8100 pathways of T2DM. This graph you can see in Figure 1. Then we create a Bayesian Networks basis on this graph. And using this network we can estimate the probability of complications for a particular patient in any of his age-points of the course of diseases. Summarize we propose a new method for predicting diabetes complications basic on Bayesian Networks and graph theory.

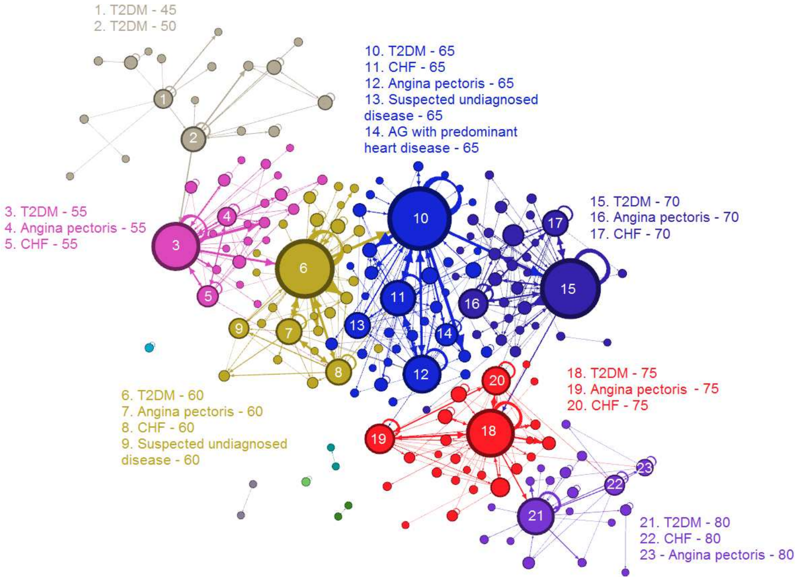

Figure 1: Graph basis on 8100 T2DM pathways. Colors are clusters that calculation using maximization modularity method. Node size is degree.

Acknowledgements

The reported study was funded by RFBR according to the research project № 20-31-70001

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Urbanization and Economic Complexity

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Extended Abstract

It is an established fact that urbanization in developed countries is accompanied by economic growth and industrialization with a mutually self-reinforced mechanism [1]. This historic pattern generated the expectation of a virtuous circle between economic growth and urbanization regardless local conditions. From classic urban economic theories to the more recent scaling approach to cities [2], the growth of urban population was routinely used as a proxy of economic growth. There are several theories aimed to explain urbanization processes. The most intriguing approach, it is rooted in the mutual indirect effect of World Trade Web (WTW) on the global urbanization processes. The dominant idea is that in open economies domestic communities (cities) can trade easily with other communities, boosting the exports, substituting industrialization and urbanization policy [3].

In this work, we couple the Economic Complexity [4,5] framework applied to WTW data with the urbanization level of more than 140 countries worldwide, between 1995-2010, to capture the fingerprint of urbanization on countries productive systems thought the lens of the exports 'similarity [6]. We notice that in rural economies the increasing of urban population creates structural changes in the exports' network [7]. It boosts the countries diversification improving the country fitness and allowing the export of more complex products. These economic transformations fade away in countries that already have high level of urban population (more than 60%), where there is no relation between the urbanization process and the fitness. Within the sub-Saharan countries, we capture the ones where the virtuous circle between economic growth and urbanization is fostering structural changes in the countries productive systems. On the other hand, within the resource export-based countries, we assess the implementation of policy leading to urbanization without any structural transformations of their export basket.

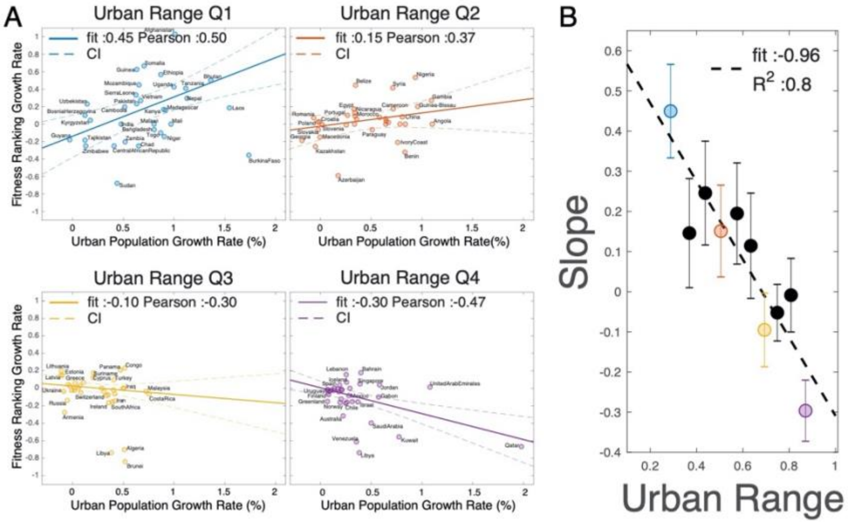

Figure 1: A Fitness ranking growth rate vs. Urbanization growth rate. The effect of urbanization growth on the transformation of the economic systems (or vice-versa) is more relevant in low urbanize countries. **B** Slope coef. of sliding widow of 25\% of the countries of Fitness Ranking Growth Rate vs. Urban Population Growth Rate. The error bar corresponds to the fit's 95\% confidence interval. The colors follow the Urban Range Scheme.

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Conductance-based constrained growth leads to emergent hierarchy

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Many complex networks are in fact coarse-grained models of modular networks, where each node represents a highly connected sub-graph that is essentially ignored for the simplicity of representation. A hidden variable model is considered for a randomly growing network, where a scalar value represents perhaps the most relevant network property of these ignored sub-graphs: their graph conductance. Being a quantification of the bottleneck of flow across the sub-graphs, the internal conductance values would naturally limit the degree of the agglomerated nodes. We have been reminded over many years ([1],[4],[3],[6]) that while scale-free growth may provide a good approximation to real-world networks, the true story is likely more complicated. Properties like hierarchy are often found in such networks, but are not present to a comparable degree in the basic stochastic growth models. The present work seeks to consider a simple mechanism by which the scale-free trend breaks down at the high end of the degree distribution (even in the infinite limit) leading to an exponential cutoff. The conceptual framing of this mechanism as a property of the underlying details of the true graph is supported for example in social networks by the work of the anthropologist Robin Dunbar [5], which posited a cap on the number of human relationships the average person can maintain at any one time. Modifying a simple preferential attachment model [2] to enforce node-dependent degree restrictions prevents hubs from overshadowing other nodes, and we find that as the average restriction gets more severe, many common measures of hierarchy increase monotonically as seen in Figure 1. We provide intuition for the results and compare heterogeneous distributions of the hidden variable, which illustrate interesting trends.

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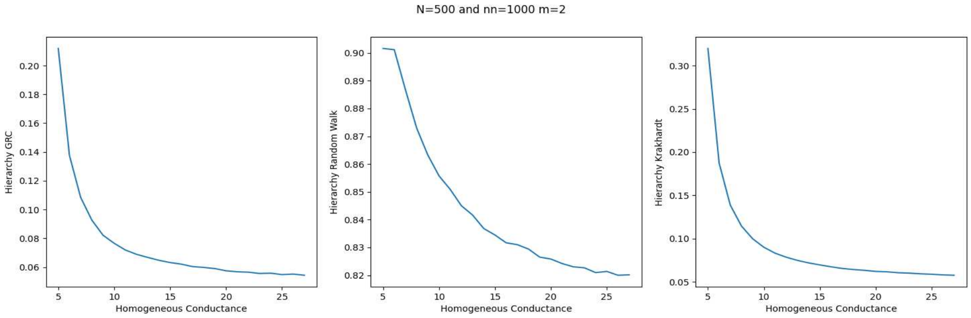

Figure 1. In the case of homogeneous internal conductance values, three common measures of hierarchy all increase as the internal node conductance decrease, restricting flow (data are averaged over 1000 runs for network size of 500).

Sustained Oscillations in Multiplex Network Epidemics

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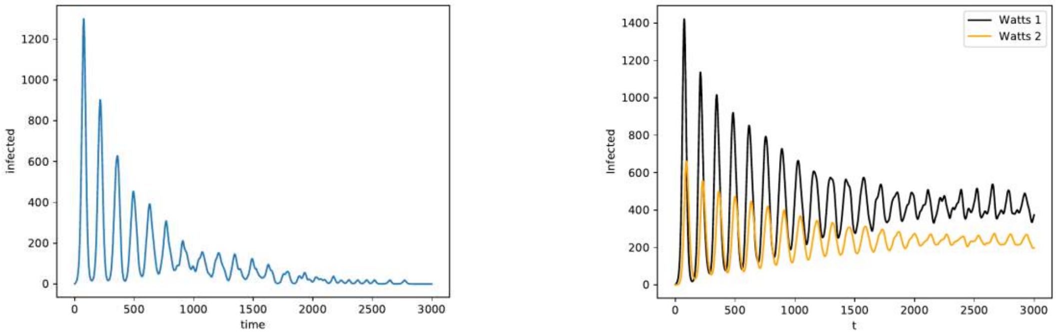
Several diseases like Measles, Influenza and many others have in common that they do not offer long lasting immunity to the patient that has recovered from it. An infected individual from those types of diseases, once recovered, presents a short term immunity, after which he is susceptible to the same disease again. In order to study such an infection we use a compartmental epidemiological model, named SIRS, on networks. Each node of the network belongs in one of the three compartments of the model. It will either be Susceptible (S), Infected (I) or have Recovered (R) from the infection. The I nodes transmit the infection to their S neighbors with probability τ, and will turn to R after a certain period of time t_I. The recovered nodes are immune for a certain period of time t_R, and after that they will become susceptible to the infection again. t_I and t_R are characteristic of the infection and the network.

However, as mentioned in [1] even though R nodes can be infected again, it is not granted that the number of infected nodes each timestep will have an oscillatory-like behavior. We look at whether having an infection in a multiplex network can result in a sustained oscillation of the number of I nodes and compare this to results of the same infection in a single network (which eventually dies out). SIRS model was applied in a multiplex network of 2 Watts Strogatz networks of $N = 10000$ nodes and $<k> = 14$, and the result was averaged over many simulations. We concluded that in multiplex networks, having different infection parameters in the two layers most of the times help the infection to survive for longer times than in a single network.



a) b)

Figure 1: Infected nodes over time, computed by applying SIRS model for an infection with transmissibility $\tau = 0.022$ to a)a single Watts Strogatz network with $N = 10000$, $<k> = 14$ and fixed times $t_I = 8$, $t_R = 70$ b)to a multiplex network of two Watts Strogatz networks with $N = 10000$, $<k> = 14$ and fixed times $t_{I,1} = 8$, $t_{R,1} = 70$ for the nodes of the first network and $t_{I,2} = 6$, $t_{R,2} = 66$ for the second.

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Simulating SIRX Model on Networks Based on Real Data

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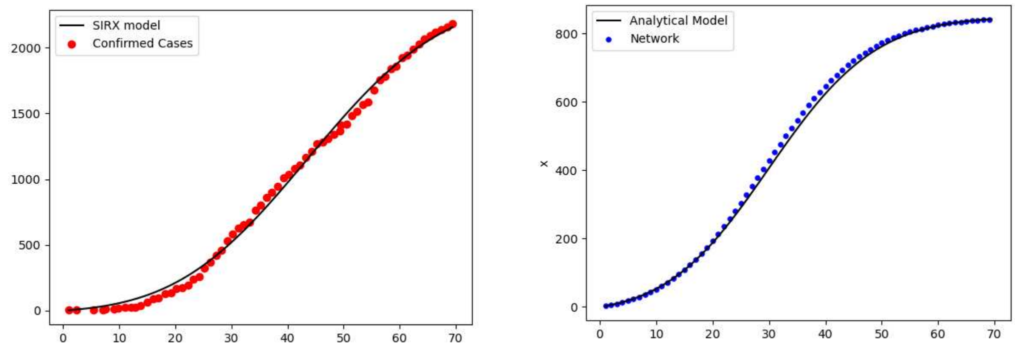
Infectious diseases, much like the current one of COVID-19, have had a huge economic and societal impact. The ability to model the transmission characteristics of an infection is critical to minimize its impact. In fact, predicting how fast an infection is spreading could be a major factor in deciding lockdown decisions, as well as the severity and strictness of the applied mitigation measures. Even though modeling epidemics is a well studied subject, most simple models do not include quarantine measures, such as those imposed in the recent pandemic. Our research is based on Brockmann's recent [1] paper, where a compartmental SIRX model that included two mechanisms was implemented. This model describes the delayed transmission of the infection during a pandemic. The first mechanism describes the social or individual behavioral changes during quarantine, and the second one considers that the symptomatic quarantined should be in state X - not transmitting the infection anymore.

A challenging question is whether by simulating the above model on networks we can have a result that fits well the analysis. Our process will be initially to find the parameters of the model that best fit the confirmed cases of a country, provided by Johns Hopkins University. Subsequently, the differential equations of the model will be solved applying the parameters that were computed on smaller population. This step is essential in order to compare the result to a computationally costly simulation on networks. Finally, we create the simulation and compare with the analytical results. Our results indicate that the analytical solution of the model fits to the confirmed cases during the first COVID-19 wave of all the countries we have tested. Moreover, the simulation fits adequately to the analytical solution.



a)

b)

Figure 1: a) Best fit of analytical SIRX model black line) to Confirmed Cases of Bosnia (red dot) over time, during days 1-70 (Day 1 is the first confirmed case day). b) X over time averaged for 1000 simulations of the SIRX model on an ER network with $< k >= 6$ (blue dot) and the results of the analysis (black line) for the parameters that were measured in a) for Romania in a model with population N = 10000

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On local and global components of the air transportation network

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Air transportation networks have been extensively studied in the network science literature. Researchers focus on airlines networks, national, regional, continental and worldwide networks using monoplex or multiplex approaches. Inspired by recent results on community-aware centrality measures [1], in this work, an extensive analysis of the topological properties of the world air transportation network is performed. Based on the community structure uncovered by the Louvain algorithm, the original network is split into local components and global components. The local components are made of the communities by removing the intercommunity links. Removing all the intra-community links and subsequent isolated nodes forms the global components. Results reported in figure 1 shows that the main local components are geographically distributed over seven areas (North America, Europe, East & Southeast Asia, Africa-West and South Asia Oceania, South America, Russia). The main global component is distributed among all these areas (figure 2). A comparative analysis of the macroscopic properties of these various networks reveal some consistencies. Indeed, density of all the components is low. However local components are all denser than the overall network. Transitivity is low and more particularly for the global component. All the networks are disassortative. Except for the Russia component, the hub dominance is relatively small. The study also reveals some dissimilarity. For example, the diameter of the local components ranges from 4 to 9 as compared to a value of 13 for the original network. The highest k-core subnetworks (k=31 and k=29) of the original network are mainly localized in the European component, and in the North America components. The maximum k-truss sub network (k=24) of the original network is in the North America component. It is followed by the European component (k=22). The remaining components exhibit low values of max k-truss. Comparative evaluation of degree and betweenness centrality measures allows to clearly identifying the reasons behind the anomalies reported in several studies [2,3]. One of the main advantages of this approach is to get a better understanding of the similarity and differences of the various regional air transportation systems. Results indicate that it is more informative than considering the world air transportation network as a single entity. Indeed, if one considers the centrality measures, it allows to clearly distinguishing airports having a regional influence from those with an international influence.

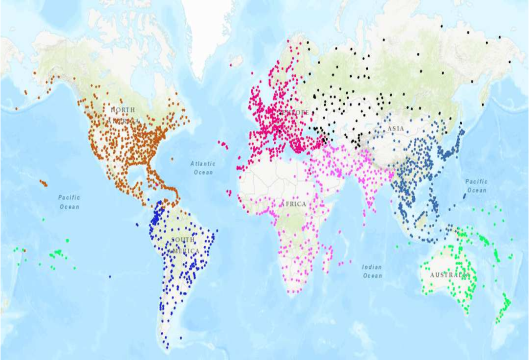

Figure 1 The 7 main local components.

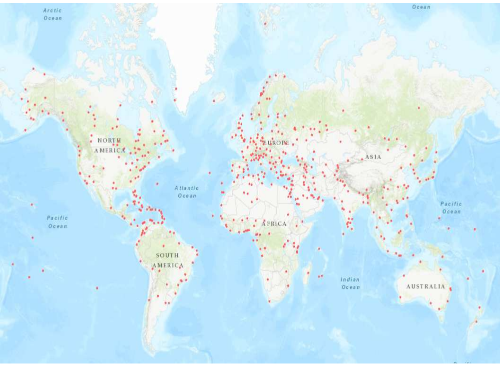

Figure 2 The main global component

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A measure of local density in complex networks

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The work [1] summarized by this abstract focuses on a specific element of the study of complex systems: the network, as a support for the representation of the diadic interactions of the system. In this field, the community structure (ie. high connected clusters) is often a major concern because it is relevant in many real-world contexts of networked systems. We propose a new measure to identify nodes that have meaningful local interactions able to give new insights into the internal organization of communities or the way communities are assembled. We are mainly interested in sets of nodes whose connection density is low compared to their external neighborhood. Little research has been carried out in this direction, and, among the studies we have identified, the various proposed tools are far from being founded on a generic approach.

We first define a weight $w(i,j)$ of an edge (i,j) of the network by:

$$w(i,j) = k \cdot |N(i) \cap N(j)| \cdot H\big(d(i), d(j)\big)$$

where k is a normalization factor, $N(i)$ is the open neighborhood of node i, $d(i)$ is the degree of node i, and $H\big(d(i), d(j)\big)$ is the harmonic mean of $d(i)$ and $d(j)$. For a given node i, the sum of the weights of the links attached to it defines a new measure $\delta(i)$:

$$\delta(i) = \sum_{i \sim j} w(i,j).$$

We weight the edges of the network with w and adapt the classical rich club algorithm [2] to the case of weighted networks by choosing an appropriate null model. Our null model breaks the $w - w$ and $\delta - \delta$ correlations. Once the first weighted-rich-club found, the process is restarted on the network from which this first rich club is removed. A second weighted-rich-club can then be identified and our algorithm *ItRich* iterates in this way to extract a sequence of rich clubs. For each extracted weighted-rich-club, we can compute a quality measure that evaluates the distance of this detected pattern from the patterns that appears in the null model. A threshold value for this quality measure then becomes a stopping criterion to the *ItRich* algorithm. This criterion is set by the user who can choose to make the output of *ItRich* more or less selective. At the end, the algorithm returns a sequence of weighted-rich-clubs, each one with a quality measure, and a set of nodes that are in no weighted-rich-clubs, called the sparse part of the network.

The sparse part of the network is divided into two distinct subsets: on the one hand, the subset of nodes whose density is too low to be included in one of the weighted-rich-clubs, and on the other hand, the subset of nodes whose δ is sufficiently high, but which are attached to a cluster of nodes whose average δ is significantly higher. We first test the performance of *ItRich* on a noisy LFR model obtained from a LFR model by adding nodes lightly connected to the classes of nodes of the initial LFR. These nodes are considered to be the sparse part of the network. The comparison between *ItRich* and the OSLOM method [3], which is a community detection algorithm that can identify homeless nodes (that do not belong to any community), shows that *ItRich* produces better results.

Various other tests are conducted on real world data, from Lusseau's bottlenose dolphins to the American college football teams, as well as Adamic's political blog network. The results highlight the *ItRich* efficiency to identify particular nodes within or between the communities, as well as the difference between *ItRich* and the k-core decompositions.

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Social Tipping Processes for Sustainability: An Analytical Framework

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Societal transformations are necessary to address critical global challenges, such as mitigation of anthropogenic climate change and reaching UN sustainable development goals. Recently, social tipping processes have received increased attention, as they present a form of social change whereby a small change can shift a sensitive social system into a qualitatively different state due to strongly self-amplifying (mathematically positive) feedback mechanisms. Social tipping processes have been suggested as key drivers of sustainability transitions emerging in the fields of technological and energy systems, political mobilization, financial markets and sociocultural norms and behaviors. Drawing from expert elicitation and comprehensive literature review, we develop a framework to identify and characterize social tipping processes critical to facilitating rapid social transformations. We find that social tipping processes are distinguishable from those of already more widely studied climate and ecological tipping dynamics. In particular, we identify human agency, social-institutional network structures, different spatial and temporal scales and increased complexity as key distinctive features underlying social tipping processes. Building on these characteristics, we propose a formal definition for social tipping processes and filtering criteria for those processes that could be decisive for future trajectories to global sustainability in the Anthropocene. We illustrate this definition with the European political system as an example of potential social tipping processes, highlighting the potential role of the FridaysForFuture movement.

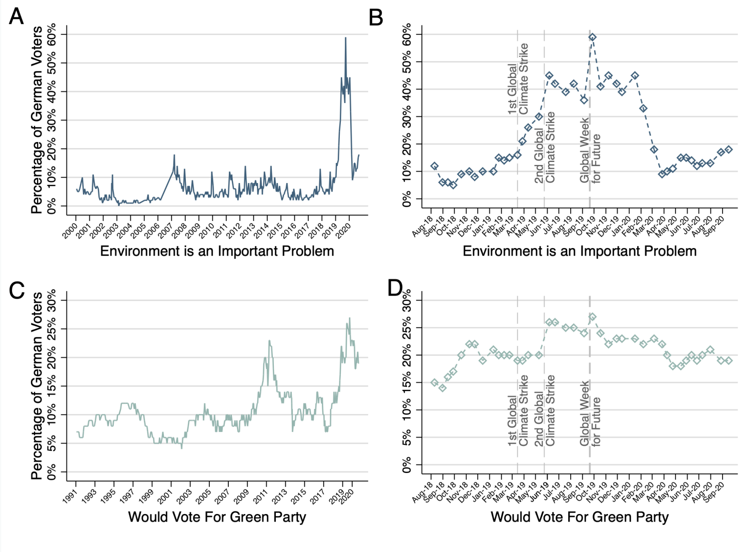

Figure 1: Potential social tipping dynamics in environment as an issue and willingness to vote for the Green Party in Germany.

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Model Analyses Used to Show the Further Importance of Biodiversity and Species Robustness for Ecosystems Resilience

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That the biotic components of an ecosystem create complex interactions appears obvious. However, this does not necessarily imply that all parts of the system are equally connected. For example, we have found that elephant while able to eat many species of plant primarily feed on a relatively select few of these species. Regardless the increased complexity of even an apparently simple ecosystem yields interesting results. We develop differential equation descriptions of the consumers and resources of theoretical ecosystems to explore the dynamics. Increasing system diversity is shown to have important effects on these dynamics. For example, for a system with disease in the resources, increasing biodiversity is shown to potentially reduce disease prevalence. The strength of coexistence of consumers and resources (species robustness) is also shown to possibly limit diseases. For these analyses we introduce a threshold quantity C_0 which assists in understanding the dynamics.

Data-driven Modelling of Public Risk Perception and Emotion on Twitter during the Covid-19 Pandemic

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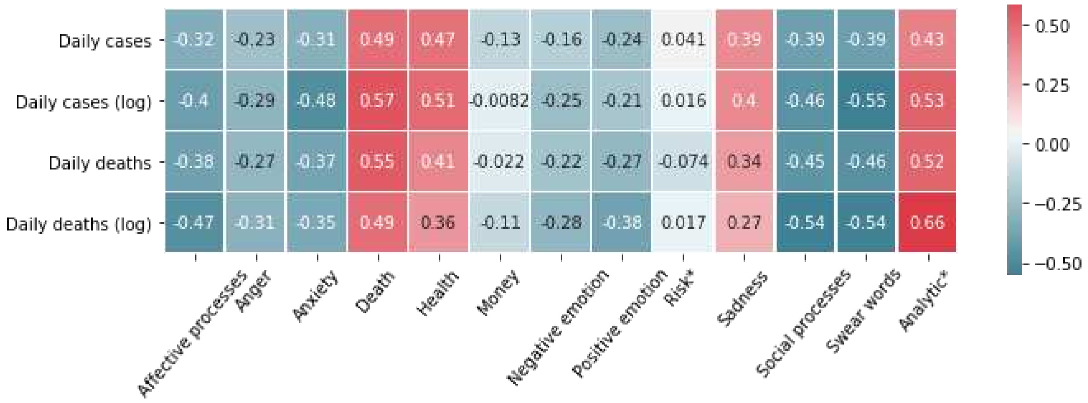
Successful navigation of the Covid-19 pandemic relies on the public's cooperation with safety measures and appropriate perception of risk, in which emotion and attention play important roles. Signatures of emotion and attention are present in social media data, thus natural language analysis of this text enables near-to-real-time monitoring of indicators of risk perception. We compare key epidemiological indicators of the progression of the pandemic with indicators of the public's perception of the pandemic constructed from ~20 million unique Covid-19-related tweets from 12 countries posted between 10th March – 14th June 2020. We find evidence of psychophysical numbing [1]: Twitter users increasingly fixate on mortality, but in a decreasingly emotional and increasingly analytic tone (see Fig. 1). Semantic network analysis based on word co-occurrences reveals changes in the emotional framing of Covid-19 casualties that are consistent with this hypothesis. We also find that the average attention afforded to national Covid-19 casualties is modelled accurately with the Weber-Fechner and power law models of sensory perception. Our parameter estimates for these models are consistent with estimates from psychological experiments [2], and indicate that users in this dataset exhibit differential sensitivity by country to the national Covid-19 death rates. Our work illustrates the potential utility of social media for monitoring public risk perception during crisis scenarios.



	Affective processes	Anger	Anxiety	Death	Health	Money	Negative emotion	Positive emotion	Risk*	Sadness	Social processes	Swear words	Analytic*
Daily cases	-0.32	-0.23	-0.31	0.49	0.47	-0.13	-0.16	-0.24	0.041	0.39	-0.39	-0.39	0.43
Daily cases (log)	-0.4	-0.29	-0.48	0.57	0.51	-0.0082	-0.25	-0.21	0.016	0.4	-0.46	-0.55	0.53
Daily deaths	-0.38	-0.27	-0.37	0.55	0.41	-0.022	-0.22	-0.27	-0.074	0.34	-0.45	-0.46	0.52
Daily deaths (log)	-0.47	-0.31	-0.35	0.49	0.36	-0.11	-0.28	-0.38	0.017	0.27	-0.54	-0.54	0.66

Figure 1: Pearson correlation coefficients between the daily proportion of words in tweets related to psycholinguistic categories (columns) and key epidemiological indicators (rows).

Acknowledgements

The authors thank Mirta Galesic, Rodrigo Leal Cervantes, R. Maria del Rio Chanona, Francois Lafond, and J. Doyne Farmer for helpful feedback and stimulating discussions.

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A Lagrangian flow network approach to atmospheric blocking

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Atmospheric blocking events, that is large-scale nearly stationary atmospheric pressure patterns, are often associated with extreme weather in the mid-latitudes, such as heat waves and cold spells which have significant consequences on ecosystems, human health and economy. The high impact of blocking events has motivated numerous studies. However, there is not yet a comprehensive theory explaining their onset, maintenance and decay and their numerical prediction remains a challenge.

In recent years, a number of studies have successfully employed complex network descriptions of fluid transport to characterize dynamical patterns in geophysical flows. The aim of the current work is to investigate the potential of so called Lagrangian flow networks for the detection and perhaps forecasting of atmospheric blocking events.
The network is constructed by associating nodes to regions of the atmosphere and establishing links based on the flux of material between these nodes during a given time interval. One can then use effective tools and metrics developed in the context of graph theory to explore the atmospheric flow properties. In particular, Ser-Giacomi et al. [1] showed how optimal paths in a Lagrangian flow network highlight distinctive circulation patterns associated with atmospheric blocking events. We extend these results by studying the behavior of selected network measures (such as degree, entropy and harmonic closeness centrality) at the onset of and during blocking situations, demonstrating their ability to trace the spatio-temporal characteristics of these events.

Acknowledgements

This research was conducted as part of the CAFE (Climate Advanced Forecasting of sub-seasonal Extremes) Innovative Training Network which has received funding from the European Union’s Horizon 2020 research and innovation programme under the Marie Skłodowska-Curie grant agreement No. 813844.

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Heterarchic Restructuring Strategies for the Repurposing of Middle-Management: Insights from Geometric Manipulation of Organizational Charts

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The contemporary evolution of the resource-based view (RBV) theory of strategic management favors the uniqueness of internal organizational resources as sources of sustainable competitive advantage (Barney, 1991). Yet, contemporary organizational restructuring strategies, when required, have focused on delayering campaigns that result in retrenchments or layoffs of supposedly uniquely endowed personnel resources which inordinately have been concentrated in the middle-management cadre of the affected organizations (Foster, Hassard, Morris, & Wolfram Cox, 2019).

The field of strategic management has traditionally considered environmental context as being important (McKiernan, 2006). Middle-management-focused restructuring strategies can thereby be portrayed as a response to the demands of a post-bureaucratic complex environment (Foster et al., 2019) featuring wicked problems derived from the interactions of a diversity of organizational stakeholders operating in dynamic environments (Teece, Pisano & Shuen, 1997). Huber (1984) has suggested that the solution to the problems of post-bureaucratic organizations would require structuring that propagates diffused decision-making, and enhanced information acquisition and distribution.

Using geometrically manipulated organizational charts, this proposal speculates that in the presence of post-bureaucratic complexity, organizational restructuring should focus on heterarchic structures that would allow the repurposing of middle managers as strategic information gatherers and distributors (instead of retrenchment). Such repurposing will enhance and encourage decision-making by dispersed from center profoundly knowledgeable managers (Deming, 1991) who are able to react more capably to environmental dynamism (dynamic capabilities).

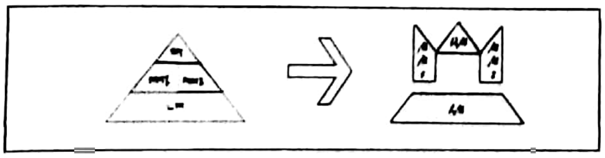
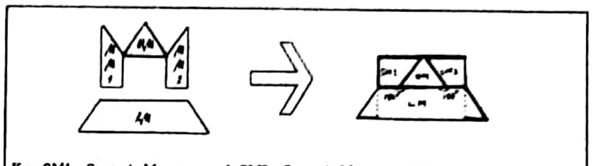


Figure 1. Middle-Management in Hierarchy



Key: SM1 – Strategic Management 1; SM2 – Strategic Management 2.

Figure 2. Middle-Management Repurposed

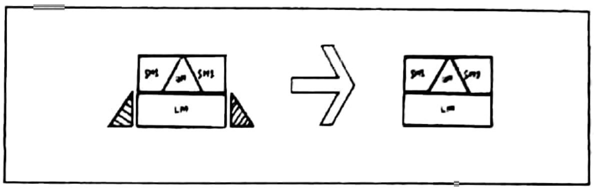


Figure 3. Strategic-Management in Heterarchy

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Rethinking Itô vs Stratonovich

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The Langevin equation is a stochastic differential equation for the velocity of a Brownian particle. In this sense, it can be considered as a physically improved counterpart of the Wiener process, the velocity of which can only be defined as a stochastic distribution. On the contrary, the velocity of the Langevin model is a function valued stochastic process, what allows to calculate the kinetic energy of the Brownian particle. In fact, this calculation has been employed as a benchmark in the history of the classical Itô vs Stratonovich dilemma. Based on it, among other arguments, there appeared in the physical literature a clear preference for the use of the Stratonovich stochastic integral, at least in this type of context. However, it is possible to prove that the resulting Stratonovich stochastic differential equation admits an uncountable number of solutions. On the contrary, the use of Itô stochastic calculus leads to a unique solution, which turns out to be the right physical solution of the problem. This mathematical fact allows us to rethink the usual conclusions that seem to derive from the traditional approach to the Itô vs Stratonovich dilemma.

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Using metadata for link prediction in bipartite complex networks

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Link prediction is a common problem that allow us to know missing links in a complex networks, unknown preferences of a user who wants that someone recommends him a movie, what a politician will vote… In our work we focus on mix-membership stochastic block models to predict links in bipartite networks [1] but adding node's metadata like an user's age, a movie's genre, a politician's state... In our approach we consider that metadata are connected with our nodes of the considered bipartite networks forming multipartite networks, and also adding an hyperparameter that tells to the model how is the importance of this metadata when we make predictions. Using our approach in synthetic networks, but with different membership-metadata correlation, we observe that for low number of observed links and some correlation, our model helps to make better predictions. But if we add observed links, we observe that metadata can't help unless threre is enough correlation. Also we found an optimal value of our hyperparameter for the prediction power of our model.

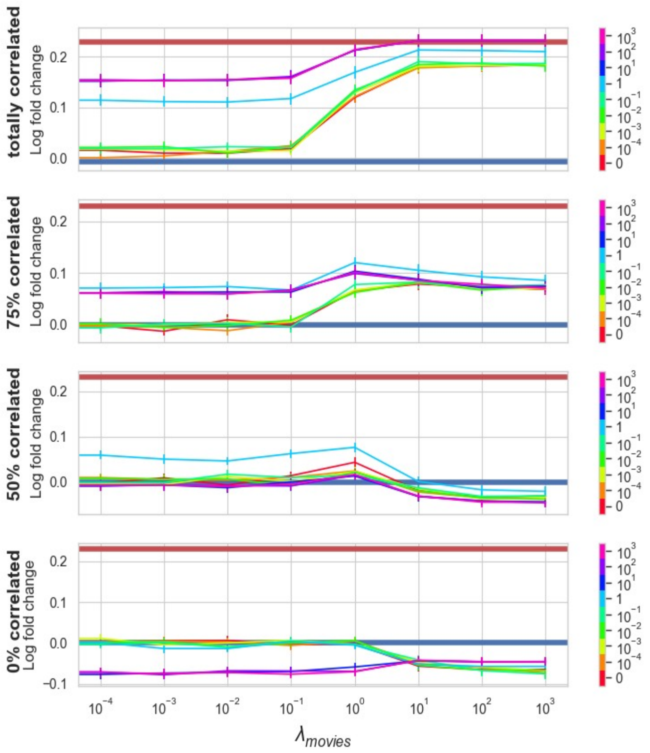

Figure 1: Log fold-changes respect the accuracy of the Mix-membership stochastic block model without prior for synthetic networks. We can see that the performance increase when data is highly correlated with the memberships, but also decrease when there is no correlation. In 75% and 50% we can see that an optimal performance for the hyperparameter exists.

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Network Opinion Diffusion With Global Optimal Solutions

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Bounded-confidence models have been widely employed to study opinion diffusion across social networks in a variety of contexts, ranging from ideological extremism to Wikipedia edit wars [1,2]. The typical approach until now has been to randomly assign initial opinion values for each node in a network, and then investigate the effect of both network structure and inter-nodal interaction thresholds on the long-term diffusion dynamics. However, this procedure fails to take into account the existence, in certain real circumstances, of a global 'optimal' solution in the opinion space which maximizes an underlying objective function. Thus, we present a modification of Hegselmann–Krause (HK) [3] diffusion where we allow nodes to exclusively update opinions towards neighbouring opinions which better maximise a predefined objective.

The model works as follows: At time step $k = 0$, each node is assigned an initial opinion drawn uniformly at random from $[0, r]$. Define a global objective function $A(x)$ such that there exists $x_{max} \in [0, 1]$ and $A(x_{max}) > A(x)$ for any $x \in [0, 1]$. At each subsequent integer time-step k, apply the HK diffusion model where each node i additionally restricts to neighbours j such that $A(x_j(k)) > A(x_i(k))$. The process is terminated when sufficient convergence is achieved. Rather than limiting ourselves exclusively to explicit algebraic functions, we make an additional modification to incorporate random event modelling. To this end, we consider a set X indexing a random variable for a fixed underlying random event. That is, a function $A : X \to M(\Omega, E)$ where the co-domain is the set of measurable functions between the sample and event spaces. The maximality condition translates to requiring the existance of an $x \in X$ such that $E[A(x)]$ is maximal over X where $E[\cdot]$ is the expected value.

In this analysis, we define A via an agent-based simulation. We consider n agents, scattered around the circumference of a unit disc in which M blocks are randomly scattered. Each agent i explores at speed $v_i \in [0, 1/10]$ (representing the agent's opinion), collecting blocks they encounter on their paths. The random variable $A(v)$ is defined to be the number of blocks collected by an agent travelling at speed v. We confirm numerically that $v = 0.1$ satisfies the required maximality condition (Fig 1).

Our main result is uncovering the insufficiency of temporally localised node update functions in achieving global convergence to the objective-maximising opinion (Fig 2). That is, when nodes consider only neighbouring opinion results from the previous time-step, convergence to optimality is unlikely to be achieved. We show that the probability of global convergence to the optimal opinion increases monotonically with the size of the *look-back* period (i.e. the number of previous time-step results each node considers when selecting positive neighbors). Additionally we explore the effects of connectedness on optimal convergence in randomly generated Barabasi-Albert networks. We find that increased connectivity, in fact, decreases the probability of optimal convergence.

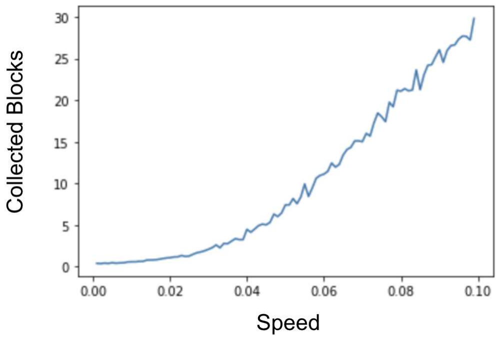

Fig. 1. Average number of blocks collected by an agent at different speeds. At each speed, the average is computed over 1000 simulations.

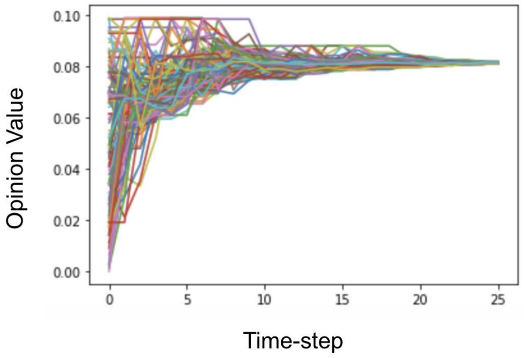

Fig. 2. Temporal evolution of individual opinions on a randomly generated scale-free network with 100 nodes. Convergence to a sub-optimal opinion is observed.

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Timing Uncertainty Encourages Group Reciprocation and Polarisation in Collective Risk Dilemmas

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Anthropogenic climate change, public health measures or even group hunting, are some of the many collective endeavours characterized by uncertain, long-term and non-linear returns. We operationalize these scenarios in a collective-risk dilemma [1], where players can contribute into a public good over a number of rounds, and will only observe their payoff when the game ends. The non-linearity of returns is modelled through a threshold that determines the risk of collective loss. This risk is able to transform a traditional public goods game, where players incur in the well-known tragedy of commons, into a coordination game, where success depends on surpassing a coordination barrier. Behavioural experiments indicate that, when the risk of collective loss is high, slightly more than half of the experimental groups are able to coordinate and avoid the dangerous threshold. However, uncertainties over environmental variables, such as the placement of the threshold, revert the game back into a prisoner's dilemma, decreasing group success. In a recent manuscript [2] we show experimentally the effect of uncertainty about the number of rounds the game will take, i.e., how much time the players have to avoid the consequences of surpassing a dangerous threshold. Surprisingly, our results indicate that, for low levels of this timing uncertainty, not only collective success does not decrease significantly, but we observe a behavioural shift. Contrarily to what happens when there is no uncertainty, participants contribute earlier and in a more polarised manner. Also, a detailed behavioural analysis of the experimental data reveals that, under timing uncertainty, participants of successful groups tend to reciprocate in a similar fashion to the group analogous of the Tit-for-Tat strategy, where players only increase their investments if the group does the same. In general, timing uncertainty appears to casts a *shadow on the future* that requires participants to respond early to encourage reciprocity among peers and ensure success as a group.

Acknowledgements

E.F.D. is supported a F.W.O. (Fonds Wetenschappelijk Onderzoek) Strategic Basic Research (SB) PhD grant (nr. G.1S639.17N) and J.G. is supported by an F.WO postdoctoral grant. This work was also partially supported by the F.W.O. project with grant nr. G.0391.13N, the FuturICT2.0 (www.futurict2.eu) project funded by the FLAG-ERA JCT 2016, and by FCT-Portugal (grants PTDC/EEI-SII/ 5081/2014, PTDC/MAT/STA/3358/2014, and UID/CEC/50021/2020).

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Social Contagion models on hypergraphs

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Our understanding of the dynamics of complex networked systems has increased significantly in the last two decades. However, most of our knowledge is built upon assuming pairwise relations among the system's components. This assumption is often an oversimplification, for instance, modern messaging systems (e.g., WhatsApp, Telegram, Facebook Messenger, among others) allow users to communicate in groups, which create a direct channel for information diffusion among all members of that given group. In other words, modern information spreading is often a one-to-many process. In the same way, team collaborations are inherently group interactions, as are some types of molecular interactions (1). Combinatorial higher-order models (2) offer a way to describe these systems, by overcoming some of the limitations of classical, lower-order network models. In a first attempt, Iacopini et al. (3) presented a model of social contagion defined on simplicial complexes and provided approximate solutions for complexes of order three, including new phenomenological patterns associated to the critical properties of the dynamics. However, the proposed model is still very constrained, both structurally and dynamically. Here we adopt hypergraphs, which relax the structural restrictions required by simplicial complexes by imposing virtually no limitation on the type, size, and mutual inclusion of interactions, thus, representing more faithfully and naturally real systems. We further incorporate explicit critical-mass dynamics, which generalizes the one modeled in (3). Moreover, we develop an analytical framework and provide numerical results for arbitrary hypergraphs, which we also support with Monte Carlo simulations. Our analyses show that the model has a vast parameter space, with first and second-order transitions, bi-stability, and hysteresis. Phenomenologically, we also extend the concept of latent heat to social contexts, which might help to understand oscillatory social behaviors. These concepts are illustrated in Fig. 1. Finally, we also mention that many interesting questions arise from our work. For instance, if one assumes that energy is proportional to the order parameter, ρ, our model might display phenomena reminiscent of a Carnot cycle for social contexts, which might help to understand abrupt changes and oscillatory patterns in social behaviors. In summary, our work unfolds the research line of higher-order models and the analytical treatment of hypergraphs, posing new questions, and paving the way for modeling dynamical processes on hypergraphs. The full paper is available at (4).

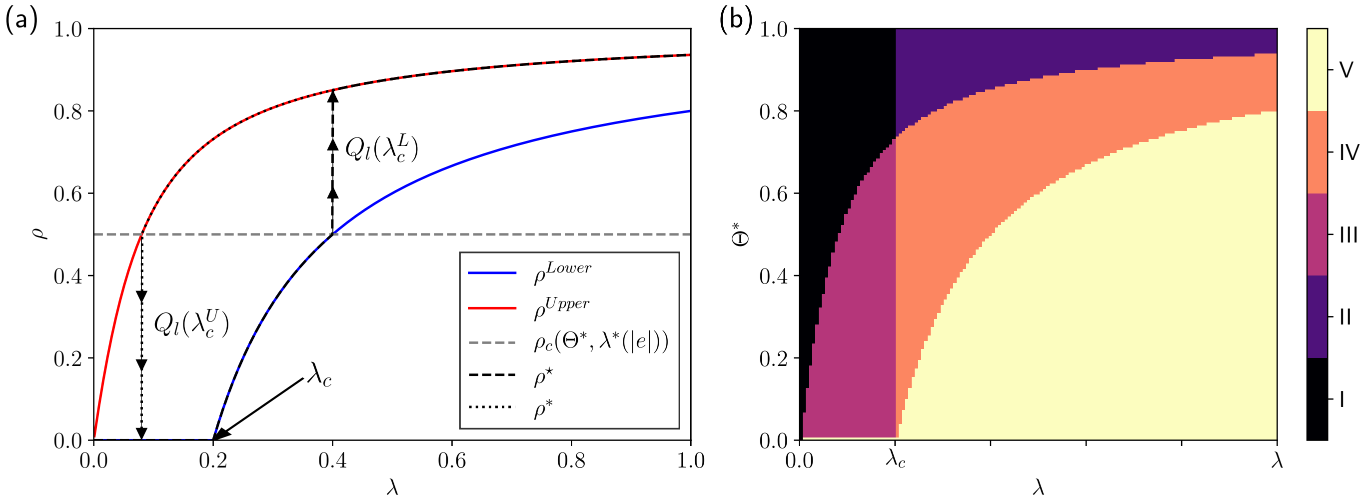

Figure 1: Results for the hyperblob (composed by a hyperedge containing all nodes in addition to a random regular network). Panel (a) shows the possible solutions for a fixed hyperedge critical-mass $\Theta^* = 0.5$. In red and blue, the upper and lower solutions (branches), respectively. The transition from the lower to the upper solution (upper to lower) occurs at the intersection of the lower (upper) solution with a value of global critical-mass, ρ_c, in which the upper solution became stable (unstable). The discontinuity is characterized by the latent heat, $Q_l(\lambda_c^L)$ or $Q_l(\lambda_c^U)$. At $\lambda_c = 0.2$, the lower solution shows a second-order phase transition. In (b) Schematic of the parameter space: Region I: the absorbing state for both the lower and upper solution; Region II: only the lower solution is stable (the global critical mass is not reached, $\rho < \rho_c$); Region III: ρ^{Upper} is stable and $\rho^{\text{Lower}} = 0$ (below the critical point); Region IV: $\rho^{Upper} > \rho^{Lower} > 0$ and both are stable (bi-stable); Region V: only the upper solution is stable (the global critical mass was reached, $\rho \geq \rho_c$).

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Data science of judicial decisions for evidence-based housing policies in Spain

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The effects of the 2007 financial crisis in the scope of housing access and loss in Spain have been devastating for a great part of the population with consequences still visible nowadays. Data available unveils the ineffectiveness of the approach undertaken by legislators and the judiciary in order to confront the complex situation. We present a methodology that aims at studying the jurisprudence by scrutinizing data from judicial decisions so to reveal systemic patterns, pillar decisions and the consequences of important legislative changes, and thus be able to evaluate those mechanisms that fail along the judiciary process.

Using a corpus of housing-related decisions that spans over the last 20 years, we focus on their textual content. We characterize each text as a distribution over topics. To do so, we make use of a network approach [1] that infers a stochastic block model [2] from the bipartite network formed by the corpus of documents and their words. Then, the blocks or communities of words detected by this procedure serve as topics for each document.

Then, once each text is expressed a weighted collection of topics, we aggregate the results over the entire corpus so to analyze the historical discursive evolution, thus finding trends and important changes. Specifically, by means of information-theory based measures of divergence [3], we are able to quantify not only the change but also the propagation of textual content in time.

Preliminary results show a major change in the textual content of decisions some time after the 2007 financial crisis, showing the extent to which the judiciary responded to the critical situation. This methodology shows that we are able to detect important social changes through historical discursive changes in the jurisprudence.

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Agentpy - Agent-based modeling in Python

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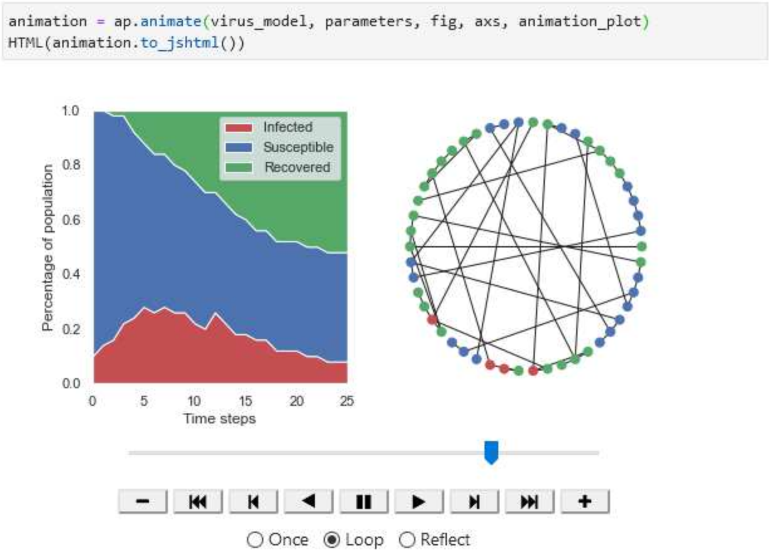
Numerous modeling and simulation tools have been developed to support the development of agent-based models (ABMs) [1]. Recent applications often require high complexity, including large numbers of agents and simulation steps, multiple environments, parameter sampling, Monte Carlo simulations, and data analysis. Existing simulation frameworks that support such complexity are arguably not as approachable and easy to use as traditional tools like NetLogo.

Agentpy [2] attempts to fill this gap by providing a simple syntax for model design, an object-oriented structure that can easily be customized, and advanced tools for experimentation and analysis. Agentpy is written in and follows the philosophy of Python 3, one of the world's most popular programming languages, and thus allows for the direct interaction with established libraries for scientific computing like NumPy, pandas, seaborn, networkx, and SALib.

While the package is in an early stage of development, it already offers a wide range of features, including the creation of custom agents, environments, and networks; the design of complex procedures; the use of standard operators on whole agent groups; experimentation with repeated iterations, varied parameters, and distinct scenarios; output data that can be saved, loaded, and re-arranged for further analysis; and tools for sensitivity analysis, interactive output, and animations (Figure 1).



```
animation = ap.animate(virus_model, parameters, fig, axs, animation_plot)
HTML(animation.to_jshtml())
```

○ Once ● Loop ○ Reflect

Figure 1: Example of an agentpy animation for a virus spread model.

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A little Knowledge is a Dangerous Thing: Excess Confidence Explains Negative Attitudes Towards Science

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Since scientific research is mostly driven by public funds and its translation impacts societies, how the lay public sees science and scientists have been subjects of pertinent interest. However an interesting paradox can be observed: the rise in science communication and outreach efforts seems to correlate with the rise of openly anti-science groups, leading to fears of a "post- truth" society. We propose a new testable and theoretical model, to understand how knowledge and confidence play a role in determining public attitudes towards science and discuss how this can inform science communication. We used The Science and Technology Eurobarometer surveys, from 1998 to 2005, in 34 European countries, comprising 84000 individual interviews, that contains a set of variables gauging, attitudes and knowledge about science. We created a new variable, an indirect measure of confidence and found that public attitudes towards science vary both with knowledge and confidence, in a nonlinear way. As confidence in one's knowledge grows faster than knowledge itself (Dunning-Kruger effect), the least positive attitudes are observed in an average knowledge but high confidence group. This corresponds to the majority of the population, across countries, years, education levels and age, and has implications for science communication and policy. Interesting and consistent differences are observed between genders and in different countries.

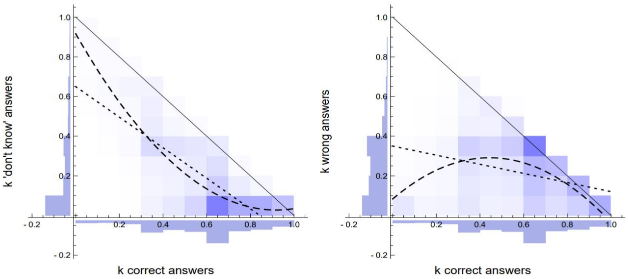

Figure 1: **Confidence grows faster than knowledge:** Upper Panel shows distribution of respondents according to the fraction of correct answers and fraction of "don't know" answers (left) or incorrect answers (right) to the knowledge questions. The dotted and dashed lines are the linear and quadratic regressions, respectively. Heat plots show how "don't know" answers (left) or incorrect answers (right) vary with k. A deviation from the diagonal (or a higher fraction of incorrect answers in intermediate knowledge bins) indicates overconfidence.

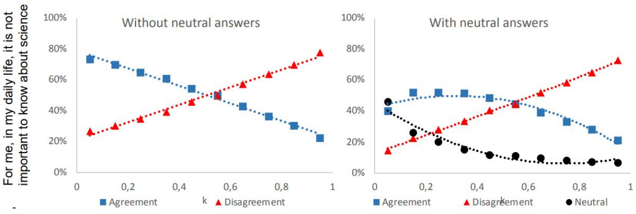

Figure 2. There is an inverted U-curve relationship between knowledge and attitudes: Relative frequencies of agreement, disagreement and neutral stance for each knowledge category for one example of attitude items.

Extraction of functional dynamic networks describing patient's epileptic seizures

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Intracranial EEG studies using stereotactic EEG (SEEG) have shown that during seizures, epileptic activity spreads across several anatomical regions from the seizure onset zone towards remote brain areas. This appears like patient-specific time-varying networks that has to be extracted and characterised. Functional Connectivity (FC) analysis of SEEG signals recorded during seizures enables to describe the statistical relations between all pairs of recorded signals. However, extracting meaningful information from those large datasets is time-consuming and requires high expertise. In the present study [1], we propose a novel method named Brain-wide Time-varying Network Decomposition (BTND) to characterise the dynamic epileptogenic networks activated during seizures in individual patients recorded with SEEG electrodes. The method provides a number of pathological FC subgraphs with their temporal course of activation. The method can be applied to several seizures of the patient to extract reproducible subgraphs. To validate the extraction, we compare the activated subgraphs obtained by BTND to interpretation of SEEG signals recorded in 27 seizures from 9 different patients. We a found a good agreement about the activated subgraphs and the corresponding brain regions involved during the seizures and their activation dynamics.

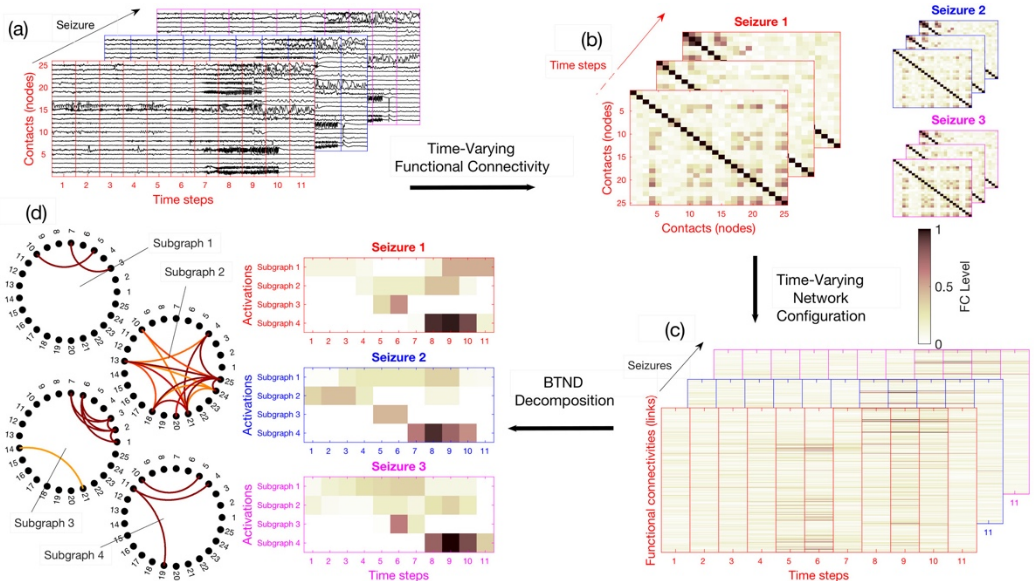

Figure 1: Overview of the joint decomposition strategy of seizures in dynamical graphs.

Acknowledgements

The authors are also at IXXI (Complex Systems Institute in Lyon). Work supported by the ACADEMICS grant of the IDEXLYON, Université de Lyon, PIA ANR-16-IDEX-0005.

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Modelling And Observing Willingness of Public Opinion Expression

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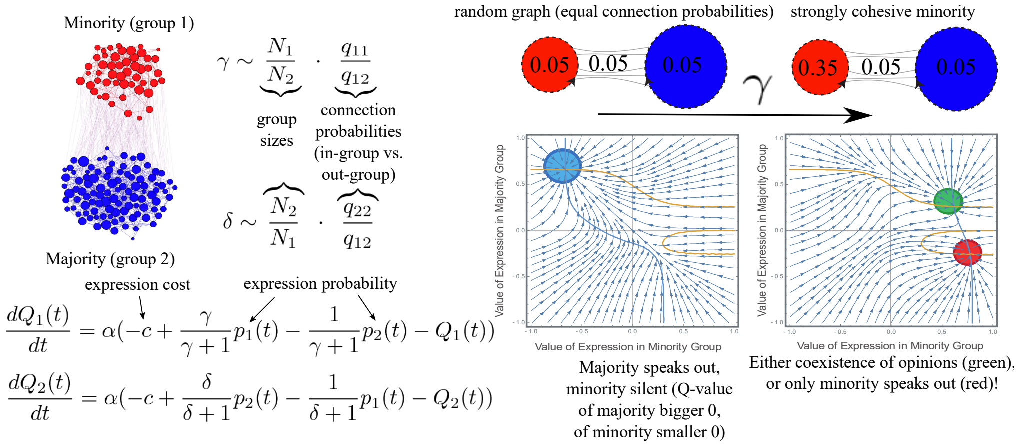
Modeling efforts in opinion dynamics have to a large extent ignored that opinion exchange between individuals can also have an effect on how willing they are to express their opinion publicly. Making one's opinion audible is important: Positions that are rarely voiced in public are improbable to be taken into consideration in, e.g., political decisions. We investigate the conditions that promote or impede opinion expression of different opinion groups in a game-theoretically grounded model with two opinion groups on a stochastic block network[1]. Agents can choose to voice their opinion publicly, or to be silent. Updating their beliefs about the opinion climate around them with the reinforcement learning algorithm of Q-learning, they get more (less) willing to publicly express their opinion if they exchange opinions with an agreeing (disagreeing) neighbor. We reduce the N-agent system in a mean-field approach to two dimensions which represent the two opinion groups, for which we carry out a bifurcation analysis over all relevant parameters. We show that increased structural cohesion (taken into account in the structural parameters γ and δ for the respective groups) and/or decreased costs of opinion expression for one opinion group can amplify its audibility in public discourse. Moreover, we identify conditions under which even opinion majorities can be driven into silence (see Figure 1). These findings gain additional traction in light of the advent of social media which reduce expression costs and facilitate connecting to like-minded others – i.e., building cohesive opinion groups. We also present a Twitter case study[2], covering the 2019 Saxonian state elections, where an opinion minority indeed turned out to be significantly more expressive and confrontative in comment sections than the majority, hence distorting the impression of public opinion on the platform in their favor.



$$\gamma \sim \underbrace{\frac{N_1}{N_2}}_{\text{group sizes}} \cdot \underbrace{\frac{q_{11}}{q_{12}}}_{\text{connection probabilities (in-group vs. out-group)}}$$

$$\delta \sim \overbrace{\frac{N_2}{N_1}} \cdot \overbrace{\frac{q_{22}}{q_{12}}}$$

$$\frac{dQ_1(t)}{dt} = \alpha(-c + \frac{\gamma}{\gamma+1}p_1(t) - \frac{1}{\gamma+1}p_2(t) - Q_1(t))$$

$$\frac{dQ_2(t)}{dt} = \alpha(-c + \frac{\delta}{\delta+1}p_2(t) - \frac{1}{\delta+1}p_1(t) - Q_2(t))$$

Majority speaks out, minority silent (Q-value of majority bigger 0, of minority smaller 0)

Either coexistence of opinions (green), or only minority speaks out (red)!

Figure 1: Model sketch. Structural parameters are ratios of group sizes times connection probabilities (top left). 2D mean-field equations are given on the lower left, yielding the phase plots on the right. If a minority increases internal connection probability (and hence increases γ), then the fixed point for which only the majority is loud disappears, and (in this example, where N_1=100, N_2=200, q_{11} from 0.05 to 0.35) either both or the minority alone are audible.

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The Ocean Environment-Bacterioplankton Nexus

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Using marine microbiome data from the Great Barrier Reef, a robust methodology for marine ecohealth signalling is introduced which considers the independent and joint probability distribution functions of oceanic physicochemical and bacterioplankton interactions quantified as transfer entropy among each system's components. Functional networks are constructed from these interactions, whose keystone nodes have the most interaction and connectivity magnitudes, and whose keystone links have the highest network-wide importance. Optimal marine ecosystems present low exponential Zipf's law scaling parameters among these interactions, corresponding to a more even distribution of environmental stressors and of species collective abundance (see Figure 1). Keystone links consistently connect a highly central and an effectively distant node, providing a more robust classification of node importance. For the bacteriome, keystone species are rare with relatively unstable abundances. A new Kleiber's law-like exponent is discovered between species pairwise interactions and abundance, where the scaling exponent is proportional to the network centrality of the microbial species. In a collective sense the Kleiber's scaling exponent is the highest for the more optimal habitats such as the Northernmost marine reefs. Overall, Marine inshore reefs are more optimal marine ecosystems likely resulting from more stable hydrodynamics and less eutrophication unlike the estuarine inshore reefs impacted by river runoff and constant wave flushing. The method provides a metric which quantifies departure from optimal ecosystem functioning by emphasizing the importance of functional organization- in terms of the interaction network topology of microbial and environmental components- rather than purely taxonomic approaches or historically derived thresholds of environmental measurements. Thus, ranking of microbes and attribution of environmental factors to ecosystem changes must be done considering the collective distribution of interactions versus the consideration of macroecological indicators that do not consider ecosystem function.

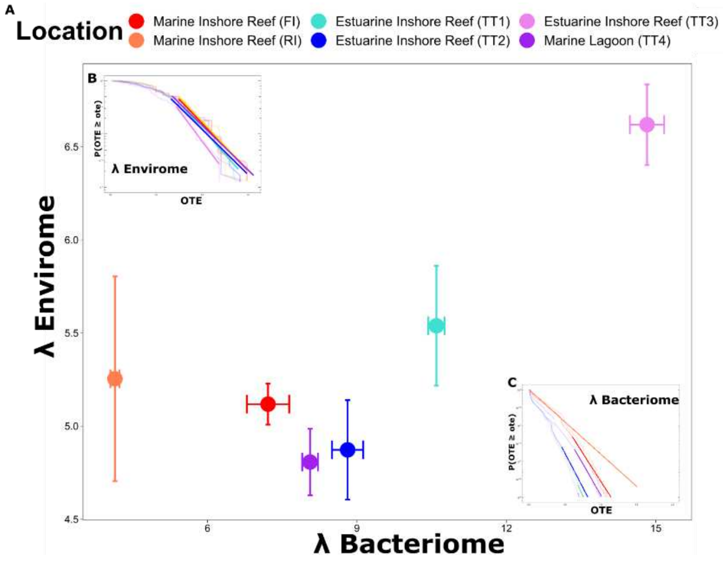

Figure 1: **(A)** Phase space showing the departure of marine habitats from optimality considering the arrangement of their envirome ($\lambda_{envirome}$) and bacteriome ($\lambda_{bacteriome}$) interactions. The closer a point is to the lower left of this space the more optimal it is considered. **(B)** The log-linear distribution of envirome interactions for each habitat. **(C)** The log-linear distribution of bacteriome interactions for each habitat.

Assessing the risk of “infodemics” in response to COVID-19 epidemics

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Our society is built on a complex web of interdependencies whose effects become manifest during extraordinary events, with shocks in one system propagating to the others to an exceptional extent. The recent explosion of publicly shared, decentralized information production that characterizes digital societies and in particular social media activity provides an exceptional laboratory for the observation and the study of these complex social dynamics, and potentially functions as a laboratory to understand, test and validate possible solutions to large-scale crises. Global pandemics are certainly an instance of such crises, and the current outbreak of COVID-19 may therefore be thought of as a natural experiment to observe social responses to a major threat that may potentially escalate to catastrophic levels, and has already managed to seriously affect levels of economic activity, and radically alter human social behaviors across the globe.

In this study [1], we analyzed more than 100 millions Twitter messages posted worldwide in 64 languages during the epidemic emergency due to SARS-CoV-2 and classified the reliability of news diffused to show that information dynamics tailored to alter individuals’ perceptions and, consequently, their behavioral response, is able to drive collective attention towards false or inflammatory content, a phenomenon named infodemics, sharing similarities with more traditional epidemics and spreading phenomena.

For each message, we identify the presence of links pointing to external websites: for each link we verify if it comes from a trustworthy source or not by aggregating information by several fact-checking databases. The number of followers of a single user is then used defines the exposure in terms of potential visualizations at first-order approximation. Exposure and reliability are useful descriptors that, however, do not capture alone the risk of infodemics. For this reason we have developed an Infodemic Risk Index (IRI) which quantifies the rate at which a generic user is exposed to unreliable news produced by a specific class of users (partial IRI) or by any class of users (IRI).

Tracking the evolution in time of the IRI across the globe, we find that, contrary to what it could be expected in principle, on the verge of a threatening global pandemic emergency, human communication activity is to a significant extent characterized by the intentional production of informational noise and even of misleading or false information. This generates waves of unreliable and low-quality information with potentially very dangerous impacts on the social capacity to respond adaptively at all scales by rapidly adopting those norms and behaviors that may effectively contain the propagation of the epidemics.

Fortunately, we also find that the escalation of the epidemics leads people to progressively pay attention to more reliable sources thus potentially limiting the impact of the infodemics, but the actual speed of adjustment may make a major difference in determining the social outcome, and in particular between a controlled epidemics and a global pandemics.

This casts new light on the social mechanics of the infodemics-epidemics interaction, and may be of help to policy makers to design a more integrated strategic approach, by suitably embedding communication and information management into a comprehensive, extended public health perspective.

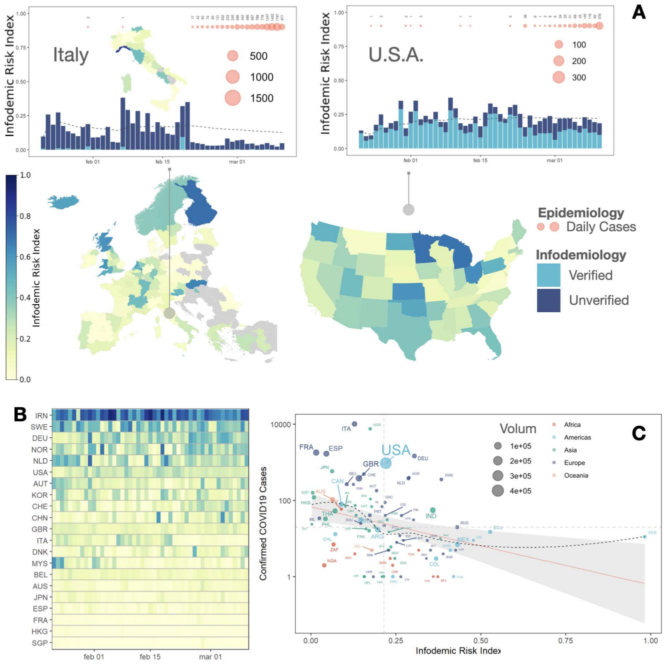

Figure 1: **Infodemic evolution is country-dependent.** (A) The infodemic risk of each country, aggregated over time, is color-coded on the maps. Note the striking drop in the Italian infodemic risk index coinciding with the first official report of non-imported epidemiological cases. (B) Risk evolution for countries characterized by a high volume of messages per day illustrating how the temporal pattern of the infodemic is strongly localized and depends on the online discourse of each individual country. (C) The number of epidemiological cases is shown against the infodemic risk index for all countries with at least one confirmed COVID19 case, illustrating a clear anticorrelation (Spearman r = -0.42) between infodemic risk and number of cases.

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Bali ancient rice terraces: A Hamiltonian approach

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In this contribution, we hypothesize that the power-law distribution of the patches clusters size distribution of the amazing mosaics, characterising several rice-growing regions, in Bali-Indonesia are a consequence of the synchronised dynamics ruled by the Subak irrigation system in that tropical island.

The resulting self-organising process is an effect led by two main mechanisms behind Subak farmers' decisions. Pest stress as a local mechanism promoting order, namely, using the same schedule within neighbouring patches. On the other hand, an antiferromagnetic interaction is set by a global mechanism, fixing a limit on the total number of cells in the same state due to water limitation. We propose a Hamiltonian formulation aimed to reproduce the relevant elements of the Subak irrigation system, which reads as:

$$H_S = -a \sum_{\langle i,j \rangle} \delta(\sigma_i, \sigma_j) + \frac{b}{N-1} \sum_{i>j} \delta(\sigma_i, \sigma_j), \tag{1}$$

where σ_i represents the state at site i, $\langle i, j \rangle$ means the sum is over the 4 neighboring sites, and the second sum counts once for all pairs of sites on the grid. a is the Pest Stress, setting the local interaction among the first nearest neighbours. Then, the pest stress acts as a ferromagnetic interaction like the well-know Potts model, promoting ordering at low temperatures. However, our Hamiltonian system balances that local interaction with a long-range antiferromagnetic contribution. The effect of the water limitation, regulated by b, has a global range of interaction. This contribution, which has the shape of a mean-field Potts model but with positive sign, promotes the system to be balanced into q states at any temperature.

In consequence, the system is driven by two main balances. The first balance is between the energy and entropy contributions. The second balance is within the energy contribution: a local Potts-like interaction and a global antiferromagnetic one. Each balance presents a phase transition.

Depending on the parameter values, our Subak Hamiltonian presents one or two phase transitions. The nature of the high-temperature transition can be critical. As a sample of our prelimininary results, in figure 1 we show the cluster-size entropy and Specific Heat for the Subak Hamiltonian for two different values of the antiferromagnetic long-range interaction, while the same intensity for the local ferromagnetic one. For the higher value of the global interaction, the system can be into three different states, and the peak of the transition moves to lower temperatures with the system size. On contrary, for the lower value of the global interaction, the transition moves to higher temperature with the system size, and only two phases are possible. Here the global antiferromagnetic contribution is too weak to balance the local ferromagnetic one.

Ultimately, our contribution is an attempt to approach the signs of criticality seen in nature as a balance of its essential mechanisms.

The path to scientific discovery: Distribution of labor, productivity and innovation in open science

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The Polymath project is the first complete example of an original research paradigm defined by M. Nielsen as “Networked science” [1]. Launched in 2009, the Polymath project is organized around a series of blogs, each of which starts with the proposition of a research question and continues through a discussion to which anybody can contribute by simply registering to the platform. The aim of this experiment of collaborative mathematics was to show of a different way to conduct research, not only through cooperation, but through a massive and completely open collaboration between hundreds of people varying from renown mathematicians to simple amateurs. Our paper investigates the collaboration and innovation dynamics of this unique mathematical experience.

Out of the 16 blogs launched so far, we collected and analyzed the posts of the five Polymath projects concluded with a collective peer reviewed publication. As in most other collaborative projects (like GitHub, Linux, Wikipedia), our study of Polymath reveals a clear labor hierarchy, with the users’ activity distributed according to a steep power law (with extremely similar slopes in the five projects) and elevate Gini indices. Secondly, we analyzed the productivity of the collaboration using multiple metrics. Figure 1, for example show the number of posts grows super-linearly (with exponent 1.46) with the increase of active users: in the line with the old saying that 1+1>2 [2]. In collaborative science, the sheer number of participants, independently from their actual activity, is a driving force for the increasing of global productivity.

Considering the content of the posts in terms of the set of mathematical concepts they contain, we confirmed that all the projects follow the typical laws of texts: the Zipf’s and the Heaps’ law [3]. The exponents are equal for the different projects, suggesting the presence of a universal growth mechanism of the debate.

We finally introduce a measure of innovation for the posts and we show again that the number of participant to the debate is important to trigger innovation. Even if in most of the projects, the largest part of innovation is produced by a handful of hyperactive users, the presence of “supportes” in the tail of distribution is an important determinant of the overall scientific productivity.

While focussed on the very specific topic of the theory of numbers, the traceability of the Polymath project makes its blogs a unique terrain to study the development of scientific discovery and this work constitutes a first dive into the potentiality of this dataset.

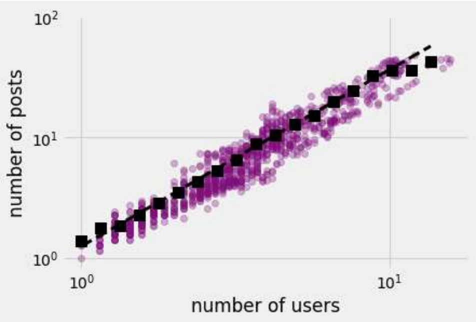

Figure 1: Super-linearity of productivity. Each point represents the number of users and the number of post aggregated on a daily base.

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The Socioeconomic Determinants of Mobility Responses to COVID-19 Mitigation Policies in Italy

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In the effort of fighting the COVID-19 pandemic, several governments world-wide have imposed unprecedented mobility restrictions and social distancing policies, as these - combined with contact tracing and isolation of cases - represent the most effective strategy to slow down the spread of SARS-CoV-2. Italy has been the first EU country to adopt such interventions, by imposing a national lockdown on March 12 that was lifted about 2 months later, once the epidemic curve had been suppressed. Here, we extensively investigate the socioeconomic determinants of the responses to mobility restrictions imposed in Italy during the full course of the first wave of the COVID-19 epidemic, from February until June 2020, through the analysis of human mobility patterns derived from anonymized and aggregated mobile phone data. To this aim, we monitored the timelines of mobility responses using several mobility metrics during 3 phases of the COVID-19 outbreak in Italy both at the province level and at the district level in 3 major cities. Through statistical modeling, we identified the association between mobility responses and several demographic, economic, and epidemiological covariates, across different spatial scales. The results show that behavioral responses were associated to varying socioeconomic factors in the different phases of the pandemic management cycle, and across different geographic scales, highlighting the complex landscape of the determinants of behavioral responses to non-pharmaceutical interventions.

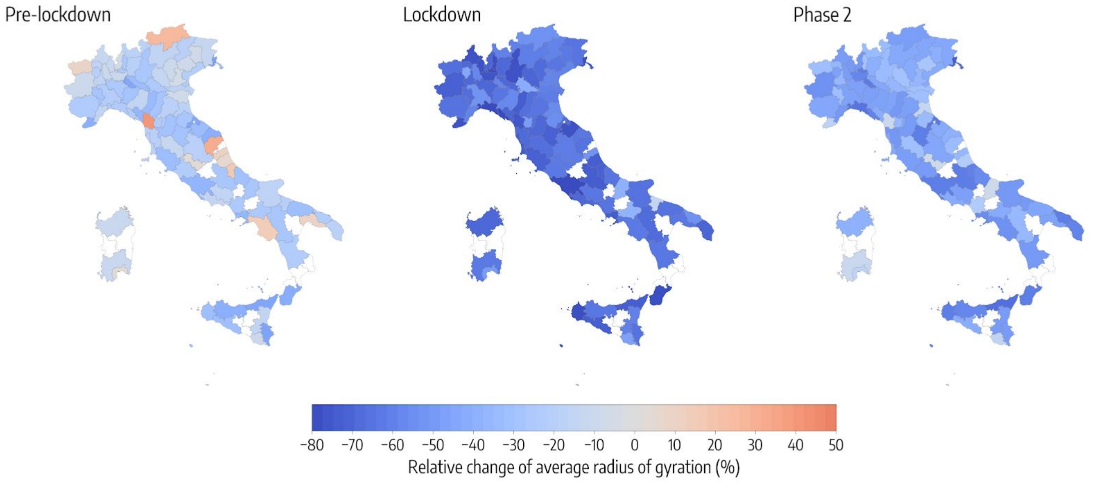

Figure 1: Each map shows the relative change of the median radius of gyration with respect to the baseline,by province, on 3 different days, one for each period under study: the Pre-lockdown (left), the Lockdown (center) and the Phase 2 (right). Provinces inwhite are not included in the analysis because of the low population sampling.

Acknowledgements

We gratefully acknowledge Cuebiq Inc. for making their data available through their Data for Good program. We acknowledge support from the Lagrange Project funded by CRT Foundation.

Photon-processed Nanocavity Networks Regulate a Thermodynamic-Chaotic State Interplay in 2D Surfaces

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Nanocavity networks in 2D surfaces are responsible for molecular confinement, where molecules are normally trapped in small size caverns [1]. Molecular confinement is responsible for a non-thermodynamic equilibrium local fluctuating–domain of trapped molecules characterised by chaotic behaviour at the boundary of 2D interphase. In this work, random walk simulations of mean escape time of only-once trapped water molecules in different size nanocavities is largely deviating from the mean escape time or repetitively trapped molecules and the mean collision time of molecules outside the cavities, where a thermodynamic equilibrium state is applied. The time differentiation inside and outside nanocavities adds a state of ordered arrangements, thus introducing an interplay between the thermodynamic (external domain) and the chaotic state (2D surface-domain). The divergence of molecular microstates from different trapping states agrees with an experimental surface entropy deviation during molecular confinement [2]. Overall, a 2D photonic-crafted surface defines a topological surface with large fractal dimension (~2.8), where the characteristic time of processes abruptly jumps from a thermodynamic state to a chaotic one.

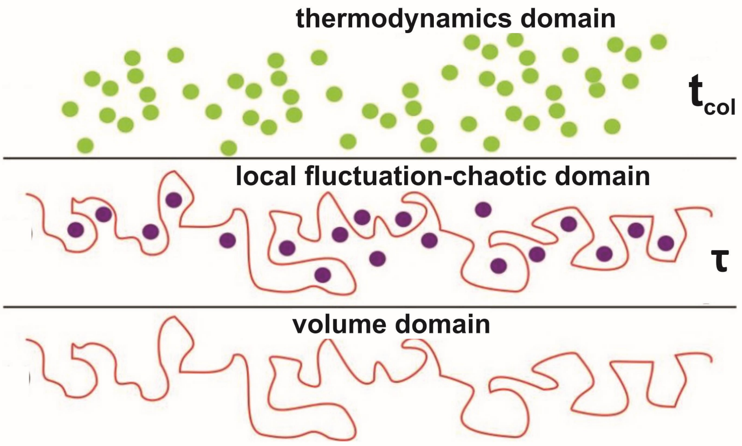

Figure 1: Schematic layout of the interphase between the photon processed 2D surface and the external domain. The time scale is determined, on the external domain, by the mean collision time t_{col} between the water and air molecules, while on the 2D surface domain, by the mean escape time τ of water molecules. There is defined a topological surface where the characteristic time of processes abruptly jumps from a thermodynamic state to a chaotic one.

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Understanding complexity of recurrences in movement data of depressed individuals

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With the ubiquity of smartphones and wearable accelerometer units, movement data has become easily procurable. The easy availability of such data makes it convenient to detect changes in physical activity patterns in real time. Such changes in physical activity levels are one of the most recognizable features of depression [1]. In this work we conduct recurrence quantification analysis to explore how recurrences of patterns in physical activity data differs between depressed and healthy individuals, collected as part of the MOOVD project [2]. We find significant differences ($p<.05$) in the mean and entropy of the diagonal line distributions and in the LAM to DET ratio [3]. These seem to suggest that the mean duration of recurrent physical activity patterns and the diversity associated with these periods are less in depressed individuals as compared to a non-depressed group. We further explore whether the changes in these quantifiers precede a transition towards a depressive episode. For this we use a sliding window approach to calculate recurrence quantifiers from actigraphy data leading up to a depressive transition [4]. The data was collected from individuals who were tapering their medication, as part of the TRANS-ID project [5].

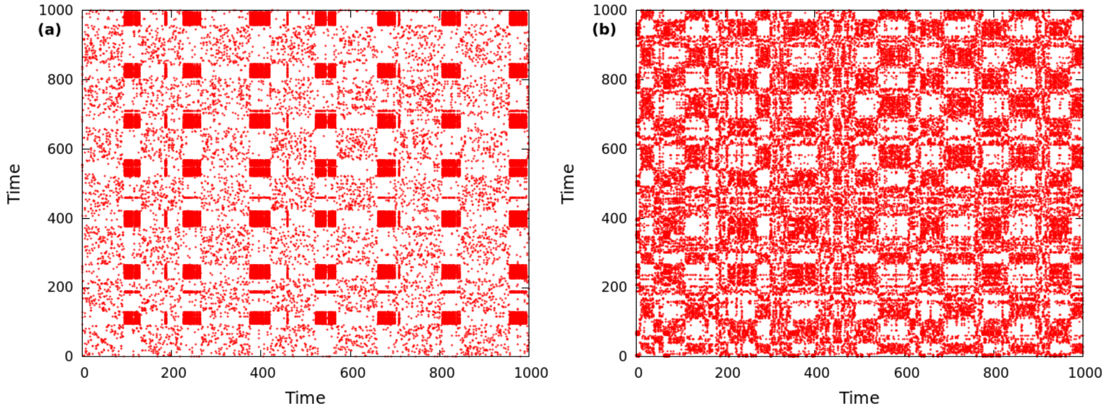

Figure: Differences in the recurrence plots derived from movement data of **(a)** healthy and **(b)** depressed individuals.

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Self-Organization In Stellar Evolution: Size-Complexity Rule

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Complexity Theory is highly interdisciplinary, therefore any regularities must hold on all levels of organization, independent on the nature of the system. An open question in science is how complex systems self-organize to produce emergent structures and properties, a branch of non-equilibrium thermodynamics. It has long been known that there is a quantity-quality transition in natural systems. This is to say that the properties of a system depend on its size. More recently, this has been termed the size-complexity rule, which means that to increase their size, systems must increase their complexity, and that to increase their complexity they must grow in size. This rule goes under different names in different disciplines and systems of different nature, such as the area-speciation rule, economies of scale, scaling relations (allometric) in biology and for cities, and many others. We apply the size-complexity rule to stars to compare them with other complex systems in order to find universal patterns of self-organization independent of the substrate. As a measure of complexity of a star, we are using the degree of grouping of nucleons into atoms, which reduces nucleon entropy, increases the variety of elements, and changes the structure of the star [1]. As seen in our previous work [2], complexity, using action efficiency, is in power law proportionality of all other characteristics of a complex system, including its size. Here we find that, as for the other systems studied, the complexity of stars is in a power law proportionality with their size - the bigger a system is, the higher its level of complexity is - despite differing explosion energies and initial metallicities from simulations and data, which confirms the size-complexity rule and our model.

Acknowledgements

We would like to thank the Assumption University Honor's Program and the Department of Biological and Physical Sciences for financial support, as well as Assumption students Thanh Vu, Simon Trcka and Lamberto Qako for help with data collection. We would also like to thank Assumption students Nicole Bramlitt and Rebecca Gilchrist for long discussions and for proofreading the paper, and to Prof. Steven Theroux, Prof. Michael Levin, Clement Vidal and Claudio Flores Martinez for valuable feedback.

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Interactions between overlapping nodes and hubs in complex networks with modular structure

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In complex networks, the degree distribution of the nodes is known to be non-homogeneous with a heavy tail. Thus, a small set of nodes (called hubs) are highly connected in the network. The community structure is another main topological feature of many real-world networks. In these networks, the nodes shared by more than one community are called overlapping nodes. They play an important role in the network dynamics due to their ability to reach multiple communities [1]. In this work [2], our goal is to characterize the relationship between the overlapping nodes and the hubs. Indeed, we suspect that hubs are in the neighborhood of the overlapping nodes. In order to investigate the ubiquity of this property, we perform series of experiments on multiple real-world networks from various origins. The aim of these experiments is to compare the set of neighbors of the overlapping nodes with the set of hubs. We compute classical measures such as the proportion of common nodes, the Rank-biased overlap (RBO) and the Pearson correlation between the two sets in order to investigate their similarities. Table 1 illustrates partial results of these evaluation for 6 empirical networks of different sizes using two different community detections algorithms (SLPA and LFME).

Network	N	*on(%)*	*S(%)*	A_n*(%)*		*r (p=0.5)*		ρ	
				SLPA	**LFME**	**SLPA**	**LFME**	**SLPA**	**LFME**
ego-Facebook	4039	3.1	17.5	59.25	71.83	0.998	0.999	0.985	0.99
ca-GrQc	5242	26.43	33.19	64.04	64.01	0.999	0.999	0.969	0.982
ca-HepTh	9877	31.36	45.2	75.32	65.17	0.999	0.999	0.99	0.996
ca-CondMat	23133	29.37	51.69	79.57	63.02	1	1	0.989	0.997
Enron Email	36692	35	48.88	73.54	70.42	1	1	0.983	0.99

Table 1. N is the network size. *on* is the fraction of overlapping nodes. S is the size of the neighborhood of the overlapping nodes. A_n is the proportion of common nodes of the two sets. r represents the Rank-biased overlap between the set of neighbors of the overlapping nodes and the set of hubs. p determines the weights of the elements. More weight is given to the first elements of both sets if p has a small value. ρ is the Pearson correlation.

Results show that there is a high overlap between the set of neighbors of the overlapping nodes and the set of hubs. It appears that a high proportion of the hubs are one-step neighbors of the overlapping nodes. Results show also that the RBO between the set of neighbors of the overlapping nodes and the set of hubs has very high values. This confirms that there is a great similarity between the two sets. Moreover, there is a very high correlation between the set of neighbors of the overlapping nodes and the hubs. All these results are a strong indication that overlapping nodes are neighbors of the highly connected.

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Investigating Longitudinal Effects of Online Recommendations with Agent-Based Simulation

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Automated recommendations are nowadays a central part of our online user experience. Today, many online services – including e-commerce sites, media streaming platforms, and social networks – use recommendations to achieve organizational goals, such as increasing sales or customer retention. However, the existing literature on the design of recommendation algorithms mostly does not consider this business-oriented perspective but focuses almost exclusively on consumers' value. The underlying assumption for doing so is that recommendations that optimally satisfy consumers' information needs are ultimately also the most valuable ones from a business perspective. In reality, however, this assumption is a severe oversimplification of the underlying, much more complex situation, since multiple stakeholders' goals must be taken into account. Consider, for example, an online hotel booking platform that charges commissions to partnering property owners whenever bookings are made through the site. When recommending hotels to consumers, an underlying machine learning algorithm might, first of all, focus on identifying hotels that match the consumer's preferences, thereby increasing the probability of booking in the first place. At the same time, however, to maximize the platform provider's profit, the algorithm might consider each viable option's profitability when ranking the items recommended to the user. Finally, the algorithm might also want to ensure that all property owners' items are recommended from time to time, to keep them partnering with the site. Ultimately, the booking platform's problem is to design a recommendation strategy that balances the potentially conflicting goals of multiple stakeholders and assures the business's profitability in the long run.

Despite their practical relevance, multi-stakeholder recommendation scenarios and longitudinal effects of recommender systems still represent two major research gaps. In our research, we employ agent-based simulation, a novel approach in this area, to model and analyze the alternative recommendation strategies effects on different stakeholders' behaviors and objectives over time. Specifically, the agents in our model include consumers, recommendation service providers that determine the strategy, and item providers, i.e., property owners in the above example. Furthermore, we include social reputation mechanisms (e.g., posts on social media sites), which may amplify consumers' publicly shared quality experiences. Our proposed agent-based model ultimately aims to capture the subtle dependencies between the objectively selected items which are recommended to users, the consumers' related quality expectations, and the feedback and transactional behavior that might arise from not matching the consumers' quality expectations over time. Moreover, we model how the actual consumer behavior, which is influenced by the perceived quality of the provided recommendations, may influence the profitability of the service providers and the item providers in the long run. Complex dynamics can emerge from the mutual interdependencies between the stakeholders, which were not adequately analyzed so far.

The first set of simulation experiments based on real-world consumer feedback data confirms the viability of our simulation approach. The experiments show that the proposed model is capable of reflecting real-world dynamics. It turns out that recommending the items with the highest expected value for consumers may not be optimal in terms of business value. At the same time, however, the model realistically encodes that optimizing only for provider profitability may lead to missed business opportunities. Our current and future works aim to better understand the extent to which social reputation mechanisms can amplify and accelerate the observed dynamics.

Statistical Physics of Complex Information Dynamics

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The constituents of a complex system exchange information to function properly. Their signalling dynamics often leads to the appearance of emergent phenomena, such as phase transitions and collective behaviors. While information exchange has been widely modeled by means of distinct spreading processes - such as continuous-time diffusion, random walks, synchronization and consensus - on top of complex networks, a unified and physically-grounded framework to study information dynamics and gain insights about the macroscopic effects of microscopic interactions, is still eluding us. Here, we present this framework in terms of a statistical field theory of information dynamics, unifying a range of dynamical processes governing the evolution of information on top of static or time varying structures. We show that information operators form a meaningful statistical ensemble and their superposition defines a density matrix that can be used for the analysis of complex dynamics. As a direct application, we show that the von Neumann entropy of the ensemble can be a measure of the functional diversity of complex systems, defined in terms of the functional differentiation of higher-order interactions among their components. Our results suggest that modularity and hierarchy, two key features of empirical complex systems - from the human brain to social and urban networks - play a key role to guarantee functional diversity and, consequently, are favored.

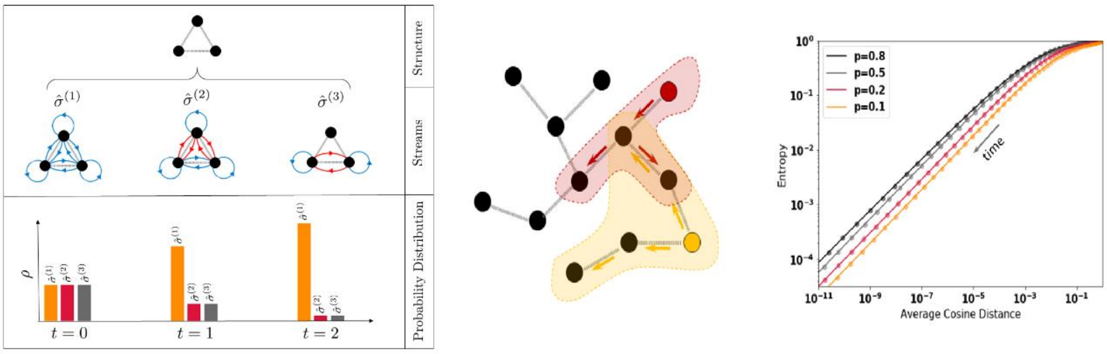

Figure 1: The figure on the left illustrates the information streams and their corresponding activation probabilities changing over time, for a simple system of 3 interacting components. The mixedness of information streams has been used as a proxy for functional diversity of the units- encoding the differentiation of higher-order interactions among them (middle and right).

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Enhancing Transport Properties In Interconnected Systems Without Altering Their Structure

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Units of complex systems communicate efficiently to function properly: e.g., allowing electrochemical signals to travel quickly among functionally connected neuronal areas in the human brain, or allowing for fast navigation of humans and goods in complex transportation landscapes. The coexistence of different types of relationships among the units, entailing a multilayer representation in which types are considered as networks encoded by *layer*s, plays an important role in the quality of information exchange among them. While altering the structure of such systems—e.g., by physically adding (or removing) units, connections, or layers—might be costly, coupling the dynamics of subset(s) of layers in a way that reduces the number of redundant diffusion pathways across the multilayer system, can potentially accelerate the overall information flow. To this aim, we introduce a framework for *functional reducibility* which allow us to enhance transport phenomena in multilayer systems by coupling layers together with respect to dynamics rather than structure. Mathematically, the optimal configuration is obtained by maximizing the deviation of system's entropy from the limit of free and noninteracting layers. Our results provide a transparent procedure to reduce diffusion time and optimize noncompact search processes in empirical multilayer systems, without the cost of altering the underlying structure.

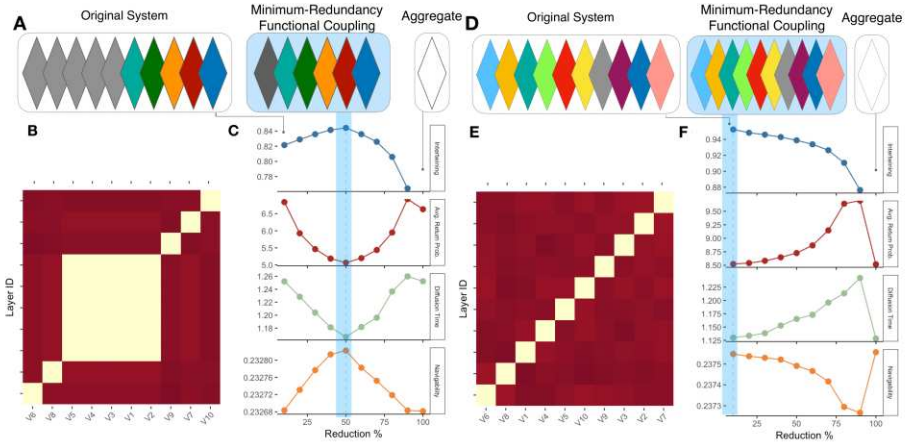

Figure 1: Reducible scenario (left): A multiplex network with 5 identical layers and 5 distinct random networks with wiring probability 0.2 is illustrated. Its transport properties – e.g. average return probability, diffusion time and navigability – are improved after coupling its layers according to the proposed framework (Minimum-Redundancy Functional Coupling). Irreducible scenario (right) A multiplex network where layers are uncorrelated random networks with wiring probability 0.2 is presented. Here, the transport properties are not enhanced by functional coupling because spectral diversity is maximized when the original system is not functionally aggregated.

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Multiscale Statistical Physics of the Human-SARS-CoV-2 Interactome

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Protein-protein interaction (PPI) networks have been used to investigate the influence of SARS-CoV-2 viral proteins on the function of human cells, laying out a deeper understanding of COVID-19 and providing ground for drug repurposing strategies. However, our knowledge of (dis)similarities between this one and other viral agents is still very limited. Here we compare the novel coronavirus PPI network against 45 known viruses, from the perspective of statistical physics. Our results show that classic analysis such as percolation is not sensitive to the distinguishing features of viruses, whereas the analysis of biochemical spreading patterns allows us to meaningfully categorize the viruses and quantitatively compare their impact on human proteins. Remarkably, when Gibbsian-like density matrices are used to represent each system's state, the spectral entropy reveals the existence of clusters of viruses at multiple scales. Overall, our results indicate that SARS-CoV-2 exhibits similarities to viruses like SARS-CoV and Influenza A at small scales, while at larger scales it exhibits more similarities to viruses such as HIV1 and HTLV1.

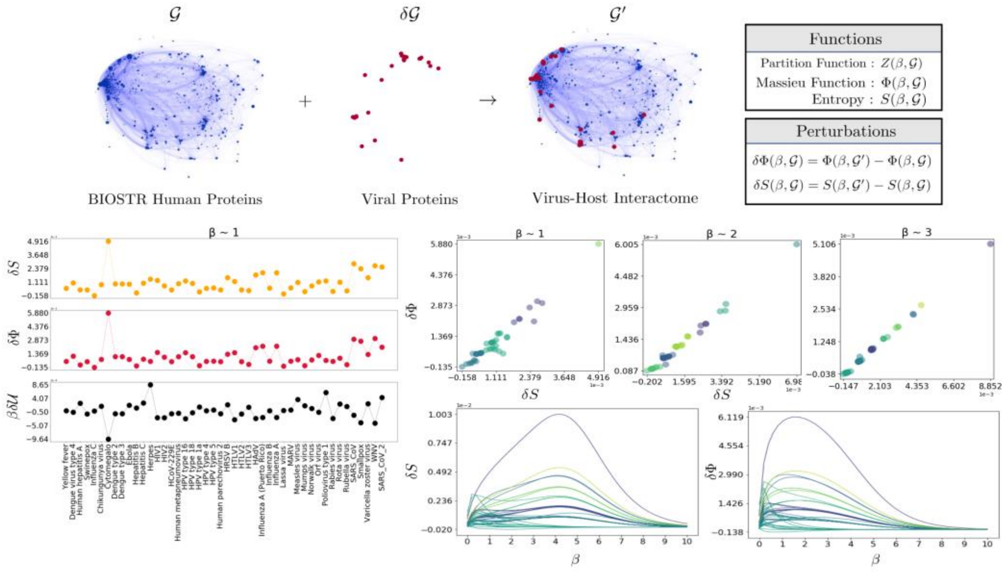

Figure 1: On the top, the BIOSTR human interactome is targeted by viral proteins, considered as microscopic perturbations, to build the virus-human interactomes. The interdependence is reflected in the macroscopic functions of the network (right-hand side tables), including the thermodynamic and dynamic features considered in this study. Interacting with the viral nodes perturbs the macroscopic properties of the human PPI network (bottom-left panel). Based on the perturbations, k-means algorithm is used to cluster the viruses at different scales corresponding to distinct choices of β (bottom-right panel).

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Shock diffusion in a multilayer supply chain network

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Abstract

The flow of goods and services between geographic regions in an economic system is enabled by supply chains. Supply chains are composed of buyers and suppliers of goods and services interacting with each other to meet the consumption needs or final demand for all products within an economy. When mapped for the entire economy and geographic locations of a country, supply chains form a spatial network of interactions among suppliers and buyers. They are typically characterized by a high connectivity due to trade and complex interdependencies among different economic sectors. This high connectivity makes supply chain networks vulnerable to cascading failures produced by exogenous shocks. The need to better understand the response of supply chains to shocks- sudden changes in supply or demand- has become increasingly evident with recent catastrophic events, such as the coronavirus disease 2019 (COVID-19) pandemic. The pandemic has exposed the fragility of basic-need products' supply chains in various countries around the globe.

In this study, we explore the exposure and fragility of United States (US) cities and economic sectors to intranational supply chain shocks. Supply chains in the US have been severely disrupted by the global pandemic, suggesting that cascading failures may be a consequential issue within the country. We use a multiregional input-output dataset to build the supply chain network of products and services in the US economy. To better capture the supply chain interactions within (intralayer) and between (interlayer) economic sectors, we use a multilayer network representation, where nodes are geographic regions, layers are economic sectors and links are economic transactions between regions and sectors. The diffusion of shocks in the multilayer supply chain network are modeled using a network cascade model. The model simulates the diffusion of a shock as a discrete process where the shock starts at a source node and propagates to other nodes and layers through sectoral interdependencies. A shock to the source node in this case represents a perturbation to the intermediate demand of goods and services by an economic sector in a geographic region. By using the model to simulate individual shocks to every node in the network, we are able to identify the most fragile and exposed nodes in the multilayer supply chain network. Although our results are for supply chains in the US, the methods are general and could be used with data for other countries.

Our results show that the size of cascading failures, measured as the total number of collapsed nodes for a given shock, varies widely depending on the shock's severity and the impacted nodes' buffering capacity. The ratio between the buffering capacity of a node and the severity of a shock is termed the node's failure level. By varying the failure level of a node, we find that the response of supply chains to shocks exhibits a threshold-like behavior. Below a certain failure level, the total number of impacted nodes increases rapidly for any source node in the network. Based on this failure level analysis, we find that the most fragile geographic locations tend to be primarily in the central United States. These are regions that specialize in food production and manufacturing. The fragility risk of nodes, measured by the intersection of the fragility of a node and its exposure to shocks, is heterogeneous across regions and sectors. This suggests that interventions aiming to make the supply chain network more robust against cascading shocks are likely needed at multiple levels of network aggregation.

Self-organization, Big Data, and the dynamics of opinion formation: A view from the Complex Systems perspective

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Guiou Kobayashi (UFABC), José Artur Quilici-Gonzalez (UFABC)

Opinion formation has acquired a new dynamics under the influence of media tools incremented by Big Data resources. Carefully designed algorithms allow the mining, organizing, modelling, and manipulation of individual and public opinion. Here, we investigate an apparent conflict in studies of the supposed self-organization characteristic of public opinion guided by media and Big Data resources. On the one hand, assuming that these tools have the power to manipulate public opinion, they would severely diminish (or even eliminate) its spontaneous self-organizing characteristic. On the other hand, the existence of various manipulations with different levels and contexts could dilute each attempted manipulation, allowing self-organization to prevail in the dynamics of public opinion. To investigate this apparent conflict, two aspects of self-organizing process are considered: (a) *Primary self-organization*, which involves the encounter, ideally by chance, between elements with independent behaviour. In the absence of a central controller, a fragile form of organization might then emerge, due to their spontaneous interaction/communication. (b) *Secondary self-organization*, in turn, involves learning procedures to adjust the communication amongst system elements, in order to create stable and resilient patterns of behaviour/communication, strengthening its functionality. A model of *secondary self-organization*, applied to studies of the dynamics of public opinion, is proposed grounded on a Complex Systems methodology, according to which: (1) Meaningful informational patterns are the fundamental units of communication; (2) Informational patterns might emerge from recurrent collective communication expressing habitual resilient *dispositions*; (3) the collective flow of communication might bring about unexpected, self-organized emergent novelties; (4) resilience plays a fundamental role in the dispositional process of communication among rational agents; (5) collective communication might involve moral agents with sufficient autonomy to rationally regulate what is supposedly of cultural, ethical, or social interest. Our hypothesis is that Big Data tools might help with the implementation of the proposed methodology to investigate the dynamics of opinion, by means of a complex network simulation, according to presuppositions (1)-(5).

Authors:

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Title: Unraveling the interplay of the urban form, mobility and social mixing in the light of the COVID19 pandemic

Abstract

The COVID-19 pandemic has left no country untouched affecting people's routines over the globe. The mobility of the population is identified as a fundamental driving force for the dissemination of the COVID-19 at both regional and local levels. This work dissects the integrated impact of urban form and human mobility in the spreading of COVID-19 within cities. Namely, systematically exploring the effects of human mobility imposed by the diverse urban patterns in regards to the distribution of population and job locations. To this end, we first present novel insights of the interaction between inhabitants' mobility behavior and their places of residence in 21 cities, characterizing their urban structures ranging from monocentric to polycentric forms. Inhabitants in more polycentric cities have more homogeneous distribution of radius of gyration. Further, we measure population's response to travel restrictions via changes in the distribution of travel radii with and without the quarantine scenario. Next, we model the early-stage and time-varying reproduction numbers as a combination of urban form and mobility predictors in eleven cities. By introducing the newly proposed mobility measures, generalized linear models achieve good performance both for the early-stage (rho = 0.98) and daily reproduction numbers (rho = 0.86). Our study informs the value of mobility-defined urban form in the spreading of a pandemic in diverse cities. These dynamic measures merit great attention for scenario analysis of urban mobility coupled with containing the epidemic spreading.

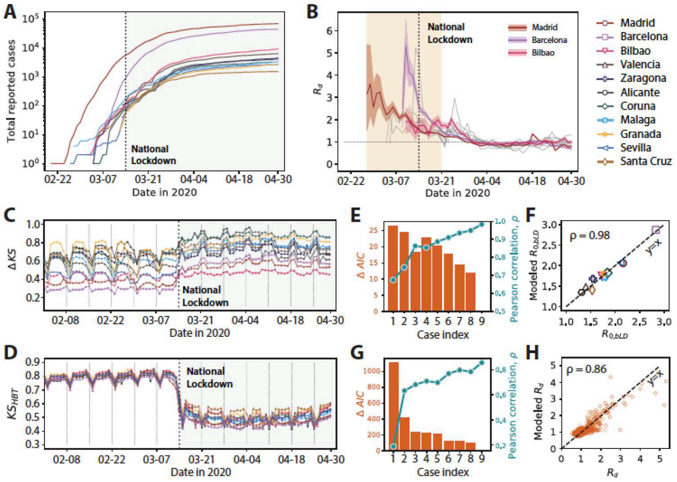

Figure 1: Modeling of reproduction number of COVID-19 in the 11 Spanish cities.

Effect of memory, intolerance, and second-order reputation on cooperation

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The understanding of cooperative behavior in social systems has been the subject of intense research over the past few decades. In this regard, the theoretical models used to explain cooperation in human societies have been complemented with a growing interest in experimental studies to validate the proposed mechanisms. In this work, we rely on previous experimental findings to build a theoretical model based on two cooperation driving mechanisms: second-order reputation and memory. Specifically, taking the donation game as a starting point, the agents are distributed among three strategies, namely, unconditional cooperators, unconditional defectors, and discriminators, where the latter follow a second-order assessment rule: shunning, stern judging, image scoring, or simple standing. A discriminator will cooperate if the evaluation of the recipient's last actions contained in his memory is above a threshold of (in)tolerance. In addition to the dynamics inherent to the game, another imitation dynamics, involving much longer times (generations), is introduced. The model is approached through a mean-field approximation that predicts the macroscopic behavior observed in Monte Carlo simulations. We found that, while in most second-order assessment rules, intolerance hinders cooperation, it has the opposite (positive) effect under the simple standing rule. Furthermore, we show that, when considering memory, the stern judging rule shows the lowest values of cooperation, while stricter rules show higher cooperation levels.

Acknowledgements

C.X. acknowledges financial support of the National Natural Science Foundation of China (NNSFC) under Grant No.61773286 and support of China Scholarship Council under Grant No. 201808120001. C.G. and Y.M. acknowledge partial support from Project No. UZ-I-2015/022/PIP, the Government of Aragón, Spain, FEDER Funds, through Grant No. E36-17R to FENOL, and from MINECO and FEDER funds (Grant No. FIS2017-87519-P). The funders had no role in study design, data collection, and analysis; decision to publish; or preparation of the manuscript.

Community structure in the World Trade Network based on communicability distances

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International trade is based on a set of complex relationships between different countries that can be modelled as a dense network of interconnected agents. A long-standing problem in this field is the detection of communities, as it reveals how the network is internally organized, highlighting the presence of special relationships between nodes, that might not be revealed by direct empirical analyses.

In this framework, a specific role is assumed by the distance between nodes. In the economic field, a network perspective is based on the idea that indirect trade relationships may be important [1]. A measure of the distance between nodes that also considers indirect connections is therefore crucial to catch interconnections between nodes. In this work, we focus on two measures of distance, or metrics, on the network: the Estrada communicability distance [2] and the vibrational communicability distance [3]. They both go beyond the limits of the immediate interaction between neighbours and they look simultaneously, albeit differently, at all the possible channels of interactions between nodes. We propose a specific methodology that exploits such metrics to inspect the mesoscale structure of the network, in search for strongly interacting clusters of nodes. Using these metrics we group nodes whose mutual distances are below a given threshold, i.e. whose interactions are stronger than a given value. Then we identify the optimal partition according to a maximum quality function criterion. Unlike the classical modularity function, we adapt the partition quality index proposed in [4] for general metric spaces, exploiting the additional information of the network's metric structure. Among all the different partitions we get at different thresholds, we select the one providing the maximum quality index, according to the criterion described in [4].

Our proposal is efficient from a computational viewpoint. Indeed, given the specific distance matrix, we can easily evaluate the optimal solution varying the threshold. We cluster nodes going beyond the interactions between neighbours and considering all possible channels of interaction between them. The approach turns out to be particularly suitable when applied to a dense network like the World Trade Network.

Numerical results depict the structure of the economic trade, detecting main relevant communities. Features and properties of each community can be exploited to compare the characteristics of different clusters and to detect the most central countries inside the single community as well in the whole network.

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Signed backbone extraction from intrinsically dense weighted networks

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Networks provide useful tools for analyzing diverse complex systems from natural, social, and technological domains. Growing size and variety of data such as more nodes and links and associated weights, directions, and signs can provide accessory information. Link and weight abundance, on the other hand, results in denser networks with noisy, insignificant, or otherwise redundant data. Moreover, typical network analysis and visualization techniques presuppose sparsity and are not appropriate or scalable for dense and weighted networks. As a remedy, network backbone extraction methods aim to retain only the important links while preserving the useful and elucidative structure of the original networks for further analyses.

Here, we provide the first methods for extracting signed network backbones from intrinsically dense unsigned weighted networks. Utilizing a null model based on the hypergeometric distribution and iterative proportional fitting procedure; we propose *significance filter* and *vigor filter*. *Significance filter* eliminates links whose weights do not significantly deviate from their expected values under the null model and infers the sign of remaining edges. *Vigor filter* enables the elimination of links that might be deemed statistically significant but not sufficiently intense and allows establishing signed weights for the backbone links.

Empirical analysis on migration, voting, temporal interaction, and species similarity networks reveals that the proposed filters extract meaningful and sparse signed backbones while preserving the multiscale nature of the network. The resulting backbones exhibit characteristics typically associated with signed networks such as reciprocity, structural balance, and community structure. The developed tool is provided as a free, open-source software package.

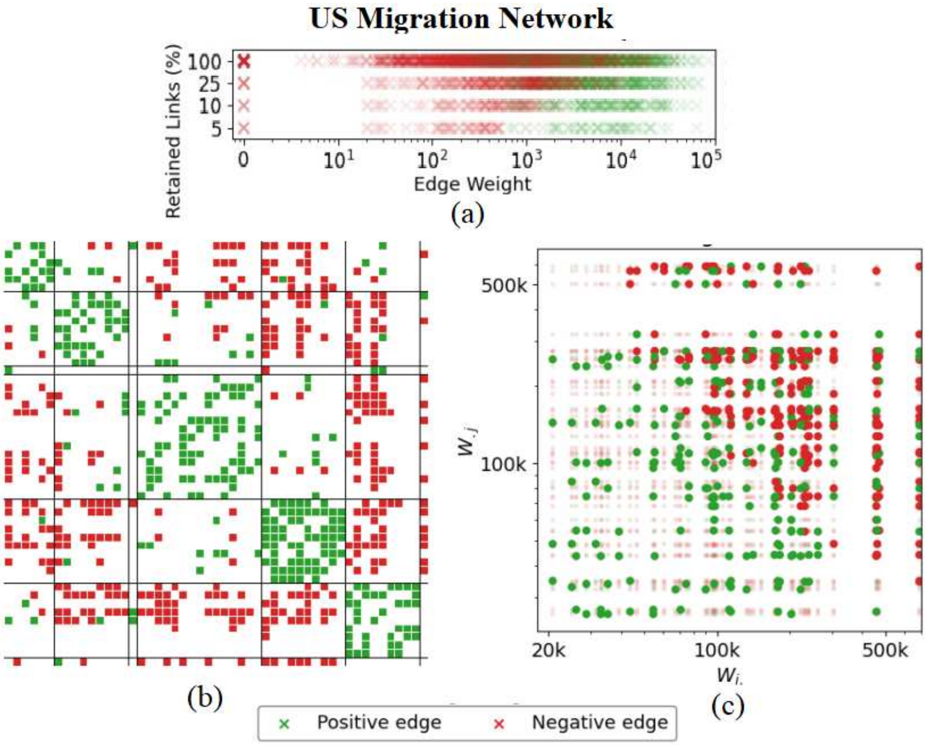

Figure 1: (a) Original weights of the retained edges, (b) Block structure of the extracted backbone (c) Original strength distribution of the retained dyads

Mediating Artificial Intelligence Developments through Negative and Positive Incentives

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The field of Artificial Intelligence (AI) is going through a period of great expectations, introducing a certain level of anxiety in research, business and also policy. This anxiety is further energised by an AI race narrative that makes people believe they might be missing out. Whether real or not, a belief in this narrative may be detrimental as some stake-holders will feel obliged to cut corners on safety precautions, or ignore societal consequences just to "win". Starting from a baseline model [1] that describes a broad class of technology races where winners draw a significant benefit compared to others (such as AI advances, patent race, pharmaceutical technologies), we investigate here [2] how positive (rewards) and negative (punishments) incentives may beneficially influence the outcomes. We uncover conditions in which punishment is either capable of reducing the development speed of unsafe participants or has the capacity to reduce innovation through over-regulation. Alternatively, we show that, in several scenarios, rewarding those that follow safety measures may increase the development speed while still ensuring safe choices. Moreover, in the latter regimes, rewards do not suffer from the issue of over-regulation as is the case for punishment. Overall, our findings provide valuable insights into the nature and kinds of regulatory actions most suitable to improve safety compliance in the contexts of both smooth and sudden technological shifts.

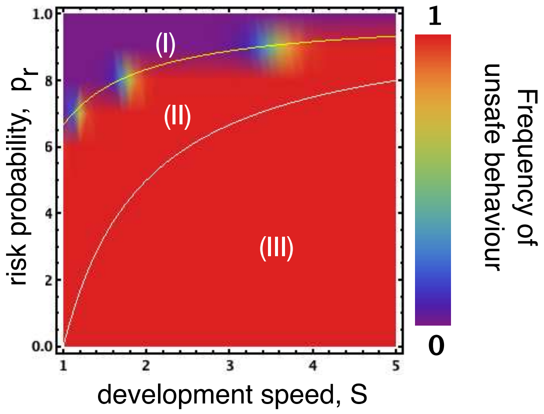

Figure 1: Frequency of unsafe behaviour as a function of development speed and the disaster risk, in absence of incentives (see Ref [1]). In regions (**I**) and (**III**), safe and unsafe/innovation, respectively, are the preferred collective outcome and are selected by natural selection, thus no regulation being required. Region (**II**) requires regulation as safe behaviour is preferred but not selected. This talk is meant to explore how to promote safe behaviour in this dilemma region using incentives (peer reward vs peer punishment) - see preprint in Reference [2].

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Urbanization – rather than local policy – drives pandemic-induced mobility reduction

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It is well-known that Covid-19 has had different effects across socioeconomic classes. In a developing context, where economic inequalities are stark both within and between cities, Covid-19 presents particularly hard socioeconomic quandaries as poorer residents (often in the informal sector) are both less likely to have jobs that can be teleworked or social safety nets. Nonetheless, the Colombian government in the early stage of the pandemic instituted a strict quarantine system wherein municipalities directed residents to concentrate their essential travel on certain days of the week, corresponding to their national ID number/gender. Interestingly, the implications of localized policies varied dramatically – e.g. some municipalities allowed up to 50% of the population out/day (Bogotá allowed males/females out on even/odd days), while others allowed as low as 10% out/day (ID-based restrictions). However, it is at this point unknown how comparatively effective these policies were in limiting mobility empirically, especially considering that the smallest, usually poorer cities imposed some of the most severe limitations.

We draw upon geolocated call detail records (CDRs) from Colombia to compare mobility changes within and across cities. In particular, we compare changes in trip frequency and daily distance travelled from basal to pandemic levels, as well as detect disruptions in established (work) commute patterns. We find that:

- municipality population (which is associated with higher wealth, labor formality, and economic complexity) is a much stronger driver of aggregate levels of mobility disruption than municipality-level policy severity (Figure 1);
- within cities, higher socioeconomic status is (as expected) associated with more dramatic mobility reduction and more commute disruption;
- workers from low income areas of the city were especially more likely to forego their established pre-pandemic commute during the pandemic if the commute destination was either in a wealthier area or a formal employment hub (bottom figure panel).

This last result points to a critical gap between cities' abilities to reduce mobility. Formal commercial/industrial employment centers (overrepresented in larger cities) have more capacity to shut down as per government directives to limit disease spread, while informal work is much more likely to carry on as usual.

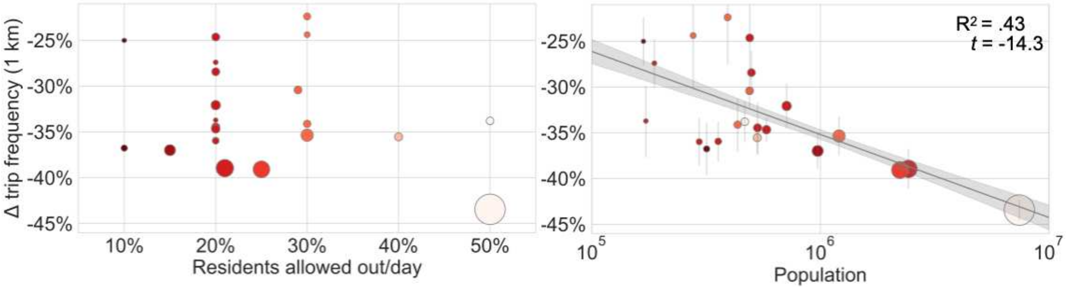

Figure 1: Municipality-level mean change in daily frequency of 1 km trips for 22 principle cities in Colombia (shade corresponds to policy severity, with redder circle representing less residents allowed out/day; size corresponds to population).

Using classical and quantum computational mechanics to characterise elementary cellular automata

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Distinguishing between random and complex processes is typically a resource-intensive task that has been made possible with the use of computational mechanics. Under the umbrella of complexity science, computational mechanics provides a framework to construct provably minimal classical models of stochastic processes, whose memory requirement is known as the statistical complexity. The statistical complexity is indicative of the minimal amount of information that must be stored about the past of a process to replicate its future [1, 2, 3] or to put it in a different perspective, it highlights the degree of structure within a stochastic process captured by the classical model's internal states [4, 5].

The extension to the quantum regime offers a refinement to traditional classical models [6, 7, 8] as it can host the internal states (now quantum states) in a non-orthogonal manner. The analogue of statistical complexity, known as the quantum statistical memory, was shown to be robust to perturbations of the process and is hence a more stable measure of structure than the classical measure, which can change discontinuously under infinitesimal variations to a process' underlying probability distribution. However, since quantum models were designed with a direct dependence on the analogous minimal classical models, the quantum inference protocol was introduced to mitigate this reliance, hence negating dependence on classical inference algorithms [9]. The statistical complexity and quantum statistical memory indicate that random processes have (provably) zero complexity and complex processes have a (positive) non-zero complexity, allowing the distinguishing between random and complex processes.

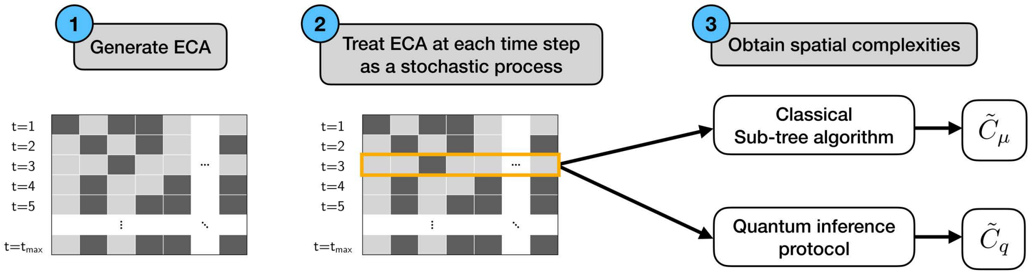

Figure 1: We extract the classical statistical complexity and quantum statistical memory of each time step of the ECA to better understand how structure changes with different rules.

Given the ability to distinguish between random and complex processes, we can now turn our attention to elementary cellular automata (ECA), which is a dynamical system capable of generating a a full diversity of behaviour that ranges from random to complex [10, 11].

In our work [12], we explore ECA through the lens of the sub-tree algorithm [1] and quantum inference protocol. Our results demonstrate that complexity measures can identify four well-established rules that reside in Wolfram's classes [13]. We then show that the line between random rules and complex rules is blurred when we use complexity measures to identify underlying structure in the ECA as not all random-looking rules have zero complexity but instead exist in a spectrum between pure random rules and pure complex rules. These rules were suggested to exhibit complex behaviour, in which our results affirm. Our results form a key step to resolve the difficulty in properly classifying ECA rules as many random-looking rules suggest varying degrees of presence of complex behaviour.

Inferring the Complexity of Quantum Causal Modelling

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Complex, stochastic processes underpin quantitative science. It is therefore of paramount importance to study and understand the behaviour of such processes for the crucial twin purposes of modelling and prediction. These tasks are typically resource-intensive, motivating the need for methods that ameliorate these requirements. A promising recent development to this end [1, 2], using a cross-disciplinary blend of tools from quantum and complexity science, has highlighted that quantum simulators can operate with much smaller memories than the minimal possible classical models [3, 4, 5], while providing equally accurate predictions.

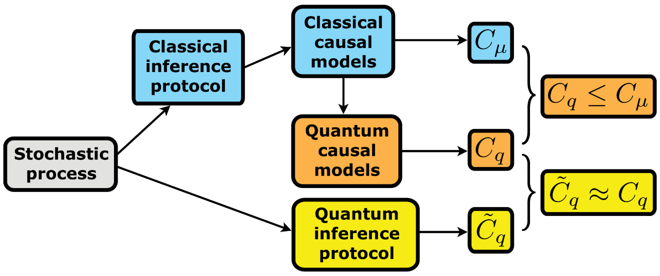

Figure 1: The quantum inference protocol negates the requirement of classical causal models to estimate $\tilde{C}_q$, the quantum statistical memory of a stochastic process.

The benefits of these quantum simulators are immediately apparent – we can use quantum technologies to construct simulators of complex stochastic processes that function with reduced memory requirements relative to optimal counterparts. Within complexity science, the minimal amount of information that must be stored about the past of a process to replicate its future is considered to be a measure of structure in the process, called the *statistical complexity* [3, 4, 5]. Presently, these efficient quantum models are designed with prior knowledge of the minimal classical model, necessitating the use of classical model inference algorithms when applied to real data.

In this work [6], we show that the quantum analogue of statistical complexity is robust to perturbations of the process, and is hence a more stable measure of structure than the classical measure, which can change discontinuously under infinitesimal variations to a process' underlying probability distribution. This allows us to introduce the quantum inference protocol for estimating the quantum measure of structure in a stochastic process directing from a time-series formed from observations of the process. Our protocol can be used to both blindly infer efficient quantum models of a given pattern or time series, and bounds on the associated structural complexity. We also show that our protocol is robust to statistical imperfections arising from finite data as it avoids inheriting errors introduced by classical inference algorithms that are associated with a non-smoothly-varying classical statistical complexity. Our results form a key step in the application of this emerging field to world world systems using quantum technologies.

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Complex dynamics emerge from disorder in neuromorphic nanowire networks

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The human brain provides a prototype for how diverse collective dynamics and functionality can emerge from a complex network of relatively simple, non-linearly interacting components [1]. Neuromorphic networks formed by self-assembly of polymer-coated inorganic nanowires (Figure 1) mimic these ingredients, with the non-linear switching of nanoscale junctions coupled by a disordered, recurrent network topology [2]. Experimental conductance time-series unveiled rich electrical switching dynamics and a phase transition between a low-conducting quiescent and highly-conducting active state. Near this phase transition, networks were found to exhibit cascades of activity with power-law distributed sizes and life-times. These scale-free avalanches are consistent with criticality, mirroring statistics of neural activity [1]. A physically motivated junction model, on a nanowire network topology, reproduced these features under constant stimuli. Even richer behaviour was found under periodic driving signals, with a controllable transition between periodic and chaotic dynamics. The role of network heterogeneity on dynamics was investigated by performing simulations on a randomly diluted lattice topology, with bond probability reduced towards the percolation threshold. In the ordered limit (regular lattice) the scale-free property of avalanches disappeared and irrespective of stimuli, only stable dynamical attractors were observed. As network disorder increased, the range of possible dynamical behaviours was maximised and the onset of critical-like, power-law distributed avalanches was observed. This suggests that the complex network structure may be crucial to the observed emergent collective dynamics of neuromorphic nanowire networks experimentally. These results may be utilised to optimise dynamics of nanowire networks for information processing applications in neuro-inspired frameworks, such as reservoir computing.

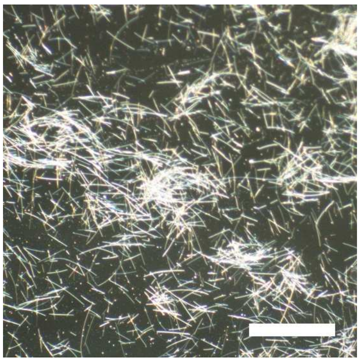

Figure 1: Optical microscope image of disordered Ag nanowire network (Scale bar: 50μm)

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Hierarchies of importance estimates in temporal network epidemiology

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Temporal network epidemiology is a theory for the effects of structures in both the timing and network of contacts. A key question in the field is how to identify influential individuals for disease dynamics. One rationale starts from the observation that influential individuals can infect many others and easily get infected themselves. Let D_i be the expected number of nodes that has i as an ancestor in an outbreak. Let U_i be the probability i gets infected at all. Then D_iU_i is a natural universal importance measure, and D_i and U_i are informative quantities per se.

Analogous to the centralities for static networks, we can gain understanding by constructing approximate measures of D_i and U_i that are intuitively related to the network structure. Two quantities that are seemingly good predictors of D_i and U_i are the downward and upward reachabilities d_i and u_i. These are defined as the expected number of nodes connected by (forward or backward) time-respecting paths.

We study the relations among D_i, U_i, d_i, and u_i for over 100 empirical temporal networks. For D_i and U_i, we scan the entire parameter space of the susceptible-infectious-recovered (SIR) model of diseases that gives immunity upon recovery [1]. Remarkably, the correlations between D_i and d_i, and U_i and u_i, ranges from very high to slightly negative (Fig. 1). We will discuss the network-structural reasons for these failures of our intuition and the implications for practical identifications of influential individuals.

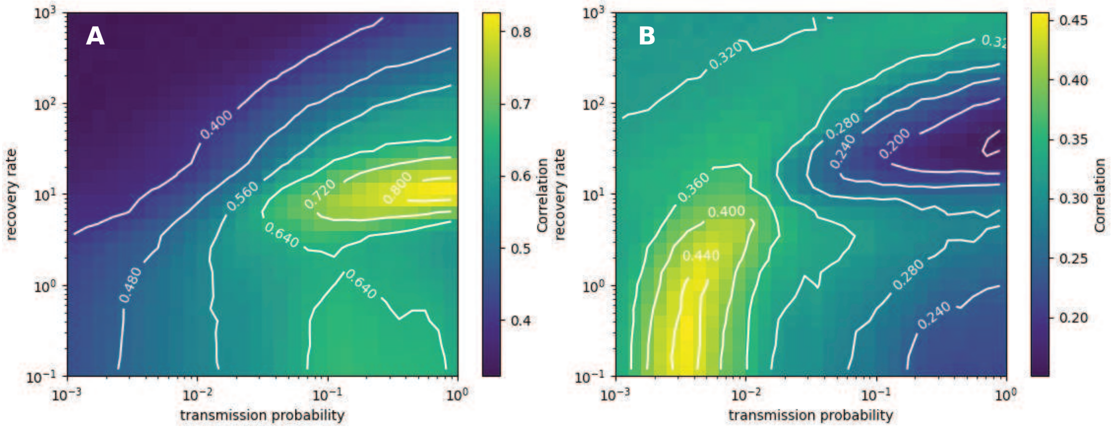

Figure 1: The Kendall correlation coefficient of U_i and u_i (A) and D_i and d_i (B). We calculate U_i and D_i for the SIR model over 10^6 averages per parameter value. The data represents human proximity in a hospital [2].

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Additive noise changes the dynamic topology of neuronal networks

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The brain is a complex system with a diverse hierarchy of spatial and temporal scales. Single neurons at a spatial scale of tens of micrometers interact with each other building a mesoscopic self-organised entity at a spatial scale of few millimetres. This entity is called neuronal patch, neural column in the cortex or just neural population. Moreover, single neurons evolve at various temporal scales, ranging from few milliseconds to hundreds of milliseconds and the mesoscopic neural population evolves on a slower range of time scale between 20 milliseconds and 1 second.

The diverse temporal scales of mesoscopic population activity can be observed experimentally in electroencephalographic data (EEG) measured as voltages on the scalp. Their corresponding power spectrum reflects well the different neural time scales and reveals the neural state of the cortex. In general anaesthesia, the EEG power spectrum accompanies the state of consciousness (i.e. the ability to respond to external stimuli) of the subject during surgery. For instance, in human surgery, increasing the concentration of the anaesthetic drug propofol changes the power spectrum characteristically and allows to detect the concentration at which the subject loses consciousness (i.e. the subject is not able to respond to external commands anymore).

The presented talk shows, in the first part, a system a of stochastic delayed ordinary differential equations, that describes the neural activity of the network of cortex and the thalamus in mammalian brain[1]. The system is driven by external white noise that represents input from brainstem structures. Numerical simulations show that decreasing the noise level describes well experimental EEG data observed during surgery and the decreasing noise level induces a breakdown of functional connectivity in the model. The results indicate that loss of consciousness is strongly correlated to denoising the brain and its functional fragmentation. In a second part of the talk, analytical results are shown that describe how additive noise induces system changes in networks [2].

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Mass Cycling in Weighted Real-World Food Webs and Economic Networks.

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We analyse the cycling of mass in over 200 real-world aquatic weighted food webs, that quantify feeding relationships between groups of species. The majority of matter cycling described through Finn Cycling Index (FCI) can be traced back to microorganisms that assimilate dead organic matter. This microbial loop recycles a significant fraction of primary production. We show how the very skew distribution of FCI at the network level originates from approximately lognormal distributions of distinct groups of nodes.

We use multiple regression to explain the node values of FCI. The indirect effects of detrital nodes, trophic level and bilateral reciprocity of flows around the node in question play significant roles. Imports and respirations relative to the total system throughflow complement reciprocity in predicting the value of FCI of whole food webs.

We compare the cycling of mass in ecosystems and economic networks. Mass cycling in food webs with 5% geometric mean is larger than 1.7% mass cycling achieved in 2011 by the world (EXIOBASE). We study the cycling at country level in a number of mass and embodied emissions networks.

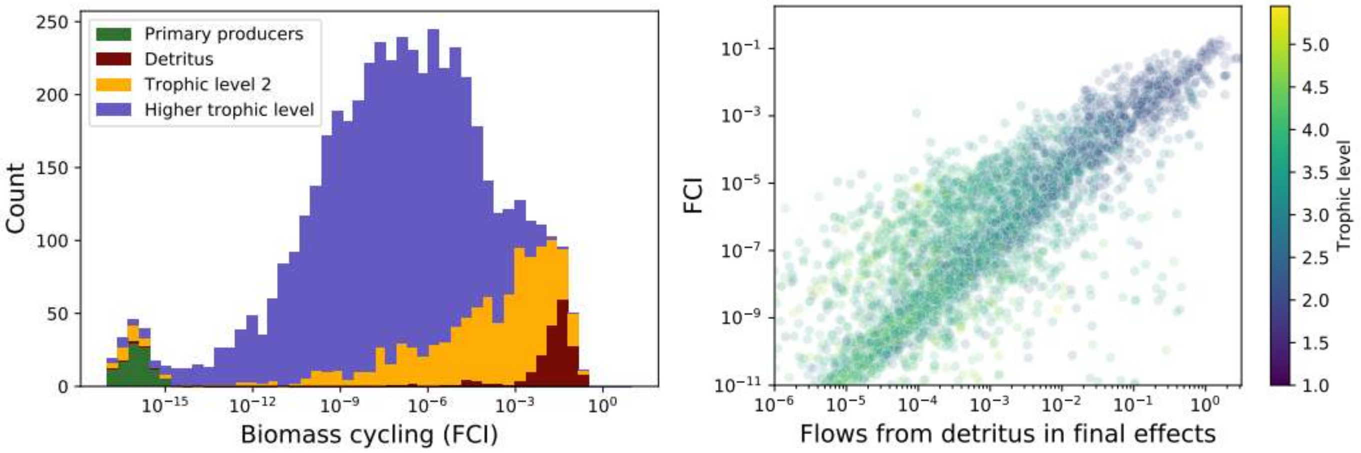

Figure 1: Value of biomass cycling measured through Finn Cycling Index for individual nodes in food webs dataset.

Left: histogram of node FCI values of primary producers (green), detritus (red), nodes at trophic level 2 to 2.5 (yellow) and higher trophic levels (blue).

Right: Node FCI values presented against sums of final effects between the given node and detrital nodes. Colours represent node trophic level.

Phase transitions in systems with quenched and annealed randomness: Nonlinear q-voter model analysis

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We compare two versions of the nonlinear q-voter model: the original one [1], with annealed randomness, and the modified one, with quenched randomness [2]. In the original model, each voter changes its opinion with a certain probability ε if the group of influence is not unanimous. In contrast, the modified version introduces two types of voters that act in a deterministic way in case of disagreement in the influence group: the fraction ε of voters always change their current opinion, whereas the rest of them always maintain it. Although both concepts of randomness lead to the same average number of opinion changes in the system on the microscopic level, they cause qualitatively distinct results on the macroscopic level. We focus on the mean-field description of these models. Our approach relies on the stability analysis by the linearization technique developed within dynamical system theory. This approach allows us to derive complete, exact phase diagrams for both models. The results obtained in this study indicate that quenched randomness promotes continuous phase transitions to a greater extent, whereas annealed randomness favors discontinuous ones. The quenched model also creates combinations of continuous and discontinuous phase transitions unobserved in the annealed model, in which the up-down symmetry may be spontaneously broken inside, see Fig. 1(a), or outside the hysteresis loop, see Fig. 1(b). The analytical results are confirmed by Monte Carlo simulations carried out on a complete graph.

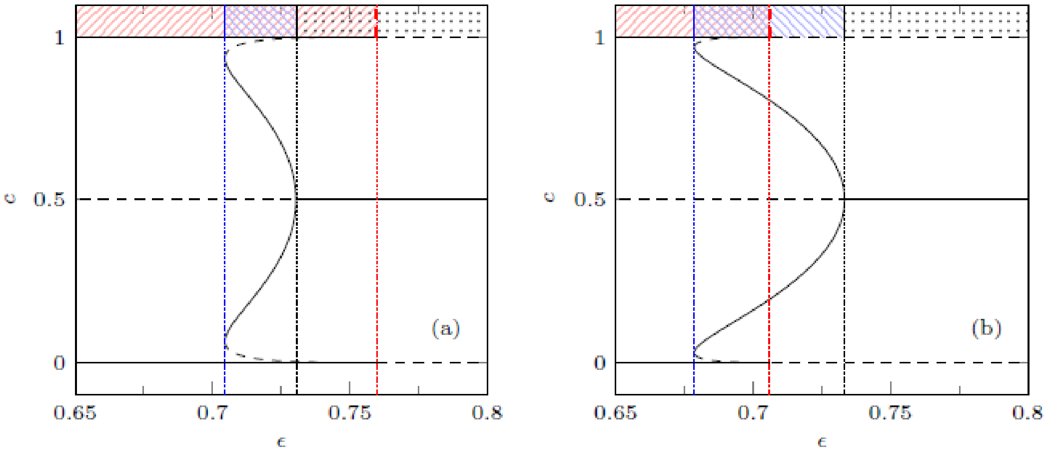

Figure 1: Schematic phase diagrams of the nonlinear q-voter model under the quenched approach for two different values of the influence group size q. The concentration of voters with one of two possible opinions is denoted by c, whereas the control parameter by ε.

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Complexity in the Military Domain: An Analytical Framework for Modeling Complex Tactical Decisions

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This presentation describes a recent study that explored the possibilities of using automated decision aids leveraging artificial intelligence (AI) to support human warfighters making weapons engagement decisions during complex tactical operations. The research applied a mission engineering approach with model-based system engineering foundations to develop an analytical framework for evaluating the use of automation for the different functions within the tactical kill chain. The framework provides a method to evaluate the risk involved in automating particular tactical decisions while addressing the decision timeline which is dictated by the threat complexity. A naval air and missile defense use case was used to demonstrate the framework and assess the automation needs for kill chain decisions according to threat complexity.

As current trends in naval warfare shift towards automated combat weapon systems, the U.S. Navy is focusing its strategies towards AI capabilities that reduce the time a warfighter needs to act decisively. Complex tactical situations require automated decision aids to support battle management as warfighters become overwhelmed with shorter decision cycles, greater amounts of data, and more technology systems to manage. To date, much emphasis has focused on data acquisition, data fusion, and data analytics for gaining situational awareness of the battlespace. However, a new frontier and opportunity exists for using this data to develop decision options and to predict the consequences of a military course of action.

This research studied the naval air and missile defense mission as a use case and produced systems engineering models of the tactical kill chain to establish system, functional, and operational foundations for the study. The project developed a conceptual architecture that could be modified to study different human-machine teaming arrangements by varying levels of automation for each key decision within the kill chain. The project developed methods for evaluating the risk associated with automating the different kill chain decisions and for determining the decision timeline based on threat complexity. The objective was to study and demonstrate how increased levels of automation can expedite the kill chain, providing a tactical advantage in air and missile defense.

The research performed a modeling and simulation (M&S) analysis to compare the naval air and missile defense kill chain at low levels of automation ("without" AI) with the kill chain at high levels of automation ("with" AI), by assessing improvements based on time. Three threat use cases were modeled—representing a low stress scenario (with a long decision timeline), a moderate stress scenario (with a medium decision timeline), and a high stress scenario (with a very short decision timeline). The M&S results revealed the need to develop an agile decision system architecture that can respond to the operational mission's threat complexity, allowing different levels of automation to be implemented based on the threat situation.

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CCS2020 – Submission for oral presentation

Hypernetworks and the Science of Design

Abstract

Herbert Simon called design a science of the artificial. The person that designs a completely new system is the first scientists of that system because before a system exists there can be no observations of its behaviour and no empirical data about it. The focus in this presentation is on the design and management of social systems and socio-technical systems. An essential feature of design is assembling parts to make wholes. The list of parts before assembly can be represented by a simplex. Simplices can have many vertices and have a geometric realisation in multidimensional space: <a> is a vertex, <a,b> an edge or line, <a,b,c> a triangle, <a,b,c,d> an tetrahedron, and so on. A simplex with an assembly relation is a hypersimplex. A collection of hypersimplices is a hypernetwork. Hypernetworks generalise networks. They include but are not restricted to diadic relations, enabling multiadic relations to be represented as the support for the multilevel multidimensional dynamics of complex social and technical systems. Design is a process to build new systems satisfying changing requirements and constraints. Problems and solutions coevolve. The representation of designed system grows as more information and detail are added, and as vague generations are instantiated by parts and subsystems that are fully described. Design -the creation of artifical system - will be presented as a proven problem-solving methodology in the application of complex systems science. It will be shown that hypernetworks are necessary to support the design of complex multilevel social and socio-technical systems.

Keywords

Design
Complexity
Multilevel Systems
Social Systems
Socio-technical Systems
Simplices
Hypersimplicies
Hypernetworks

Leverage points in the financial sector for seafood sustainability

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Can finance contribute to seafood sustainability? This is an increasingly relevant question given the projected growth of seafood markets and the magnitude of social and environmental challenges associated with seafood production. As more capital enters the seafood industry, it becomes crucial that investments steer the sector toward improved sustainability, as opposed to fueling unsustainable working conditions and overexploitation of resources. Using a mixed-methods approach that combined content analysis, qualitative examples and shareholder network analysis, we mapped where different financial mechanisms are most salient along a seafood firm's development trajectory and identified three leverage points that could redirect capital toward more sustainable practices: loan covenants, stock exchange listing rules, and shareholder activism. We argue that seafood sustainability requirements need to be integrated into traditional financial services and propose key future avenues for academic, policy, and practice communities. While our study focuses on the role of finance in seafood, the insights developed are of high relevance and applicable to other sectors as well.

The Blue Acceleration: The Trajectory of Human Expansion into the Ocean

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Does humanity's future lie in the ocean? As demand for resources continues to grow and land-based sources decline, expectations for the ocean as an engine of human development are increasing. Claiming marine resources and space is not new to humanity, but the extent, intensity, and diversity of today's aspirations are unprecedented. We describe this as the Blue Acceleration – a race among diverse and often competing interests for ocean food, material, and space, with a sharp acceleration characterising the onset of the 21st century. We use case descriptions to explore how this new reality manifests and what it entails for the emergence of new challenges and interconnected risks. We argue that, in an increasingly connected world, limits to the Blue Acceleration may be set by emerging systemic risks rather than predictable finite limits of ocean resources. We discuss current ocean governance processes and point out the mismatches between the rate of change in ocean claims and the slow pace at which new policy is being developed. With the UN Decade of Ocean Science for Sustainable Development about to begin, we conclude by highlighting future pathways to promote a sustainable and equitable ocean economy, with a focus on the beneficiaries and financiers of this Blue Acceleration.

Analysis of the ethnicity network using surname data

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Various ethnic and racial features are needed for understanding social phenomena and biological problems. However, there are costal and methodological limitations in classifying and analyzing ethnicity and race in modern society. In this study, we would like to address the method of how to extract ethnic data using surname data and the examples applied analysis.

We use the ORBIS 2016 dataset, which includes surname-nationality data of company executives and individual shareholders of 35 million cases in 203 countries. With this dataset, we build a surname-nationality classifier [1] using a Recurrent Neural Network. And to classify surname-ethnicity by defining a country with language culture and racially unique characteristics as the origin of the ethnicity [2].

With this classifier, we interpret each social phenomenon as the perspective of ethnicity. The results of classifying and extracting ethnic network [1] using our classifier and mapping them to African maps are the same as Figure1. And we visualize European countries' spatial ethnic distribution in a similar way [2]. We also apply it to interpret international trading between countries. And we will show the captured evidence that the ethnic network was activated in events such as the U.S.-China trade war.

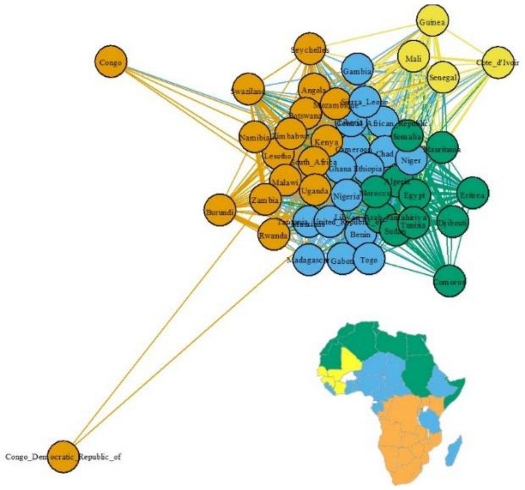

Figure 1: Ethnic Network in Africa extracted using the surname-ethnicity classifier

Our study presents a way to extract and interpret ethnic network in social phenomena using a large-scale of surname data and machine learning. We expect that this method can be applied in various fields that require information about ethnicity.

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Cardiac Dynamics from ECG: A Multiplex Recurrence Networks approach

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The Electrocardiogram (ECG) is a record of the electrical activity of the heart which serves as the first step in diagnosis of a cardiac abnormality. To detect and associate specific features linked to diseases is the thrust of research, aimed at the development of automated diagnostic tools. However, most of the existing studies use single-lead ECG data (from a single electrode), and focus only on diseases such as Arrhythmias and Chronic Heart Failure. The attempts to analyze full 12-lead ECG have been few, because of the short duration of data (few minutes) and lack of extensive training data that Machine Learning approaches require. Moreover, these approaches reveal little to no information of how a disease actually affects dynamics of the cardiac system. Based on Dynamical systems theory, studies on the nature and extent of chaos in cardiac systems already exist, and we use that insight to construct Multiplex Recurrence Networks (MRNs) from multi-lead ECG. These MRNs highlight spatio-temporal features of the cardiac dynamics which are quantified using layer similarity/dissimilarity measures in addition to the standard complex network measures. Based on the analysis of patient data from Bundle Branch Block, Dysrhythmia, Myocardial Infarction and Cardiomyopathy, we show that the cardiac dynamics manifests abnormalities in a multitude of ways that can be understood best with a set of measures that quantify different levels of structural complexity in the MRN. These results can lead to better classification and diagnosis algorithms that outperform existing ones. Since the framework developed can be used for any multivariate data, it may find applications outside of physiological data analysis.

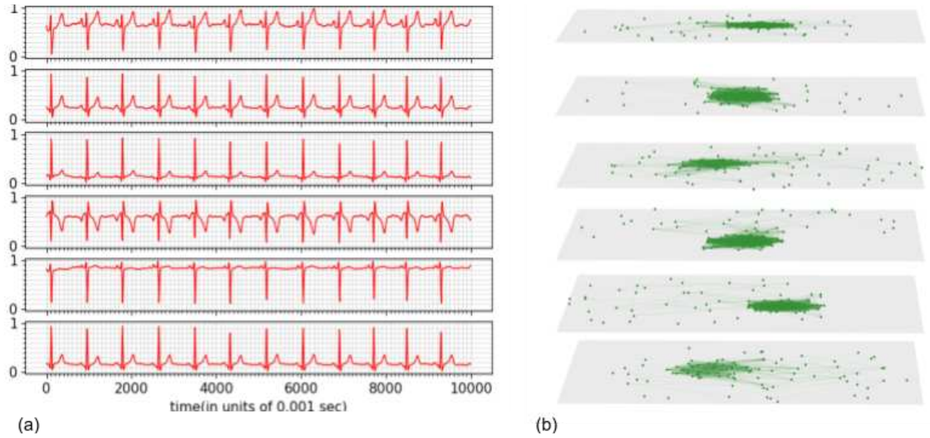

Figure 1: (a) Six-lead ECG data, and (b) corresponding Multiplex Recurrence Networks, for a healthy person. Nodes on the MRN are points in time and links among them are established based on their proximity in embedded phase space.

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Explosive synchronization in multilayer dynamically dissimilar networks

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The phenomenon of explosive synchronization, which originates from hypersensitivity to small change in coupling strength caused by some form of frustration prevailed in various physical and biological systems, has been shown to lead events of cascading failure of the power grid to chronic pain or epileptic seizure in the brain. Furthermore, networks provide a powerful model to understand and predict the properties of a diverse range of real-world complex systems. Recently, a multilayer network has been realized as a better suited framework for the representation of complex systems having multiple types of interactions among the same set of constituents. This article shows that by tuning the properties of one layer (network) of a multilayer network, one can regulate the dynamical behavior of another layer (network). By taking an example of a multiplex network comprising two different types of networked Kuramoto oscillators representing two different layers, this article attempts to provide a glimpse of opportunities and emerging phenomena multiplexing can induce which is otherwise not possible for a network in isolation. Here we consider explosive synchronization to demonstrate the potential of multilayer networks framework. To the end, we discuss several possible extensions of the model considered here by incorporating real-world properties.

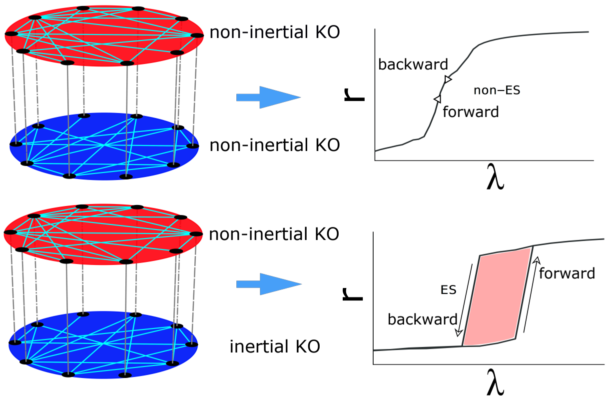

Figure 1: Schematic representation of a multiplex network whose two layers follow the same dynamics, namely, non-inertial Kuramoto Oscillators (KO) and take up continuous route to achieve synchronous state. However, in other case when the dynamics follows non-inertial KO in one layer and inertial KO in other layer, both the layers then prompt to ES.

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Parallel Implementation of Networks Properties Revealed from Matrix Functions

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Abstract: Networks are all around us and their properties are studied through their associated matrices: the adjacency matrix, the graph Laplacian. Both matrices have been well studied from an algebraic point of view, but when it comes to real network, the matrix dimensions increase extremely, which leads to think about faster processing. A useful notation in the analysis of complex networks based on spectral analysis is the communicability between nodes, temporal communicability and in general the overall communicability of the network, which are expressed as the exponential of the adjacency matrix and its invariants. There exist a lot of method for the calculating the exponential of a matrix, and one of the bests is *scaling and squaring* [Higham, 2005]. In this presentation we will use a computational strategy proposed by Benzi & Simoncini [2017], in the evaluation of the exponential of the matrix, which is based in the Kronecker product, which is more appropriate for large dimensions. The numerical tests for real networks (social networks, communication networks and genetic networks) with matrix dimensions, which vary from thousands to millions, are performed in shared memory environment using OpenMP C++ and are compared with Matlab R2011b and R codes.

Acknowledgements

The numerical tests are performed in the shared memory environment using OpenMP C++ in an AMD 32 core computer at the Institute for Mathematics and Scientific Computing at the University of Graz.

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Directed Networks in Hyperbolic Space

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Many experimentally observed undirected networks have small diameter, large clustering coefficient and power-law degree distributions. Random geometric graphs in hyperbolic space have similar properties [1,2] and thus are well suited for modeling of experimentally observed datasets. Until now, only undirected graphs have been considered within this hyperbolic framework, while there exist many practically important examples of networks with similar topological properties for which the directionality of connections is crucial. Among possible examples are networks of free associations of English [3] and Russian languages, i.e. networks in which nodes are words, and the role of connections is played by associations between them, measured experimentally by interviewing native speakers. This motivates us to study directed geometric graphs in hyperbolic space in search for possible simple models with properties similar to those observed in experimental directed networks.

We discuss several approaches to generating such stochastic directed networks, starting with a naive approach directly generalizing the results of the paper [2], however it does not explain the bidirectional connections observed in real networks.

An alternative approach is to study nearest neighbour network on a hyperbolic disk, which is constructed as follows. Distribute points on a disk at random with a given density, and then connect each point to its m nearest neighbors. We study topological properties of these networks in the limit of large disk size as a function of density of points and parameter m. It turns out that for all densities and large enough size of the disk, the networks have a distinct shell-core structure: in the core of the network (i.e., far from the boundary of the disk) the network is reminiscent of a random geometrical graph in Euclidean space, with Poissonian distribution of the in-degree of nodes. In turn, at the periphery (in the shell) in-degree strongly (exponentially) depends on the spatial coordinate of the node in a way similar to the behavior of undirected graphs studied in [1,2]. Moreover, the ratio of the sizes of the core and the shell strongly depends on the density of the points, so that there is a sharp crossover between core-dominated regime at low densities and shell-dominated regime at high densities. In the shell-dominated regime, all the typical properties of the undirected random geometrical graphs (power law degree distribution, logarithmically low density, and large clustering coefficient) are recovered.

Acknowledgements

The authors are grateful to D. Krioukov, P. van der Hoorn, and S. Nechaev for many fruitful discussions. This work is supported by RFBR grant 18-29-03167.

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Forestation to Mitigate Climate Change: Impacts on Regional Employment Distribution--Picking Winners and Losers

***M. Kaufman*[1]**, *S. Kaufman*[1] *& M. Salling*[1]

Complex social-ecological systems shift constantly in response to individuals, organizations, and government decisions. Policy makers need to anticipate system-wide consequences to both targeted and non-targeted system components, to avoid costly or irreversible mistakes. However, complex joint outcomes of individual and collective decisions are difficult to predict. Scenarios can help anticipate system-wide responses to specific interventions. We illustrate their use with a policy to set aside land for forestation in an economic region, to mitigate climate change. Does this policy affect the number of jobs at locations losing development space?

We use a dynamic model with 4 nonlinearly estimated parameters to anticipate regional distribution of jobs in time, using publicly accessible data. With Northeast Ohio (NEO) and Dallas-Fort Worth (DWF) 2001-2015 data (Kaufman et al. *Applied Network Science* 4(1) (2019) 1-17), by 2015 the actual-predicted correlations were .98 (NEO) and .99 (DWF) for municipal job shares of the regional total. Here we consider removing land from access to development to plant trees Northeast Ohio. Forestation requires specific locations (Matthews et al. *Landscape ecology*, *29*(2) (2014) 213-228): at the edge of existing forests trees grow faster and reduce fragmentation, enhancing ecosystem diversity. We identified NEO forests to which trees can be added, and forest-adjacent vacant commercial/industrial land, some of which would likely be redeveloped with industrial uses. NEO commercial/industrial acreage and respective number of jobs per locality are similar ($r=0.93$, $p<0.01$), so land "lost" to forestation is roughly directly proportional to jobs lost. Let $AF_{t,x}$ be the forested area of locality x at time t. Then the difference $af_{t,x}$ between the forestation area and the regional mean is $af_{t,x} = \frac{AF_{t,x}}{\sum_y AF_{t,y}} - \frac{1}{N}$, where N is number of localities in the region. The fraction of jobs $n_{t,x}$ changes by $-af_{t,x}$. Thus as a locality's forestation area goes above the regional mean, its jobs share declines. The dynamic equation for how employment redistributes in the region from t to t+1 is $n_{t+1,x} - n_{t,x} = \left(P_{t,x} - \bar{P}_t\right)n_{t,x} - af_{t,x}$, where $P_{t,x}$ is the market potential at x, at time t: $P_{t,x} = \sum_y q_{x,y} n_{t,y}$ and q is matrix of inter-localities interactions. We estimate model parameters with 2012-2013 data. In 2014 we withdraw vacant commercial/industrial land and anticipate NEO jobs location for 2014-2040. We illustrate results at 3 localities. Solon—thriving outer suburb—gets forestation above the regional average. Shaker Heights—quasi-dormitory inner-suburb—gets below-average forestation. We compare employment predictions for the forestation scenario (blue line, Figure 1) to "no action" (red line). Solon's regional share of jobs drops while Shaker Heights' share goes up, akin to packing urban centers and reducing urban sprawl—a positive outcome. However, jobs in 12% of other NEO small localities disappear, e.g. Cuyahoga Heights Village (Figure 2). Thus employment "winners" (e.g. Shaker Heights) and "losers" (Solon and Cuyahoga Heights Village). Our results can inform regional plans.

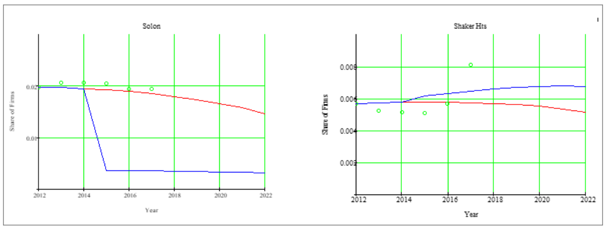

Figure 1: Employment, Solon & Shaker Heights

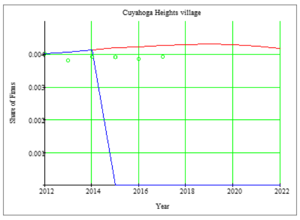

Figure 2: Employment, Cuyahoga Hts

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A study on the distribution tendency of everyday words on online social networks using stochastic processes

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In this study, how the comments change depending on the content and the number of reports in daily news media such as “weather information” and “traffic information” is influenced by news using mathematical models of social phenomena. We thought that it might be possible to consider whether it is due to nature or not. In this paper, we considered information that is easily referred to on OSN, such as “weather” and “traffic” in Japanese, and that is easily searched and refer- enced.The results in Fig. 1 are the results and parameters obtained by fitting the results on the bulletin board (Blog: 5ch) using the mathematical model (the model approximated by the mean field) also used in [1].

D is a probability of direct propagation, and P is a parameter of the prob- ability of propagation indirectly. Also, Cadv_T indicates the probability due to TV coverage time, and Cadv_n indicates the probability due to News. During this calculation period, the results were assumed to be abruptly mentioned after June 2019 and inferred that they were indirectly mentioned due to news. Using this method, we would like to discuss the diffusion of speech on online social media using parameters fitted to the diffusion process of information related to daily life by a model using a stochastic process.

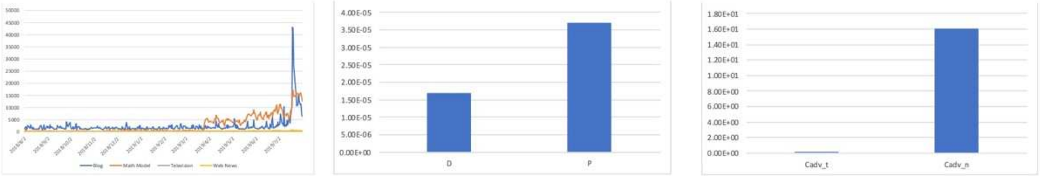

Figure 1: 2018/8-2019/7 : Number of mentions of `` weather " on the bulletin board (Blog: 5ch) in Japanese within 2018 / 8-2019 / 7 and Fitting Parameta Result

Acknowledgements

This research is also the result of a joint research project with Akira Ishii Laboratory, Faculty of Engineering, Tottori University (FY 2019). It also serves as a research outcome in the 2017~2019 Leading Initiative for Excellent Young Researchers (LEADER).

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Sentiment analysis for text information of major news media on online social networks

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In this research, YouTube was selected in the world due to restrictions on data acquisition of various media.

Various OSNs (Online Social Networks) are available for real-time video distri- bution. News media with one of the leading TV and newspaper media has published news frag- ments on YouTube. Another feature is that real-time distribution is performed. It was also hypothesized that the distribution of opinions in the news media in each country, the difference in coverage of the same news content, and the distribution of opinions on the difference in the us- ers who commented were possible. In this abstract, we will show the trend of news that Huff- post has played particularly many times. The left side in Fig. 1 has the highest number of views, but it is observed that there is little influence or negative opinion related to popular movie works, and there is an extremely positive opinion tendency. In the graph on the right, it was observed that opinions were extremely concentrated in neutral. Other major news media that gather large-scale comments are known to tend to be gathered positively or neutrally about information reminiscent of everyday life such as animals and children. In this paper, we will discuss various cases.

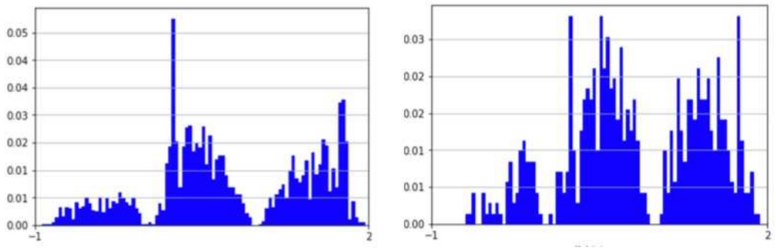

Figure 1: (Left Side) 21 Mini Elsas Star In An Epic Supercut Of 'Let It Go' Huffpost :Distribution of negative, positive and neutral comments (CDF) (Right Side) Little Boy Catches Fish with Toy Rod Huffpost :Distribution of negative, positive and neutral comments (CDF): Data acqui- sition period: Comments acquired from the video upload date to 2019/5/12

Acknowledgements

This research is also the result of a joint research project with Akira Ishii Laboratory, Faculty of Engineering, Tottori University (FY 2019). It also serves as a research outcome in the 2017~2019 Leading Initiative for Excellent Young Researchers (LEADER).

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Within-Subject Changes in Network Connectivity Occur During an Episode of Depression: Evidence from a Longitudinal Analysis of Social Media Posts

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Network theory of mental illness posits that causal interactions between symptoms give rise to mental health disorders. This is thought to occur because positive feedback loops between symptoms trigger cascades of further symptom activation. Increasing evidence suggests that depression network connectivity is therefore a risk factor for transitioning and sustaining a depressive state. However, much of the evidence comes from cross-sectional studies that estimate networks across groups, rather than within individuals. We used a novel method to construct personalised depression-relevant networks from social media data to test the hypothesis that network connectivity is linked to depression severity and increases during a depressive episode.

We analysed Twitter data from 946 participants who retrospectively reported the dates of any depressive episodes they experienced in the past 12 months and self-reported current depressive symptom severity. Daily Tweets were subjected to textual analysis, which allowed us to construct personalised, within-subject, depression networks, based on 9 a priori text features previously associated with depression severity. We tested for associations between network connectivity and current depression severity and, in participants who experienced a depressive episode in the past year, we tested if connectivity increased during the dates of a self-reported episode (N = 286).

Significant bivariate associations were found between current depression severity and 8/9 of the text features examined. In line with our hypothesis, individuals with greater depression severity had a significantly higher overall network connectivity between these features than those with lesser severity ($\beta = 0.008$, SE = 0.003, $p = 0.002$). Importantly, we observed within-subject changes in overall network connectivity associated with the dates of a self-reported depressive episode ($\beta = 0.03$, SE = 0.009, $p = 0.005$).

The connectivity within personalized depression networks changes dynamically with changes in current depression symptoms. Social media data provides a fruitful, albeit noisy, source of data to test key within-subject predictions of network theory.

Opinion dynamics as associative diffusion

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A central paradigm in modeling opinion dynamics is based on the notion of “information diffusion” - the idea that opinions spread like viruses through social networks, diffusing between individuals, communities, and countries. Empirical cases of opinion spread on social networks, such as diverging stances towards vaccines or climate change, cannot be fully explained by these social contagion processes alone. In a model proposed by Goldberg & Stein [1], agents observe each other’s behaviors, but this does not directly lead to simple or complex contagion. Instead, agents only increase their association between the behaviors observed. In this work, we extend the associative diffusion model of [1], designed for the spread of behavior specifically, to study the diffusion and distribution of opinions. Unlike behaviors, people might express negative opinions and these opinions can be negatively associated. In our updated model, we do not find the binary polarized structures observed by [1], but instead, we find various groups of individuals holding similar world views, expressed as the same association structures and matching opinions, see Fig. 1. Investigating the discrepancies between our findings and the model in [1] suggests that their binary polarized structure is largely a result of the assumptions and choices made in the implementation of the Goldberg & Stein model, for which, we argue, we offer a more suitable alternative. By offering a model of opinion dynamics that integrates a dimension of meaning, this research shows that the clustering of opinions may arise due to the emergence of bundled associations, a proxy for meaning or culture, and offers an explanation for the slow but ever-changing composition of opinions in society.

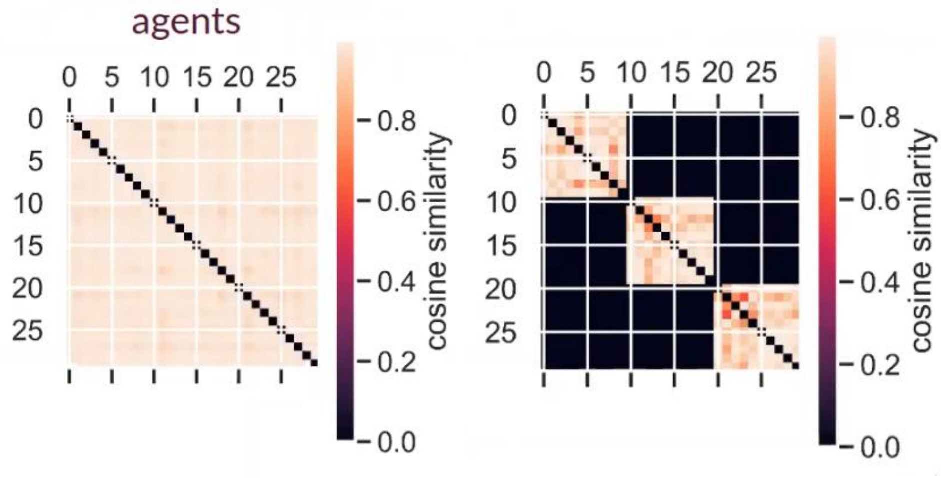

Figure 1: Number of clusters emerging from allowing different types of associations to form: (left) only positive associations as in [1] imply a single, large cluster, while (right) permitting both positive and negative associations lead to multiple (2-3) clusters forming

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Emergent social norms and their interaction with other means of behavioral control in complex and adaptive agent societies

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In agent societies, social norms emerge from interactions and sharing of information between members of a society [1]. Social norms play a crucial role in many contexts in which (human) agents interact and make decisions, such as politics or organizations. Topics of emergence and enforcement of such norms have been studied in various fields, e.g. multi-agent systems [2]. The economic literature has studied the interplay between exogenously defined social norms and incentive mechanisms, but has widely failed to properly address the emergence of social norms [3]. We follow this line of research and aim at (better) understanding how *social norms that emerge in agent societies* interact with other means to control behavior.

Based on the *NK*-framework [4], we set up a complex adaptive system that represents an agent society with multiple interacting entities working on a complex set of interdependent binary decision tasks. Agents operate on pairwise-correlated performance landscapes which together form the task environment of the agent society. Agents interact with their peers in social networks and share information about their past actions, which creates desirable behavioral patterns. We refer to these patterns as *emergent social norms* and model agents to include them in their decision rules. Along with complying to emergent social norms, agents aim at maximizing their performance-based incentives, and apply the approach of goal programming to balance the two objectives. In the proposed complex adaptive system, social norms are *recursive* in that they emerge from the agents' previous actions, and, once formed, can feed back to influence the further decision-making process of agents.

Our results suggest that emergent social norms tend to have an adverse effect on the system's performance, unless the agents are operating on highly correlated performance landscapes. If parameterized properly, incentive mechanisms can help to offset the potential performance loss: for agent societies facing highly (moderately) complex tasks, incentives based on team (individual) performance tend to lead to a higher system-level performance.

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Self-Healing Strategy for Improving Robustness in Limited Resource

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Many real networks have a common topological structure called scale-free (SF) which is vulnerable to malicious attacks [1]. Moreover, these complex systems are frequently exposed to nature and man-made disasters. To overcome the serious problems, resilience-based system design attracts much attention recently. In particular, the concept of resilience means not only to absorb disturbance but also to reconstruct a system with adaptive capacity [2]. Thus, we propose a self-healing method based on enhancing loops for improving robustness in reconstructing to be a better structure as distinct from SF instead of recovering. Because removing all loops make network into tree structure which is fragmented easily by any attacks [3]. Furthermore, enhancing loops is effective on constructing the optimally robust onion-like structure [4]. First, rings are created as the simplest loop to maintain the larger connectivity in limited resource of links. Then, loops are enhanced on the rings by adding remaining healing links between extended neighbors of damaged nodes in distributed local process. We assume that some links emanated from removed nodes can be reused for healing. For several systems such as air-traffic, power-grid and Internet, in comparison with the conventional method [5], the reconstructed network by our method obtains both higher robustness of connectivity and efficiency of paths with a better structure than original one (see Fig.1).

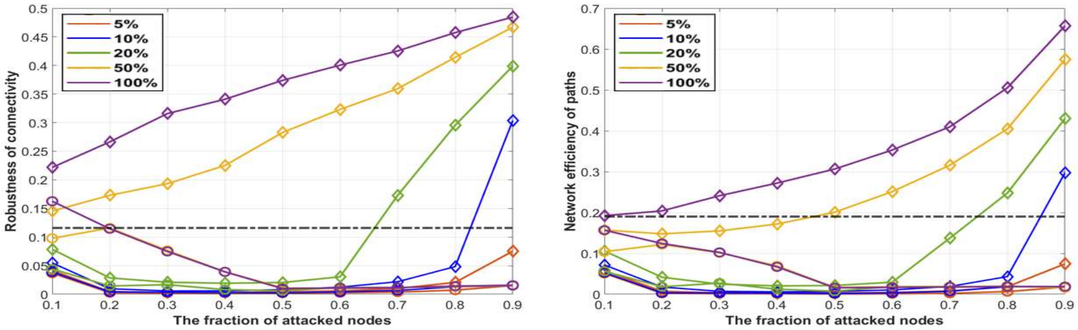

Figure 1: Result of our proposed (marked by diamond) and conventional (marked by circle) methods for air-traffic network. Colors are corresponded to 5~100% of reused links for healing. Black dot-dash line represents the result in the original network before attacks.

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This research is supported in part by JSPS KAKENHI Grant Number JP.17H01729.

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Win-Stay-Lose Shift as a Self-Confirming Equilibrium in the Iterated Prisoner's Dilemma

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Evolutionary game theory assumes that players are able to replicate a highly scored player's strategy through genetic inheritance, but in terms of learning, it is often difficult to recognize a strategy just by observing the behavior. In this work, we consider players with memory-one stochastic strategies in the iterated prisoner's dilemma, with an assumption that they cannot directly access each other's strategy but only observe the actual moves for a certain number of rounds. Based on the observation, the players have to infer the resident strategy in a Bayesian way and adjust their own strategies accordingly. By examining the best-response relations, we argue that players can escape from full defection into a cooperative equilibrium supported by Win-Stay-Lose-Shift, provided that the cost of cooperation is low and the observational learning supplies sufficiently large uncertainty.

Acknowledgements

This work was supported by Basic Science Research Program throughthe National Research Foundation of Korea (NRF) funded by the Ministryof Education (NRF-2020R1I1A2071670).

Teaching Recurrent Neural Networks to Modify Chaotic Memories by Example

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The ability to store and manipulate information is a hallmark of computational systems. Recent efforts have made progress in modeling the representation and recall of information in neural systems. However, precisely how neural systems learn to modify these representations remains far from understood. Here we drive a recurrent neural network (RNN) with examples of translated, linearly transformed, or pre-bifurcated time series from a chaotic Lorenz system, alongside an additional control signal c that changes value for each example. By training the network to replicate the Lorenz inputs, it learns to autonomously evolve about a Lorenz-shaped manifold, and to continuously interpolate and extrapolate the translation, transformation, and bifurcation of this representation far beyond the training data by changing the control signal. Finally, we provide a simple but powerful mechanism for how these computations are learned, enabling the principled study and precise design of RNNs.

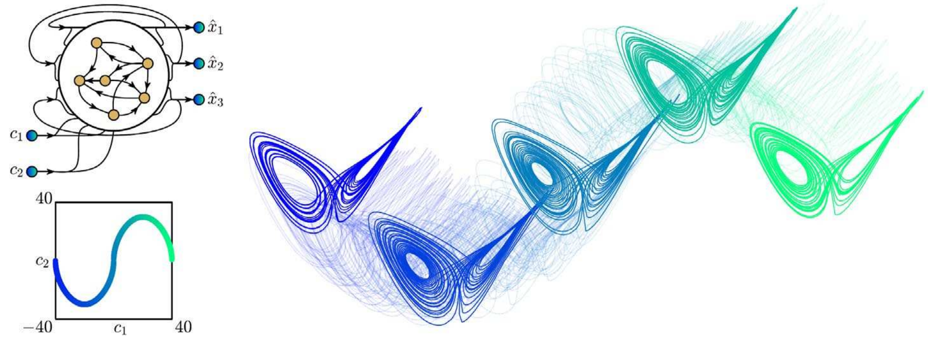

Figure 1: Flight of the Lorenz. A reservoir trained on Lorenz attractor inputs that are translated along the x_1 and x_3 directions evolves autonomously along a Lorenz-shaped chaotic attractor. We change the x_1 and x_3 position of its representation by changing the inputs c_1 and c_2, respectively.

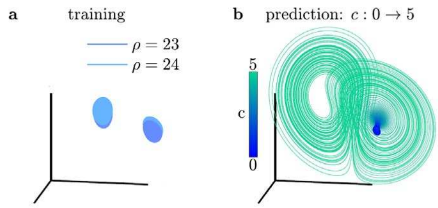

Figure 2: (a) Training data of the Lorenz system before bifurcation, that drive the reservoir when ρ=23 at c=0, and ρ=24 at c=2. (b) The reservoir accurately predicts the bifurcated Lorenz when c=5.

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MULTI-SCALE NETWORK RULE-BASED STOCHASTIC PROCESSES

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Abstract. In this article we combine the novel mathematical concept of a hierachical hypergraph with the idea of ruled-based stochastic processes. The hierachical hypergraph structural concept is immensely important when dealing with the mathematical abstraction of the idea of 'multi-scale composition' in general. Classical graphs as systems descriptions, and therefore also network theory, lack the ability to describe the structure of multi-scale systems. However, hierachical hypergraphs can describe such a system completely in a consistent way. A typical multi-scale description starts from the lowest level, the basic system components, like atoms in chemistry, or individuals in a sociological or epidemiological context. As upper levels in this hierachy, we can then define molecules, molecules of molecules (chemistry, biochemistry), or groups, and groups of groups (ecology, sociology, economy) etc. The hierachical hypergraph covers the static description of such a multi-scale complex system, but not the dynamical part, the time evolution. For the time evolution we define a process (both deterministic and stochastic) which is event-driven, and defined for each level of the hierachy. A typical such event structure are collision events, leading to classical reaction kinetics for chemical systems in case of a single level hierachy only. But we also consider deterministic updates, like a daily update of information, like stock prices, for example, or a mix of updates for different rules.

We discuss also some applications, mostly those related to novel models of the Covid-19 pandemic.

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Date: October 12, 2020.

The Emergence of the Inter-Organisational Adversarial Network in Strategic Patenting

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Much of the research on networks using patent data focuses on citations and the collaboration networks of inventors, hence regarding patents as a positive sign of invention. However, patenting is, most importantly, a strategic action used by companies to compete with each other. This study sheds light on inter-organisational adversarial relationships in patenting for the first time, with a specific focus on patent opposition. Patent opposition is a legal action that a company (or individual) can take to challenge the validity of a patent within a certain period (usually 6 – 9 months) after grant. If an opposition is 'successful', the opposed patent is revoked and cannot take effect in any of the signatories. Companies thus oppose patents owned by rival companies clearly intending to hinder their innovation activities.

We constructed and analysed the network of companies connected via patent opposition relationships that occurred between 1980 and 2018. The network comprises of 11,480 nodes (companies) and 26,433 directed edges (opposition relationships). We found that the network exhibits a heavy-tailed, power-law-like degree distribution and assortative mixing, making it an unusual type of topology compared to social networks with positive or negative relationships. We argue that adversarial (or rivalry) relationships are substantially different from positive or negative (e.g., dislike, conflict,…) relationships. A patent opposition occurs when the opposing company is aware of (and feel threatened by) the high value of a patent owned by the opponent company. Indeed, opposed patents tend to have a high citation counts, which is a widely used metric to capture the patent value. We identified a few triadic motifs in the opposition network (Figure 1), and further investigated how these patterns have emerged over time, by conducting a temporal network motif analysis [1], with patent co-ownership among the companies also considered. By regarding opposition as a negative relationship and co-ownership as a positive relationship, the results identified the 'structurally imbalanced' triadic motifs (in the context of the balance theory [2]) and the temporal patterns of the occurrence of triads formed by a mixture of these two types of relationships. Our findings indicate that the mechanisms of the emergence of the inter-organisational adversarial relationships may differ from those of other types of negative relationships hence necessitating further research.

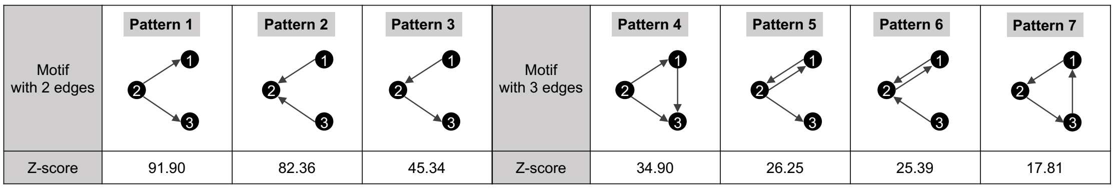

Figure 1: Triadic motifs identified in the opposition network

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Predicting Future Pairs of Acquirer and Acquiree Companies by Using Information of Companies' Relationships and Network Positions

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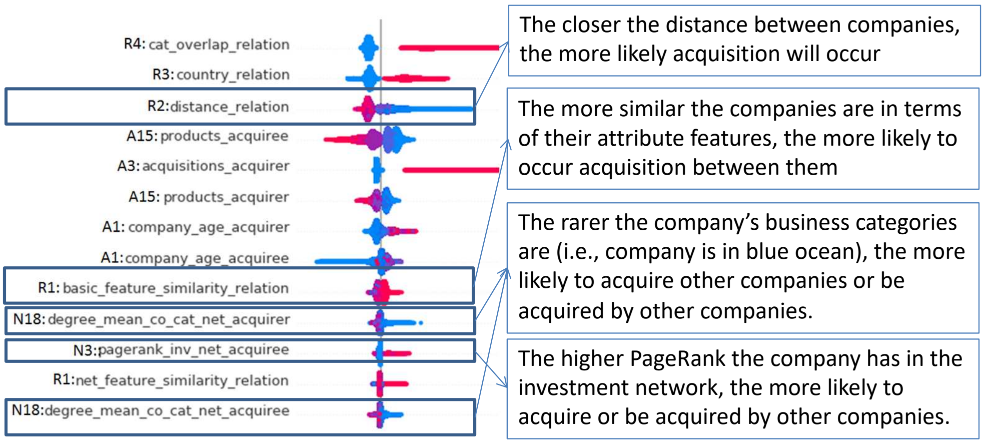
This study aims to realise the prediction of future inter-company acquisitions, and gain insights into the essential factors that contribute to the prediction. Existing models are to predict either acquirers or acquirees, but not both. Here, we constructed a classifier to predict the future pairs of acquire and acquiree companies. The major challenges lie in the following two issues. First, acquirees are often young and/or small start-ups with no good financial records to capture their values. Second, although companies usually consider several acquiree or acquirer candidates before actual acquisition, information of negative examples (i.e., the cases of the non-occurrence of acquisition), which is necessary for the classifier's learning, is not publicly available. To tackle these issues, we incorporated not only companies' attribute features (e.g., age, size,…), but also relational features (i.e., features representing the similarity and closeness between an acquirer and an acquiree) and network features (i.e., centrality scores (such as PageRank) of each company in the investment network). Furthermore, we generated negative examples by identifying companies that were similar to those found in positive examples. (Details are omitted here due to space constraints.)

We tested our model on the Crunchbase data [1] (2000 – 2018), and evaluated the results by applying the Shapley additive explanation (SHAP) [2]. Figure 1 shows the top 13 features that were identified as being highly influential to the prediction. In the figure, "R"s are relational, "A"s are attribute, and "N"s are network features. The results suggest that the similarity / closeness of companies and companies' positioning in their network are highly informative when predicting future acquisitions.



The closer the distance between companies, the more likely acquisition will occur

The more similar the companies are in terms of their attribute features, the more likely to occur acquisition between them

The rarer the company's business categories are (i.e., company is in blue ocean), the more likely to acquire other companies or be acquired by other companies.

The higher PageRank the company has in the investment network, the more likely to acquire or be acquired by other companies.

Figure 1: SHAP [1] value features for 2017 prediction model and interpretation of the results

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Policy and Innovation Spreading on the Global City Network

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Only a fast and global transformation towards decarbonization and sustainability can keep the Earth in a civilization-friendly state. Cities play an important role in this transformation: they are responsible for a dis-proportionally large part of greenhouse gas emissions, and simultaneously are one of the main drivers of sustainable policy innovation and adoption. Learning from each other to reduce, prepare for and react to the coming environmental changes, they can be conceptualized as nodes in a globe-spanning network. This network model may be approximated by the global air traffic network, political and trade relations, and other city-to-city connections. Such a learning network model may also yield insights into the social tipping dynamics that are so urgently needed to control the human impacts on the Earth System [1].

The aim of this study is identifying whether network-based transmission effects are dominant in sustainability policy adoption by by cities, and which networks have the highest prediction power for this spreading process. For this purpose, we analyze the spreading of several municipal policies and innovations related to sustainability transformations as contagion processes on such inter-city networks. We extract several networks, comprising different types of city interconnections, from empirical data. Examples investigated as spreading innovations are the implementation of Bus Rapid Transit public transport systems (see Figure 1), and membership in a sustainability organization. The spread of these urban technology and policy innovations are then investigated using a dose-response-contagion approach [2], combined with surrogate data methods [3].

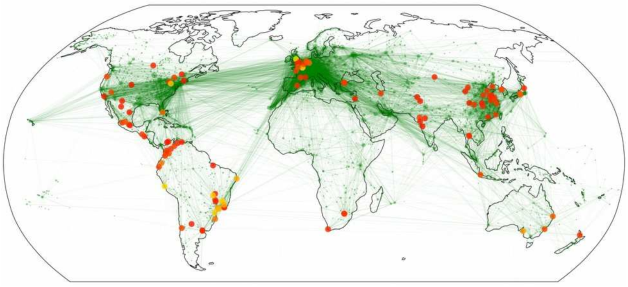

Figure 1: Spread of the Bus Rapid Transit System, from 1971 (yellow) to 2016 (red), superimposed with the global air route network (green).

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Design is not an Optimization Problem

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The process of designing a product is supposed to answer two questions: what solution should we pick for a particular product and why that is a good solution. We argue that approaching design as a mathematical optimization problem is misleading, particularly for design of complex systems. We propose an alternative, open-ended and cyclical approach in form of a Model-Compute-Learn loop. Across three Naval Engineering case studies this approach not only identifies the best solutions, but provides a comparison of robustness of these solutions and reveals the emergent physical mechanisms which drive the solution change. Thus we show how physics can inform and be informed by design problems.

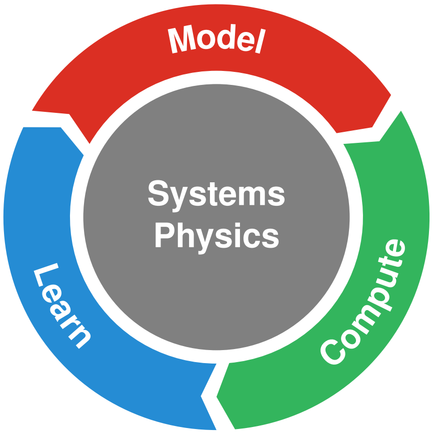

Figure 1: Systems Physics investigation consists of three stages: making mathematical modeling choices, performing computations, and learning from the computational results in order to refine the model on the next iteration.

Acknowledgements

This work was supported by the U.S. Office of Naval Research Grant Nos. N00014-17-1-2491

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Age contact matrix reconstruction from online and representative samples

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Social face to face interactions act as one of the most important routes of transmission during the current COVID-19 pandemic. Furthermore, social interactions mark the diffusion of infection throughout different segments of the population. Despite the importance of such data, currently the scientific community is in need of data collection methods that are privacy respecting, representative, while detailed enough to allow dynamical observations, even on an aggregated level. To answer this challenge, we coordinate a data collection campaign in Hungary aiming to follow the social mixing patterns of people in different age groups in real time during the pandemic. The Hungarian Data Provider Questionnaire (MASZK) [1] was released in late March 2020 during the initial phase of the COVID-19 outbreak in Hungary and it is an ongoing effort to anonymously collect age contact matrices of a voluntary population online. It has reached over the 2% of the population, moreover, it is accompanied with a nationally representative data collection via telephone survey on 1500 respondents each month.

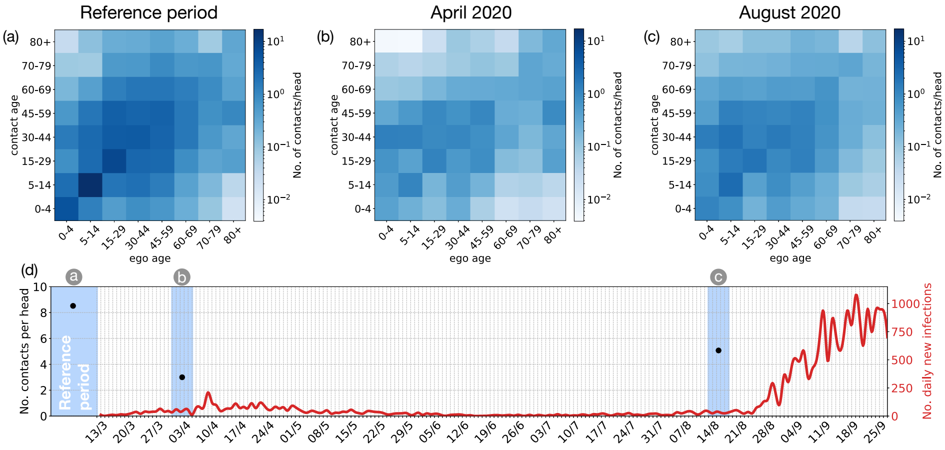

Figure 1: Age contact matrices recorded from representative telephone survey data for (a) the reference period (before 13th March 2020); for (b) early period of the COVID-19 pandemic; and (c) right before the second wave of the pandemic in Hungary. Panel (d) shows the evolution of the numberof daily infections in Hungary (red solid line) and the average number of contacts (black dots) during the observed periods (blue shaded rectangles).

Via the combination of these two matching datasets we provide a new methodology to dynamically reconstruct close-to-representative age contact matrices from the non-representative online samples using iterative proportional weighting along the most important dimensions affecting the contact pattern of people. This unique data collection and methodology could lead to an important step towards a more precise modeling of epidemic spreading, which could contribute to the reduction of the medical and economic burden of the actual pandemic.

Acknowledgements: The authors are very thankful for the COVID-19 development team lead by Vilmos Bilicki from the Department of Software Development at the University of Szeged [1]. This work was done in the framework of the Hungarian National Development, Research, and Innovation (NKFIH) Fund 2020-2.1.1-ED-2020-00003. JK was supported by the Premium Postdoctoral Grant of the Hungarian Academy of Sciences.

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Equation of state for pollution in aire

Atahualpa S. Kraemer, Abraham Nava Mireles

Around the world, millions of people die directly from air pollution each year. Understanding the behavior of pollutants with respect to environmental factors can help reduce this problem. In this work, the dependence of pollutant levels as a function of humidity was analyzed. A decrease in Ozone, SO_2, particles $PM_{2.5}$ and PM_{10}, was observed. Using the Langmuir adsorption model we were able to obtain an equation of state for the amount of pollutants as a function of humidity, pressure, and temperature. This oversimplified theoretical model seems to reproduce the trend curve reasonably well.

Seeking to be Influential in Network

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According to the concept of eigenvector centrality, a node is influential if it is connected with influential neighbors [1]. Hence a reasonable strategy of an actor in a social network is to make acquaintances with influential partners. The related process of social stratification is at the center of sociological research [2]. Here we report results of our new algorithm designed as to mimic the time evolution of a social network, where actors adopt this strategy. Additional condition is that the number of neighbors remains limited. The detailed algorithm and the results of the simulation are reported in [3]. Here we only mention main results. Three stages of the time evolution are identified. During the first stage, which is relatively short, agents increase their eigencentrality from an initial random state. At the end of this stage, a minority group of actors emerges which remain active during the second stage; inactive actors are blocked. This stage is much longer and it ends at an absorbing state, where some subset of the active group remain active forever and the time evolution is stopped. These three stages are shown in Fig. 1, where the fraction R of active agents is plotted as a function of time. Exemplary curves are shown for different initial fractions of active actors. The results of simulations indicate, that the character of the time evolution of the system does not depend in this initial fraction. Further, the final fraction of active agents in the last stage decreases with the system size. This result is consistent with old sociological theories, formulated without mathematical modeling [4]. There is also an analogy of our model results on first two stages of evolution with processes of formation of oligarchies, where after turbulent conflicts some group of actors seizes power [5].

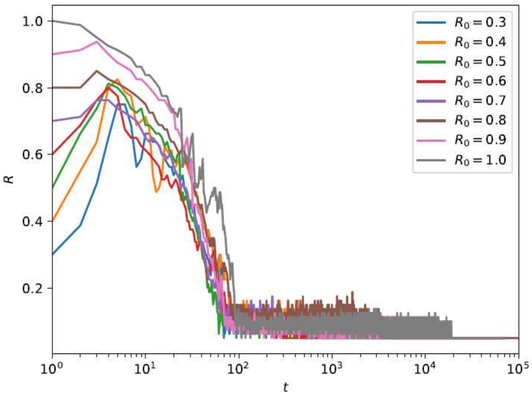

Figure 1: The fraction R of active actors vs time. A time step is an update of agents' state in a random order. These results are obtained for 80 nodes.

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Pleasing can solve the problem of disagreement for indirect reciprocity

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Indirect reciprocity is an important mechanism for promoting cooperation among self-interested agents. Simplified, it means you help me, therefore somebody else will help you (in contrast to direct reciprocity: you help me, therefore I will help you). Indirect reciprocity can be achieved via reputation and norms. Strategies relying on these principles can maintain high levels of cooperation and remain stable against invasion, even in the presence of errors. However, this is only the case if the reputation of an agent is modeled as a shared public opinion. If agents have private opinions and hence can disagree if somebody is good or bad, even rare errors can cause cooperation to break apart [1]. We study a solution for this private assessment problem, where agents act in accordance to others' expectations of their behavior (i.e. pleasing them) instead of being guided by their own, private assessment. As such, a pleasing agent can achieve better reputations than previously considered strategies when there is disagreement in the population. Our analysis shows that pleasing significantly improves stability as well as cooperativeness, especially for three well-known strategies standing (L1), stern judging (L6) and staying (L7) [2]. And pleasing is effective even if only the opinions of few other individuals are considered and when it bears additional costs.

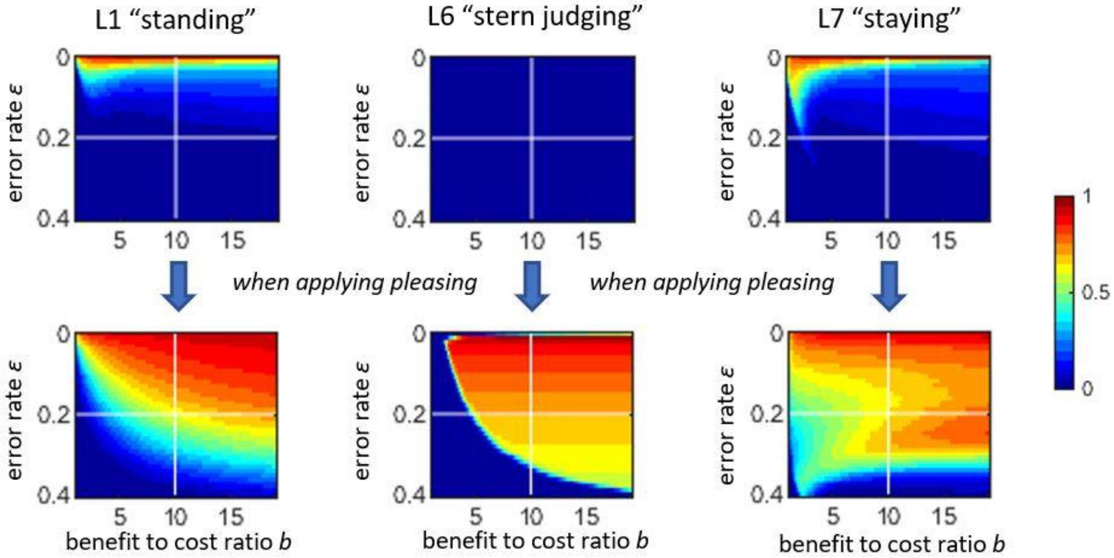

Figure 1: Abundance of cooperation under evolutionary pressure, for the three most successful strategies across error rates and benefit to cost ratios. Simulations with population size 50, iterations 10^6, observation probability 0.9

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On the relation between transversal and longitudinal scaling in cities

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Empirical evidence has been shown that some urban variables scale non-linearly with the city population size. More specifically, some socio-economic variables, such as the number of patents, wages and GDP, show a super-linear behaviour with the population of the city. On the other hand, infrastructure variables, such as the number of gas stations and length of streets, scale sub-linearly with the city population, generating a scale economy. However, does this scaling properties observed in a system of cities (transversal scaling) also work for individual cities in different stages of their growth process (longitudinal scaling)? The answer to this question has important policy implications, but the lack of suitable data has so far hindered rigorous empirical tests. The work that will be presented was developed looking at the evolution of two urban variables, GDP and water network length, for over 5500 cities in Brazil. It will be shown that longitudinal scaling exponents are city-specific, however they are distributed around an average value that approaches the transversal scaling exponent provided that the data is decomposed to eliminate external factors, and only for cities with a sufficiently high growth rate. This result adds complexity to the idea that the longitudinal dynamics is a micro-scaling version of the transversal dynamics of the entire urban system.

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Earth System Interactions Amplify Human Impacts on Planetary Boundaries

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The planetary boundary framework presents a 'planetary dashboard' of humanity's globally aggregated performance on a set of environmental issues that endanger the Earth system's capacity to support humanity. While this framework has been highly influential, a critical shortcoming for its application in sustainability governance is that it currently fails to represent how impacts related to one of the planetary boundaries affect the status of other planetary boundaries. Here, we surveyed and provisionally quantified interactions between the Earth system processes represented by the planetary boundaries and investigated their consequences for sustainability governance. We identified a dense network of interactions between the planetary boundaries. The resulting cascades and feedbacks predominantly amplify human impacts on the Earth system and thereby shrink the safe operating space for future human impacts on the Earth system (Figure 1). Our results show that an integrated understanding of Earth system dynamics is critical to navigating towards a sustainable future.

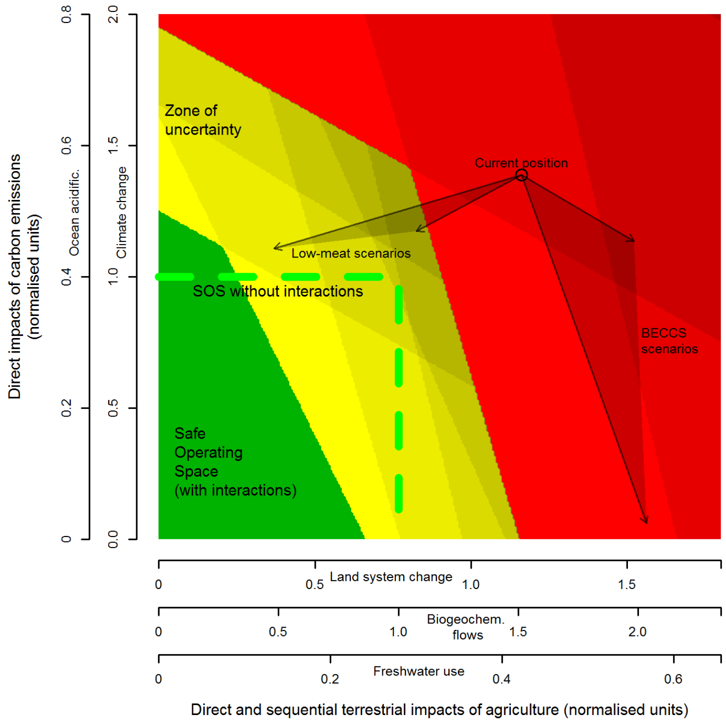

Figure 1: Effects of interactions between planetary boundaries on the shape of the safe operating space for human impacts on the Earth system

Resilience as pathway diversity: linking systems, individual, and temporal perspectives on resilience

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Approaches to understanding resilience from psychology and sociology emphasize individuals' agency but obscure systemic factors. Approaches to understanding resilience stemming from ecology emphasize system dynamics such as feedbacks but obscure individuals. Approaches from both psychology and ecology examine the actions or attractors available in the present, but neglect how actions taken now can affect the configuration of the social-ecological system in the future. Here, we propose an extension to resilience theory, which we label "pathway diversity", that links existing individual, systems, and temporal theories of resilience into a common framework (Figure 1). In our theory of pathway diversity, resilience is greater if more actions are currently available and can be maintained or enhanced into the future. Using a stylized model of an agricultural social-ecological system, we show how pathway diversity could deliver a context-sensitive method of assessing resilience and guiding planning. Using a stylized state-and-transition model of a poverty trap, we show how pathway diversity is generally consistent with existing definitions of resilience and can illuminate long-standing questions about normative and descriptive resilience. Our results show that pathway diversity advances both theoretical understanding and practical tools for building resilience.

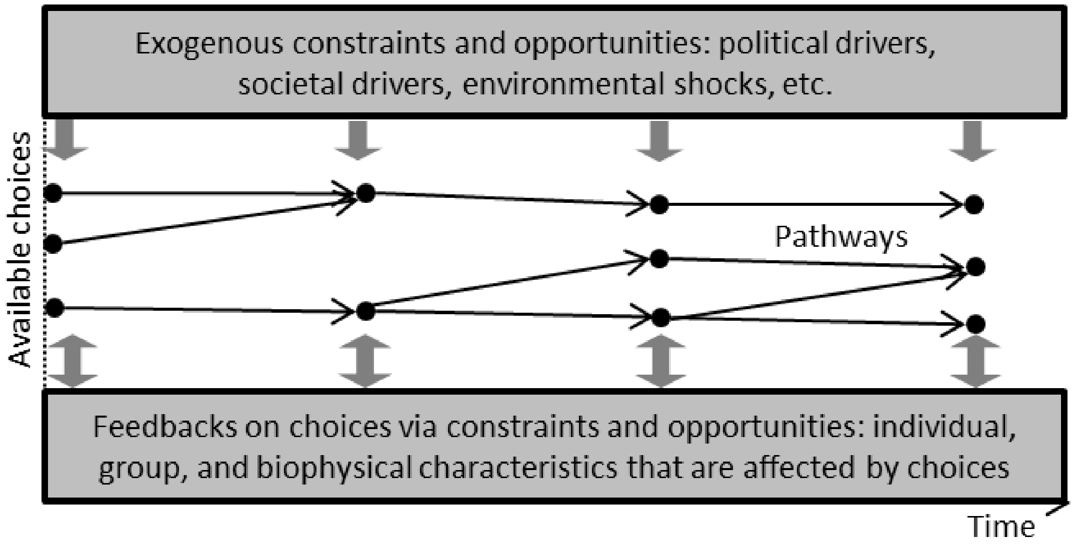

Figure 1: Pathways and pathway diversity. The diversity of future pathways is constrained and enabled by exogenous and endogenous drivers and endogenous feedbacks.

Data and main statistical features for pedestrian mobility through a citizen science project

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We study the GPS data from 260 students' pedestrian journeys to reach their schools. Pedestrian mobility patterns around up to 10 different schools of the Barcelona Metropolitan Area are analyzed. The work is part of Bee-Path, an interdisciplinary citizen science project that has introduced citizen science participatory practice as part of education and learning activities in schools. A data representation through maps already provides valuable insights on urban structure. Diffusion of the pedestrians' movement is also characterized, showing a super-diffusive regime, almost ballistic. Pedestrian velocities are described with a log-Normal Distribution and the logarithmic Ornstein-Uhlenbeck process appears to be a good candidate for modelling. Stops duration statistics can be described on a weighted double exponential law. The movement orientation is also obtained, giving information about the direction of the movement flow towards schools. Finally, we calculate the turning angle memory, often used to model random walks and animal movement. A family of symmetric distributions on the circle is used to describe it, obtaining practically a Wrapped Cauchy distribution. By treating schools separately, the fit parameters can reveal information on how oriented and straightforward the movement is, hinting at possible difficulties of access to schools due to urban structure. Being a follow up from previous studies [1], the results confirm the potential of citizen science practices to reach new data to build better mobility models.

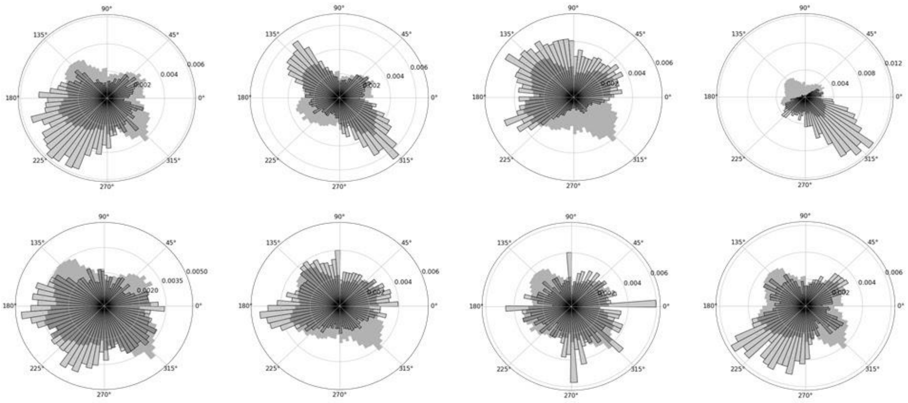

Figure 1: Polar Histogram of students' orientation for different schools.

Acknowledgements

This work was partially supported by MINEICO (Spain), Agencia Estatal de Investigación (AEI) and Fondo Europeo de Desarrollo Regional (FEDER) through grant FIS2016-78904-C3-2-P (JP) and PID2019-106811GB-C33 (FL and JP); by Generalitat de Catalunya (Spain) through Complexity Lab Barcelona (contract no. 2017 SGR 608; FL and JP).

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Cliques and a New Measure of Clustering

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Clustering, or “transitivity”, measures the relative frequency with which two neighbours of a given node are also neighbours of one another. Many real-world networks display higher levels of clustering than would be expected if those networks were random [1-4], but also have significant topological structures on *more than* three nodes that may perform precise specialized functions [5-7, Figure 1]. We develop a new generalized clustering coefficient that can detect this hidden higher-order structure. We use exact subgraph enumeration to build a fast implementation for groups of up to five nodes and apply our measure to 15 years of data on U.S. airline route networks to provide new insight into the strategic behaviour of firms. Our work complements the recent paper by Yin-Benson-Leskovec [8], and we draw careful comparisons with their approach for several theoretical network models, and on empirical data.

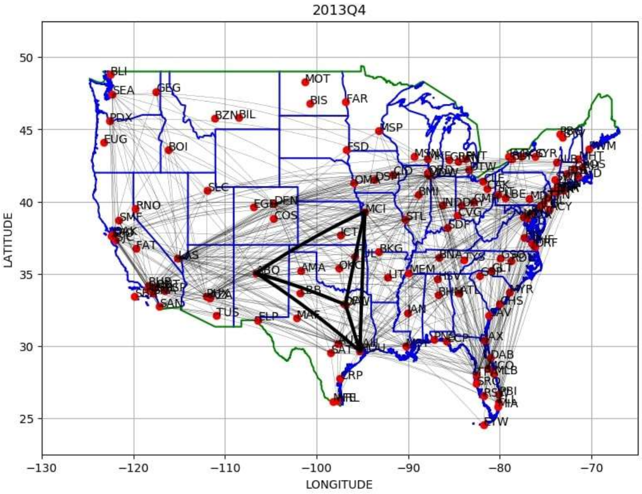

Figure 1: The Albuquerque–Dallas–Houston–Kansas City maximal 4-clique in Southwest Airlines’ network in 2013Q4 is one example of a completely-connected set of four nodes.

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Vehicular traffic under conditions of dynamic assignment and instantaneous network state information as a complex system

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The proposed contribution addresses vehicular traffic on large networks. Typically what is considered is a regional sized network, such as the Ile-de-France network in which the number of daily car trips exceeded 14.5 million in 2018. In order to carry out a trip a traveler chooses his departure time and path, the result of which is called traffic assignment. The standard behavioral assumption for departure time and path choice is that the traveler minimizes his travel cost (travel time + monetary cost). The travel cost expresses the network supply, which depends on the traffic assignment. Since paths which are attractive in terms of their cost attract much demand and thus see their attractiveness diminish, traffic assignment must be viewed as an equilibrium process, which can be calculated as a fixed point [1]. The fixed point is not necessarily unique, a fact liable to induce chaotic behavior in path choice [2]. The choice of departure time need not be stable as shown in [3]. The impact of travel information systems on assignment dynamics was analyzed in [4] and leads to possibly chaotic behavior. The new systems of information (vehicle-to-vehicle communication, internet/portable operators, crowd sourcing) provide instantaneous travel time and network state information. They provide a communication both instantaneous and long-range between travelers in the network. When the path choice is determined based on such information, strong nonlinear feedback and dis-utilities occur [5]. [6] considers the impact of various types of information on combined departure and path choice in a simple setting, showing potential chaotic behavior. The object of the contribution is to analyze vehicular traffic as a complex system when the dynamic assignment process is governed by instantaneous travel time and traffic state information. The traffic flow model is simplified but recaptures essential features (travel time, congestion, competition for intersection resources). The proportion of travelers benefiting from instantaneous network information constitutes a parameter of the study. Travelers who do not benefit of instantaneous information rely on historical information.

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Behaviour of partially ordered discorectangles obtained by random sequential adsorption: Consideration of one- and two-dimensional problems

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The random sequential adsorptions (RSA) of identical elongated particles (discorectangles) on a line [1] and on a plane [2] were studied numerically. Off-lattice models were considered. The problems were analyzed for a wide range of discorectangle aspect ratios (length-to-width ratios) $\varepsilon \in [1; 100]$. The particles were partially ordered along a given direction and the connectivity between them was performed assuming a core-shell structure [3].

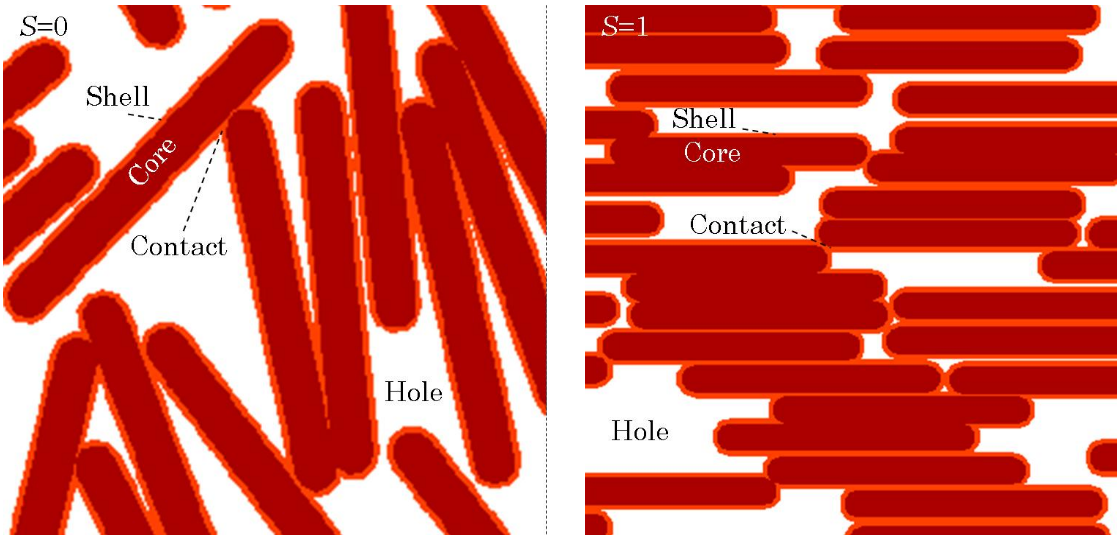

Figure 1: Examples of two dimensional jamming patterns for $\varepsilon=10$ at different order parameters, S

The kinetics of the changes of the order parameter, S, the packing density, φ, and the percolation width of the shell, δ, were analyzed. The values of ε and S significantly affected the packing density φ_j at the jamming state. Noticeable cusps in the $\varphi(\varepsilon)$ and $\delta(\varepsilon)$ dependencies were explained by the competitions between the particles' orientational degrees of freedom and the excluded volume effects.

Acknowledgements

We acknowledge funding from the National Research Foundation of Ukraine (Competition "Support for research by leading and young scientists", Project No. 2020.02/0138) (NL, MT, NV), and the Russian Foundation for Basic Research, Project No. 18-07-00343 (YuT).

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Uncovering Hidden Dependency in Weighted Networks via Information Entropy

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Interactions between elements, which are usually represented by networks, have to delineate potentially unequal relationships in terms of their relative importance or direction. The intrinsic unequal relationships of such kind, however, are opaque or hidden in numerous real systems. For instance, when a node in a network with limited interaction capacity spends its capacity to its neighboring nodes, the allocation of the total amount of interactions to them can be vastly diverse. Even if such potentially heterogeneous interactions epitomized by weighted networks are observable, as a result of the aforementioned ego-centric allocation of interactions, the relative importance or dependency between two interacting nodes can only be implicitly accessible. In this work [1], we precisely pinpoint such relative dependency by proposing the framework to discover hidden dependent relations extracted from weighted networks. For a given weighted network, we provide a systematic criterion to select the most essential interactions for individual nodes based on the concept of information entropy. The criterion is symbolized by assigning the effective number of neighbors or the effective out-degree to each node, and the resultant directed subnetwork decodes the hidden dependent relations by leaving only the most essential directed interactions. We apply our methodology to two time-stamped empirical network data, namely the international trade relations between nations in the world trade web (WTW) and the network of people in the historical record of Korea, Annals of the Joseon Dynasty (AJD). Based on the data analysis, we discover that the properties of mutual dependency encoded in the two systems are vastly different.

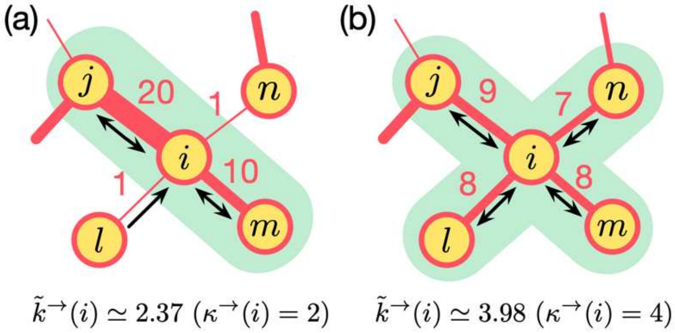

Figure 1: In this example illustrating two different weight distributions, the red edges with different widths represent the original weighted networks and the black directed edges represent the resultant directed subnetwork from our method.

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Fibration symmetries uncover the building blocks of biological networks

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The unifying organizing principle of physical systems is the principle of symmetry. Since life is an emergent property of physics, can life be similarly understood by the same symmetry principles that describe atoms, phases of matter and all elementary particles and fundamental forces in the tangible Universe?

We found that genetic networks exhibit fibration symmetry[1], which have never been observed in physical systems. We were able to deconstruct the network into synchronized parts, which gave us an opportunity to study genetic networks in a novel way and uncover their building blocks based on the function rather than the statistical significance. Further, we were able to classify the building blocks into topological classes of input trees characterized by integer branching ratios and complex topologies with golden ratios of Fibonacci sequences representing cycles in the network. From this idea we show that the core functional logic of discovered genetic circuits arises from a fundamental symmetry breaking of the interactions of the biological network [2]. Observed genetic circuits, ubiquitous across species, are surprising analogues to the emblematic circuits of solid-state electronics: starting from the transistor and progressing to ring oscillators, current-mirror circuits to toggle switches and flip-flops.

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The Role of Geography in the Complex Diffusion of Innovations

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The urban–rural divide is increasing in modern societies calling for geographical extensions of social influence modelling. Improved understanding of innovation diffusion across locations and through social connections can provide us with new insights into the spread of information, technological progress and economic development. In this work, we analyze the spatial adoption dynamics of iWiW, an Online Social Network (OSN) in Hungary and uncover empirical features about the spatial adoption in social networks. During its entire life cycle from 2002 to 2012, iWiW reached up to 300 million friendship ties of 3 million users. We find that the number of adopters as a function of town population follows a scaling law that reveals a strongly concentrated early adoption in large towns and a less concentrated late adoption. We also discover a strengthening distance decay of spread over the life-cycle indicating high fraction of distant diffusion in early stages but the dominance of local diffusion in late stages. The spreading process is modelled within the Bass diffusion framework that enables us to compare the differential equation version with an agent-based version of the model run on the empirical network. Although both model versions can capture the macro trend of adoption, they have limited capacity to describe the observed trends of urban scaling and distance decay. We find, however that incorporating adoption thresholds, defined by the fraction of social connections that adopt a technology before the individual adopts, improves the network model fit to the urban scaling of early adopters. Controlling for the threshold distribution enables us to eliminate the bias induced by local network structure on predicting local adoption peaks. Finally, we show that geographical features such as distance from the innovation origin and town size influence prediction of adoption peak at local scales in all model specifications.

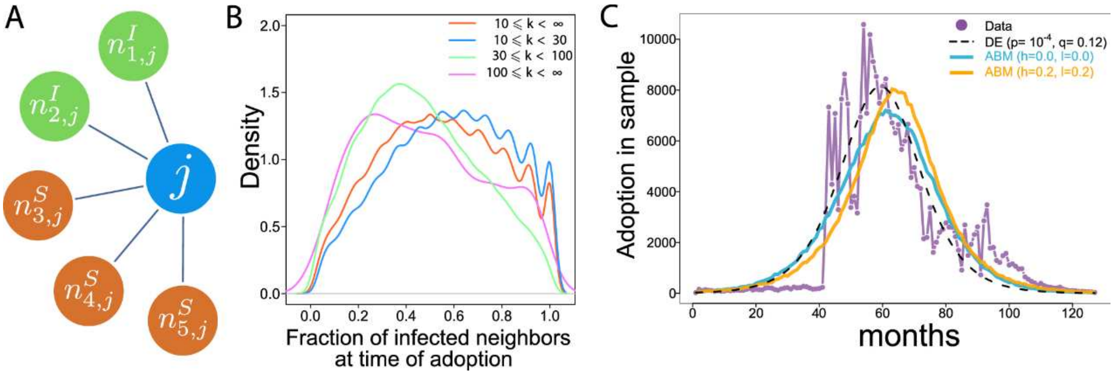

Figure 1: Model of complex contagion. (A) Network topology and peers influence in the Bass ABM. A sample individual *j* has two infected neighbors n^I_j who have already adopted the innovation and three susceptible neighbors who have not adopted yet n^S_j. (B) The distribution of adoption thresholds. Fraction of infected neighbors at time of adoption illustrate that most individuals adopt when half of their neighbors have already adopted. This fraction is smaller for high degree (*k* >30) individuals. (C) ABM adoption curves assuming linear (in blue) and non-linear (in orange) functions of infected neighbor ratio predict slower adoption than Bass DE.

Remotely sensed socioeconomic correlations of urban patterns

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Cities have become the economic bedrock of modern nations and this transition will likely be continued in the coming years as an estimated three billion people will move into cities by 2030. Nevertheless, while urbanisation can entail economic dynamism and social development, it can also create enormous social challenges. The management of natural hazards and pollution, the exclusion of the poor from the city's socioeconomic fabric and the subsequent surge of social and economic inequalities have become some of the pressing issues that modern metropolises need to address. Solutions to address these issues requires however both spatially fine-grained socioeconomic information as well as a detailed understanding on how wealth and the underlying urban topology are entangled.

Our aim is to contribute to this challenge [1] by training a deep learning model to predict the socioeconomic status of a given location from its aerial image and in turn interpret its activation maps in terms of the underlying urban topology. More precisely, we first overlay three publicly available datasets, providing a complete description of five French cities in terms of socioeconomic and land use data, as well as aerial imagery. Subsequently, after merging the aerial imagery (Fig.1a) with the corresponding socioeconomic maps, we train a Convolutional Neural Network (CNN) model, to predict accurately the socioeconomic status of inhabited tiles. Next, by relying upon a gradient-weighted class activation mapping (Grad-CAM) for computing attribution maps [2], we generate high resolution class discriminative activation maps (see Fig.1b and c), which are projected back onto the original image and overlaid with land use data (Fig.1d). We thus generate empirical statistics on the features used by our model to predict socioeconomic status in terms of land use classes (Fig.1e and f).

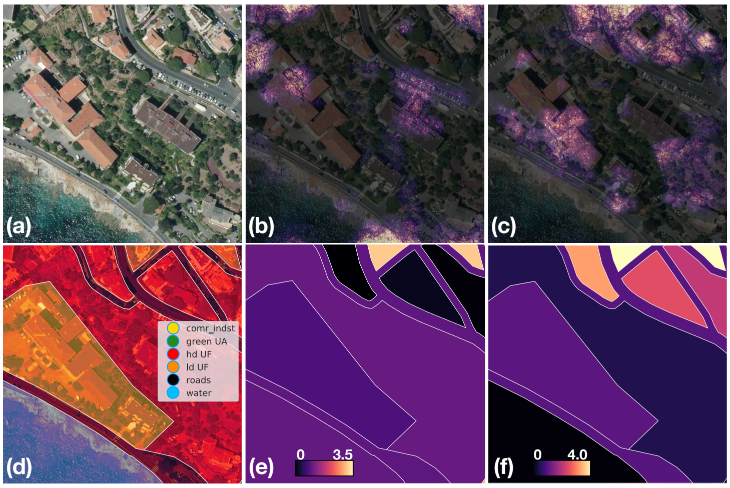

Figure 1: Model interpretability studies using Guided Grad-CAM (GGC). From an aerial tile (a), GGC computes activation maps for the poorest (b) and wealthiest (c) socioeconomical class. The activation maps are then overlaid with the tile's tesselation into urban classes polygon (d) to compute the normalised ratio of activations per polygon for the poorest (e) and wealthiest (f) class.

This framework enables the inference of socioeconomic status at scales rarely seen before, while also indicating precisely the predictive features contained in the actual urban environment. Furthermore, it allows for the observation of distinct city-to-city patterns of correlations between urban topology and the distribution of wealth, what we will report in our presentation.

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Adaptive spike response model: Learning with spiking neural networks beyond synaptic plasticity

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The complex processes of learning and memory *in vivo* often involve simultaneous alterations in synaptic strength and intrinsic excitability of the constituent neurons [1]. However, such synergy is rarely explicitly manifested in the bottom-up training of spiking neural models, partially because of conceptual and computational difficulties. Here we incorporate the combined plasticity mechanisms into a spike response model (SRM [2]), by which postsynaptic responses therein may deviate from stereotyped properties and evolve into arbitrary, yet self-consistently determined kernels for adaptation to imposed activity. We develop a general framework for reconstruction of adaptive SRMs as a neuroinspired generative model of event sequence data. It provides a descriptive approach to generate the observed timing of spiking activity of a set of interconnected neurons with nonparametric response kernels determined by event timing data. We further illustrate the potential of this neurally inspired model by two examples, neural synaptic connectivity reconstruction and time-series extreme event forecasting. Our approach provides a new conceptually simple but effective generative model for recognizing and exploiting event timing patterns in a broad variety of applications.

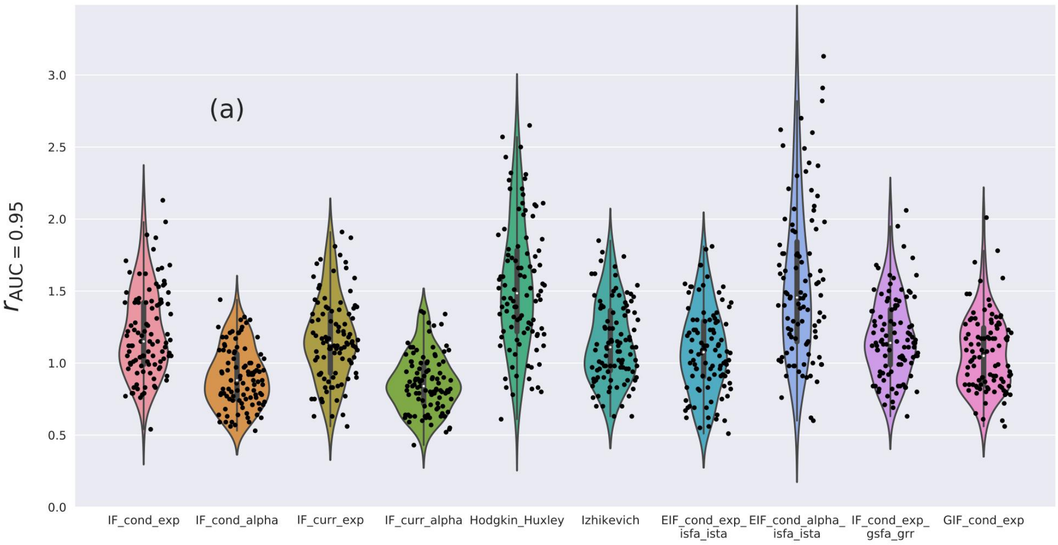

Figure 1: Violin plots of critical relative data size for synaptic connectivity reconstruction

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This work was partially supported by AMED under Grant Number JP20dm0307009.

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Taming Network Inference: Optimal Information Flow Model

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The detection of causal interactions between variables is of great importance when inferring complex networks but also remains challenging due to the high-dimensionality and nonlinearity of observational time series with a limited sample size. Convergent cross mapping (CCM) based on nonlinear state space reconstruction, as a network inference model, made substantial progress by measuring how well historical values of one variable can reliably estimate states of other variables. Here, we investigate the ability of an Optimal Information Flow (OIF) model to infer bidirectional causality and validate the model on a mathematically simulated predator-prey model, a real-world sardine-anchovy-temperature system and a multispecies fish ecosystem by comparing that to CCM. The validation work demonstrates that the proposed OIF model performs better than CCM since it provides a larger gradient of inferred interactions, higher point-value accuracy with smaller fluctuations and no requirement of convergence. Besides, OIF offers broad ecological information by extracting predictive causal networks of complex ecosystems from time-series data in the space-time continuum. Therefore, OIF is a robust model in estimating predictive causality (also in terms of computational complexity) due to the explicit consideration of synchronization, divergence and diversity of events that define model sensitivity, uncertainty and complexity. The accurate inference of species interactions allows to predict biodiversity changes as a function of climate and other anthropogenic changes. This has practical implications for defining optimal ecosystem management such as fish stock prioritization and marine protected area delineation based on the derived collective multispecies assembly.

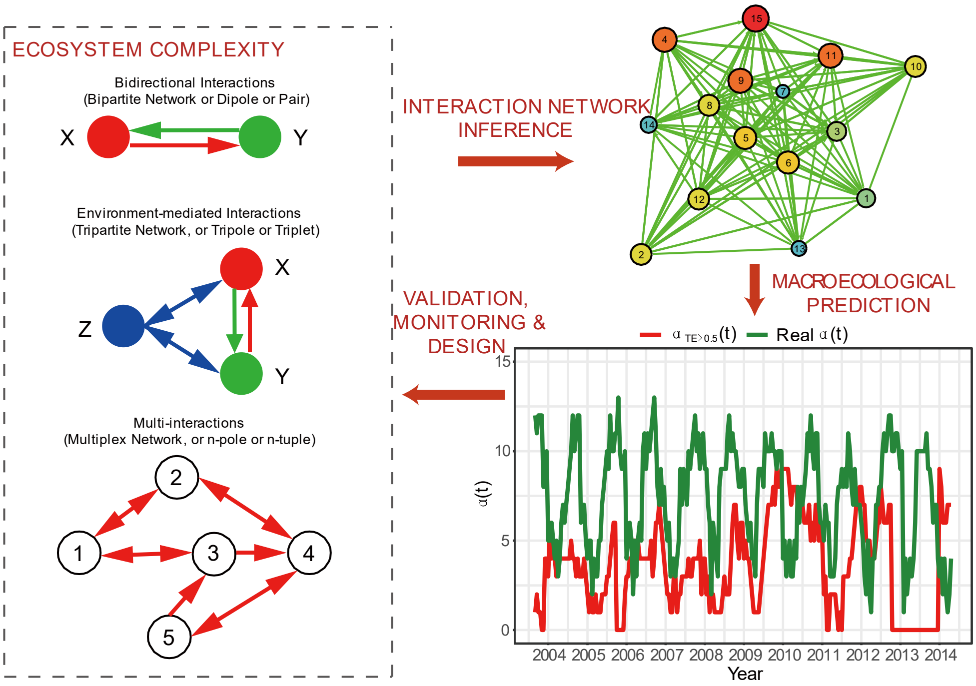

Figure 1: Causal Interaction Detection and Predictive Networks Inference

Rethinking Infrastructure Network *Criticality* for Climate Resilience: Inputs from Complexity Sciences and Disaster Risk Theory

Sarah Lindbergh and John Radke

Critical infrastructure (CI) functions and spatial boundaries are often implicit premises which can result in misalignments between CI resilience goals and their societal utility. Furthermore, the historical legacy and institutionalization of CI, powered by national security issues, has resulted in technocentric approaches of infrastructure systems that can be counterproductive to disaster risk reduction. Through a literature review, this paper argues that rethinking concepts of infrastructure network criticality quantitatively and qualitatively is a necessary step to address this misalignment and to apply the current paradigm shift which defines CI, beyond hardware, as sociotechnical and socioecological systems. Rethinking these concepts of criticality requires a reexamination of infrastructure networks functions and spatial boundaries. Complementary approaches to CI resilience are harnessed within two large and sometimes disconnected bodies of literature: complexity sciences and disaster risk theories. Complexity sciences have significantly advanced quantitative definitions of infrastructure criticality by modeling interconnectivity and extracting network level metrics of vulnerability and resilience. At a conceptual level, complexity sciences further revolutionized our understanding of CI as complex adaptive systems through the idea of ecological resilience and panarchical cycles of stasis and change. Nevertheless, the application of ecological resilience to CI risk management still struggles to recognize and assess sociotechnical functions of complex systems, for which disaster risk theories have a latent potential to address, notably within concepts of social construct of risk and the vulnerability paradigm. This theoretical bridge helps realign infrastructure network criticality with CI services and ecological resilience goals. In a practical level, it converges contributions from multiple fields and provides direction for assessing sociotechnical network exposure to climate change threats and identifying network-level organizational stakeholders to support CI collaborative risk governance.

Keywords: critical infrastructure, conceptual gaps, vulnerability paradigm, sociotechnical systems, ecological resilience, bridging disciplines

Network Symmetry Extraction

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Most literature on measuring the symmetry of networks uses graph automorphism algorithms to find the automorphism group, and defines either the number of elements in the automorphism group or the number of nodes involved in the automorphism group as a measure of the level of symmetry of networks. However, this type of measure has two problems: first, it is a measure for exact symmetry, meaning that it fails to capture a large group of approximate symmetries of networks (for example, a lattice with one missing edge still has a high level of symmetry, intuitively speaking, but according to the present symmetry measure it may have zero symmetry); second, in real-world networks, most of the automorphism transformations found are composed of local permutations, for example two degree-one nodes attached to the same node are symmetric to each other. Therefore if a network has many automorphism transformations it could mean that the network has a lot of local symmetries, instead of global symmetries. For example, a lattice has translational and reflectional symmetries, both of which are global. To overcome these problems, we introduce a new measure of the level of symmetry of a given network with adjacency matrix A:

$$\mathrm{S} = \min_{Q}(||\mathrm{A} - \mathrm{QAQ}^{T}||),$$

where Q is a permutation operator with properties det(Q) = 1 and $QQ^T = I$, and ||·|| is order-1 norm. QAQ^T is the resulting adjacency matrix after a permutation of the node sequence. In order to restrict the symmetries we find to global symmetries, we limit Q such that trace(Q) = 0, meaning that all nodes are involved in the permutations. The difference between A and the permuted adjacency matrix $\hat{Q}A\widehat{Q^T}$ with permutation $\hat{Q}$ = argmin($||A - QAQ^T||$) is a measure of how close $\hat{Q}$ is to exact symmetry.

Figure 1 shows S for networks with N = 100 nodes, generated from three different network models: Erdös Rényi (ER), Random Geometric Graphs (RGG), and Stochastic Block Models (SBM), as a function of the number of edges M. For ER networks (blue) and RGGs (orange), when they are empty (M = 0) or complete (M = 5,000), they have complete symmetry, which is reflected by S = 0. When half of the potential edge slots are filled (M = 2,500), the networks have the least level of symmetry, due to the high uncertainty of edge placements.

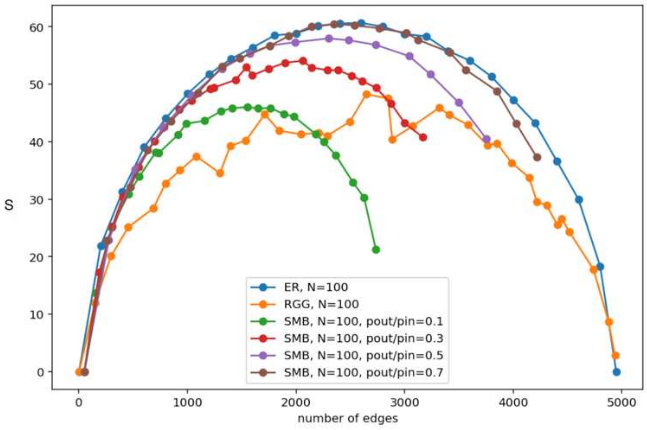

Figure 1: S for networks with N = 100 nodes, generated from three different network models.

Contrastive Learning Approach for Phase Diagram Construction of the Random Walk Model with Volume and Surface Reinforcement

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Random walk with volume and surface reinforcement is a discrete random walk on a lattice proposed to model a wide range of polymer interaction potentials. Volume reinforcement controls short-range interaction with visited lattice points while surface reinforcement describes longer-range interaction with neighbors of visited volume. The model exhibits rich morphological behavior for different values of parameters. However due to non-markovian nature of the walk it is hard to investigate phase transitions analytically or using traditional finite-size scaling methods. We propose a deep learning technique based on contrastive learning scheme to analyze ensemble of relatively short random walk trajectories. In contrastive learning scheme deep learning model tries to differentiate between two given microstates and tell whether they were generated at the same macroscopic conditions or not. It implicitly defines distance metric between microstates, which allows effectively classify phases and construct sketch of a phase diagram without a priori knowledge of exact number of phases.

Acknowledgments

This research was supported in part through computational resources of HPC facilities at NRU HSE and by BASIS Foundation grant 19-1-1-48-1.

Bursting Dynamics and Signatures of Criticality across the Sleep-wake Cycle

F. Lombardi[1]*, M. G. Extremera*[2]*, J. Wang*[3]*, X. Zhang*[3]*, P. Bernaola-Galvan*[2]*, P. Ch. Ivanov*[3,4]*. (1) Institute of Science and Technology (IST) Austria, A-3400, Klosterneuburg, Austria, lombardif00@gmail.com. (2) University of Malaga, Malaga, Spain. (3) Boston University, Boston, MA, USA. (4) Harvard Med. School and Division of Sleep Medicine, Brigham and Women Hospital, Boston, MA, USA*

Sleep periods exhibit numerous intermittent transitions among sleep stages and short awakenings, with fluctuations within sleep stages that may trigger micro-states and arousals. Despite the established association between dominant brain rhythms and emergent sleep stages, origin and functions of sleep-arousals and sleep-stage transitions remain poorly understood. Empirical observations of intrinsic fluctuations in rhythmic cortical activity, and the corresponding temporal structure of intermittent transitions in sleep micro-architecture, raise the hypothesis that non-equilibrium critical dynamics may underlie sleep regulation at short time scales, in co-existence with the well-established homeostatic behavior at larger time scales. In this talk, I will discuss recent results on the dynamics of dominant cortical rhythms across the sleep-wake cycle that support such hypothesis [1, 2]. I will focus on cortical theta and delta rhythms in rats, which are associated with arousals/wakefulness and sleep respectively. I will show that intermittent bursts in theta and delta rhythms exhibit a complex temporal organization: Theta-burst durations follow a power-law distribution, whereas delta-burst durations follow an exponential-like behavior. Such features are typical of non-equilibrium systems self-tuning at criticality, where the active phase is characterized by bursts with power-law distributed sizes and durations, while quiescent periods (inactive phase) are exponentially distributed. By interpreting theta-bursts as active phases and delta-bursts as inactive phases of the cortical activity in the sleep-wake cycle, I will then draw a parallel with other non-equilibrium phenomena at criticality, and demonstrate that theta-bursts exhibit a peculiar organization in time described by a single scaling function (Gamma distribution) and closely reminiscent of earthquake dynamics [1, 2]. Overall, such results constitute a fingerprint of critical dynamics underlying the complex temporal structure of intermittent sleep-stage transitions at the behavioral level, and complement previous observations of critical behavior at the neuronal level (we find similar scaling exponent).

Acknowledgements (optional)

FL acknowledges support from the European Union's Horizon 2020 research and innovation program under the Marie Sklodowska-Curie Grant Agreement No. 75441.

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Leader Identification through Networks of Conversational Interruptions

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Leaders are often identified in empirical studies by either their position in an organizationally defined hierarchy or by sociometric survey. However, such methods conflate behavioral antecedents and outcomes, including subjective co-participant attributions, with assessment of behaviors themselves. In this study, we propose the "interruption network" as a model of small group structure based on a nonverbal behavior—conversational interruptions—that has been previously validated as a correlate of social status. A directed, weighted edge exists in an interruption network $i \rightarrow j$ representing the number of times j interrupted i (Figure 1A, B); a "leadership" or "vote" network based on co-participant leader nominations is shown in Figure 1C. In simulation studies, randomizing edge directions within node pairs suggests that interruption network edge direction accounts for substantial variance in leader emergence while retaining the association between speaking time and leadership. Network motif analysis reveals hierarchical, nontransitive mesoscale structures (triad 021C: $i \rightarrow j \rightarrow k$; $p = 0.00$). Comparison of exponential random graph models finds that leadership attributions contain a male bias (vote network in-degree; $\hat{\beta} = 1.061$, $p < 0.001$) not found in the interruption networks (weighted in-degree; $\hat{\beta} = 0.075$, $p = 0.136$). We conclude that while it is often reported that male group members emerge more as leaders than female group members, the difference may be more attributional than behavioral.

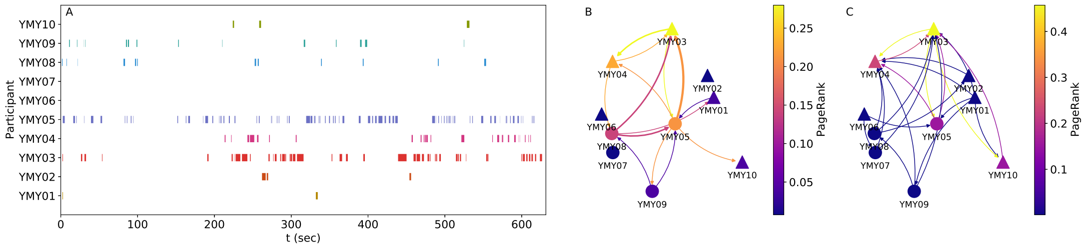

Figure 1: Diarized speaking data for an example group, with speaking events marked by horizontal bars delimited by the start and stop time of the speaking event (A), along with the corresponding interruption network (B) and vote network (C). Female participants are represented by circles and male participants by triangles, arc thickness is proportional to edge weight, and node and out-edge colors are mapped to PageRank centrality.

Acknowledgements

The research described herein was sponsored by the U.S. Army Research Institute for the Behavioral and Social Sciences, Department of the Army (Grant No. W911NF-17-1-0221). The views expressed in this presentation are those of the author and do not reflect the official policy or position of the Department of the Army, DOD, or the U.S. Government. Preprint: https://psyarxiv.com/m8y5n.

Analysis of Couped Dynamic Model for Malaria Spreading between Human being and Mosquito with Infected Immigrants

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In this study, we assume that the recovered human population does not generate permanent immunity. Therefore, they become susceptible class after losing their immunity. In this model, we use mathematical modelling techniques and non-linear dynamic system to analyze the SIRS model for human population and SI model for mosquito population. We compute the disease-free equilibrium and derive the basic reproduction number (R_0) by using the next generation matrix. Moreover, the local stability of the model is computed by using the Jacobian Matrix. The result shows that the per capita rate of loss of immunity in humans contributes to the stability of the model. The infected migration rate for human also contributes to both the stability of the model and the basic production number (R_0).

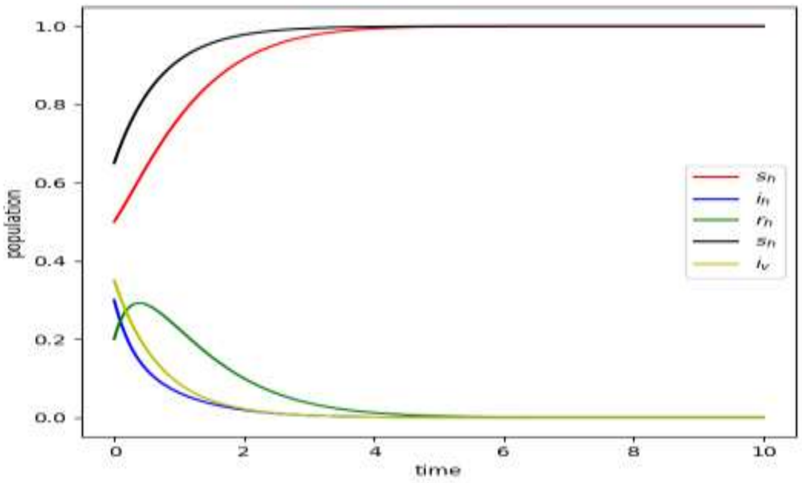

Figure 1: Numerical simulation of the model with respect to time for parameter values $a = 1$, $g = 3$, $r = 0.5$, $d = 1.2$, $b = 2$, $c = 0.05$, $e = 0.7$, $w = 0.5$, $s = 1$, $s_h = 0.5$, $i_h = 0.3$, $r_h = 2$, $i_v = 0.65$, $s_v = 0.35$, and $R_0 = 0.20806$.

Acknowledgements

This research was supported by the Basic Science Research Program through the National Research Foundation of Korea (Grant No. NRF-2020R1A2C1005334).

Opinion Formation and Spread: Does Randomness of Behaviour and Information Flow Matter?

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Recently, the model of multi-choice opinion dynamics based on Latané theory [1] was proposed [2, 3, 4]. Each actor is characterized by his/her opinion, persuasiveness and his/her supportiveness. The system evolution depends on the social temperature *T*, and the exponent *a* tuning the long-range interaction among actors. Increase of temperature increase the randomness of actors actions while increase of alpha decrease the effective range of interaction. With computer simulation we check influence of the model control parameters on spatial distribution opinions, spatial distribution of social impact and size of the largest cluster formed among agents sharing the same opinion. The system exhibits complex and non-monotonous behaviors in both, *T* and *a* parameters.

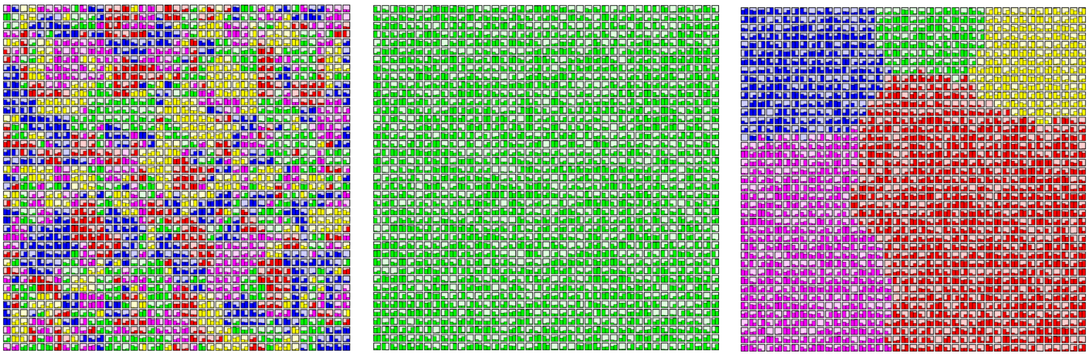

Figure 1: Examples of the spatial distribution of opinions for five opinions available in the system . From left to right: T=0, α=6; T=1, α=2; T=1, α=3.

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Informed design of future integrated developments using complexity science

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Contemporary urban design is primarily driven by intuition and heuristic methods. Every year, more people move to urban areas in record scale and cities have grown dense and vertical to accommodate this unabated trend. This increasing density has encouraged cities like Singapore to design vertically integrated developments that comprises hospitals, supermarkets, shopping complex, public transportations, restaurants, parks, and other community facilities. However, the current design approaches do not account for, nor tap into the complexity of the system under study. As a complex system, a city and its people interact seamlessly effectively bringing cities to "life" [1]. The growth and life of the city have also been postulated to depend on its ability to serve as a facilitator for social interactions [1]. Three common factors that reveal the interaction between inhabitants and the built environment are: mobility, co-presence, and spatial configurations [2]. Given that, an informed design must therefore take into account the interplay between these factors. Specifically, looking at cities through the lens of complex adaptive systems will help design cities and microcosms of cities like integrated developments with efficient allocation of facilities, space use, and connectivity. This study aims to use a range of tools and methodologies borrowed from complexity science—especially network science and computational social science—to achieve a certain level of informed design. A case study is conducted in one of Singapore's largest and most recent public integrated development—Kampung Admiralty [3], *kampung* meaning village in the Malay language—where the residents and facility users are tracked for two weeks using a custom mobile app that records barometric pressure, accelerometer, and Bluetooth scans from the beacons placed in the building and its vicinity. A spatial network analysis of Kampung Admiralty shows that the node with the highest betweenness centrality is the community lift lobby at level-1 that allows reachability to any place in the building with an average travel distance of 50 meters, which validates the design intention of the architects. The spatial network of Kampung Admiralty also shows evidence of the small-world property with a broad degree distribution due its vertical integration through various modes of vertical mobility [4]. The date-driven results will help inform future designs of integrated developments and hopefully establish a framework for evidence-based designs.

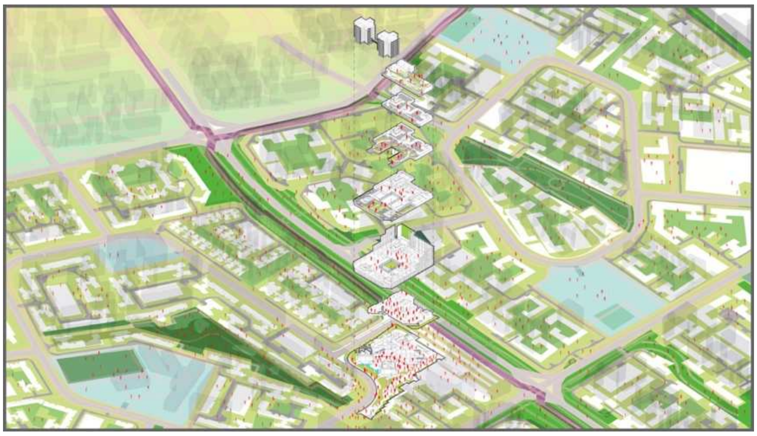

Figure 1: 3-D projection of Kampung Admiralty

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XDFA - Software To Evaluate Detrended Fluctuation Analysis And Related Time Series Measures

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xdfa is a software package to compute Detrended Fluctuation Analysis (DFA), and related methods, on time series. The core of the package is written in C++ for performance reasons with interfaces available for python, octave and R. The purpose of the package is to provide a uniform calling convention together with ensuring the numerical stability of the methods used.

In the context of complex systems the observable time series of several quantities are the result of many small part interactions and often exhibit long range dependency, also called long memory. A model for a long memory stochastic process is the fractional Brownian motion, where a single parameter H (Hurst exponent) controls persistence of the time series. The original work from Peng et al [1] has introduced DFA in order to estimate the Hurst exponent of a time series. This method is widely used in several scientific fields like econophysics, geophysics, biophysics and others.

In Detrended Fluctuation Analysis trends at all scales are removed from the integrated time series and the the behavior of the residuals is studied. In other variations like the Detrended Moving Average the trend is evaluated using moving averages [2]. In the previous cases the residuals are taken using the norm-2 metric. It is possible to evaluate the trend using other norms in to study the multifractal properties of the time series [3]. Other extension deal with the comparison between two time series, in a scheme similar to the covariance/correlation analysis using the Detrended Fluctuation Analysis as the basis, that correspond to the Detrended Cross Correlation Analysis [4,5].

The main goal of the xdfa software package is to have the code that deals with all these different methods in a single place and with a common interface.

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Diffusion Speed of the Node2vec Random Walk on Networks

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Random walks on networks, which are usually formulated as first-order Markov processes, are a prevailing tool for constructing various stochastic algorithms to obtain information from network data. The node2vec algorithm [1] provides a flexible biased random walk framework for graph machine learning, which can be applied to tasks such as node classification and link prediction. The behavior of node2vec in these applications is contingent on two parameters that control how a random walker explores the entire network. Here, we examine properties of the node2vec random walk both theoretically and numerically. The node2vec random walk can be formulated as a second-order Markov chain, which can be reduced to a first-order Markov chain using the so-called memory network formalism. We exploit this correspondence to write down the transition probability matrix in the state space of directed edges, and then analyze the stationary probability, relaxation speed in terms of the spectral gap of the transition probability matrix, and coalescence time [2]. In particular, we show that node2vec random walk accelerates diffusion when walkers are configured to avoid back-tracking (by making the value of parameter α small) and also avoid visiting neighbors of the previously visited node (by making the value of parameter β small) to a certain degree. We have observed this tendency consistently for different diffusion speed measures (i.e., spectral gap and coalescence time) and across different empirical and model networks (see Fig. 1 for two examples). Finally, we discuss the application of the node2vec random walk to analyses of epidemic processes on networks.

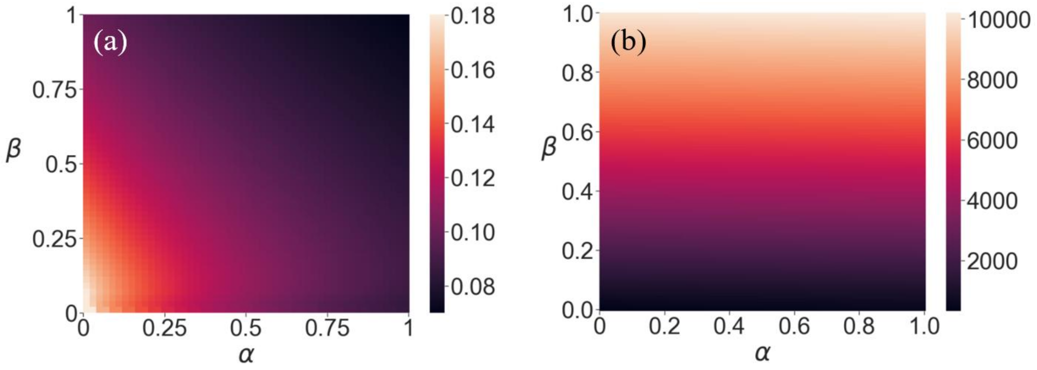

Figure 1: (a) Spectral gap for the node2vec random walk on an email network from Enron Corporation [3]. (b) Mean coalescence time of two node2vec random walkers in the network composed of two cliques each having 100 nodes and a single edge connecting the two cliques.

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Interpretations of Complexity of Social Systems in Inter- and Multi-disciplinary Research

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In most general sense social systems can be treated as "complexity of complexities" thus all kinds of research relating to complexity have become attractive for all areas of social science. The ideas drawn from the discourse on complexity have been applied in social studies as mathematical models, analogies, metaphors, and other linguistic constructs.

A multitude of interpretations of complexity has emerged, and a new inter- and multi-disciplinary approach is needed. Following this observation, a survey of applications of the utterance complexity in broadly defined social studies is proposed. It is based on an assumption that any uniform complexity theory is not achievable. The only realistic approach it to conduct more profound hermeneutic study of occurrences of the term complexity in social research.

Three aspects of proposed approach to the complexity of social systems have to be reminded: relations between qualitative and quantitative approaches, narratives concerning complexity and its related terms, and the role of hermeneutics. First, the opposition qualitative vs. quantitative methods of research sometimes exposed in social sciences is artificial. Second, as a consequence of the first, attention is focused on narratives on complexity, including both their qualitative and quantitative components. Third, understanding social theory and practice requires a more profound inter- and multi-disciplinary hermeneutical analysis.

A variety of interpretations of the notion of complexity leads a very peculiar situation. In order to develop computable models, in many works on the complexity of social systems, the "society" is presented as a set of interacting elements: non-divisible points/balls/nodes and networks of interactions between those elements, etc. which are often based on excessively simplifying, if not trivialized assumptions about the complexity of components and of their interactions. On the other extreme, we can find a multitude of works in social studies - sociology, management, environmental studies, economics and finance where the complexity of social phenomena is described with more or less sophisticated qualitative characteristics of complexity depicted with analogies and metaphors with a various degree of relevance to reality. Facilitating communications and understanding between representatives of both streams of discourse on the complexity of social systems seems necessary. For instance, a physicist applying the Ising models in studying the complexity of more or less abstract social systems could have problems in finding a common language with a follower of complexity ideas developed, for example, by Luhmann and Cilliers. Worse, they are not able to understand each other, the scientific value of ideas of their partners. It may be concluded that such a situation makes it impossible to search for synergy resulting from the exchange of their experience.

This paper is addressed to both groups of authors. It is designed to help them to communicate with each other, to develop mutual understanding, and to encourage them for a multi-disciplinary and inter-disciplinary cooperation which seems, and it will be proved in this paper, inevitable in the studies of all aspects of the complexity of modern society.

The main aim of the paper is to present a comprehensive survey of research with the use of the term complexity in studying broadly defined social systems. This aim embodies three supporting purposes. The first one is to develop a universal interpretation of social systems, which constitutes a kind of the foundation of both quantitative and qualitative studies. It is not a comprehensive ontological study of social systems but just an introductory description allowing for studying the situations when they are described as complex. The second supporting aim of this paper is to develop a new typology and a preliminary survey of interpretations of the notion complexity and associated terms in broadly defined studies of society. The third supporting aim is to facilitate understanding between specialists applying mathematical models of the complexity of social systems with specialists in broadly defined social sciences.

Using pandemics to improve now-casting models

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Online searches have been used as a tool for close to real-time study of different health-related behaviours, including identifying disease outbreaks. However, many models have been criticized for ignoring whether such activity is related to an actual disease. Here we propose a methodology to disentangle online search behaviours that are driven by actual disease from others that can be caused by other motives, including media-driven curiosity or information seeking. It is known that information seeking becomes less common as pandemics progress, so we argue that selecting search terms during the worst possible moment, with highest media hype, can help to understand which searches are more associated with the disease and which are prompted by media exposure. We use Google Trends and apply this methodology to two pandemic respiratory infectious diseases: 2009-H1N1 (in the United States) and COVID-19 (in Spain). We found that search-terms cluster into three groups, one more associated with cases (C1), another highly correlated with media reports (C2) and a noisier third (C3, not shown). We observed the same pattern for both diseases, showing that it is possible to identify differences in search-patterns online, and that these are consistent in time and across countries. We tested whether the differently clustered search-terms could now-cast seasonal influenza and the Spanish COVID19 second wave. By using both Random Forest and Linear Regression, we show that, contrary to common believe, less data can be better and that previous clustering and manual selection can help model performance. Our system is flexible and general enough to be applied to other diseases, or different phases (ex. seasonal events), and human activities that spread on networks.

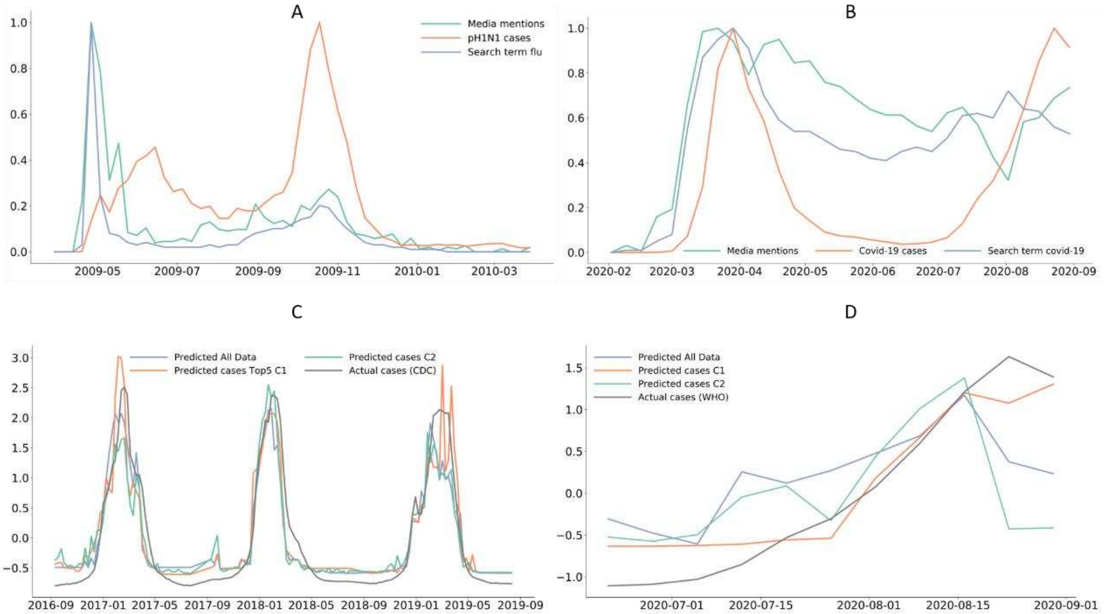

Figure 1: **A -** Media versus flu activity (max-scaled) in the United States for 2009-H1N1. **B -** Media versus disease activity (max-scaled) in Spain for Covid-19 pandemic. **C -** USA CDC ILI model with a fit of R^2=0.82 on average and standard deviation of 0.12 (C1) versus R^2=0.71 and standard deviation of 0.17 when using all data (not shown). **D** – results obtained for Spain with a R^2=0.91 using the cluster more correlated with cases (C1) versus a R^2=0.43 using all data (not shown).

Multifractal analysis of eigenvectors of smallworld networks

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Many real-world complex systems have small-world topology characterized by the high clustering of nodes and short path lengths. It is well-known that higher clustering drives localization while shorter path length supports delocalization of the eigenvectors of networks. Using multifractals technique, we investigate localization properties of the eigenvectors of the adjacency matrices of small-world networks constructed using Watts-Strogatz algorithm. We find that the central part of the eigenvalue spectrum is characterized by strong multifractality whereas the tail part of the spectrum have $D_q \rightarrow 1$. Before the onset of the small-world transition, an increase in the random connections leads to an enhancement in the eigenvectors localization, whereas just after the onset, the eigenvectors show a gradual decrease in the localization. We have also analyzed the impact of change in average degree and network size on D_q. We have verified an existence of sharp change in the correlation dimension at the localization-delocalization transition.

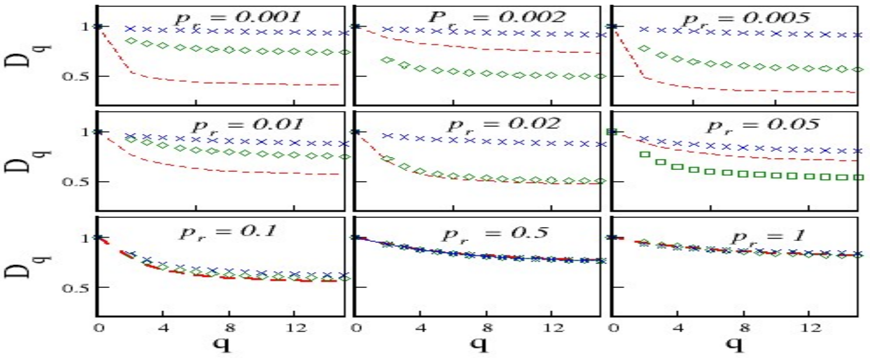

Figure 1: Multi-fractal dimension (D_q) vs q of tail part (blue) and the central part (green and red) of eigenvalue spectrum for different rewiring probabilities.

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Socially Responsible Investing in the Global Ownership Network

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We connect the corporate ownership network to the network of financial instruments that inject money into the ownership network. The ownership network in our data consists of 66 million nodes (i.e., companies and their shareholders) and over 90 million ownership links among them. The previous studies on the network of corporate ownership and control emphasize the importance of roles played by banks and other financial institutions in the network [1-4]. However, it is left unanswered where the financial institutions collect the capital from so that they can inject cash into the capital market (i.e., corporate ownership network). We therefore look into ETFs and mutual funds as the financial instruments through which the investors (individual and institutional alike) supply money in the shareholding network. In this way, we extend the existing research on corporate control in the ownership network to the network of investment funds purchased by investors (such as central banks) from asset managers and other the institutional investors.

The analysis of the shortest path from asset management companies to a munition company reveals that no asset manager either in the US or Japan directly invests in any Chinese munition companies with one link of ownership. That is, no Chinese munitions company's stock was included in the ETFs or mutual funds listed in the US and Japanese markets. However, almost all the asset managers have at least one path through which their equity stakes eventually reach a Chinese munitions company with the second or further apart links in the global ownership network.

This result points to an important social consequence, namely causing the disparity between the power of corporate control and the stewardship responsibility. In the ideal world where the investors who strive for socially responsible investing should be empowered by their own equity stakes to make positive impacts on corporate activities related to the ESG issues. However, our analysis suggests that two obstacles encourage decoupling of equity stakes and social responsibilities so that socially responsible investors become incapable of making positive impacts with their investing strategy. The first obstacle is the fact that ETFs and other similar financial instruments separate capital and corporate control. The second obstacle is the complexity of ownership network itself. While the investors may have the potential to control munition companies, the complexity of the ownership network is likely to prevent the investors from knowing its own potential.

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Interpersonal Synergies Dominate Over Intrapersonal Synergies in a Cooperative Slackline Task

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This study aimed to explore the interpersonal coordination of pairs cooperating to stand up in balance on a slackline through the study of inter and intrapersonal synergies (Fig. 1). For this purpose, acceleration time series of the slackline as well as of both legs and the center of mass of performers were recorded. Inter and intrapersonal synergies were assessed by the Uncontrolled Manifold, and subsequently, they were organized by their strength proximity using the Hierarchical Cluster Analysis. Additionally, the Detrended Fluctuation Analysis was computed to study the kinematic variability of the synergetic elements and find potential stabilizing roles among performers. Synergies were identified at inter and intrapersonal levels with a higher hierarchical dominance of the former. Inter and intrapersonal stabilizing roles were evidenced among performers, revealing greater kinematic control of free leg and the center of mass in those performers with more training experience and higher task performance. This exploratory study of interpersonal coordination found an embedded organization between inter and intrapersonal synergies within every unique pair-environment interaction, which depended on how affordances constrained the emerged stabilizing roles between performers. Pairs established a dominantly proprioceptive communication to form a co-adaptative whole and cope with an unstable environment.

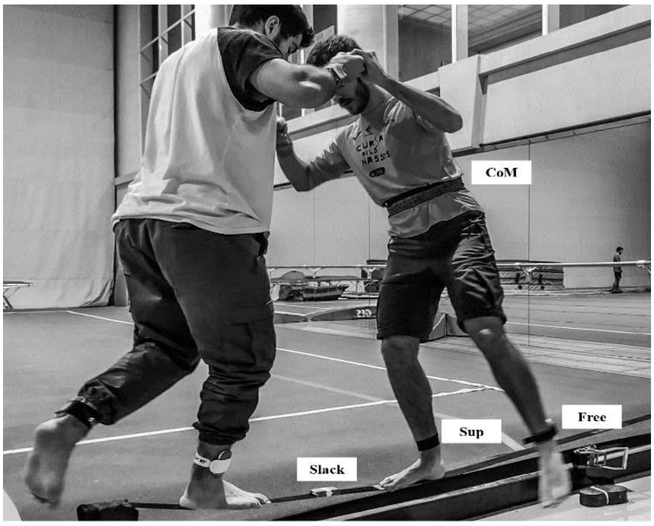

Figure 1: Slackline cooperative task

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Restricted Boltzmann Machines for feature extraction: A stopping criterion using Hamming Distance

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Abstract

Restricted Boltzmann Machines (RBMs) are stochastic neural networks which are capable of learning a probability distribution over its set of inputs. This characteristic allows them to be useful in many different and complex tasks, the most popular of which are dimensionality reduction, feature learning, classification and collaborative filtering. Nowadays, the RBMs have gained much interest as they are studied in many different versions and scientific fields, using multiple types of data. The use of RBMs in so many scientific fields, has raised our interest in further study and improvement.

The main version of RBM consists of two layers, a visible and a hidden. The visible layer contains the visible nodes corresponding to the input data and the hidden layer, which tries to capture latent dependencies, allowing the correct reconstruction of the initial data. While the RBM is being trained, its parameters are also updated, until a stopping point is reached, where the log likelihood function finds a maximum and the model parameters are optimal. Computing analytically the log likelihood function and its gradient in each training step is intractable, therefore the Contrastive Divergence (CD) algorithm was invented to estimate it numerically. However, the CD algorithm is a biased estimator of the log likelihood gradient, so the derived approximation of the log likelihood function in each training step, using Annealed Importance Sampling technique, may not be a safe choice for evaluating the training process. For this reason, most of the times a maximum iteration limit is imposed to terminate the training procedure.

With all of this in mind, we decided to explore the stopping criteria used in RBMs training. So, this study aims to introduce a new stopping criterion, which is based on the Hamming Distance. In particular, the proposed criterion computes the Hamming Distance between the input data and the reconstructed data from the model, in each training step. This new criterion proposes an optimal stopping point at a time when the rate of change of the Hamming distance becomes insignificant and beyond this point further improvement of the Hamming Distance value will be negligible.

In addition, our criterion was compared with known methods currently used for the termination of the training process, such as log likelihood function estimation and maximum iterations limit. More specifically, simulations have been made where the training process is stopped by either criterion (log likelihood and our proposed stopping criterion) and then the optimal model parameters are stored and the reconstructions of the test set are created to be fed into a softmax classifier. At this point, it should be mentioned that the log likelihood function was estimated based on Annealed Importance Sampling technique, as in real size RBMs the direct computation of log likelihood is intractable, introducing an unbearable computational burden compared to our proposed criterion. The comparison of these two termination methods in terms of stopping epoch, total computational time, classification accuracy, highlighted the advantages and the drawbacks of each method respectively, concluding that our method saves time and has smaller variance.

In addition, simulations have been done where a maximum iteration limit is imposed to terminate the training process. In this case, the classification accuracy in every training step is calculated to evaluate the training progress. Surprisingly enough, the classification accuracy does not seem to improve when a large number of training epochs is used, after an initial increase in the early epochs, the curve starts to flatten, at the point of our termination criterion. Finally, we showed by simulations the robustness of our criterion as compared to the log likelihood stopping criterion, when modifying the model hyperparameters. The log likelihood criterion, when using a small learning rate, appears to have difficulties founding the maximum value that terminates the training process.

The evaluation of the stopping criteria was performed using many benchmark datasets, such as MNIST and OCR to ensure that we have come up with consistent results. Based on our study, we believe that the proposed stopping criterion for RBMs training is useful and has potential for further improvement in the future.

Synchronization dynamics on non-normal networks

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Nature offers a wealth of systems where basic unities multiply and non-linearly interact with each other to eventually exhibit a synchronous behavior. In particular, biology displays a vast assortment of examples, from myocyte cells coordinating the heartbeats to the synchronous firing pattern of coupled neurons.
The importance of self-organized collective behaviors in many biological systems has triggered the interest of scientists since long time, leading to the study of stability and, consequently, robustness of the synchronous state. In this context, a well-know mathematical tool has been developed, the Master Stability Function (MSF) [1], through which it is possible to investigate, among other parameters, the role that different interacting topologies have in the stability of the synchronized behavior [2]. It has been shown, for example, that long-range links enhance the possibility of synchronization [3] or that asymmetry can reduce it [4].

In this work, we studied the phenomenon of synchronization on non-normal networks, i.e., networks having a strong degree of directionality and a hierarchical structure, which appear to be ubiquitous in real scenarios [5]. At variance with the classical MSF approach, here we performed a stability analysis for the Jacobian matrix averaged on a period of the synchronous solution [6], studying in this way the stability as a function of the graph Laplacian eigenvalues (see the figure). In particular, to capture the non-normality effect, we complement the MSF analysis by taking into account the pseudo-spectrum [7]. We found (blue dots) that due to the non-normality of the network, the perturbed eigenvalues become unstable, despite the fact that the spectrum is stable, hence impeding the synchronization of the system. In the small boxes we plot a function $d(t)$ indicating the difference between the behaviors of each oscillator: we observe that when the network is symmetric (green) the system synchronizes ($d(t) = 0$), while in the non-normal case (blue) it does not. Such an outcome is consistent with our previous results for the pattern formation problem and states that linear analysis could be not sufficient once non-linearity and non-normality are at play [8]. This shows that non-normal networks are more difficult to synchronize if compared with their symmetric analogues. Moreover, by repeating the analysis with a classical MSF approach, we have corroborated our result by showing that non-normality may impede synchronization, even with a negative MSF, as in the case above. We have validated our results by considering several "real-world networks" of biological interest, e.g., the *C. elegans* neuronal network.

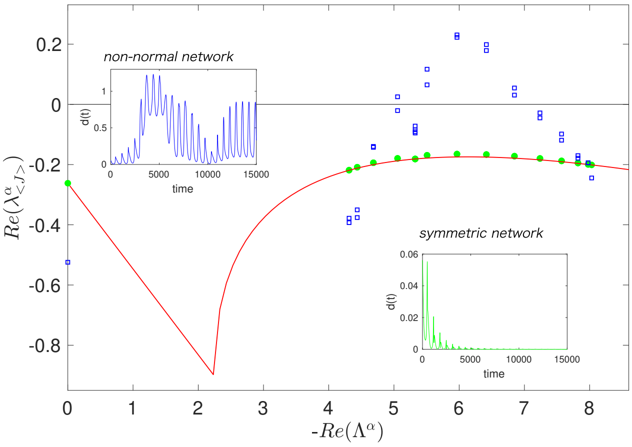

Fig. 1. The perturbed eigenvalues (i.e., the pseudospectrum, blue dots) become unstable due to the non-normality, even though the spectrum is all negative (green dots). In the small boxes we plot a function $d(t)$ indicating the difference between the behaviors of each oscillator: we observe that when the network is symmetric (green) the system synchronizes ($d(t) = 0$), while in the non-normal case (blue) it does not. Hence, by looking at the spectrum, we should expect synchronization, while, due to the non-normality of the network, the system does not synchronize.

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Five rules for friendly rivalry in iterated Prisoner's Dilemma

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Theory of repeated games is one of the most fundamental mathematical frameworks that has long been studied for understanding how and why cooperation emerges in human and biological communities. If the prisoner's dilemma (PD) game is repeated with sufficiently high probability, cooperation becomes a feasible solution because a player can reward and/or punish the co-player in subsequent rounds. This is known as direct reciprocity, one of the most well-known mechanisms for the evolution of cooperation.

According to recent understanding, most of classical strategies for direct reciprocity fall into one of two classes, 'partners' or 'rivals'[1]. A 'partner' is a generous strategy achieving mutual cooperation even under a noisy environment. Rival strategies, on the other hand, is more stringent against the co-player. If a player uses a rival strategy, it is guaranteed that the player's payoff is never be less than the co-player's. A schematic diagram of the strategy space is shown in Fig. 1.

Partners and rivals have different working conditions: For example, partners show good performance in a large population, whereas rivals do in head-to-head matches. A natural question would be on the possibility that a single strategy is *both* a partner and a rival simultaneously. If such an ideal strategy (called "friendly rival") exists, mutual cooperation is realized while assuring that the player is never be beaten by any kind of opponents.

In this work [2], by means of massive super-computing, we show that a tiny fraction of friendly rival strategies indeed exist among deterministic memory-three strategies for the iterated PD game. In particular, we focus on one of the friendly rivals, named CAPRI, because it can be described by simple five rules, which implies great potential importance in understanding and guiding human behaviour.

We also demonstrate that our friendly rivals exhibit evolutionary robustness for *any* population size and for *any* benefit-to-cost ratio. This property is demonstrated by evolutionary simulation in which CAPRI overwhelms other strategies under a variety of environmental conditions.

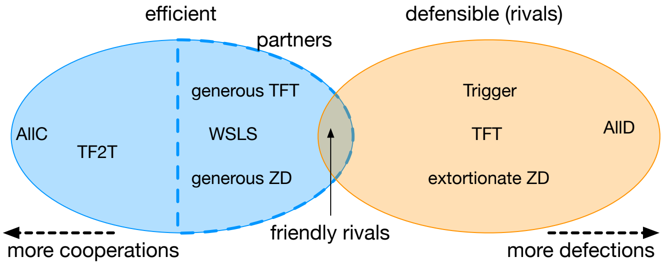

Figure 1: A schematic diagram of the strategy space. Strategies that tend to cooperate (defect) are shown on the left (right). The blue (red) ellipse represents a set of partner (rival) strategies. We found that the intersection, called "friendly rivals", indeed exists and shows an excellent performance in evolutionary game.

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Trends in urban flows: from Wi-Fi data to pedestrians' route choices

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The accurate estimation of human activity in cities is one of the first steps towards understanding the structure of the urban environment and estimating them with confidence is crucial for decision-making in numerous applications [1,2]. Detecting general trends in the flow of people between spatial locations is neither obvious nor an easy task due to the high cost of capturing these movements without compromising the privacy of those involved. Using data generated (2017-2019) by a network of sensors (Wi-Fi enabled devices) installed at around 1000 locations, we constructed a daily footfall (FF) signal by location (Figure 1.a) and derived a series of results to characterise each area in terms of two features: Core activities and Pedestrian flows / route complexity between two locations.

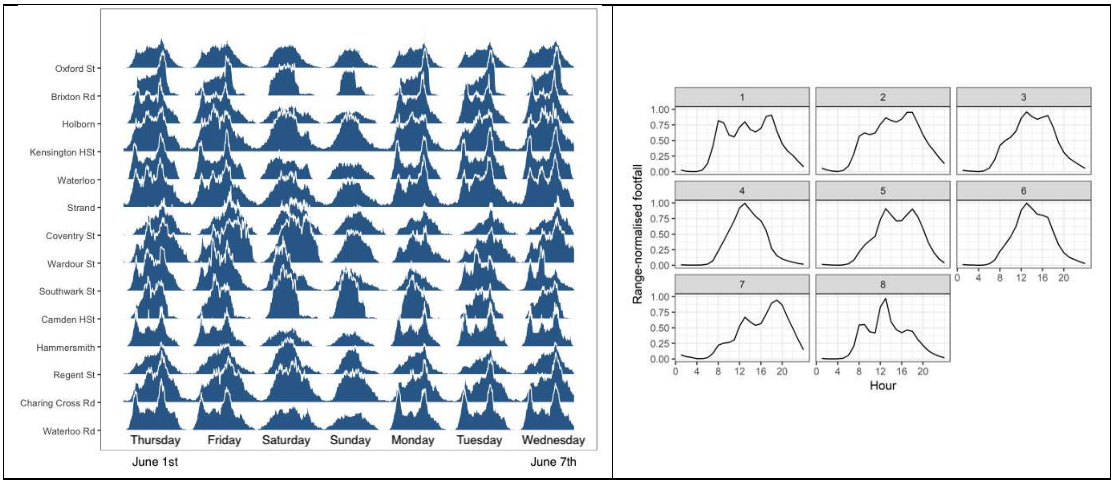

Figure 1: a) A week of measures at fourteen London locations where it is clear that different locations produce different FF signals; b) Weekday clustering of FF signals. Again, there's a clear distinction between locations, depending on their particular core activities

Core Activities. We produce the typical weekday/weekend signal for each location and then cluster them (using a Dynamic Time Warping approach) and found a core of eight canonical FF signals that tell us a story about the activities around these locations (Figure 1.b). For example, cluster 1 is a typical job location (FF peaks at morning/lunch/afternoon). **Pedestrians Flows and route complexity**. Without tracking people, we provided a measure (based on the concept of Local Transfer Entropy [3]) to determinate the most likely direction for the flow of people between locations, relating the number of pedestrians reaching location S1from S2 (and vice versa) by measuring the uncertainty between both signals. We noticed that for ~40% of the pair's locations, the flow profiles were the same between S1⟷S2 or meaningless (LTE≤0). To complete our analysis, we performed a semantic exploration over the walking directions (from the Google API) from S1 to S2 and then derived a route complexity score S, based on an assigned weight to each common word W_i and its associated distance d_i: S = $\sum_{i=1..12} W_i/d_i$. This S, in conjunction with the LTE flows, explains the different local dynamics observed in areas with the same FF profiles and with the same walking distance between them. In conclusion, in these nearby locations, street configuration and core activities (and not distance), are the drivers behind the FF footprints observed.

Identifying risk profiles in the London's public transport system

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Public transport networks are a key element in the survival of modern cities and their inhabitants. It is therefore of paramount importance to be able to identify which areas in the network are the most vulnerable to disruptions through a prompt and an effective risk assessment. Due to the complex nature of these networks, detecting the high risk areas is not always an obvious nor an easy task. One can identify transport hubs in the system that are not related to crowdedness but to the way they connect parts of the systems to each other spatially and temporally. These hubs, or brokers, have the potential to create more in the case of an accidental or a planned failure. Using detail spatial-temporal individual records from London's Underground transport network during 2012, an using a novel methodology to the field of Big Data (Local Transfer Entropy [1,2]) we derived alternative measures of disruption to the system. After the analysis, we produce two main outputs: 1) A comprehensive temporal profile of the volume of people that, minute by minute, is in each one of the stations (Fig. 1a). This corresponds not only to the individuals getting in/out of the transport network but also its transient population. 2) A complete spatiotemporal risk profile (Fig. 1b) that highlights the so-called hubs in the system. These provide relevant candidates for testing risk management scenarios. Our analysis is revealing those high-risk areas given by spatiotemporal correlations, which is in contrast with previous assumptions focussed on crowdedness.

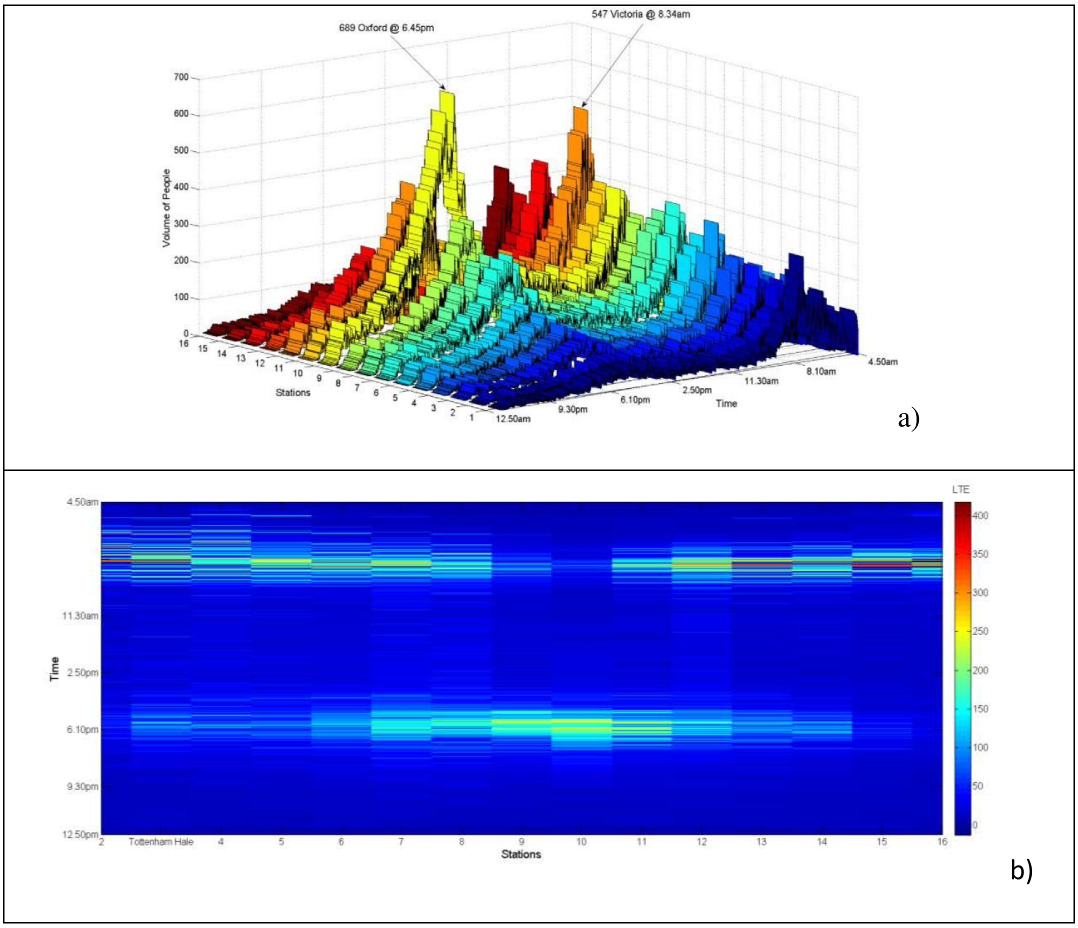

Figure 1: Volume of people (a) and Information profile (b) from the Victoria line in a typical weekday. In b, the areas with larger LTE values (red) are the ones identified as possible spatial-temporal points serving as hubs of information in the network.

Bosons Outperform Fermions: The Thermodynamic Advantage of Symmetry

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The recent miniaturization of heat engines to the nanoscale introduces the possibility of engines that harness quantum resources. The analysis of quantum engines provides important insight into how their efficiency compares to classical analogues and deepens our understanding of thermodynamic mechanisms at the quantum scale. We examine a quantum Otto engine with a harmonic working medium consisting of two particles to explore the use of wave function symmetry as an accessible resource. It is shown that a bosonic working medium displays enhanced performance when compared to distinguishable particles, while a fermionic working medium displays reduced performance. To this end, we explore the trade-off between efficiency and power output and the parameter regimes under which the system functions as engine, refrigerator, or heater. Remarkably, the bosonic system operates under a wider parameter space both when operating as an engine and as a refrigerator.

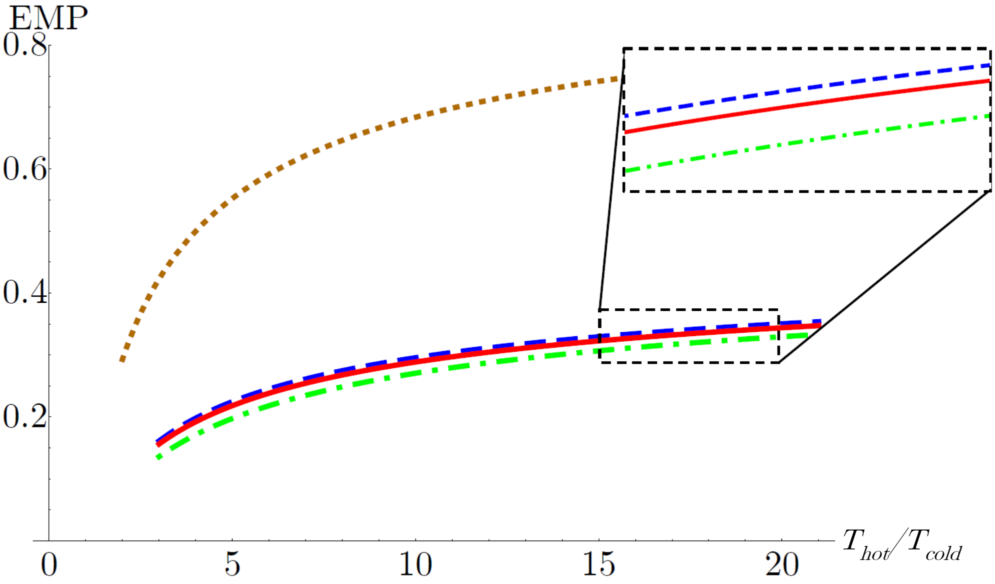

Figure 1: Efficiency at maximum power for a quantum Otto engine with a working medium of two boson (blue, dashed), distinguishable particles (red, solid), and fermions (green, dot-dashed). The classical, quasistatic limit of the EMP is given by the Curzon-Ahlborn efficiency (brown, dotted).

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Directed Percolation with Non-Unitary Quantum Cellular Automata

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In classical physics and computer science, cellular automata (CA) provide a powerful framework for investigating the emergence of large-scale complex structures from local dynamical rules [1]. Similarly, complex dynamics of quantum many body systems have been studied using Quantum Cellular Automata (QCA) [2], in which the cellular update rules are implemented by localizable unitary maps.

In this work, we develop a non-unitary QCA model, where the unitary rules are replaced by local completely-positive (CP) trace-preserving maps. This generalization of QCA enables exploration of non-equilibrium dynamics of quantum many-body systems with dissipation and decoherence. We construct a non-unitary QCA that in the fully dissipative limit reduces to Domany-Kinzel Cellular Automaton (DKCA) [3] - a classic model of directed percolation in one dimension. We simulate the dynamics of the model using infinite Time Evolving Block Decimation (iTEBD) for mixed states [4] verifying that the evolution agrees with the classical probabilistic DK dynamics. We then add small unitary rotations on the cells conditional on the state of their neighbors, exploring the effect of quantum corrections to the phase diagram of the DKCA. The presence of unitary rotations generates quantum entanglement in the steady state of the model, which we quantify using N-concurrance and negativity.

In addition to providing a novel framework for exploring fundamental non-equilibrium phenomena in quantum many body systems, non-unitary QCA models can be used for developing new applications for quantum devices operating in the presence of environmental noise. Non-unitary QCA is physically realizable in atomic physics platforms with regular lattice structures, such trapped ions, superconducting qubits and arrays of Rydberg ensembles [5]. The entanglement generated in the steady states of non-unitary QCAs can be exploited in quantum information processing and metrology applications.

Acknowledgements

This research was funded in part by the Australian Research Council Centre of Excellence for Engineered Quantum Systems (Project number CE170100009).

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Deterministic Diffusion

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Dynamical systems on the entire axis with discrete time are defined by the recurrence relation

$$x_{n+1} = \mathrm{f}(x_n), \qquad (1)$$

where f(x) is a real function given on the entire axis and x_0 is a given initial value. Equation (1) determines a trajectory $(x_0, x_1, ..., x_n, ...) = \mathrm{x}$ in the dynamical system (1) according to the initial value x_0 and the form of the function f. For the dynamical systems admitting the chaotic behavior of trajectories, the problem of construction of the entire trajectory or even of determination of the values of x_n for large n is quite complicated because, as a rule, the numerical calculations are performed with a certain accuracy and the dependence of the subsequent values of x_n on the variations of the previous values is unstable. Moreover, from the physical point of view, the initial value x_0 is specified with a certain accuracy. Therefore for the investigation of the behavior of trajectories for large values of time, we can analyze not the evolution of system (1) but the evolution of measures on the axis generated by this evolution.If a probability measure μ_0 (a normalized measure for which the measure of the entire axis is equal to 1) with density ρ_0 : μ_0 (A) $=\int_A \rho_0 dx$ is given at the initial time, then, for a unit of time, system (1) maps this measure into μ_1 : μ_1 (A) = μ_0 (f^{-1}(A)), where f^{-1} (A) is a complete preimage of the set A under the map f . The operator F that maps the density ρ_0 of the measure μ_0 into the density ρ_1 of the measure μ_1 is called a Perron–Frobenius operator [1]. The investigation of the asymptotic behavior of the density $\rho_n = F^n\rho_0$ as n → ∞ is reduced to the investigation of the behavior of the semigroup F^n . There are examples of dynamical systems (1) with locally stretching maps f for which the densities ρ_n are asymptotically Gaussian as n → ∞ independently of the choice of the density of the initial probability measure. In this case, it is said that deterministic diffusion occurs in the dynamical system (1). We consider examples of dynamical systems with deterministic diffusion [1,2]. We restrict ourselves to the so-called lifting dynamical systems with piecewise linear functions f (x) in (1).We briefly consider the mechanisms of appearance of the anomalous deterministic diffusion in the process of transportation in long billiard channels with spatially periodic structures [2,3]. We will consider a new dynamical system of type (1) with two-dimensional phase space covered by regular hexagons or regular triangles.

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Interdisciplinary Analysis of Automated Psychological Profiling and Conduct Prediction Using Big Data Techniques

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The objective of this paper is to investigate, from an interdisciplinary complex systems perspective, studies according to which automated psychological profiles, using digital tracks of social networks users, can predict their conduct. Such a statement seems to challenge the conception that humans are autonomous beings capable of intentional actions, since it presupposes that it is possible to calculate which interactions would be more likely to produce the desired results (especially for advertising purposes) only from the data available in a platform for digital interactions limited to 140 characters in natural language. Inspired by studies that challenge the accuracy of the big five models of human psychological profiling, we will seek to: (1) critically analyse the epistemological assumptions underlying personality tests and their alleged capability to predict the conduct of users of digital social networks, and (2) investigate the scope and possible limits of computational models and big data techniques (Clustering, LDA and Sentiment analysis) for text content analysis on Twitter. We will try to show that, even if predictive models are able to anticipate consumer actions in certain contexts, the social conduct of moral agents is not reduced to consumption options, which makes the moral agents conduct difficult to predict, especially over long time scales.

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In search for the social hysteresis – the symmetrical threshold model with independence on random graphs

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We study the homogeneous symmetrical threshold model with independence (noise) by pair approximation and Monte Carlo simulations on Erdős-Rényi and Watts-Strogatz graphs. The model is a modified version of the famous Granovetter's threshold model: with probability p a voter acts independently, i.e., takes randomly one of two states ±1; with complementary probability 1−p, a voter takes a given state, if a sufficiently large fraction (above a given threshold r) of individuals in its neighborhood is in this state. We show that the character of the phase transition, induced by the noise parameter p, depends on the threshold r, as well as graph's parameters. For $r = 0.5$ only continuous phase transitions are observed, whereas for $r > 0.5$ discontinuous phase transitions also are possible. The hysteresis increases with the average degree $\langle k \rangle$ and the rewriting parameter β. On the other hand, the dependence between the width of the hysteresis and the threshold r is nonmonotonic. The value of r, for which the maximum hysteresis is observed, overlaps pretty well with the size of the majority used for the descriptive norms in order to manipulate people within social experiments. We put the results obtained within this paper into a broader picture and discuss them in the context of two other models of binary opinions: the majority-vote and the q-voter model. Finally, we discuss why the appearance of social hysteresis in models of opinion dynamics is desirable.

Accidental vs. Preferential Attachment in Citation Networks

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The seminal work of Derek de Solla Price [1] constitutes one of the first observations of a very natural fact that as far as the growth of citations networks is concerned, "success breeds success". In more modern terminology, this may be referred to as the preferential attachment rule or Matthew's Effect [2]. It turns out that, however, a pure rich-get-richer fails to describe the sophisticated structure of citations networks. In our approach, we follow the previous attempts [3,4] for mixing preferential and random rules.

In this presentation, we discuss how to modify the preferential attachment rule so that it can reproduce a real citation network better. Combining the above-mentioned preferential and accidental rules we have obtained the exact formula for the degree distribution:

$$P(k) = \frac{1}{-\rho m + m + 1} \frac{\left(\frac{m}{\rho} - m\right)_{1+\frac{1}{\rho}}}{\left(k + \frac{m}{\rho} - m\right)_{1+\frac{1}{\rho}}},$$

where k is the node degree, m is number of edges being added in each iteration, ρ is the probability of using the preferential rather than random attachment rule and $(k)_n$ is the Pochhammer symbol.

Our analytical results were validated by means of numerical simulations as well as the real data from DBLP database [5].

Acknowledgements

The project was funded by POB Research Centre Cybersecurity and Data Science of Warsaw University of Technology within the Excellence Initiative Program - Research University (ID-UB).

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Multiscale Performer‑Audience Physical Synchrony in Joint Music Performance

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Previous studies have shown that physical coordination among musicians characterizes their joint performances [1,2]. This report presents an analysis of the physical synchrony between performers and audiences, aiming to test the hypothesis that audiences' subtle physical activities are linked to those of performers, reflecting the way they experience different modes of performance. The experiment involved the *Portorius string Quartet*, which performed movements from Mozart and Haydn quartets as well as improvised pieces in different performance modes. Specifically for the repertoire works, they performed the same piece twice with two performance modes: (a) “strict” mode (strictly following every textual instruction while aiming for the best and most expressive performance), and (b) “let-go” mode (with a creative, improvisatory approach, allowing more risk-taking and spontaneous expressive gestures) [2]. The performance was attended by forty-two audience members. We measured the performers’ head motions with inertial measurement units (IMUs) attached on their forehead, and the audiences’ body fluctuations with IMUs contained in the smartphones that the audiences wore around their neck [3]. We evaluated physical synchrony of each musician-audience pair on the time-frequency space via the wavelet transform coherence (WTC) of their acceleration norm time series. By averaging the coherence values, we obtained the summary coherence measure of *how much each member of audience was in sync with the musicians on average, at each time scale (1/frequency)* for each piece. Repeated measures ANOVA comparing the let-go and strict modes at each time scale revealed that, while the performer-audience synchrony was higher for the strict than for the let-go mode in the shorter timescale (around 1 second; from musical point of view more strictly metronomical, often less expressive performance mode), in the longer timescale of the order of ten seconds the let-go mode synchrony dominates (from musical point of view allowing for more spontaneous expressive gestures). These results suggest that collective music experience is embodied in a multiscale adaptive dynamical interaction process between the performers and audiences and indicate that this process is sensitive to the degree of creativity involved in the music making. Furthermore, the results support the utility of physical sensing technologies in capturing subtle but important aspects of collective music experience, and potentially helping to improve it through feedback.

Acknowledgements

We thank the Guildhall School of Music and Drama for allowing us to use their facilities and for the help of their IT team support. This study was supported by JST-COI Grant Number of JPMJCE1309 and by KAKENHI Grant Number JP20H03553 from JSPS/MEXT, Japan.

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Can a Financial Crisis Cause a Structural Damage to Economic Indicator Linkages? A Linear Stochastic Approach

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The purpose of this work is to investigate the influence of a financial crisis to the structural model of the economy. Research interest of how a financial crisis interferes on major economic indicators, lead us to check whether there are noticeable changes on linkages of endogenous economic variables behaviour over time. The Great Recession of 2008 (Subprime Mortgages Crisis) is chosen to be investigated. Main American economic indicators abstracted from the area of monetary policy and macroeconomics, are chosen to be investigated. Market reactions on changes of the above variables are mentionable and loudly stated by research. Moreover, central banks policies joint with government economic planning is focused on such indicators to abhor crisis. But is the explanatory power of these endogenous variables stable over time, and more over how are they affecting the outcomes of an analysis if the crisis period is included in dataset.

Our approach is based on a period from 2000 to 2019. The 2008 crisis period is considered to yield from 01/01/2008 to 30/06/2009. Our research approach is based on calculating cross correlation matrices, cluster investigation and then Principal Components Analysis. Continuing with the PCA findings we construct a VAR model, and we imply Impulse Analysis on it. The methodology is applied first on the entire data set and then on the period before and after the crisis neglecting on purpose the crisis period. Our goal is to check the hypothesis that a major crisis can affect the linkages between major economic variables and the model that defines the economic policies. The findings of cross correlations indicate a severe change of the impact on some variable pairs. A possible discontinuity existence coincides with the crisis, we could say that market just before crisis is balancing on a “saddle equilibrium point” in a mathematical sense.

As we can observe from our findings this large perturbation, is likely to cause a major structural damage to the state economy. Thus, time is needed after a major crisis to redefine the prior existing model to make a new guideline for the future.

Identification of skill in an online game: The case of Fantasy Premier League

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In all competitions where results are based upon an individual's performance the question of whether the outcome is a consequence of skill or luck arises. We explore this question through an analysis of a large dataset of approximately one million contestants playing Fantasy Premier League, an online fantasy sport where managers choose players from the English football (soccer) league. This contest is of considerable complexity due to both the stochasticity of the underlying game upon which it is based but also the colossal number of permutations available to managers in terms of decision-making. In spite of this, we show that managers' ranks over multiple seasons (over 13 years) are correlated (see Fig.1) and analyse the actions taken by managers to increase their likelihood of success. The prime factors in determining a manager's success are found to be long-term planning and consistently good decision-making in the face of the noisy contests upon which this game is based. Similarities between managers' decisions over time that result in the emergence of 'template' teams, suggesting a form of herding dynamics taking place within the game, are also observed. Taken together, these findings indicate common strategic considerations and consensus among successful managers on crucial decision points over an extended temporal period and offer an insight into the underlying laws which quantify the likelihood of success for the managers in the complex system of fantasy sports.

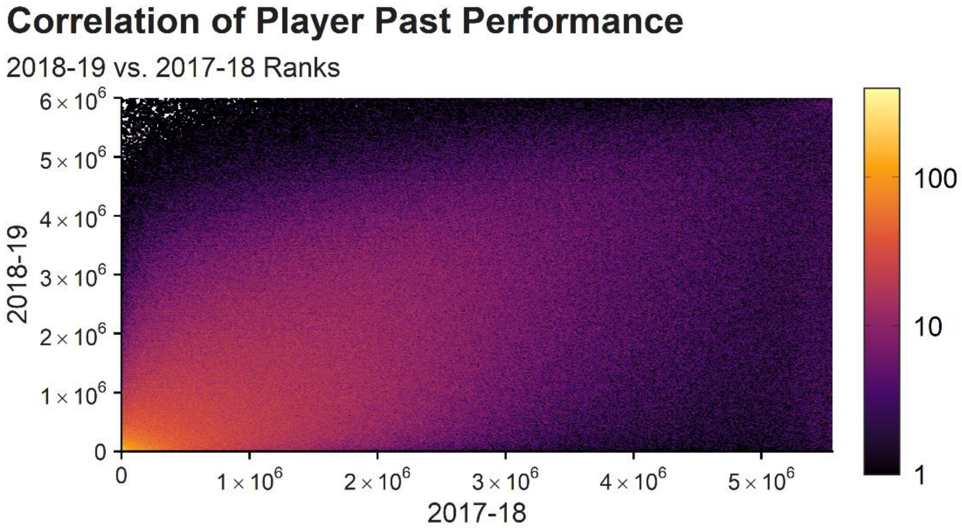

Figure 1: Relationship between the performance of users over editions of FPL. We show the relationship between user rank in two specific seasons (2018/19 and 2017/18) where a considerable correlation is observed, the bins are of width 5,000 with the color highlighting the number of users in each bin.

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Quantifying Uncertainty in a Predictive Model for Popularity Dynamics

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The ease with which individuals may now access online content has revolutionized the way in which information is consumed with social media platforms and online opinion boards being two paradigmatic examples of how information is generated, transmitted and finally absorbed. Modern information communication allow users to both become informed on topics and to easily interact online with each other, which may lead to further discussion in a cascade-like manner. The ability to accurately forecast which online content will become popular has attracted a lot of attention with recent literature focussing on developing methods based upon the theory of self-exciting point processes. Unlike homogeneous Poisson processes, the occurrence of previous events in such processes increases the future rate of activity, which can produce a `snowballing effect' leading to heavy-tailed distributions of cascade sizes, as observed in empirical data . An example of such a process is the Hawkes process, the application of which has been used to both model and predict the evolution of such cascades.

In this talk we will firstly introduce an analytically tractable approach to fully describe the aforementioned Hawkes process using branching processes. Using the results obtained from this analysis we then turn our attention to the question of predictability in systems with dynamics of this type. We show that our probabilistic interpretation enables the calculation not only of analytical predictions of future popularity but also of levels of confidence in these values. We conclude by highlighting the applicability of this approach to modelling the dynamics with which online content propagates by applying our model to empirical social media cascades.

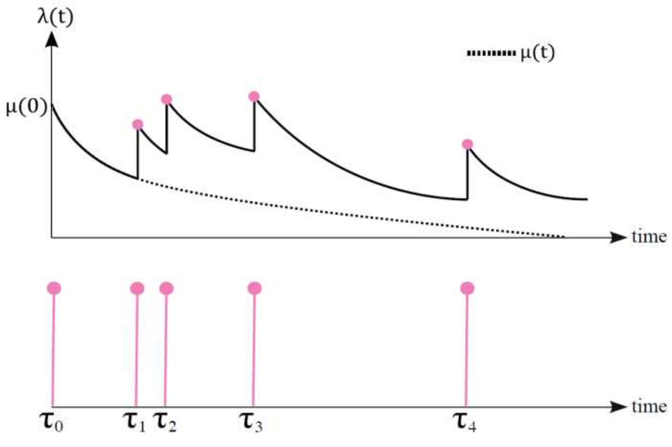

Figure 1: An example Hawkes process. The top panel shows the intensity function $\lambda(t)$ along with the background intensity $\mu(t)$ without any self-excitation shown by the dashed line. The bottom panel shows the corresponding event sequence of five events at times τ_i.

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The hierarchical route to the emergence of leader nodes in real-world networks

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A large number of complex systems, naturally emerging in various domains, are well described by directed networks, resulting in numerous interesting features that are absent from their undirected counterparts. Among these properties is a strong non-normality, inherited by a strong asymmetry, which stands out as a universal signature that characterizes such systems and guides their underlying hierarchy. In this talk, we consider an extensive collection of empirical networks and analyze their structural properties by using tools such as the entropy rate borrowed from information theory. A ubiquitous feature is observed amongst such systems as the level of non-normality increases (see Fig. 1). Several highly directed substructures aiming towards a terminal (sink or source) node, namely a node with only incoming or only outgoing edges, uniformly emerges. Such spontaneous occurrence is characterized by a threshold in the non-normality which yields terminal nodes, denoted here as leaders, detected by a sudden collapse of the entropy measure. Based on the networks' structural analysis, we develop a null model to capture features such as the aforementioned transition. Furthermore, depending on the relative number of leader nodes, the empirical networks' domains may be classified from more anarchic to more autocratic. Also, we show that the nodes' role at the pinnacle of the hierarchy is crucial in driving the dynamical processes in these systems. Taken together, these results pave the way for a deeper understanding of the architecture of hierarchical empirical complex systems and the processes taking place on them.

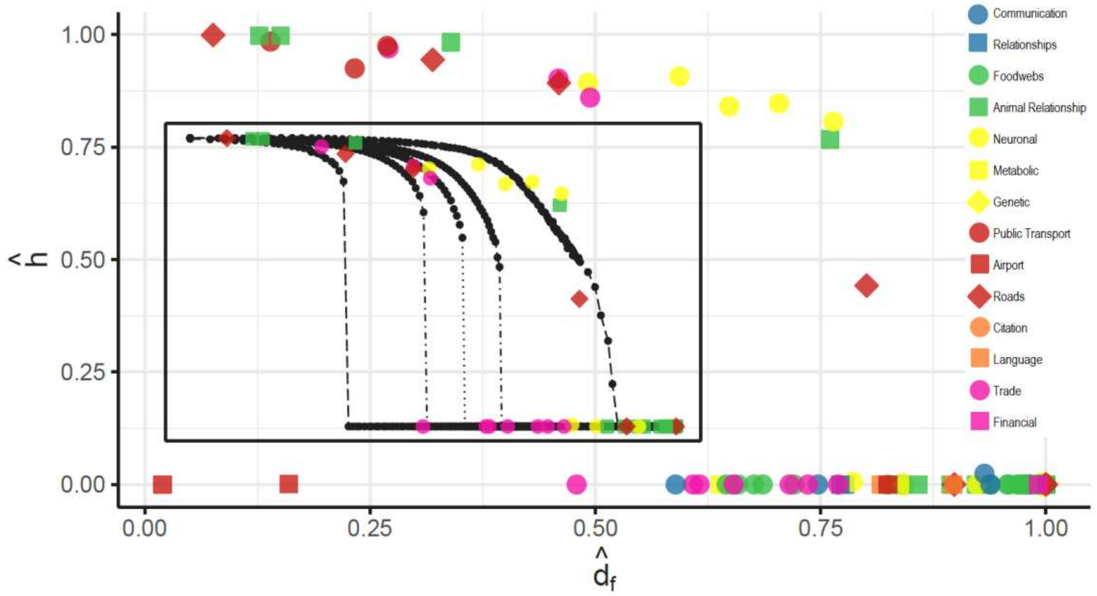

Figure 1: The collapse of relative entropy rate $\hat{h}$ as non-normality, represented by Henrici's departure $\hat{d}_f$, reaches a threshold indicates the emergence of leader nodes. In the inset, we show how our null model reproduces the transition in four domains of the 125 analyzed networks.

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Productive Ecosystems and the Arrow of Development

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Economic growth is associated with the diversification of economic activities, which can be observed via the evolution of product export baskets. Exporting a new product is dependent on having, and acquiring, a specific set of capabilities, making the diversification process path-dependent. Taking an agnostic view on the identity of the capabilities, we derive a probabilistic model for the directed dynamical process of capability accumulation and product diversification of countries. Using international trade data, we identify the set of pre-existing products, the product *Ecosystem*, that enables a product to be exported competitively. We construct a directed network of products, the Eco Space, where the edge weight corresponds to capability overlap. We uncover a modular structure, and show that low- and middle-income countries move from product communities dominated by small Ecosystem products to advanced (large Ecosystem) product clusters over time. Finally, we show that our network model is predictive of product appearances.

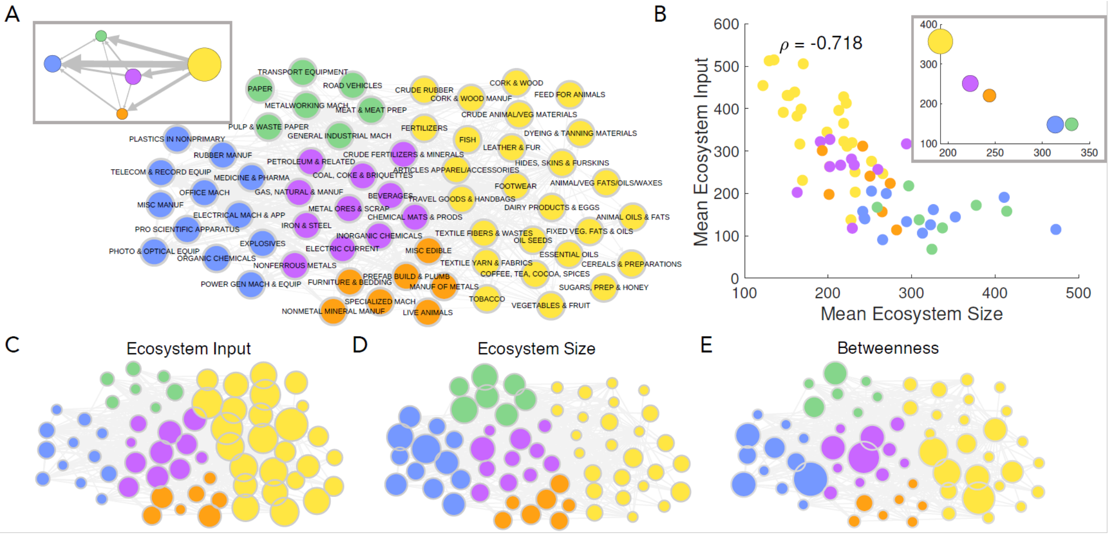

Figure 1: (A) Visualization of Ecosystem network at a 2-digit product division level (63 divisions). The directed edges correspond to product diversification paths estimated from export data. Nodes are coloured by node community. In the inset, we show the overall network aggregated to the community level. (B) The relationship between Ecosystem input (out-degree) and Ecosystem size (in-degree) at node and community (inset) level. (C-D) We can clearly see that the large Ecosystem input products (which are input to many other products) are located on the right and large Ecosystem size products (which require many inputs) are located in the left. Hence, the arrow of development often follows this right to left trajectory. (E) High Ecosystem input and size products are stepping stone products.

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Critical Synchronization Dynamics of the Kuramoto Model on a Large Human Connectome

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The hypothesis, that cortical dynamics operates near criticality also suggests, that it exhibits universal critical exponents which marks the Kuramoto equation, a fundamental model for synchronization, as a prime candidate for an underlying universal model. Here, we determined the synchronization behavior of this model by solving it numerically on a large, weighted human connectome network, containing *804092* nodes, in an assumed homeostatic state. Since this graph has a topological dimension $d < 4$, a real synchronization phase transition is not possible in the thermodynamic limit, still we could locate a transition between partially synchronized and desynchronized states. At this crossover point we observe power-law–tailed synchronization durations, with $\tau_t \simeq 1.2(1)$, away from experimental values for the brain. For comparison, on a large two-dimensional lattice, having additional random, long-range links, we obtain a mean-field value: $\tau_t \simeq 1.6(1)$. However, below the transition of the Connectome we found global coupling control-parameter dependent exponents $1 < \tau_t \le 2$, overlapping with the range of human brain experiments [1]. We have also studied the effects of additive Gaussian noise and the region of ultra-slow eigen-frequencies, where human brain operates and found similar results as before, the control-parameter dependent exponent suggests extended dynamical criticality below the transition point [2].

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Evolution of Coordination in Pairwise and Multi-player Interactions via Prior Commitments

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Upon starting a collective endeavor, it is important to understand your partners' preferences and how strongly they commit to a common goal. Establishing a prior commitment or agreement in terms of posterior benefits and consequences from those engaging in it provides an important mechanism for securing cooperation. Resorting to methods from Evolutionary Game Theory (EGT), here we analyze how prior commitments can also be adopted as a tool for enhancing coordination when its outcomes exhibit an asymmetric payoff structure, in both pairwise and multiparty interactions. Arguably, coordination is more complex to achieve than cooperation since there might be several desirable collective outcomes in a coordination problem (compared to mutual cooperation, the only desirable collective outcome in cooperation dilemmas). Our analysis, both analytically and via numerical simulations, shows that whether prior commitment would be a viable evolutionary mechanism for enhancing coordination and the overall population social welfare strongly depends on the collective benefit and severity of competition, and more importantly, how asymmetric benefits are resolved in a commitment deal. Moreover, in multiparty interactions, prior commitments prove to be crucial when a high level of group diversity is required for optimal coordination. The results are robust for different selection intensities.

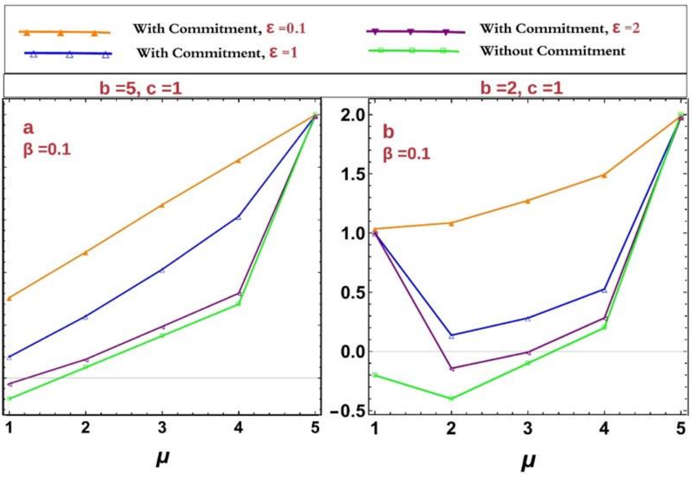

Figure 1: Prior Commitment significantly improves the population social welfare and coordination, especially when the cost of arranging it is not too high (see [1] for more details). Parameters: b, c: cost and benefit of coordination; β: intensity of selection, ε: cost of arranging commitment.

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Chaotic Transients and Hysteresis in an α² Dynamo Model

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The dynamics of the solar magnetic field can be studied using the mean-field dynamo theory, which is based on the approximation of two scales, which suggests that the magnetic field consists of a large-scale field with small-scale fluctuations. The large-scale field can be generated by the α² effect, related to the fluid's kinetic helicity. In the dynamo model, the α² effect is responsible for the regeneration of both the poloidal and toroidal components of the field. The presence of chaotic transients in a nonlinear α² dynamo is investigated through direct numerical simulations of the 3D magnetohydrodynamic equations. By varying the parameter that controls the injection of kinetic helicity into the domain, a hysteretic blowout bifurcation is conjectured to be responsible for the transition to dynamo, leading to a sudden increase in the magnetic energy of the attractor. This high-energy hydromagnetic attractor is suddenly destroyed in a boundary crisis when the helicity is decreased. Both the blowout bifurcation and the boundary crisis generate long chaotic transients that are due, respectively, to a chaotic saddle and a relative chaotic attractor.

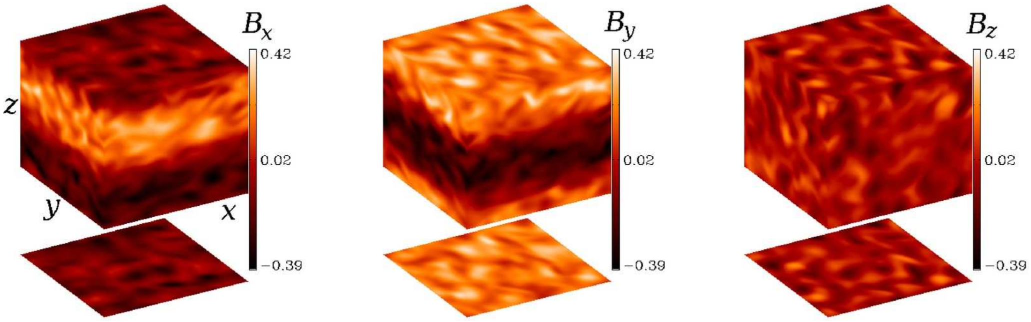

Figure 1: Intensity plot of magnetic field.

Acknowledgements

Oliveira, D. N and Rempel, E. L acknowledge financial support from Brazilian agencies CAPES and CNPq. Chertovskih, R acknowledges support from the Fundação para a Ciência e a Tecnologia (R&D Unit SYSTEC: POCI-01-0145-FEDER-006933/SYSTEC funded by ERDF — COMPETE2020 — FCT/MEC — PT2020 extension to 2018, UID/EEA/00147/2020 and NORTE-01-0145-FEDER-000033 supported by ERDF — NORTE 2020) as well as the Russian Science Foundation (project no. 19-11-00258 carried out in the Federal Research Center “Computer Science and Control” of the Russian Academy of Sciences, Moscow, Russian Federation).

Complexity In Psychological Self-Ratings: Implications For Research and Practice

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Psychopathology research is changing focus from group-based ‘disease models’ to a personalized approach inspired by complex systems theories. This approach, which has already produced novel and valuable insights into the complex nature of psychopathology, often relies on repeated self-ratings of individual patients. So far it has been unknown whether such self-ratings, the presumed observables of the individual patient as a complex system, actually display complex dynamics. We examine this basic assumption of a complex systems approach to psychopathology by testing repeated self-ratings for three markers of complexity: memory, the presence of (time-varying) short- and long-range temporal correlations, regime shifts, transitions between different dynamic regimes, and, sensitive dependence on initial conditions, also known as the ‘butterfly effect’, the divergence of initially similar trajectories. We analysed repeated self-ratings (1476 time points) from a single patient for the three markers of complexity using Bartels rank test, (partial) autocorrelation functions, time-varying autoregression, a non-stationarity test, change point analysis and the Sugihara-May algorithm. Self-ratings concerning psychological states (e.g., the item ‘I feel down’) exhibited all complexity markers: time-varying short- and long-term memory, multiple regime shifts and sensitive dependence on initial conditions. Unexpectedly, self-ratings concerning physical sensations (e.g., the item ‘I am hungry’) exhibited less complex dynamics and their behaviour was more similar to random variables. Psychological self-ratings display complex dynamics. The presence of complexity in repeated self-ratings means that we have to acknowledge that (1) repeated self-ratings yield a complex pattern of data and not a set of (nearly) independent data points, (2) humans are ‘moving targets’ whose self-ratings display non-stationary change processes including regime shifts, and (3) long-term prediction of individual trajectories may be fundamentally impossible. These findings point to a limitation of popular statistical time series models whose assumptions are violated by the presence of these complexity markers. We conclude that a complex systems approach to mental health should appreciate complexity as a fundamental aspect of psychopathology research by adopting the models and methods of complexity science. Promising first steps in this direction, such as research on real-time process-monitoring, short-term prediction, and just-in-time interventions, are discussed.

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Information and Communication Technologies Management in Digital Libraries

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This study aims examine the critical factors that should be considered by Digital Libraries in managing the complexity of the lifecycle of their resources for information systems, cloud computing infrastructure and information technology governance with a focus on organizational performance. The use of complex network technology is evolving toward comprehensive solutions to manage IT using a single repository and a single interface, dramatically reducing the costs and complexity of managing their computational resources. Faced with the emergence and speed of growth in the information economy, organizations have an urgent need to adopt IT governance best practice. The main drivers of the digital transformation are the globalization of markets, products, and resourcing; electronic information and knowledge intensity; and the geometric increase in the level of complexity of networking and connectivity. Information technology is involved with all operational procedures of the organization and, increasingly, is affecting the ability to offer services, influencing the efficiency, quality innovative capacity. The ability to leverage the potential of the technology is becoming increasingly critical to the success of Digital Libraries operations. The main tool to acquire this ability is to develop an effective organization of IT, Figure1, focusing on three key areas:

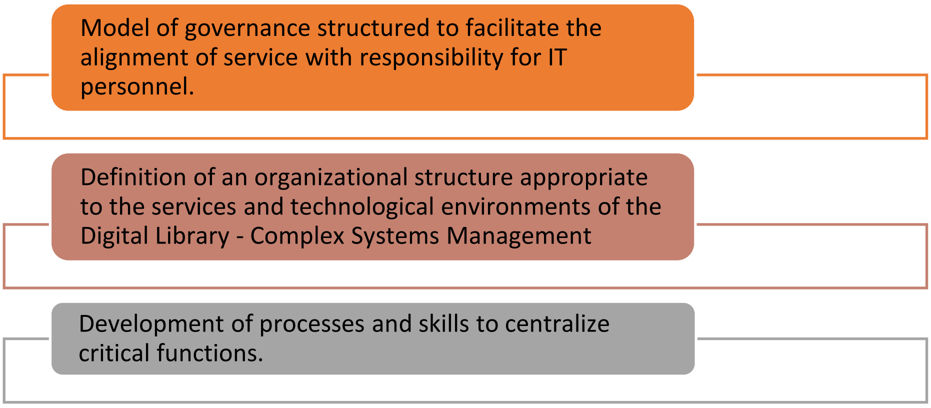

Figure 1 - IT Organization Focus and Complex Systems

This research proposes to examine the critical factors that should be considered by Digital Libraries in managing the lifecycle of their resources for information technology, cloud computing infrastructure and IT governance with a focus on complex networks systems.

Keywords: Information and Communication Technologies Management. Complex Networks. Information Systems. Digital Library. Technology Governance.

Acknowledgment: FAPESP Process: 2019/01128-7

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Complex Network Research Data Mining

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Research data mining requires the use of information systems and complex methods of searching, accessing, retrieving, and appropriating information on the web of data. Platforms such as Google Scholar Google, Elsevier, JSTOR, ResearchGate, ScienceDirect and the ones provided by commonly used universities identified with search terms. The challenge is to ensure that researchers are being exposed to the state of the art networked knowledge production. This study aims to analyze the process of searching and retrieving information, reflect on the role of information systems in the search result and the informational skills of the researcher in view of the quality of information retrieved. This research aims to analyze the complexities associated with data mining in research activities and to reflect on the search, access, retrieval and use of information tools in the Data Web. Researchers need to develop digital skills in the use of information systems and computational resources in the process of organizing information and knowledge. With the help of technology, they must cross-reference information of the materials found, broadening the search within your area and in other areas where the subject matter may have been studied.

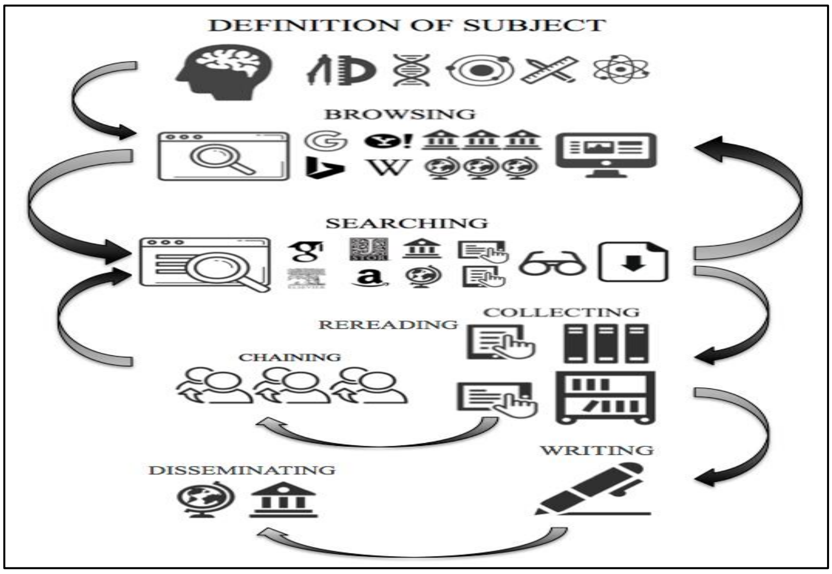

Fig. 1. Diagram of academic activities in reference research. Source: Author.

The activity diagram (Figure 1) exemplifies the process of academic creation using the Internet and shows how navigation and research are intertwined and of different natures. While navigation is geared towards a broader search, the search is more objective in getting the results.

Acknowledgment: FAPESP Process: 2019/01128-7

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Data Web Information Retrieval: the role of *Infographics in the Covid-19 Pandemic*

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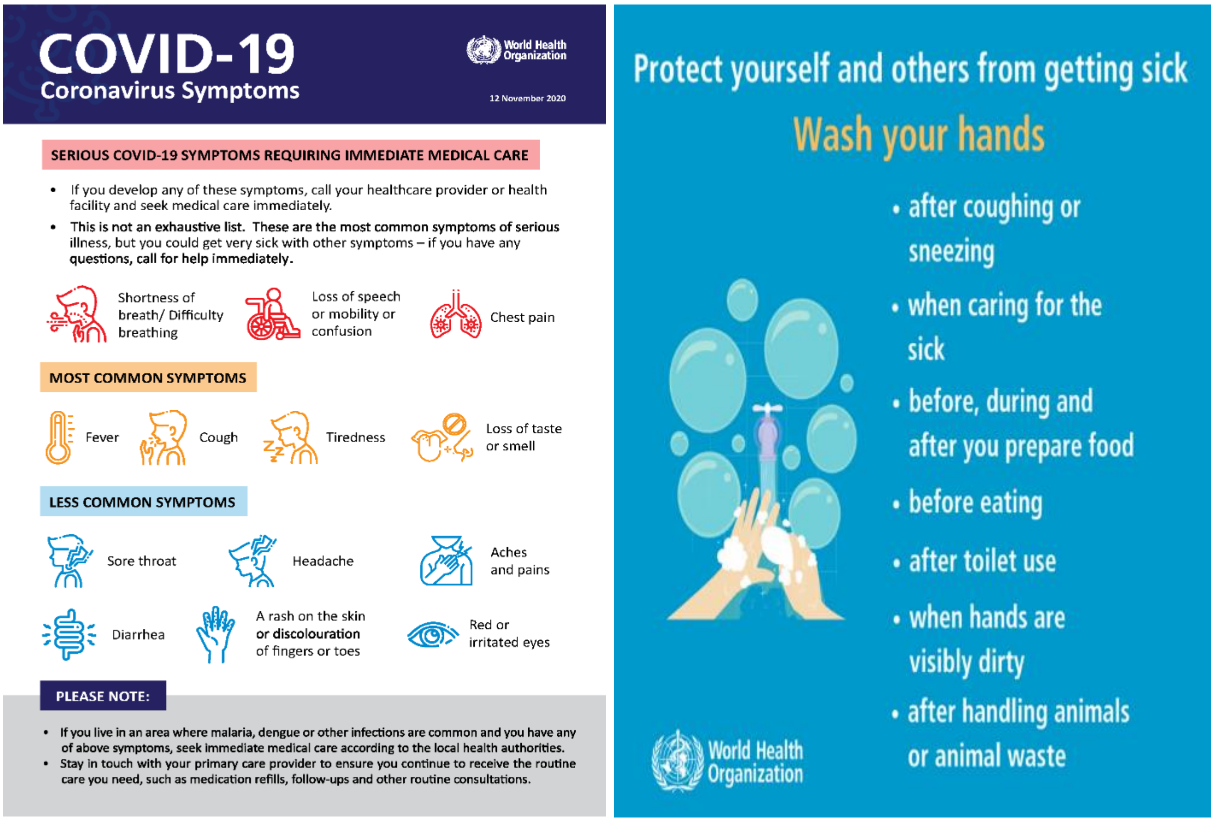
Owing to the new coronavirus and to the COVID-19, new words and concepts are being incorporated into our daily lives, and into linguistics as well. In an environment flooded with terms such as *new normal, flatten the curve, asymptomatic, comorbidity, community spread, herd immunity, lockdown, quarantine, social distancing, live* (as in live video or live streaming), and *work from home*, a new glossary has been made ordinary and assimilated by society. Times of crisis are usually harbingering of jumps in intellectual and technological innovation, as illustrated by the two world wars and by the coronavirus pandemics, Figure 1.



COVID-19
Coronavirus Symptoms
World Health Organization
12 November 2020

SERIOUS COVID-19 SYMPTOMS REQUIRING IMMEDIATE MEDICAL CARE

- If you develop any of these symptoms, call your healthcare provider or health facility and seek medical care immediately.
- This is not an exhaustive list. These are the most common symptoms of serious illness, but you could get very sick with other symptoms – if you have any questions, call for help immediately.

Shortness of breath/ Difficulty breathing
Loss of speech or mobility or confusion
Chest pain

MOST COMMON SYMPTOMS

Fever
Cough
Tiredness
Loss of taste or smell

LESS COMMON SYMPTOMS

Sore throat
Headache
Aches and pains
Diarrhea
A rash on the skin or discolouration of fingers or toes
Red or irritated eyes

PLEASE NOTE:

- If you live in an area where malaria, dengue or other infections are common and you have any of above symptoms, seek immediate medical care according to the local health authorities.
- Stay in touch with your primary care provider to ensure you continue to receive the routine care you need, such as medication refills, follow-ups and other routine consultations.

Protect yourself and others from getting sick

Wash your hands

- after coughing or sneezing
- when caring for the sick
- before, during and after you prepare food
- before eating
- after toilet use
- when hands are visibly dirty
- after handling animals or animal waste

World Health Organization

Figure 1: Infographic: protect yourself. Source: **World Health Organization**

A bibliographical research of publishers' databases in infographics, especially in the context of the production of descriptive documents reveals an almost complete inexistence of materials. In the aftermath of the closing down of cultural institutions such as museums and libraries, and of the emergence of news reports focused on the topics of the pandemics and social distancing, our research was redirected to the output of infographics by organs and entities involved in the divulging of information. We consider that this exploratory research, carried out in a virtual and remote format, presents results that justify the such technical and theoretical treatment related to the effect caused by the coronavirus and/or COVID-19.

Keywords: Librarianship. Coronavirus. COVID-19. Infographic

Acknowledgment: FAPESP Process: 2019/01128-7

Implementation of Singular Spectrum Analysis and Convergence Cross Mapping Algorithm in Financial Time Series

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Abstract

Are capital market prices the product of a stochastic processes or are they determined by deterministic chaos? Is there a non-linear causality between them? We are addressing these questions by studying two basic time series: the closing prices of the S&P 500 index which is one of the main indicators of the US capital market and the volatility index (VIX) of the New York Stock Exchange. With the help of Takens theorem (Takens 1981), Singular Spectrum Analysis and the Convergent Cross Mapping (CCM) algorithm as described in (Huffaker et al. 2017) we deal with these questions in the present framework. Implementing those relative new tools in the financial sector, we try to gain a new perspective on the financial indexes and try to take an alternative approach in the field of understanding the financial time series. An effort is made also to show that a prediction on the basis of next day values is feasible.

In order to achive that we examine the daily prices of the indexes for the period 2000 to 2019. The selection of the specific period is based on the fact that it contains the Financial Crisis of 2007-2008, an event that caused a major collapse in the financial sector. This perspective that could provide another insight in the financial data from the point of view of complexity theory, is relatively new and it is getting much attention among financial analysts, as there are many major successive predictions. The CCM algorithm, despite the fact that is computational costly and its results are highly sensitive to several parameters, can provide via lagged embedding time series, another causality measure avoiding the stochastic process procedure which is implemented in the Granger Causality test. The distinctive characteristic of the financial time series, which is noise, can affect the analysis and conclude in controversial results. This matter will be addressed in the conclusion sector of the present paper.

Keywords: Nonlinear analysis, R, Chaos, Correlation dimension, Singular Spectrum Analysis (SSA), Convergent Cross Mapping (CCM)

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AI-Square: Artificial Intelligence for Artificial Immunity

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Threats to the cyberspace are increasingly complex, and new approaches for attacks prevention, detection and investigation are required [1]. We propose AICS2: Artificial Intelligence for Cyberspace Security, to address the two core challenges: 1) define a new model for anomaly detection, GAD, the Graph-based model for Anomaly Detection; 2) build the new Artificial Intelligence primitives to identify and characterize cmoplex attacks in system logs and network traffic [2,3]. The target environment of AICSS2 is able to generate complex, heterogeneous log information matching individual actions. Out of these logs, behaviour graphs can be extracted to model the individual users, services and systems.

The GAD (Graph-based model for Anomaly Detection) framework entails 3 layers: data layer (data lake), analysis layer (execution of the core of attack detection algorithms) and knowledge layer (learning from the expert for data annotation, control or evaluation). Artificial Intelligence algorithms are highly specific of the expected properties of attack detection. A strong requirement for GAD is the availability of explicit, explainable, input and output layers representing actual artefacts from the system to be protected. This coupling enables the support of explainable Artificial Intelligence, which is critical in attack detection systems to enable cyber-investigator intervene rapidly for preventing the attacks from spreading and finalizing it.

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Macro Consequences of Micro Behaviours in Epidemics

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The increasing complexity of social relations, coupled with more integrated transportation systems, makes the spread of epidemics increasingly frequent and severe, making the prevention and containment more difficult. In this context, computational resources that make it possible to capture the individual behavior of heterogeneous agents, and their complex micro characteristics, are essential to quantify the dynamics and mechanisms of contagion and spread of diseases. The economic literature, unfortunately, still explores the macro effects of these epidemics based on epidemiological models such as SIR, without, however, evaluate the micro fundamentals of individuals' behavioral decisions or contagion mechanisms, such as the type or number of contacts between individuals. Limitations that this work tackle by using an agent-based model (ABM), with demographic and census data parameters to incorporate social economics epidemiological characteristics differences for classes of people, to incorporate an individual behavior approach for each of these classes, and also for business and government, increasing the capabilities of the model to reproduce direct and indirect effects of interventions in the dynamics of infections and the economy. Therefore, by basing the model on the daily micro-foundations of the lives of individuals, i.e., their social interactions, such as: using public transport, attend school, working, as well as various decisions such as isolation, it generates epidemiological, social, and economic dynamics at the macro level. The model, from an epidemiological point of view, for COVID-19, captures these dynamics with a SEIRD model. From a social point of view, the macro-dynamics incorporate the changes in perceptions of well-being that include general satisfaction with life, with the family, and the health system. From an economic point of view, the model captures macro-dynamics through the assessment of specific changes in the economy with proxies like the labor market with the reduction in working hours, loss of employment or closing of businesses, and requests for subsidies or grants. This work aims to support improvement in forecasting and management of the evolution of epidemics; and in the development of new approaches to mitigate its economic consequences, leading to the optimize public and private resources and lives saved, potentially filling a gap in the literature.

Statistics and stochastic interest rate models for climate change mitigation

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High future discounting rates favor inaction on present expending while lower rates advise for a more immediate political action. A possible approach to this key issue in global economy is to take historical time series for nominal interest rates and inflation, and to construct then real interest rates and finally obtaining the resulting discount rate according to a specific stochastic model. Extended periods of negative real interest rates, in which inflation dominates over nominal rates, are commonly observed, occurring in many epochs and in all countries. This feature leads us to choose a well-known model in statistical physics, the Ornstein–Uhlenbeck model, as a basic dynamical tool in which real interest rates randomly fluctuate and can become negative, even if they tend to revert to a positive mean value. By covering 14 countries over hundreds of years we suggest different scenarios and include an error analysis in order to consider the impact of statistical uncertainty. We find that only 4 of the countries have positive long-run discount rates while the other ten countries have negative rates. The results provided increase the priority of confronting global actions such as climate change mitigation. We extend the analysis by first allowing for fluctuations of the mean level in the Ornstein–Uhlenbeck model and secondly by considering modified versions of the Feller and lognormal models. In both cases, results remain basically unchanged thus demonstrating the robustness of the results.

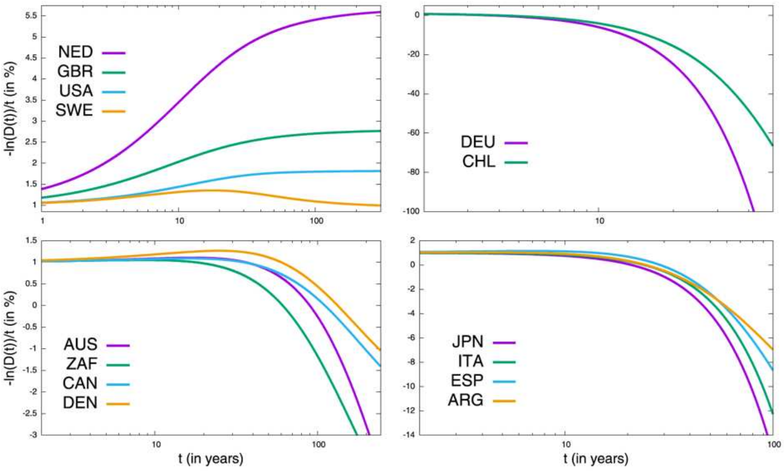

Figure 1: The logarithmic discounting rate as a function of time for several countries.

Acknowledgements

This work was partially by MINEICO (Spain), Agencia Estatal de Investigación (AEI) and Fondo Europeo de Desarrollo Regional (FEDER) through grants FIS2016-78904-C3-2-P and PID2019-106811GB-C33; by Generalitat de Catalunya (Spain) through Complexity Lab Barcelona (contract no. 2017 SGR 608).

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Gender-based pairings influence cooperative expectations and behaviours: A citizen science public experiment

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The study explores the expectations and cooperative behaviours of men and women in a lab-in-the-field experiment by means of citizen science practices in the public space. It specifically examines the influence of gender-based pairings on the decisions to cooperate or defect in a framed and discrete Prisoner's Dilemma game after visual contact. Overall, we found that when gender is considered behavioural differences emerge in expectations of cooperation, cooperative behaviours, and their decision time depending on whom the partner is. Men pairs are the ones with the lowest expectations and cooperation rates. After visual contact women infer men's behaviour with the highest accuracy. Also, women take significantly more time to defect than to cooperate, compared to men. Finally, when the interacting partners have the opposite gender they expect significantly more cooperation and they achieve the best collective outcome. Together, the findings suggest that non verbal signals may influence men and women differently, offering novel interpretations to the context-dependence of gender differences in social decision tasks.

Figure 1: Behavioural domains by gender pairing. The number in each cell shows the normalised value; the standardised mean difference is calculated as the difference in means between groups for each behavioural domain divided by the standard deviation of each behavioural domain.

Acknowledgements

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Fluctuations in System of Coupled Oscillators induce Micro-Correlations

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In the Kuramoto model of infinitely many globally coupled phase oscillators with different frequencies, beyond the synchronization transition the oscillators separate perfectly into two groups: an ordered one locked to the mean field, and a disordered one rotating at different frequencies. This picture is not exact for finite-sized ensembles, where the mean field fluctuates due to the finite-size effects. We demonstrate that these fluctuations lead to cross-correlations in the disordered group on a microscopic scale. We derive the properties of the cross-correlations analytically under an assumption of white noise fluctuations of the mean field. For finite ensembles where mean field fluctuations are not delta-correlated, cross-correlations are explored numerically in a model that involves active and passive tracer-type oscillators.

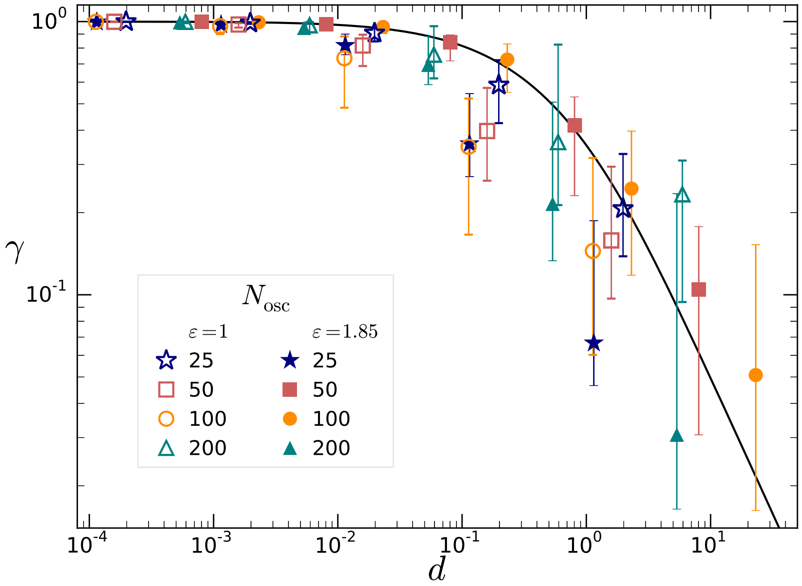

Figure 1: Comparison of the observed cross-correlation in sub- and supercritical ensembles (open and filled symbols, respectively) of different ensemble sizes Nosc compared with the analytical model (solid line).

Acknowledgements

This talk and the corresponding paper were developed within the scope of the IRTG 1740 / TRP 2015/50122-0, funded by the DFG/ FAPESP. A. P. was supported by the Russian Science Foundation (grant No. 17-12-01534). The authors thank D. Goldobin, R. Cestnik, M. Wolfrum, O. Omel'chenko, D. Pazó, H. Engel, and R. Toenjes for helpful discussions.

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Effect of limb dominance on knee extensor torque complexity during fatiguing intermittent isometric contractions

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Muscle force (or torque) output exhibits constant inherent fluctuations. These fluctuations possess a statistically irregular temporal structure, or “complexity”, which reflects the ability to modulate motor output rapidly and accurately in response to task demands and provides significant insight into motor control. Neuromuscular fatigue reduces the complexity of muscle torque output, as quantified by decreased approximate entropy (ApEn) and more Brownian fluctuations in detrended fluctuation analysis (DFA) α.

Long-term preferential use of the muscles of one side of the body is associated with changes in motor unit control and discharge properties. As motor units transduce synaptic input from the nervous system into muscle force, such changes could have implications for muscle torque fluctuations and complexity. This study aimed to determine the effect of limb dominance on muscle torque complexity during fatiguing contractions. It was hypothesised that adaptations from long-term preferential use of participants’ dominant limb would lead be associated with different motor control strategies, as quantified by the rates of change in ApEn and DFA.

Nine healthy participants performed, on separate days, intermittent isometric contractions (6 s contraction, 4 s rest) of their dominant and non-dominant knee extensors, to task failure at 50% of their maximal voluntary contraction. Complexity was quantified using ApEn, which characterises the regularity of a time-series, and DFA α, which characterises the long-range fractal correlations and noise colour in a time-series.

Time to task failure did not differ between the dominant and non-dominant limbs ($P = 0.63$). Muscle torque complexity, as measured by ApEn ($P = 0.51$) and DFA α ($P = 0.36$), did not differ between the dominant and non-dominant limbs at the start of contractions. ApEn significantly decreased and DFA α significantly increased as fatigue developed, and reached common values in both limbs at task failure. The rate of decrease in ApEn and increase in DFA α did not differ between the limbs.

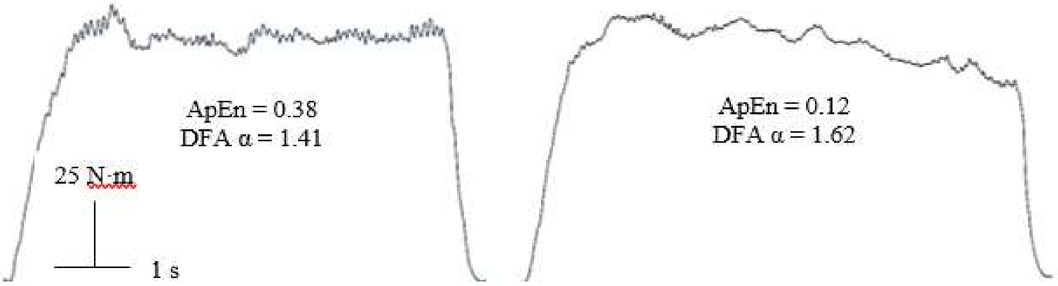

Figure 1. Raw torque outputs from the dominant limb of a representative participant.

In contrast to the hypothesis, limb dominance had no effect on motor control strategies and the rate of the fatigue-induced loss of muscle torque complexity. These results suggest that the adaptability of motor control, which measures of complexity are thought to reflect, is similar in both the dominant and non-dominant limbs under basal conditions and is maintained equally well during fatiguing contractions. Moreover, the common values attained at task failure indicate that the adaptive capacity of each limb was reduced to the same extent.

THE BRANCH OF ECONO-BYOPHYSICS AS A PREREQUISITE OF THE DEVELOPMENT OF THE CONCEPTION OF ELECTRONIC CURRENCY

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Abstract. Last modern age is characterized by the enormous development of the various integrative scientifical systems. The Human being is not only a complex biological system but also a socio-economical one that interacts with all factors including also the social aspects and finally the result is the well developed healthy, educational and social Human individual as a component of the complex system of the society. The classical Latin phrase "Mens sana in corpore sano" explains the harmony and the equilibrium of the Human being with the environmental medium. The complex theory of equilibrium is a main purpose of the study of complex dynamical systems.

The recent paper aims to study the complex analysis of the quantitative mathematical expression of the cost as the functional dependence of the molar mass of the chemical substance that is the constituent component of the products. The human being who is the driving force of the development of the society as a complex system and as a consumption potential of the goods stays namely on this study of this quantitative analysis of the price. The integrative World globalization of all processes is explained by the common solution of the complex problems of political and economical aspects within the limits of this integrative form of the political unions like the European Union. These formations have the final result of the utilization of the common currency like euro with the regarding of the respective common use of the energy resources, solutions of the strategic big problems like ecological problems, pandemic situations, macroeconomical aspects, etc.

All the above mentioned aspects stay on the creation of the modern scientifical platforms like econophysics, biophysics, bioeconophysics, sociophysics, social dynamics, etc., that have the aim of the deep complex study of the socio-economical processes by the application of the classical theory of physics and mathematical statistics.

The database of medical substances with therapeutic effect (electronic Drug bank database) stays on the base of the creation of this quantitative dependence of the price as the function of the molar mass of the substances both of food nature and of another nature like clothes and various types of products of energetical and material origin. The choosing of this Drug bank database is explained by the various large scale of the values of molar masses from possible minimal values till very big biological molecules with high molar masses (>100 kDa). The theory of physiological receptors which have the interaction and the regulation functions at the biochemical and energy levels uses the fundamental first law of thermodynamics that is not only pure physical law but also of universal character. This quantitative description is performed by the complex integrative application of the bases of econophysics, biophysics, pharmacology and the pharmaceutical kinetics theories which lead to the creation of the new scientifical conception of econo-biophysics (bioeconophysics), (biosocioeconophysics), etc.

The following stages of this complex study are performed: 1. The obtaining of quantitative estimation of the price of one mole of medications; 2. The obtaining of the dependences of half-life time as the function of the molar masses of medications; 3. The research of the dependences of activation energy of receptors as the result of the interaction with ligand's medications with various molar masses; 4. The quantitative estimation of the quantity of receptors by the dependences of the prices of one gram as the function of the mass of one medication's form; 5. The obtaining of the quantitative law of the interval of time of administration doses of medications.

These expressions could be extended not only at the medical level but also at the large scale of all social processes and could serve as the prerequisite of the final estimation of the cost as the function of molar masses of the substances and could serve for the creation of the World electronic currency with the measurement unit of Joule/mole which is able to solve effectively the global processes.

Key words: bioeconophysics; half-life; molar mass; activation energy; price of one mole; microeconomical state; dose administration interval of time; electronic universal World currency.

Shock propagation in supply and demand constrained input-output economies

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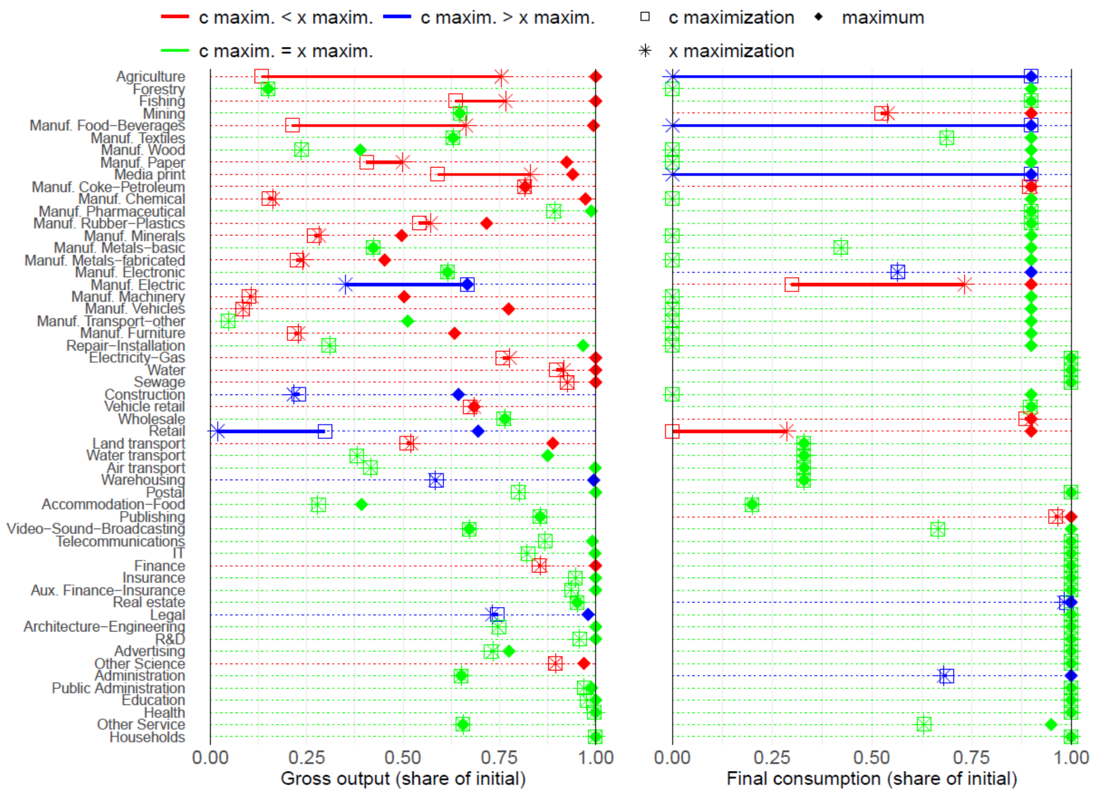
Social distancing measures adopted to combat the COVID-19 pandemic have created severe disruptions to economic output. During lockdown firms are required to shut down or substantially reduce their economic activity if they cannot comply with social distancing rules and are located in non-essential industries. Another source of negative direct shocks arises from changed consumption behavior of individuals to avoid infectious exposure. The shocks to the economy are highly industry-specific and therefore affect firms in heterogeneous ways [1]. Since firms are embedded in production networks, these direct shocks will propagate upstream (due to reduced demand to suppliers) and downstream (due to reduced supply for customers) [2]. We show that standard IO models which allow for binding demand and supply constraints yield infeasible solutions when applied to empirical data from the United Kingdom. We then introduce a mathematical optimization procedure which is able to determine optimal and feasible market allocations, giving a lower bound on total shock propagation. We find that even in this best-case scenario network effects substantially amplify the initial shocks. To obtain more realistic model predictions, we study the propagation of shocks out of equilibrium by imposing different rationing rules on firms if they are not able to satisfy incoming demand. Our results show that overall economic impacts depend strongly on the emergence of input bottlenecks, making the rationing assumption a key variable in economic predictions.

Figure 1: Economic impacts on industries resulting from optimization method.



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Analysis of Brazilian Agricultural Production through Complex Networks

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In this work, the complex systems approach was used to analyze Brazilian agricultural production using data from the 2006 Agricultural Census, which consists of 258 different products present in all 137 Brazilian mesoregions. For this purpose, we used a different approach of Hidalgo (2007) for visualizing the network, despite having used the same computational tool from these authors. The generated network offered an important visualization of the country's agricultural production, showing aspects that could not be perceived outside the global scope. We indicate that aspects such as the spatial distribution of the agricultural products, and their respective productive arrangements, and regional economic dynamics, as influential vectors on the weight of the proximity measure. This approach to agriculture production allows us to show the Brazilian regional agriculture production network and understand the main factors associated with these productions. These results highlighting important aspects that can be pertinent to the design and evaluation of public policies in the context of food security and sovereignty in Brazil.

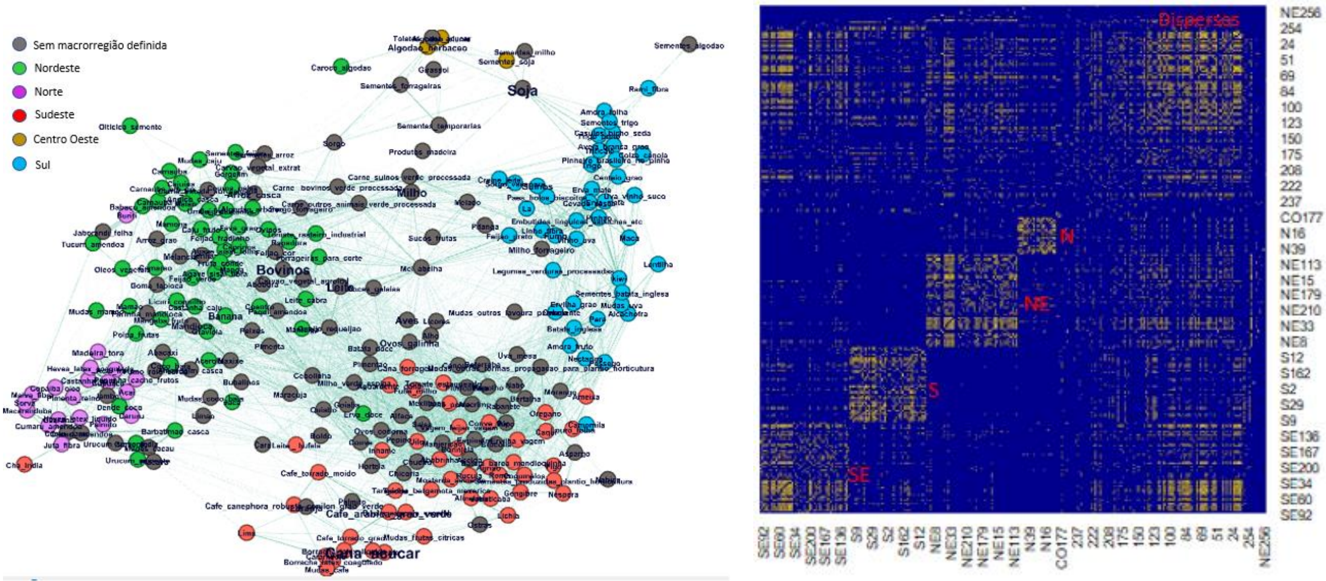

Figure 1: Spatialization of the network agriculture products in the 5 major Brazilian regions

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A Novel Methodology for Epidemic Risk Assessment: the case of COVID-19 outbreak in Italy[1]

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The prediction of the future developments of a natural phenomenon is one of the main goals of science, but it remains always a great challenge especially when the phenomenon that one is observing involves people that can have a feedback reaction on the observed quantities. This is particularly true in the case of epidemics, especially with the COVID-19 outbreak that the world is suffering in this period. We propose a novel data-driven framework for assessing the a-priori epidemic risk of a geographical area and for identifying high-risk areas within a country. Our risk index is evaluated as a function of three different components: the hazard of the disease, the exposure of the area and the vulnerability of its inhabitants. As an application, we discuss the case of COVID-19 outbreak in Italy. We characterize each of the twenty Italian regions by using available historical data on air pollution, human mobility, winter temperature, housing concentration, health care density, population size and age. We find that the epidemic risk is higher in some of the Northern regions with respect to Central and Southern Italy. The corresponding risk index shows correlations with the available official data on the number of infected individuals, patients in intensive care and deceased patients, and can help explaining why regions such as Lombardia in particular, but also Emilia-Romagna, Piemonte and Veneto, have suffered much more than the rest of the country. Although the COVID-19 outbreak started in both North (Lombardia and Veneto) and Central Italy (Lazio) almost at the same time, when the first cases were officially certified at the beginning of 2020, the disease has spread faster and with heavier consequences in regions with higher epidemic risk. Our framework can be extended and tested on other epidemic data, such as those on seasonal flu, and applied to other countries. We also present a policy model connected with our methodology, which helps policy-makers to take informed decisions.

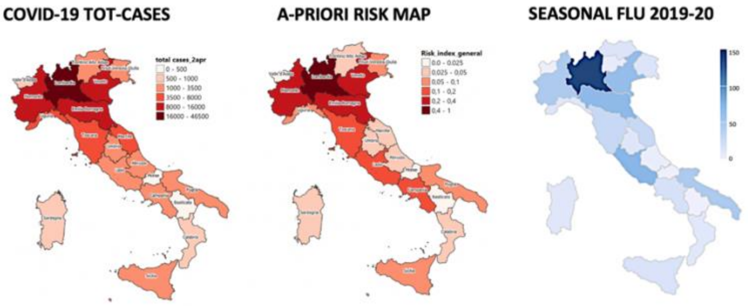

Figure 1: (a) Spatial distribution of COVID-19 total cases in Italy; (b) A-priori risk map; (c) the most struck regions from 2019-2020 seasonal flu according to the ISS data. The geographical correlation with the risk map is evident for both the epidemic flus.

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Why Lot? How Sortition could help Representative Democracy

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In this study we present a new analytical model of a Parliament and investigate the beneficial effects of the selection of legislators by lot in order to reduce some of the drawbacks of modern representative democracies. Resorting to sortition for the selection of public officers used to be in the past a popular way of taming factionalism in public affairs. Factionalism is assumed to be detrimental since public officers tend to favour their own faction instead of pursuing the general interest. In this respect our mathematical model shows in a rigorous way how it is possible to improve the efficiency of a Parliament by introducing the use of sortition to select part of its members. It will be shown that, starting from a Parliament working with two parties (or coalitions), where the costs of representative democracy are quite apparent through the detrimental effects of party discipline, one can beneficially move towards a Parliament where independent, randomly selected legislators sit alongside elected members. In particular, we show that increasing the number of independent legislators up to a critical point enhances the efficiency of the Parliament and puts into check the factionalism likely to arise from party discipline.

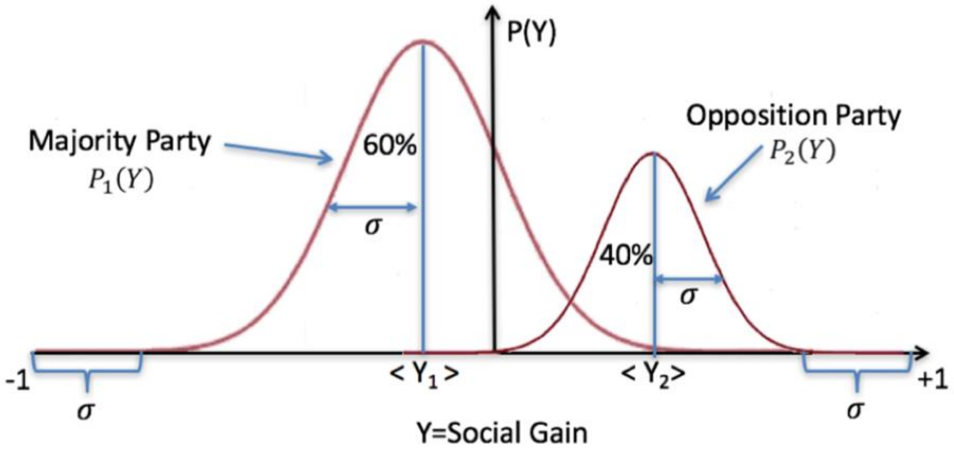

Figure 1: Gaussian distributions of legislators belonging to the two parties $P_1(Y)$ and $P_2(Y)$. The two curves also represent the distributions of proposals coming from the two parties.

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http://www.pluchino.it/parliament-ita.html

Abstract

We have performed the comparative spectral analysis of structural connectomes for various organisms using open-access data. Our results indicate new peculiar features of connectomes of higher organisms. We found that the spectral density of adjacency matrices of human connectome has maximal deviation from the one of randomized network, compared to other organisms. Considering the network evolution induced by the preference of 3-cycles formation, we discovered that for macaque and human connectomes the evolution with the conservation of *local clusterization* is crucial, while for primitive organisms the conservation of *averaged clusterization* is sufficient. Investigating for the first time the level spacing distribution of the spectrum of human connectome Laplacian matrix, we explicitly demonstrate that the spectral statistics corresponds to the critical regime, which is hybrid of Wigner-Dyson and Poisson distributions. This observation provides strong support for debated statement of the brain criticality.

Spreading of Performance Fluctuxations on Real-World Project Networks

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Understanding the role of individual nodes is a key challenge in the study of spreading processes on complex networks. In this work we propose a novel metric, the reachability-heterogeneity (RH), to quantify the vulnerability of each node with respect to a spreading process on a network. We then introduce a dataset consisting of four large engineering projects described by their activity networks, including records of the performance of each activity; such data, describing the spreading of performance fluctuations across activities, can be used as a reliable ground truth for the study of spreading phenomena on networks. We test the validity of the RH metric on these project networks, and discover that nodes scoring low in RH tend to consistently perform better. We also compare RH and seven other node metrics, showing that the former is highly interdependent with activity performance. Given the context agnostic nature of RH, our results, based on real-world data, signify the role that network structure plays with respect to overall project performance.

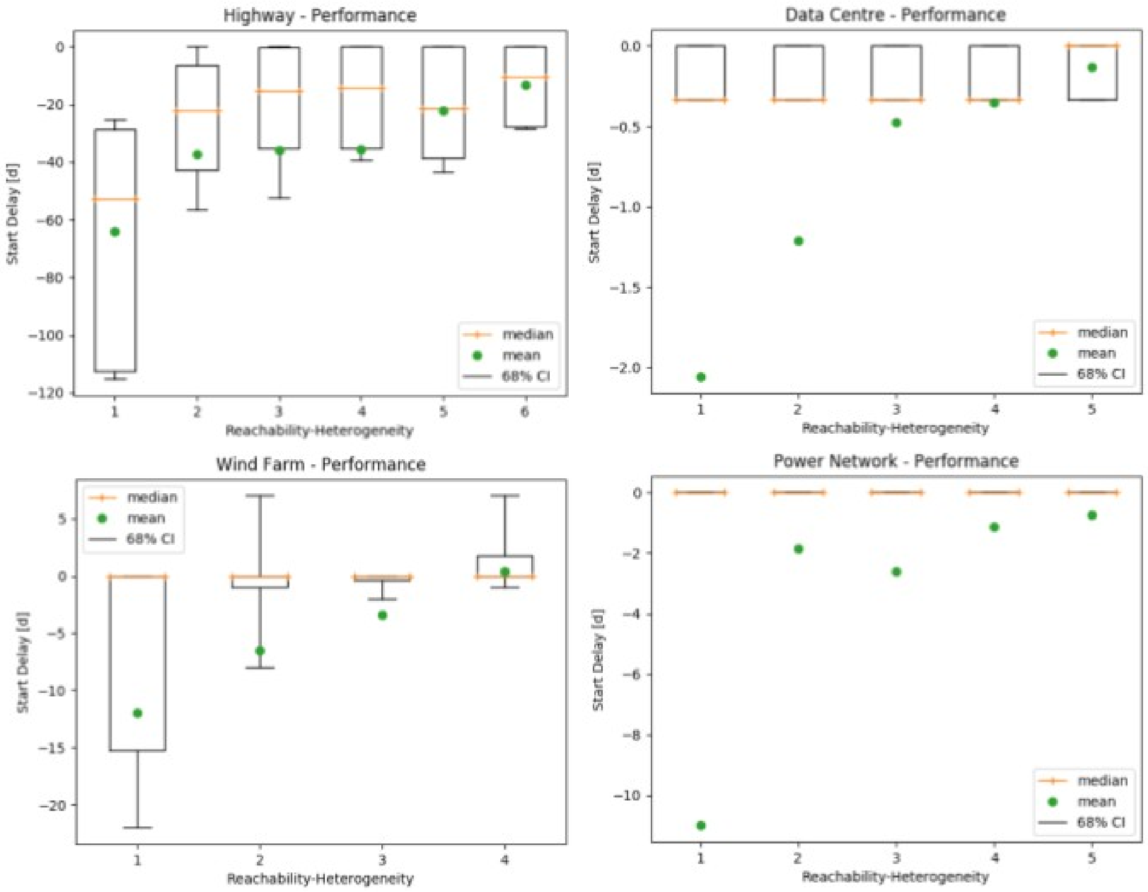

Figure 1: For each activity of each project, we report Start Delay (in days) and RH score (at the node level). Data are binned uniformly along the RH dimension to mitigate noise. A trend emerges in all four datasets with higher RH values corresponding to longer delays, i.e., worse performance.

Different kinds of chimera states in a network of locally coupled Stuart-Landau oscillaotrs

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We discuss the occurrence of different kinds of chimera states such as transient amplitude chimera, stable amplitude chimera and imperfect breathing chimera states in a locally coupled network of Stuart-Landau oscillators. In an imperfect breathing chimera state, the synchronized group of oscillators exhibit oscillations with large amplitudes while the desynchronized group of oscillators oscillate with small amplitudes and this behavior of coexistence of synchronized and desynchronized oscillations fluctuate with time. The existence of imperfect breathing chimera state is confirmed through the localized set approach and by finding the relative phases of the oscillators. The choice of cluster initial condition has been found to support the presence of the above mentioned dynamical states including amplitude chimera state and imperfectly breathing chimera state. Then we have analyzed the stability of the amplitude chimera states under various circumstances, including variations in system parameters and coupling strength, and perturbations in the initial states of the oscillators. For an increase in the value of the system parameter, namely the nonisochronicity parameter, the transient chimera state becomes a stable chimera state for a sufficiently large value of coupling strength. In addition, we also analyzed the stability of these states by perturbing the initial states of the oscillators. We find that while a small perturbation allows one to perturb a large number of oscillators resulting in a stable amplitude chimera state, a large perturbation allows one to perturb a small number of oscillators to get a stable amplitude chimera state. We have also found that the transient time of the amplitude chimera state increases if the system of oscillators are coupled through nonlocal interaction.

Acknowledgements

The work of K. P has been supported by the DST-SERB, Government of India, for providing financial support through National Post Doctoral Fellowship under the grant No. PDF/2018/000783.

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Analysing the footprint of a terrorist group to detect its fragmentation and mobility patterns

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Boko Haram is one of the deadliest jihadist organisations on the planet. At its current rate, Boko Haram takes part in roughly one event every 10 hours, taking the lives of nearly 11 people daily. Yet, little is known concerning Boko Haram's internal structure or frequently travelled paths. Here, we apply a novel technique based on mobility patterns to analyse consecutive Boko Haram events to detect the mobility of the group [1]. Our work leverages a database of 3,800 events from the Armed Conflict Location & Event Data Project (ACLED) in which Boko Haram has been involved since the organisation became violent 10 years ago. Assuming that travel costs and reduced familiarity with unknown locations limit the mobility of Boko Haram members, we model the fragmentation of the group based on their footprint. We construct a spatial network (Figure 1) based on the proximity of the terrorist events and detect edges which are frequently crossed by distinct group cells. Our results show that Boko Haram is a rather fragmented organisation in which at least 50-60 decentralised cells, capable of committing numerous and repetitive attacks against government and civilian targets. Our methodology also allows measuring the number of cross-border trips by Boko Haram, which is the number of times that our model predicts that a cell was active in two consecutive events located at a different side of a country border. Although the number of international border crossings varies according to the mobility of Boko Haram cells, our method shows that for a high and medium mobility scenario, roughly one-third of the journeys of a Boko Haram cell cross an international border, mostly between Nigeria and Cameroon or between Nigeria and Niger and that cross-border crossings have become more frequent.

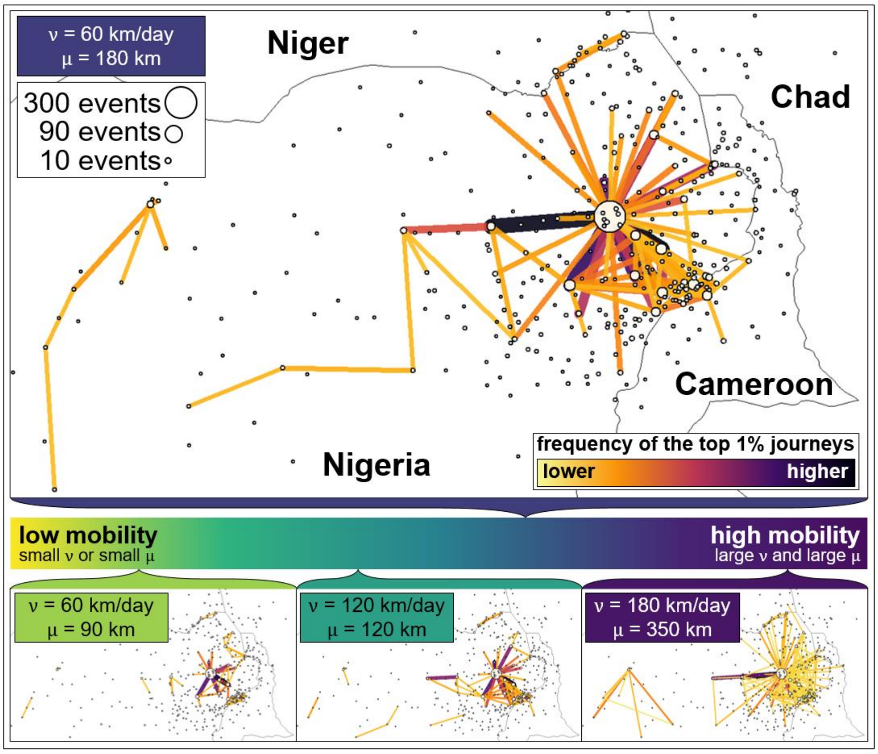

Figure 1: Spatial network of Boko Haram paths according to different levels of mobility.

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A co-evolution agent-based model for systems of cities and transportation networks integrating top-down governance through game theory

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The evolutionary theory for systems of cities at the macroscopic scale proposed by [1] suggests the existence of co-evolutionary dynamics in the trajectories of cities and their environment. In particular, transportation infrastructure connecting cities can in some cases co-evolve with them [2]. Understanding such processes is crucial for sustainable planning at large scales. The issue of the interplay between bottom-up emergence of urban dynamics and top-down planning of infrastructures is in that context relevant to study. We propose in this contribution a model of co-evolution for cities and transportation networks, with a focus on how transportation networks evolve. More particularly, we extend the model of [3] by introducing top-down governance agents which decide on investments in transportation links. The model simulates population trajectories of cities and network link speed trajectories, with two main modules: (i) spatial interaction modeling to determine growth rates of cities, and (ii) governance modeling for network evolution. Using a game-theoretic approach, macroscopic agents (such as governments or planning authorities) arbitrate stochastically between national and international investments, following a payoff-matrix considering optimal accessibility gains and collaboration costs, with probabilities obtained under the assumption of mixed strategies in a Nash equilibrium. Network investments are used to increase effective link speed by fixed increments. The model is applied to synthetic systems of cities, in a stylized configuration of two neighbor countries of comparable size. We systematically study model behavior with the OpenMOLE platform for model exploration and validation [4]. First exploration results suggest a strong qualitative influence of propensity to collaborate on trajectories of the full system, and that intermediate levels of international investments may be more optimal in terms of accessibility gains at fixed costs. In comparison to null model behavior obtained running the base model from [3], the introduction of top-down governance decisions also changes considerably model behavior. We also show that initial spatial conditions such as urban hierarchy significantly influence model outcomes [5]. This work illustrates how co-evolution models at this scale can be refined, opening research possibilities towards more complex or multi-scale models.

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Measuring Network Features under Uncertainty

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We propose a new methodological framework for data-based network reconstruction, which accounts for the uncertainty about the connectivity [1]. The nodes of the networks considered in our study represent interacting dynamical systems which are the components of a complex system. The network reconstruction problem is to derive the topological structure of the interactions between the components, relying on temporal data produced by each component. A wealth of methods has been developed to reconstruct the network connectivity using observations about the component's dynamic (see e.g. [2]). Generally, the presence of a link between components is evaluated using a connectivity metric (e.g. correlation, mutual information) which results in a functional network structure. Typically, a threshold on the connectivity level is used to filter the unlikely links, obtaining a particular structure. The choice of the threshold is usually guided by an arbitrary heuristic. Preferably, using more sophisticated statistical analysis, a set of *p-value* are computed to evaluate the significance of the connectivity with respect to null-models. However, this process still incurs in the problem of multiple testing [3]. We discuss the impact of these issues on some important network analysis.

In this work, we propose an alternative probabilistic approach which overcomes these limitations and offers a different perspective on structural connectivity. The fundamental topological descriptors are replaced, even at the level of single nodes, with appropriate probability distributions. Employing a Bayesian procedure we derive for every i and j the posterior probability p_{ij} that the node i is linked to the node j, given the *p-value* from the traditional analysis. The probabilities p_{ij} can be arranged in the adjacency matrix A of the network. Although this matrix appears as a weighted adjacency matrix with values in the interval $[0, 1]$, the entries are not weights, but they represent the existence probability of the corresponding edge. The result is a complete graph whose edges *might* exist with a certain probability. Therefore, the observed complex network is an actual realization of the possible configurations described by the "fuzzy network" model. Under this probabilistic perspective, also the network descriptors must be redefined as random variables. A natural way to recover the descriptive information is to consider the whole distribution or a suitable statistic. For example, it doesn't make sense to ask for the degree of a node, because each node can have all possible degrees at the same time, with a certain probability. Consequently, we have defined the "fuzzy" counterpart of some structural descriptors such as the node degree and the network degree distribution, the distance, the clustering coefficient, and the connectivity. For each of them, we present the analytical probability distribution and the main statistics (see *Figure 1* for an example). We applied this framework to various well-known real and synthetic networks and compared the results with the before mentioned reconstruction techniques.

The method proposed, is able to reveal the structural features of a complex network from time-series data, without the explicit reconstruction of the network and accounting for the uncertainty in the connectivity.

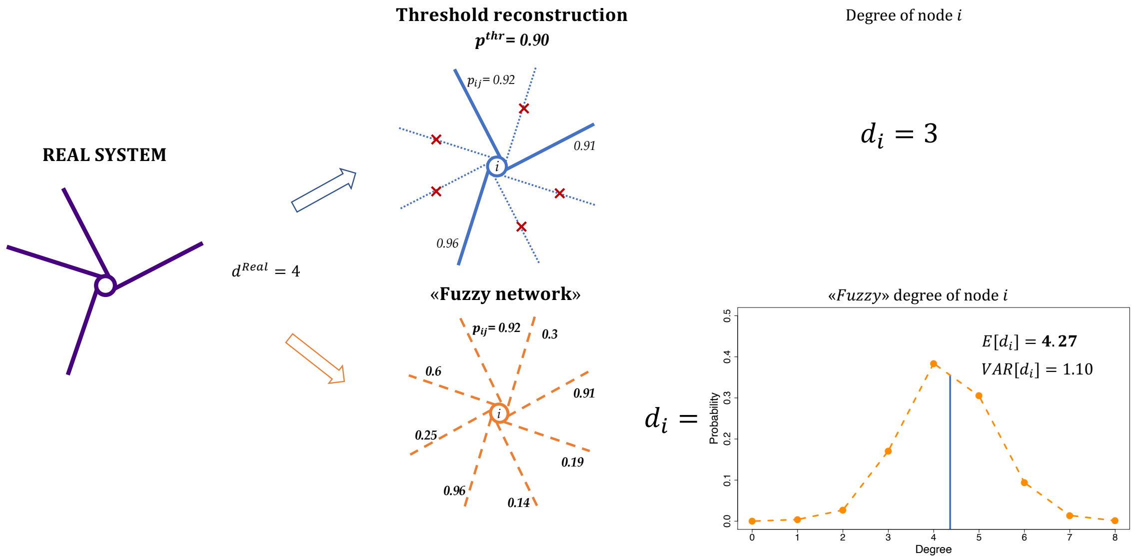

Figure 1: **Example of (fuzzy) network descriptor: the degree.**
This example shows a node i and its edges, under the traditional reconstruction methodology using a threshold (fixed at $p^{thr} = 0.9$) (above) and under the proposed probabilistic methodology (below). In the former case, the node has a deterministic degree equal to 3. In the latter case the degree is a random variable whose distribution depends on the values p_{ij}. The node expected degree is closer to the "real" node degree than the classical degree d_i.

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Environmental conditions and human activity nexus. The case of Northern Italy during COVID-19 lockdown

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During COVID-19, the draconian countermeasures adopted to mitigate the spreading of Sars-CoV-2, including the forced closure of schools, public facilities and workplaces, drastically reduced the vehicle traffic and the industrial activities, providing an unprecedented setup for testing sustainability policies. Capitalizing on powerful tools such as partial correlation, Granger causality and Bayesian state-space models, we propose a complex-causal analysis to investigate the relationship between 16 environmental conditions and human activities variables. We statistically proved that, concomitantly with the reduction in both the mobility and the energy demand, the NO_2 average concentration significantly decreases during the lockdown in 2020 when compared against the same period in 2019. On the one hand, causal analysis points out the influence of the human activities on the NO_2 concentration as well as the possible influence of meteorological conditions, such as precipitation and wind speed, that could cause variation on air pollution. On the other hand, even though the results of the Bayesian state-space model seem to reveal a clear causal impact of the lockdown on the NO_2 concentration, given the current data availability the strength of evidence for the Bayesian causal analysis might be debatable, to say the least. We argue that, despite the relaxation of a broad spectrum of human activities during the lockdown, the *backbone* of human activity – including, for instance, the supply chain of essential goods and commodities – has never really stopped. This fact proves the efficiency of the region in providing indispensable services during emergencies but, at the same time, it suggests that a lockdown could be not enough in changing pollutants concentrations and, consequently, in being regarded as a strategy for pollution control and climate change mitigation.

Therefore, policy strategies more effective and economically sustainable than lockdowns must be considered for pollution control and climate change mitigation. Our analysis, framed within a systemic view, and strongly based on causality, makes our results grounded on statistical physics and applied math, demonstrating the relevance of integrative complex-data analysis for sustainability investigations.

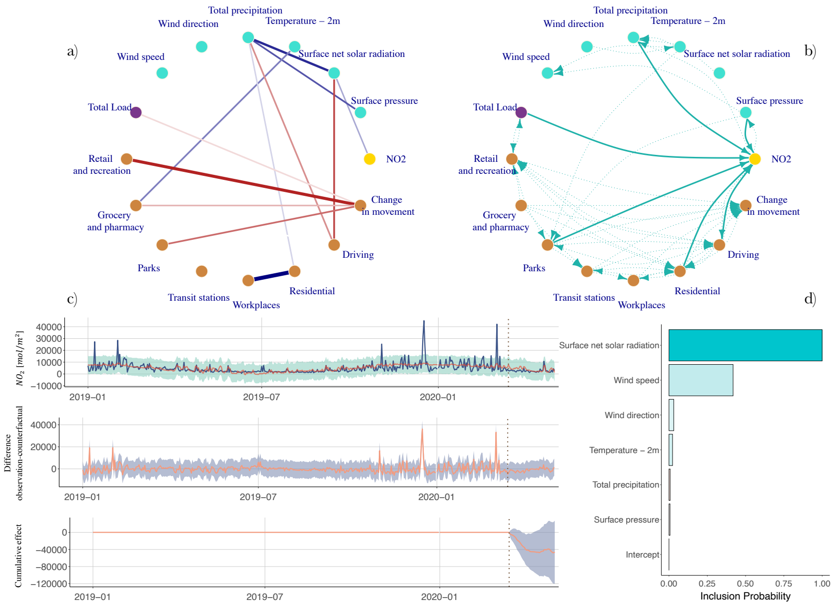

Figure 1: **Causal analysis for the time course of the 16 observables. a)** Partial correlation network: each node corresponds to a variable, the color encodes the type of variable (meteorology, energy, mobility, NO_2); blue edges represent the negative partial correlation, while red edges represent positive partial correlation; the thickness of the edges is proportional to their partial correlation value. **b)** Granger causality network: the arrows are oriented in the causal direction; the variable which have a causal impact on NO_2 are better highlighted with solid edges. **c)** Bayesian state-space model: The top panel shows the data and a counterfactual prediction for the lockdown period. The middle plot shows the difference between observed data and counterfactual predictions. The bottom plot is the cumulative effect of the lockdown. **d)** Probability of inclusion for the regressors; light-blue bars represents negative coefficients, while red bars represents positive coefficients. Note that only the meteorological regressors can be used for the counterfactual prediction, since they are the only variables not influenced by the lockdown intervention.

Hierarchy and Centrality: Two Sides of The Same Coin?

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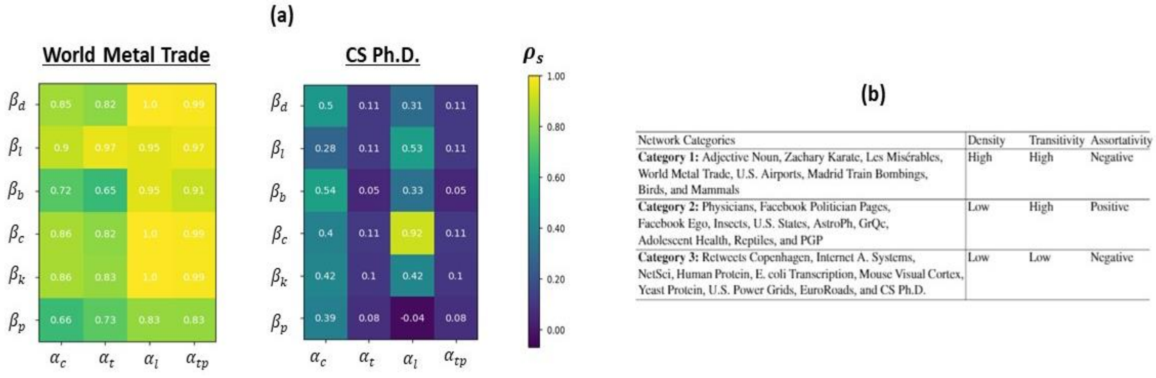
Identifying influential nodes that can spread information throughout a network, suppress disease outbreaks, or fail terrorist attacks is a fundamental issue. Centrality and hierarchy measures come forth in quantifying node influence. The former leverages dynamics while the latter exploits the hierarchical structure of networks. Several works have been devoted to centrality measures, however, the relationship between hierarchy and centrality measures is still unexplored. In this work, an empirical analysis is conducted to investigate the interplay between hierarchy measures, centrality measures, and the network topology [1]. Three questions are examined. (1) Do hierarchy and centrality measures provide similar information? (2) How does the network topology affect their relationship? (3) Which are the most orthogonal hierarchy and centrality measures? To answer these questions, 6 centrality and 4 hierarchy influential measures are used to quantify the interactions in 28 real-world networks. In order to answer the first question, correlation and similarity analyses are conducted on all the combinations of hierarchy and centrality measures for each network. Results show that hierarchy and centrality measures behave differently, with a range of correlation from high to low as shown in Fig 1 (a). To answer the second question based on correlation/similarity measures, categorization of the networks using the *k*-means algorithm is performed. Inspection of the macroscopic topological properties of the networks reveals that density and transitivity play a major role. If both are high, hierarchy and centrality are well correlated and pretty similar. On the contrary, if one of them is low, hierarchy and centrality measures are quite dissimilar and uncorrelated. Finally, to answer the third question, the Schulze voting method is used. Networks are voters and the hierarchy and centrality combinations are the candidates. It appears that the combination *k*-core, betweenness is the most orthogonal.



Network Categories	Density	Transitivity	Assortativity
Category 1: Adjective Noun, Zachary Karate, Les Misérables, World Metal Trade, U.S. Airports, Madrid Train Bombings, Birds, and Mammals	High	High	Negative
Category 2: Physicians, Facebook Politician Pages, Facebook Ego, Insects, U.S. States, AstroPh, GrQc, Adolescent Health, Reptiles, and PGP	Low	High	Positive
Category 3: Retweets Copenhagen, Internet A. Systems, NetSci, Human Protein, E. coli Transcription, Mouse Visual Cortex, Yeast Protein, U.S. Power Grids, EuroRoads, and CS Ph.D.	Low	Low	Negative

Figure 1: (a) Heatmaps of the Spearman's correlation (ρ_s) for the various combinations of hierarchy α_i and centrality β_j measures of 6 real-world networks. The hierarchy measures are α_c= *k*-core, α_t= *k*-truss, α_l = LRC, and α_t = triangle participation. The centrality measures are β_d = Degree, β_l = Local, β_b = Betweenness, β_c = Current-flow Closeness, β_k = Katz, and β_p = PageRank. (b) Categories of networks with their aggregated topological characteristics.

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Chaos, Complexity and Complex Systems Thinking to Help Understand and Stop COVID-19 and its Global Disruption.

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The pandemic of COVID-19 emerged from the complex dynamic nonlinear interactions of the novel corona virus, disrupting global health, society and the economy in expected, unexpected and unprecedented ways. Chaos, complexity and complex systems thinking should help understand and stop this complex and dynamic 21st century problem.

An online search for chaos, complexity, complex systems, COVID-19 yielded
Websites and webpages:
Santa Fe Institute: "What does complexity science tell us about COVID-19?" The Damage we are not attending to" Scientists who study CS offer solutions to the pandemic."
NECSI - Analysis, Reports, Policy, practical advice, Endcoronavirus.org: All you need to CRUSH COVID-19, Harvard, MIT, UCLA, etc. CCNR NE Univ - network science and coronavirus, Complexity Digest: papers, discussions, conferences, books on COVID-19.
Medical journals
The Lancet EClinical Medicine, Bradley "Systems Approach to COVID-19," CMAJ Letter Rambihar "Chaos, complexity and complex systems to contain and manage COVID-19," BMJ Letters, Rambihar "Who dropped the ball with COVID-19?"etc., many clinical reports.
Science and other journals:
Scientific American: Clifford Brangwinne "How a Landmark Physics Paper from the 1970s Uncannily Describes the COVID-19 Pandemic," Phil Anderson "More Is Different" - "different levels of complexity require new ways of thinking" with "COVID-19 exponential replication leading to global transformation and disruption from healthcare, society to the economy." Faies Jafar "Applying Complexity Theory to the Coronavirus Crisis," Cristina-Marina Păcurar and Bogdan-Radu Necula "An analysis of COVID-19 spread based on fractal interpolation and fractal dimension."
Newspapers ad newsletters:
Atlantic newspaper March, 2020: Tufekci "America's Coroanvirus response failed because we did not understand the complexity of the problem," and failed messaging and leadership. Guardian March 2020: Taleb, Bar-Yam "The UK coronavirus policy may sound scientific- it isn't. UK theorising about complexity and getting it wrong." Forbes April 2020: Bedzow "Wake Up Call For Industry Leaders: The Time To Think About COVID-19 As A Complex Adaptive Challenge Is Now."
Blogs:
Martin: "How Complexity Theory can Help Decision-Making making in chaotic times - Cynefin model, Snowden and Blignault: Cognitive Edge Webinar April " Reflections on Complexity, Chaos and COVID-19," Strazewski: AMA April 4, 2020 Public Health " What's ahead on COVID-19,?" N Christakis - "the U.S. should have been better prepared," Resnick "How chaos theory helps explain the weirdness of the Covid-19 pandemic," Rickards "The Daily Reckoning "Complex Systems Collide, Markets Crash; Applying complexity theory to the corona virus crisis- systems flip from complicated to complex.".

Conclusion: Chaos, Complexity and Complex Systems thinking are widely reported to help understand and stop COVID-19 and its global disruption. This included: lack of complexity thinking leading to the emergence and global spread of the virus, Reports and science advocating early and sustained intensive actions to flatten and crush the curve, examples of mitigation of disruption of health, society, business and economy, emergence of novel unexpected critical clinical and other features, description as chaos, complex and fractal, and applications to manage and stop Covid-19 and its global disruption.

From Cos to Cosmos and now Covid-19: 30 Years Teaching Health Professionals Chaos, Complexity and Complex systems.

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Background and purpose:

This poster is a review of 30 years of experience and advocacy in this field and not new research. Chaos and Complexity, considered the science for the 21st century by Stephen Hawking and the science for a complex world by the Santa Fe Institute, should apply to medicine, health, education and now global challenges like COVID-19. It describes complex dynamic social, economic, biologic, behavioral and other interactions leading to health and disease, and between health professionals, patients and society. These exhibit nonlinearity, sensitive dependence, feedback, adaptation, uncertainty, self-organization and emergence, and were used to achieve change as adaptive, dynamic, co-evolving and co-learning.

Results:

30 years teaching, using, and advocating for thinking chaos, complexity and complex systems in medicine (Cos), health, and everything else (Cosmos), and now covid-19 included:
Lectures: 1991 Univ West Indies, 2000 Trinity College and Newton Inst for Mathematical and Physical Sciences, Cambridge U UK, 1990- present - U of Toronto and other universities.
Publications, Presentations/abstracts/posters various conferences in US, UK, Canada, WI: 1993 Chaos in Medicine and Medicine out of this World 1994 Editorials/Commentary Canadian J Cardiology 1993 Jurassic Heart: From the Heart to the Edge of Chaos, 2000 Creating a Pandemic of Health using chaos and complexity, 2020 Society for Chaos Theory in Psychology and Life Sciences, 2020 10 th Int Complex Systems Society Conf 2020.
Books: CHAOS From Cos to Cosmos: a new art science and philosophy of medicine, health…and everything else. CHAOS Based Medicine: the response to evidence, Tsunami Chaos Global Heart: using complexity science to rethink and make a better world.
Global networking and advocacy for complexity thinking in medicine, health and society. Health promotion/Preventing premature heart disease and book South Asian Heart, Book Chapter using complexity science for community health promotion.
Projects on Complexity in Health and Diversity at The Scarborough Hospital and community Complexity to rethink/transform medical education for the 21st century, with McMaster med education as complexity, Proposal for Thinking Complexity for Educating Health Professionals for the 21st century (response to Lancet 2010 Report).
Letters to the Ed/Posts on using chaos, complexity and systems approach to prevent, contain and manage Covid-19 – CMAJ 2020, Who dropped the ball with COVID-19? BMJ 2020, etc.

Conclusion:

Health professionals were taught chaos, complexity and complex systems over a 30 year period 1990-2020, to understand and manage the complex dynamic 21st Century interactions of medicine, health, society and disease, starting in 1990 with Medicine (Cos), advocating using this for everything else (Cosmos) and in 2020 to manage, contain and stop Covid-19.

Notes: The Poster is highly visual with imagery from fractals, chaos and complexity, and adapted from Posters at U of Toronto Conference “Creating a Pandemic of Health” “Medical Education Conference at Sunnybrook Hospital” 2015, “30th Annual Society for Chaos Theory in Psychology and Life Sciences Conference,” Fields Institute of Mathematics, University of Toronto, July 2020, and 10th International Complex Systems Society Conf July 2020.

Integrating Climate Network Analysis with Machine Learning to Predict South Asian Monsoon

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The accurate prior information of the south asian monsoon helps the government and farmers to mitigate agricultural losses and proper planning of water resources. However, the forecasting of south asian monsoon is a challenging task due to the involvement of complex nonlinear dynamics and its variability over time. In this work, we developed a method to predict the mean seasonal, intraseasonal and meteorological region wise south asian monsoon using evolving climate networks combined with machine learning. The climate networks are constructed using daily surface air temperature data (SATA) from 1948 to 2009 .The SAT captures the underlying dynamics between the ocean and the atmosphere due to heat exchange and other local processes. We used the various network measures i.e, local degree, local clustering coefficient, and average link distance measures as a predictors for machine learning algorithmn. We implemented the modern machine learning regression technique, i.e., extra trees regressor, to predict mean seasonal, intraseasonal and region wise south asian monsoon. Based on our testing results, Our new method can forecast the mean seasonal monsoon in average 45 days in advance with median deviation of 3.6%. For intraseasonal monsoon months median deviation vary from 2.78 to 7.92 with lead-time from 45 to 135 days. In case of meteorolgical subdivison region, the median deviation vary from 5 to 20 %. The forecasting results show the method is competitive with the other methods used for forecasting south Asian monsoon.

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Anticipating stochastic calculus. Optimal investment strategies under insider trading

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In this work we study the presence of insider information in a non-adapted version of the simple problem of portfolio optimization in a financial market.

We consider three different anticipating stochastic integration theories: the Russo-Vallois Forward, the Ayed-Kuo, and the Hitsuda-Skorokhod integrals.

We analyze a specific formulation of the insider trading problem for the bank account and for the stock. We compute the optimal portfolio, i.e., the optimal investment strategy for each case, and compare the results obtained.

The results suggest that the Ayed-Kuo and the Hitsuda-Skorokhod integrals provide a solution that seems to be counterintuitive in the financial sense, while the Russo-Vallois integral gives a financially meaningful investment strategy for this problem.

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Eur. Phys. J. Special Topics **229**, 841–849 (2020)

https://doi.org/10.1140/epjst/e2020-800232-7

THE EUROPEAN
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Regular Article

Acoustic emissions in compression of building materials: q-statistics enables the anticipation of the breakdown point

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Received 17 December 2018 / Received in final form 10 March 2019

Abstract. In this paper we present experimental results concerning Acoustic Emission (AE) recorded during cyclic compression tests on two different kinds of brittle building materials, namely concrete and basalt. The AE inter-event times were investigated through a non-extensive statistical mechanics analysis which shows that their complementary cumulative probability distributions follow q-exponential laws. The entropic index q and the relaxation parameter $\beta_q \equiv 1/T_q$, obtained by fitting the experimental data, exhibit systematic changes during the various stages of the failure process, namely (q, T_q) linearly align. The $T_q = 0$ point corresponds to the macroscopic breakdown of the material. The slope, including its sign, of the linear alignment appears to depend on the chemical and mechanical properties of the sample. These results provide an insight on the warning signs of the incipient failure of building materials and could therefore be used in monitoring the health of existing structures such as buildings and bridges.

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A complex and adaptive system model of a stylized delegation relationship with hidden-action

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Following a procedure introduced by Guerrero and Axtell [1], and Leitner and Behrens [2], we transform the standard economic model for delegation relationships with hidden-action, which was first described by Holmström [3], from a closed-form (mathematical) model into an agent-based model, which follows the tradition of complexity economics. With our approach, we deviate from rather "heroic" assumptions, which are typically included in similar models, such as rational and homogeneous agents [1], and implement a complex system version of the hidden-action problem with two types of agents, namely a supervisor and an employee. We characterize agents by (i) limitations in their cognitive capacity (e.g., in terms of limited processing power and limited memory/storage) and the (ii) availability of information about the environment. However, we endow agents with learning capabilities so that they can learn the missing pieces of information over time (with varying accuracy). In the model, the supervisor delegates a task to the employee and uses an incentive system to control its behavior. While the standard model comes up with an optimal incentive scheme immediately, we observe which incentive system emerges from the complex system over time.

Our analysis focuses on how close and how fast the solution emerging from the actions and decisions of autonomous agents converges to the solution proposed by the standard model, or if even better solutions can be found, and examine how the agent's limited cognitive capacity affects performance. We investigate whether, and if so, how fast an equilibrium solution (i.e., a stable incentive scheme) emerges from our model. In relatively stable environments, we can nearly reach the optimal solution, i.e., the incentive scheme proposed by the standard hidden-action model. A stable solution, surprisingly, emerges earlier in turbulent environments. We operationalize the variations in environmental turbulence by altering the distribution's standard deviation, which we set relative to the optimal outcome x of the standard hidden-action model (second-best solution in [3]). Further, we can see that it is not the employee's but the supervisor's cognitive capacity, which affects the emergent solution's performance.

Acknowledgements

This work was supported by funds of the Oesterreichische Nationalbank (Austrian Central Bank, Anniversary Fund, project number: 17930).

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Scaling Patterns in Basic Sanitation Expenditure: the case of Brazil

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Starting in the late 20th century, the Brazilian federal government created several programs to increase the access to water and sanitation. However, although these programs made improvements in water access, sanitation was generally overlooked. While water supply, and waste collection are available in the majority of the Brazilian municipalities, the sewage system is still spatially concentrated in the Southeast region and in the most urbanized areas. The Southeast region has roughly 42% of Brazilian population and includes the cities such as Rio de Janeiro and São Paulo.

In order to explain this spatially concentrated pattern it is frequently assumed that the size of cities does really matter for sanitation services provision, specially for sewage collection. As a matter of fact, as cities grow in size, one should expect economies of scale in sanitation infrastructure volume. Economies of scale in sanitation infrastructure means a decrease in basic sanitation costs, proportional to the city size, leading also to a (expected) power law relationship between the expenditure on sanitation and city size. Using population, N(t), as the measure of city size at time t, power law scaling for infrastructure takes the form $Y(t) = Y_0 {*} N(t)^\beta$ where $\beta \approx 0.8 < 1$, Y denotes infrastructure volume and is a constant.

Many diverse properties of cities from patent production and personal income to electrical cable length are shown to be power law functions of population size with scaling exponents, that fall into distinct universality classes. Quantities reflecting wealth creation and innovation have $\beta \approx 1.2 > 1$(increasing returns), whereas those accounting for infrastructure display $\beta \approx 0.8 < 1$ (economies of scale).[1][2][3]

We verified this relationship using data from Brazilian Federal Government databases, denominated Integrated Planning and Budgeting System, and referred to hereinafter as SIOP. Preliminary results show decrease, proportional to the city size, in federal grants-in-aid to municipalities to help finance public sanitation projects. For the initial budget allocation, β was found to be roughly 0.62 for municipalities over twenty thousand inhabitants; to be roughly 0.9 for municipalities over twenty thousand inhabitants; and to be roughly 1.15 for municipalities over fifty thousand inhabitants. For the expenditure commitments, β was found to be 0.43 for municipalities over two thousand inhabitants; to be roughly 0.58 for municipalities over twenty thousand inhabitants; and to be roughly 0.6 for municipalities over fifty thousand inhabitants.[4]

Key words: complexity, scaling, self-similarity, cities.

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Indication of correlations between urban scaling and Zipf’s exponent

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Zipf's law and urban scaling are two fundamental paradigms researched in urban science. They have mostly been investigated independently and are perceived as disassociated matters. Here we present a large scale investigation about the connection between these two laws using population and GDP data from 96 countries. We empirically demonstrate that both laws are tied to each other and derive an expression relating the exponents. This expression captures the main tendency of the empirical relation between both exponents, and simulations yield very similar results to the real data after accounting for fluctuations. Our research puts forward the idea that urban scaling of GDP does not solely emerge from intra-city processes. Instead, we show that population distribution affects the scaling of urban GDP such that countries with less small cities and more metropolises (small Zipf exponent) have less pronounced increasing returns to scale of urban GDP than countries with a more uneven number of small and large cities (large Zipf exponent).

Detecting complex diversity-dependent diversification with a novel phylogenetic inference framework

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Phylogenetic trees are types of networks that describe the temporal relationship between individuals, species, or other units that are subject to evolutionary diversification. Many phylogenetic trees are constructed from molecular data that is often only available for extant species, and hence they lack all or some of the branches that did not make it into the present. This feature makes inference on the diversification process challenging. For relatively simple diversification models, analytical or numerical methods to compute the likelihood exist, but these do not work for more realistic models in which the likelihood depends on properties of the missing lineages and complex interactions of ecological phenomena at different time scales. In this talk, we study a general class of species diversification models, and we provide an expectation-maximization framework in combination with an efficient data augmentation scheme to perform maximum likelihood estimation of the parameters of the diversification process. As an illustration we consider a general diversity-dependence model where the combination of different facets of diversity and it's impact of diversification processes is studied.

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Contributions to Reinforcement Learning and Deep Reinforcement Learning using Probabilistic Boolean Networks.

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Probabilistic Boolean Networks (PBN) are a tool in Complex-Adaptive Systems theory used primarily for bioinformatics. They possess complexity, adaptability, self-organization, emergence, and self-similarity. They are sensitive to initial conditions, and react to environmental perturbations. Learning occurs in the fundamental sense of adaptation to changes; the system adapts in order to survive. This work presents an alternative means to Reinforcement Learning and Deep Reinforcement Learning through the use of PBNs as a building block of the Machine Learning (ML) system. Since PBNs are systems that satisfy the Markov Property, they can behave like an agent sensing and reacting to the environment. Stimuli in form of rewards is used to achieve the desired characteristics by reinforcing the actions that lead to states with higher expected cumulative rewards. Every node in a PBN is an agent having a set of functions defining its next state based on the current network, and the PBN is a collection of nodes and sets of states that evolve through time. Artificial Neural Network neurons are equivalent to the set of nodes of a PBNs, which have input and output states. The set of input nodes have a set of predictor functions that define the output state (like the threshold function). The learning task would be to change the transition probabilities in order to select a context (constituent BN) that represents the state in which the network has to be (steady state), where states are the goals to be achieved in the system.

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Long-term feedback mechanisms underlying societal collapse

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Based on prior work on the mathematical modelling of the societal development, and ultimately the collapse, on Easter Island [1], of the Classic Maya [2] and of the Western Roman Empire [3], we propose a framework for understanding long-term societal evolution. Analysing social systems at a large scale, in an aggregate way over a long-time span, can provide models that with significant predictive power, as has been the case with Limits to Growth. The success of the method lies in identifying feedback mechanisms that operate over centuries and that survive the numerous changes in rulers, social norms, and external threats. After studying several ancient societies, and developing mathematical models that reproduce their archaeological record, we have identified an archetypal scheme of feedback mechanisms that is common to these historical cases and proves informative for modern society as well. The key variables in the feedback mechanisms involve the complexity of a society, its resources, and a measure of returns from investments, and the framework allows for a direct interpretation of these abstract notions in concrete cases, see Fig. 1.

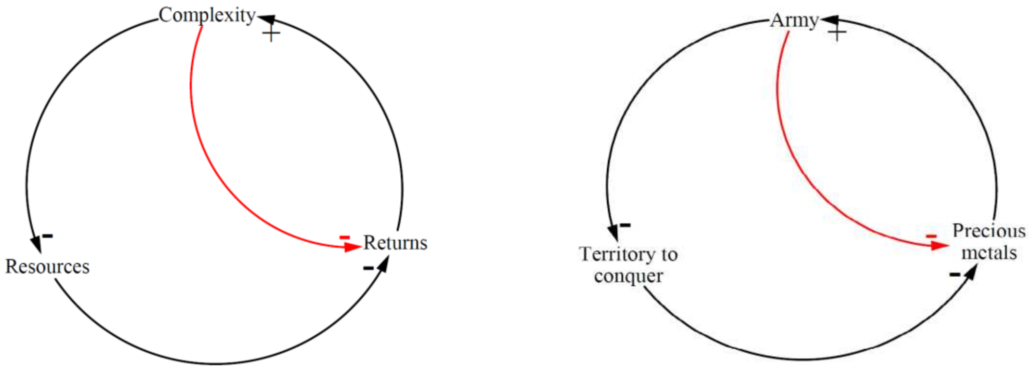

Figure 1: The causal loop diagram illustrates how complexity, resources and returns relate. With increasing complexity, resources are more rapidly depleted; the decline in resources translates to an increase in returns, which in turn lead to an increase in complexity. This represents the reinforcing feedback (outer, black) loop of the diagram. But complexity also has costs that draw on returns (red arrow). Higher complexity implies higher costs and a decline in returns, which constitutes a counter-acting loop in the diagram. In the case of the Roman Empire, the complexity is best encapsulated by the army, the resources by the territory and returns by precious metals and taxation [3].

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Historical Dynamics of the Chinese Dynasties

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We develop a framework for studying state division and unification, and as a case study we focus on modelling the territorial patterns in imperial China during periods of unity and upheaval. In contrast to prior work that relied on ordinary differential equations [1-3], we focus on discrete dynamical systems: the logistic map and a new class of maps, which we name ren maps. The critical transitions exhibited by the models depend on a parameter λ that can be used to capture the process of territorial division but also unification. We outline certain limitations of unimodal, smooth maps and propose ren maps as an alternative, which we use to reproduce the territorial dynamics over time. As a result of the modelling we propose a quantitative measure for asabiyyah, a notion of group solidarity, whose secular cycles match the historical record over 1800 years, from the time of the Warring States to the early Ming dynasty, see Fig. 1. Furthermore, we also derive an equation for aggregate asabiyyah applicable to other cases.

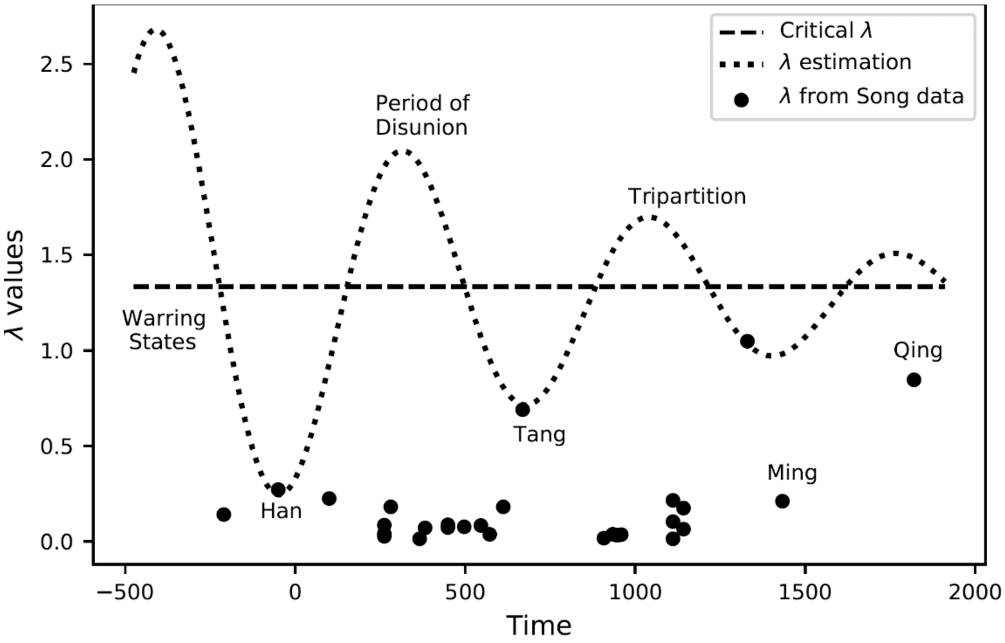

Figure 1: The evolution of the λ parameter according to the data. The λ for the dynasties (dots) indicates a single dominant dynasty in the stable periods (Han, Tang, Ming, Qing) and several in the chaotic periods. The Warring states period, the Period of Disunion, the period after the fall of the Tang and the Tripartition, all correspond to values of λ in the chaotic regime, above 4/3 (dashed line). We define asabiyyah as a constant minus λ.

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Emergence of knowledge communities and information centralization during the COVID-19 pandemic

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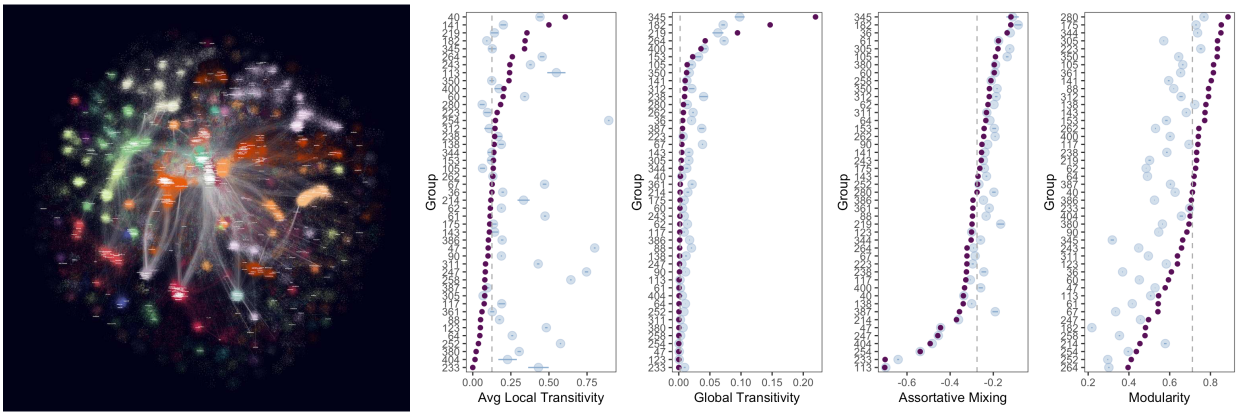
A challenging aspect of the current COVID-19 pandemic crisis is its infodemic dimension, that is, an overabundance of COVID-related information that makes it difficult for the majority of the public opinion to distinguish between reliable and unreliable sources [1]. Individuals make an active use of social media to access news as part of their personal strategy of social capital acquisition, civic engagement and political participation. Therefore, the nature of the information that is circulated and validated within an individual's digital relational sphere has a considerable impact on her/his orientations and conduct in a variety of highly sensitive matters, including public health ones [2].

Here, we develop a computational approach to gain insight on a key social feature of infodemics, that is, the structure of the knowledge communities that are endogenously formed in the process of creation, filtering and dissemination of COVID-19-related information. Using a unique data set of online activities during the COVID-19 pandemic [3] together with human coding of most influential actors, we map the global communication ecosystem from more than 200 million interactions on a popular microblogging platform (Twitter), and show that the COVID-19 infodemics present a highly characteristic community structure, shaped by ideological orientation, typology of fake news, and geographical areas of reference. This reflects complex geo-political patterns, and can be clearly distinguished from the other knowledge communities we have identified [4].



(a)**Network map**

(b)**Nontrivial connectivity patterns**

Figure 1: **(a)** Web of about 1.1 millions social interactions about COVID-19 observed worldwide between 22 January and 16 April 2020. Nodes represent about 0.4 millions user accounts and links encode their social interactions aggregated over the observational period. Nodes are colored according to their social group inferred using the Louvain method. Only nodes belonging to groups which are at least 0.1% of system size are colored, i.e., the smallest colored group consists of about 400 accounts. A label with the account name is shown for extremely active users, the one with an overall social activity of at least 3500 interactions (either active or passive). **(b)** It is tested against its configuration model preserving its connectivity distribution while washing out topological correlations. For each group separately, we measure average local and global transitivity (quantifying the tendency of accounts to local triadic closure); assortative mixing (quantifying the tendency of accounts to connect to accounts with similar number of connections); and modularity (quantifying the organization of accounts in groups within the group). Values estimated for the observed groups are encoded by solid dark points, whereas values obtained from null models and averaged across 20 independent realizations are shown with lighter markers and segment denoting the 95% variation around the expected values. Vertical dashed lines encode median values across groups. Overall, the results indicate that some measured features are not observed by chance: most of the groups are characterized by a lack of triadic relationships and a stronger organization into sub-groups, a hallmark of hierarchical organization.

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Multiple Inequalities in an Agent-Based Climate-Economy Model: Implications for the Social Cost of Carbon

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Integrated Assessment Models (IAMs) are widely used to estimate the social cost of carbon, i.e. the economic cost caused by an additional ton of carbon dioxide emissions. Such models assume full employment and aggregate demand while abstaining from a financial sector. Against this background, we create an agent-based climate-economy model as a disaggregated, behavioural approach to IAMs. It describes networks of heterogeneous consumers, banks, power plants and firms, while it is calibrated to generate patterns of growth and carbon dioxide emissions consistent with Dynamic Integrated Climate-Economy model (DICE). We pay attention to how climate change affects, notably through unemployment, three types of inequalities, namely in consumption, wealth and income. These provide an essential but overlooked link between climate-change damages and the optimal carbon tax. In the model, climate damages reduce budgets of individual consumers. By comparing three distributions of damages – proportional, uniform, and inversely proportional to individual wealth – we find that the first of these gives rise in the highest rate of firms' bankruptcies and income inequality. This translates into a lower estimate of the social cost of carbon compared to other damage distributions. Another finding is that using tax revenues to support investments in renewable energy is more equitable in income and consumption, but not in wealth, than tax rebates. This is due to more favourable employment effects. Bounded rationality in the form of habits is found to negatively affect distributional equity of a carbon tax.

Effectiveness of social distancing through the lens of agent based modelling

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With the rise of urbanization and the population flow from rural areas to denser neighborhoods, the risk of epidemic spreading is only expected to take a turn for the worse. In this work we quantitatively calculate the transmission risk of an infectious disease among individuals moving within a confined setting (office, religious site, classroom, etc), inspect methods for lowering the risk and examine the costs of such measures. Combining human mobility (Fig.1-a) and a compartmental epidemic model (Fig.1-b), we devise an agent based model consisting of pedestrian dynamics and spreading phenomena and introduce a novel definition of social distancing force.

Along with direct person-to-person transmission (Fig.1-c), we also consider indirect transmission with the footprints of the infectious pedestrians (Fig.1-d). We show that the increase in the intensity of social distancing has a significant effect on the exposure risk (Fig.1-c). Then, by classifying the population into social distancing abiders and non-abiders, we conclude that the practice of social distancing even by a minority of potentially infectious agents although results in a drastic change on the population exposure risk, hinders the effectiveness of the protocols when practiced by the rest of the population. We will also explore the parameter space of disease transmission probabilities and study the effectiveness of social distancing for different diseases.

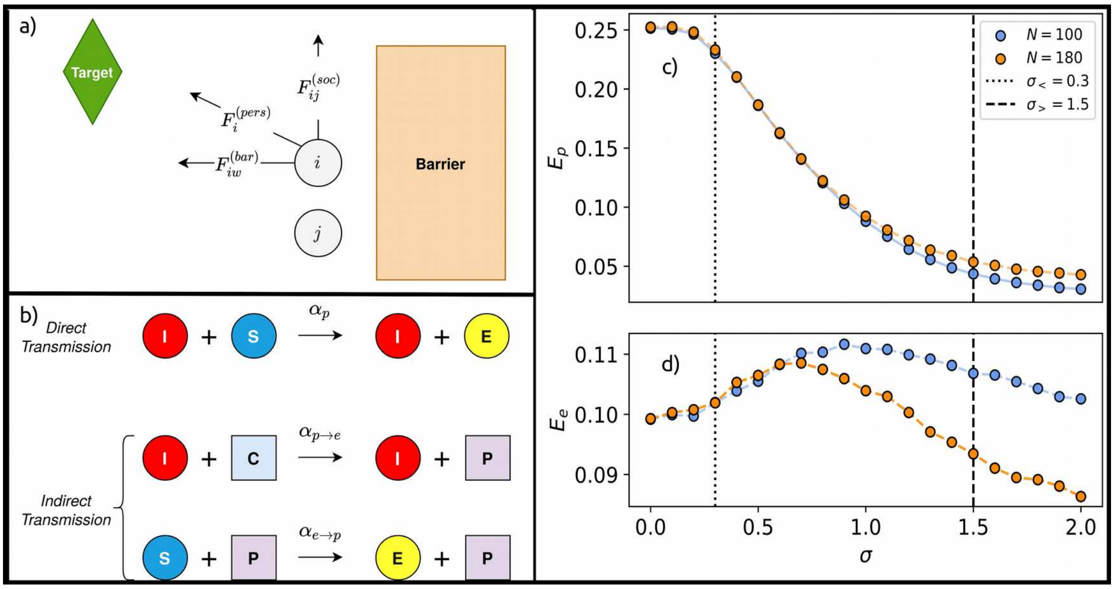

Figure 1: a) The mobility model. b) The Spreading model. Risk of infection through c) direct and d) indirect transmission for different population densities over a range of σ (social distancing force values.)

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***A preprint based on this research will soon be available on arXiv repository.**

k-means clustering method for coinfective spreading risk calculation

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We devise a systematic method for risk estimation of coinfective spreading dynamics, based on **k-means clustering**. By classifying the outbreaks into high and low risk incidents, we define the *mean outbreak size* and the *outbreak probability*.

We simulated the *Susceptible-Infectious-Recovered* epidemic model on multiple empirical temporal networks (exemplary results in Fig.1-Left and Fig.1-Middle). We classify the realizations, using k-means clustering (Fig.1-Right). By using different shuffling methods we studied each correlation's effect on hindering/enhancing the spreading phenomena. We observed that causal temporal correlations reduce the size of an outbreak, on the other hand, periodical correlations which can either decrease or increase the probability of an outbreak, have no significant effect on the size of a possible outbreak.

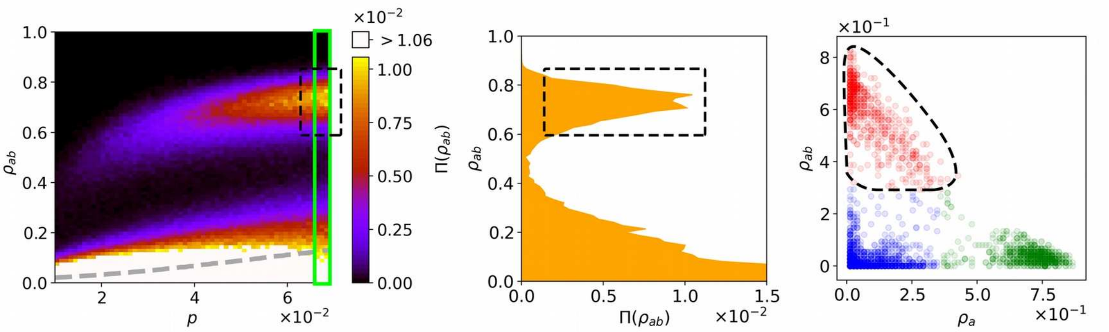

Figure 1: Systematic measurement of *mean outbreak size* and the *outbreak probability.* Left: infected population heatmap for a range of infection probability. Middle: probability distribution of infected population for infection probability=0.7. Right: k-means clustering performed on the simulation results for infection probability=0.7. red values depict high risk outbreaks. Dashed areas in all panels correspond to the same cluster of realizations.

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Cluster synchronization in systems with higher order interactions

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Cluster synchronization (a type of synchronization where different groups of nodes in the system of coupled oscillators follow distinct synchronized trajectories) on networks is a broadly analyzed phenomenon characterizing behaviors with wide areas of applicability from neuroscience to consensus dynamics. Analyzing cluster synchronization can be used to understand phenomena such as remote synchronization and the emergence of chimera states. Ideas from graph and equivariant dynamical systems theory can be applied to deduce admissible patterns of synchronization and simplify their stability analysis. However, higher order interactions may be required to describe many social, biological, and ecological systems, making it necessary to go beyond the pairwise interaction analysis to study certain phenomena such as consensus dynamics, epidemic spreading, and metabolic reactions. While complete synchronization and its stability have been analyzed very recently for such systems, and examples from consensus dynamics, where the system settles on a fixed point, have been analyzed, general cluster synchronization has not been considered. To address that, we formulate conditions for cluster synchronization based on the hypergraph structure from (external) equitable partition and symmetry perspective. Then, we show how to reduce the dimensionality of stability calculation based on the hypergraph structure for any specific pattern of cluster synchronization. A specific example of an admissible pattern of synchronization and its analysis is shown in *Figure 1*. Our results are an extension of existing cluster synchronization literature to higher order systems and could be of interest to a larger audience.

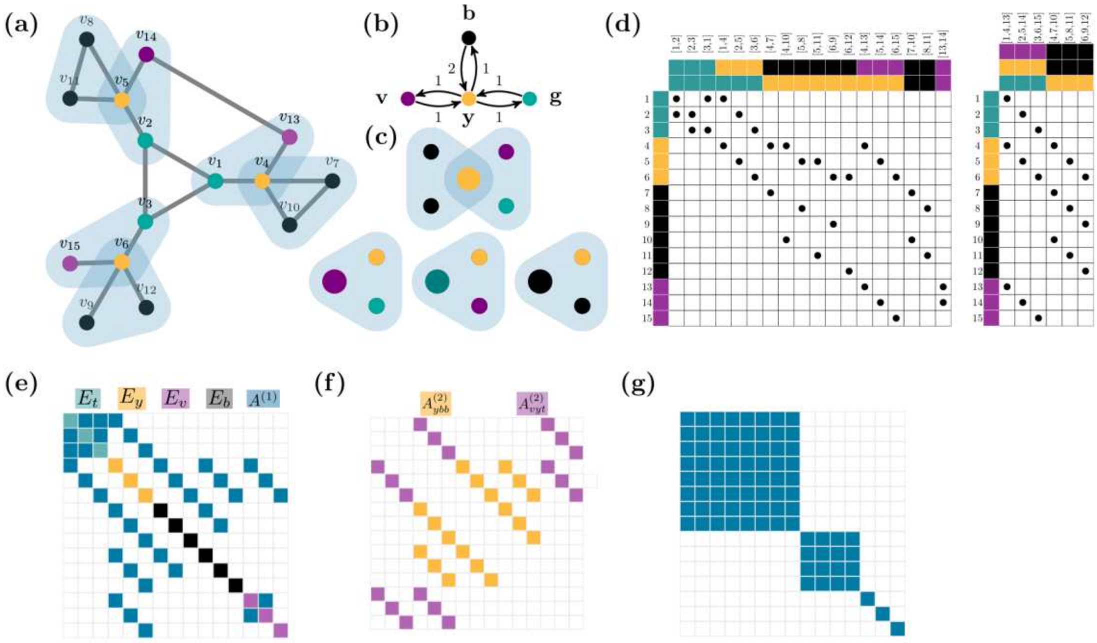

Figure 1: Example cluster synchronization pattern in a 15-node hypergraph. Colors represent distinct clusters. (a): example cluster synchronization pattern on a hypergraph, (b-c): quotient hypergraph for dyadic and triadic interactions, (d): adjacency matrices for dyadic and triadic interactions, (e-f): matrices needed to simultaneously block diagonalize self-, dyadic, and triadic interactions, (g): structure of block diagonal Jacobian.

Agenda-Setting Effects on Twitter in Brazilian Presidential Elections 2018

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In this work, we study the relationship between social media and traditional media and their impact on democratic systems. Using topic modeling techniques, we explore agenda-setting effects in the Twitter debate about the Brazilian Presidential Elections 2018. Our results reveal a complex dynamic in the transmission of the media agenda to the public with the distribution of shared media outlets aligned according to a truncated power-law, reflecting a "preferential attachment" behavior. However, the traditional media did not dominate the debate, as alternative media played an important role in the campaign. Measuring the euclidean distance of the topics found in the debate, we noticed that the titles of the articles shared in the tweets are closer to the text of tweets than the text of the articles. Nonetheless, when comparing with the complete corpus of tweets (tweets with links and without links), the text of the shared articles is closer, in a relationship of inverse proportionality with the distance of tweets to titles. We conclude a list of recommendations to address the societal challenges posed by the transformation of the media environments.

Random Matrix Theory based study of spin chains

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10th October, 2020

1 Abstract

Quantum Spin chains are fascinating objects which have a plethora of applications in various branches of physics ranging from quantum information to astrophysics [2, 3]. The idea of application of random matrices to spin systems originate through the works of Hartmann, Mahler and Hess who for the first time used ensembles to study the spectral properties of spin chains, in order to avoid solving the hamiltonians explicitly. In most of the previous works where spin chains have been studied with RMT, spectral density and extreme eigenvalue statistics have been studied for the limiting case i.e. for large dimensional hamiltonians corresponding to large chain limits. In this work we study the spectral properties of reduced density matrices of two most generic nearest neighbour qubit spin chains given by the Hamiltonians [4] and match them with finite-dimensional analytical RMT predictions which can be found in papers [5, 6].

$$H_n = \sum_{j=1}^{n} \sum_{a,b=1}^{3} \alpha_{a,b,j} \sigma_j^{(a)} \sigma_{j+1}^{(b)}, \tag{1}$$

$$H_n^{(local)} = \sum_{j=1}^{n} \sum_{a=1}^{3} \sum_{b=0}^{3} \alpha_{a,b,j} \sigma_j^{(a)} \sigma_{j+1}^{(b)} \tag{2}$$

and match them with analytical RMT predictions which be found in papers [5, 6].

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Chaotic semi-express buses in a loop

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Urban mobility involves many interacting components: buses, cars, commuters, pedestrians, trains etc., making it a very complex system to study. Even a bus system responsible for delivering commuters from their origins to their destinations in a loop service already exhibits very complicated dynamics. Here, we investigate the dynamics of a simplified version of such a bus loop system consisting of two buses serving three bus stops. Specifically, we consider a configuration of one bus operating as a normal bus which picks up passengers from bus stops A and B, and then delivers them to bus stop C, whilst the second bus acts as an express bus which picks up passengers only from bus stop B and then delivers them to bus stop C. The two buses are like asymmetric agents coupled to bus stop B as they interact via picking up passengers from this common bus stop. Intriguingly, this *semi-express* bus configuration is more efficient and has a lower average waiting time for buses, compared to a configuration of two normal buses or a configuration of two express buses. We reckon the efficiency arises from the chaotic dynamics exhibited in the semi-express system, where the tendency towards anti-bunching is greater than that towards bunching, in contradistinction to the regular bunching behaviour of two normal buses or the independent periodic behavior of two non-interacting express buses.

Enhanced Ability of Information Gathering May Intensify Disagreement Among Groups

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Today's society faces widening disagreement and conflicts among constituents with incompatible views. Escalated views and opinions are seen not only in radical ideology or extremism but also in many other scenes of our everyday life. Here we show that widening disagreement among groups may be linked to the advancement of information communication technology by analyzing a mathematical model of population dynamics in a continuous opinion space [1]. We adopted the interaction kernel approach to model enhancement of people's information-gathering ability and introduced a generalized nonlocal gradient as individuals' perception kernel. We found that the characteristic distance between population peaks becomes greater as the wider range of opinions becomes available to individuals or the more attention is attracted to opinions distant from theirs (Figure 1). These findings may provide a possible supplemental mechanism of why and how disagreement is growing in today's increasingly interconnected society, without attributing its cause only to specific individuals or events.

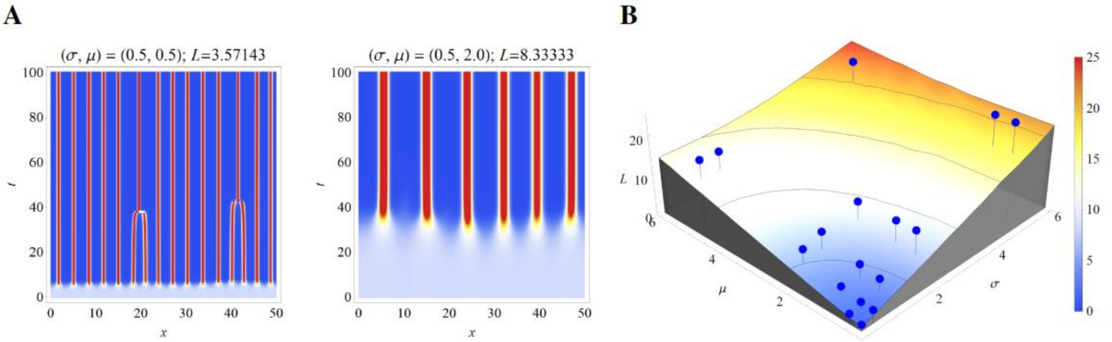

Figure 1: A: Numerical simulation results of the population dynamics of the proposed model visualized in space (x: horizontal axis) and time (t: vertical axis, going from bottom to top). Colors represent population density. Results with several different values of perception kernel parameters σ and μ are shown. **B:** Characteristic distance between population peaks (L) visualized as a function of σ and μ. The surface plot shows a critical lower bound L_c below which such perturbations would not grow. The blue dots show actual peak distances measured in numerical simulations. See [1] for more details.

Acknowledgements

This work was supported by JSPS KAKENHI Grant No. 19K21571 and the Visitors Program of the Max Planck Institute for the Physics of Complex Systems.

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Superspreading k-cores at the center of COVID-19 pandemic persistence

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The spread of COVID-19 caused by the recently discovered SARS-CoV-2 virus has become a worldwide problem with devastating consequences. To slow down the spread of the pandemic, mass quarantines have been implemented globally, provoking further social and economic disruptions. Here, we implement a comprehensive contact tracing network analysis to find the optimal quarantine protocol to dismantle the chain of transmission of coronavirus with minimal disruptions to society. We track billions of anonymized GPS human mobility datapoints from a compilation of hundreds of mobile apps deployed in Latin America to monitor the evolution of the contact network of disease transmission before and after the confinements. As a consequence of the lockdowns, people's mobility across the region decreases by ~53%, which results in a drastic disintegration of the transmission network by ~90%. However, this disintegration did not halt the spreading of the disease. Our analysis indicates that superspreading k-core structures persist in the transmission network to prolong the pandemic. Once the k-cores are identified, the optimal strategy to break the chain of transmission is to quarantine a minimal number of 'weak links' with high betweenness centrality connecting the large k-cores.

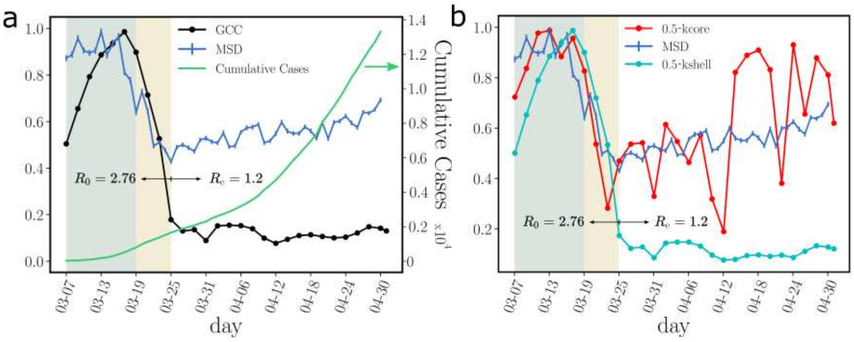

Figure 1*: Structural components of transmission networks across the lockdown*. (**a**) Evolution for different metrics in Cearà, Brazil, previous to the mass quarantine (grey area), right after the imposed quarantine (yellow area) and later. The plot shows the root mean square displacement (MSD) normalized by the maximum value over the total period (blue), the cumulative number of cases (green) and the size of the GCC normalized by the maximum value over the total period (black). The uncertainty corresponds to the standard error (SE). The mobility data is showcased in the Grandata-United Nations Development Programme map shown in https://covid.grandata.com. The initial rise in GCC is due to the lack of data before March 1. (**b**) The plot shows the 0.5-kcore size (red), the 0.5-kshell size (cyan) all normalized by their respective maximum value pre-lockdown. While the size of the 0.5-kshell is reduced drastically during the lockdown, the 0.5-kcore was not reduced as much and keeps increasing, contributing to sustain the pandemic. The 0.5-kcore seems to follow the trend in the MSD, which we plot again to show this trend.

Predicting Chaos with Electronic Reservoir Computing

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Reservoir Computing (RC) is a machine-learning-based computing paradigm which allows for the use of physical dynamical systems as computing elements. A reservoir computer consists of an input layer, a reservoir and a readout layer. The reservoir is generally a randomly connected recurrent neural network, which brings about a nonlinear transformation of the inputs onto a higher dimensional space and hence, any nonlinear dynamical system is capable of being a reservoir. A special feature of RC is that the input layer or the reservoir are kept fixed and do not require training. Only the readout is trained and this drastically reduces the computational cost. In this work [1], we aim to integrate the model-free prediction ability of RC with the intrinsic computing capability of complex dynamical systems, specifically memristive electronic systems. We demonstrate the computation through a single node reservoir made of a memristive chaotic circuit and explore the effect of the system's dynamics on its performance. The reservoir is computationally implemented and is trained for the task of approximating nonlinear polynomials and a trajectory of the Lorenz-63 dataset. The performance of the reservoir is tested based on the mean squared error between the test and target data. Subsequently, we demonstrate how the dynamics of the circuit plays a direct influence on the reservoir's hyperparameters.

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Bi-modal demand responsive ride pooling

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Commuting is an indispensable part of modern human lives. While modern cities offer various modes of transportation, considered separately, none of them is both efficient, i.e., sustainable, and convenient. A taxi service is convenient, in a sense, due to door-to-door service, but is inefficient since it usually serves one customer only. Demand responsive ride pooling (DRRP) with minibuses [1] is more efficient, but leads to undue competition with line services (LS), which provide even better pooling (average number of passengers per vehicle) but are less convenient due to fixed routes and stops. A combination of both modes, DRRP and LS, may provide an ideal solution but is challenging to organize. Here we derive conditions for efficient and convenient transportation for a bi-modal service based on a simple square-grid geometry. We relate the optimal mesh size, i.e., distance between stations, to external parameters like passenger density and traveling behavior. Our analytical results are accompanied by agent-based transport simulations. This study contributes to the general understanding of how to resolve the fundamental challenge of serving largely uncorrelated mobility demands in a sustainable way.

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V-, U-, L- or W-shaped recovery after Covid-19: Insights from an Agent-Based Model

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Following the Covid-19 pandemic, governments all over the world have been forced to impose emergency measures such as lockdowns leading to a severe loss in economic output. Whereas standard models assume a progressive return to equilibrium output after a shock, we discuss the impact of a Covid-like shock on a simple toy economy, described by the Mark-0 Agent-Based Model [1-3]. We consider a mixed supply and demand shock, and show that depending on the shock parameters (amplitude and duration), our minimal model can display V-shaped (quick recovery), U-shaped (rapid drop followed by slow recovery) or W-shaped (double dip) recoveries, and even an L-shaped output curve with permanent output loss. This latter scenario is due to the existence of a self-sustained ``bad'' state of the economy. We then discuss two policies that attempt to moderate the impact of the shock: giving easy credit to firms, and the much-debated "helicopter money" drop, i.e. injecting new money into the savings of households. We find that both policies are effective if strong enough, and we highlight their impact on inflation as well as the potential danger of terminating these policies too early. While we only discuss a limited number of scenarios, our model is flexible and versatile enough to allow for a much wider exploration, thus serving as a useful tool for the qualitative understanding of post-Covid recovery. Finally, our work highlights the importance of ABM as multi-purpose "scenario generators", which produce outcomes that are difficult to foresee due to the intrinsic complexity of macro-economic dynamics.

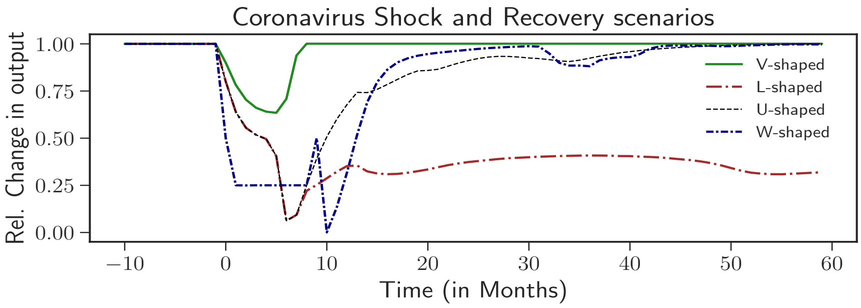

Figure 1: Possible recovery patterns following the coronavirus shock, which starts at time t=0. We show, as a function of time, the fall in output relative to the no-shock scenario.

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The Role of Modularity in the Formation of Macroscopic Patterns on Complex Networks.

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Patterns are macroscopic structures which are derived from the self-organization of a system consisting of macroscopic interacting entities. The formation of spatial patterns was originally based on the competition between fast diffusing chemicals, the inhibitors, and the slow diffusing activators [1]. This theory originally assumed a continuous space, but we now know that if one looks closely, many systems are discrete, and can be abstracted as a network. One such system is the brain, which can be described as a network of connected neurons. There has been a wealth of macroscopic patterns of activity observed in brain networks. In this work we have developed a mathematical theory which explains the crucial role of the topology of the underlying networks. Using the spectrum of the Laplacian of a network, we show that modularity can induce the formation of patterns.

Thus, our main result is that modular networks can exhibit Turing instabilities for cases where the ratio between the activator and inhibitor diffusion coefficients is close to one. Turing patterns can arise in nonlinear systems of reaction-diffusion equations involving at least two species. They form when a spatially homogeneous steady state is linearly unstable to an inhomogeneous perturbation. This can normally only occur when there is a large difference between the diffusion constants of the activator and inhibitor.

Turing instabilities are studied by linearizing about the homogeneous steady state, and calculating the dispersion relation; in the networks case this relates to the eigenvalues of the Laplacian (which represent the different spatial patterns of instability via their eigenvectors) and the eigenvalues of the Jacobian (which represent the speed at which a small perturbation will grow or shrink). For modular networks, the eigenvectors can force macroscopic patterns (see figure 1a), as reported in the brain [2].

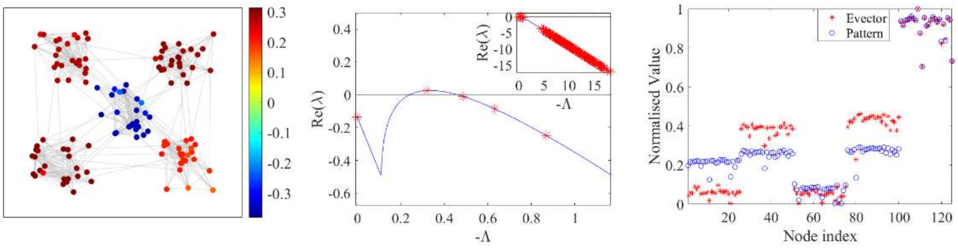

Figure 1: (a) A macroscopic pattern on a modular network (b) Plotting the normalized eigenvector of the largest eigenvalue of the extended Jacobian, with the normalized pattern. (c) The corresponding dispersion relation derived by plotting the eigenvalues of the extended Jacobian against those of the Laplacian.

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Inferring the role of contact networks in the meta-population spreading models

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The spreading phenomenon has characterized for a long time, problems arising from the diseases contagion to the diffusion of information [1]. The behaviour of the interacting agents has been usually modelled in two main ways accordingly to the size of the spatial support where the spreading occurs. On one side, we have contact network models where the interacting agents are confined in a restricted physical or virtual space where the transmission between individuals in contact with each other. On the other side, we have the meta-population formalism that makes use of reaction-diffusion equations where agents need to migrate between meta-nodes to infect individuals from other spatial patches. In the latter scenario, however, the impact that the topology of the contact network has on the spreading dynamics has been neglected or has merely been quantified through the infection rate only. In this paper, we shed light on the role that the contact networks have on the spreading processes by embedding their structure in the meta-population systems creating this way a hybrid extended model, recently known as metaplex [2], that takes into account the topological features of the contact processes. Our model is independent of the mean-field approaches that model the contact network dynamics and paves the way to a better understanding of the spreading dynamics in general.

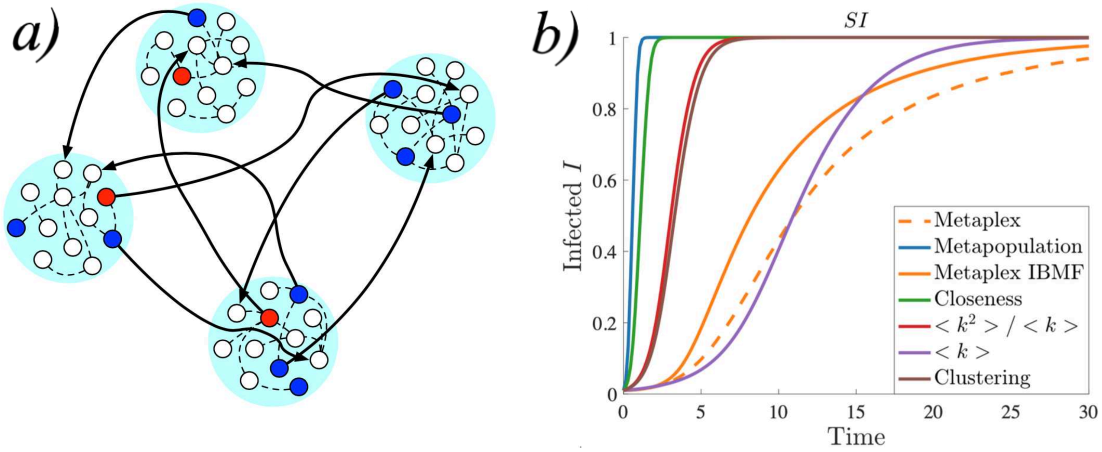

Figure 1. *(a) A schematic representation of the spreading process in the metaplex network. The single individuals who can be infected (red) or not (blue) might be in contact with each other (dashed links) once they belong simultaneously to the same spatial patch represented with the meta-node (cyan). They are also allowed to migrate from node to node (solid links) at the specific position already provided for them in the hosting node. This way, they cannot belong to more than one meta-node at a time. (b) Spreading dynamics in metaplex and meta-population in the SI model. Several approximations (in the inset) are used to infer the right contagion parameter in the meta-population model that also considers the topology of the local contact networks. It results that the mean degree of the networks constituting the meta-nodes, is the best approach, in general.*

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Citation Vectors in 3D

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The growing popularity of bibliometric indexes goes hand in hand with their critique by those who claim that scientist's impact cannot be reduced to a single number. Some even believe that such a complex reality fails to submit to any quantitative description. We argue that neither of the two controversial extremes is true. With our new agent-based model [1] we can describe the emergence of citation curves very accurately.

We assumed that some citations are distributed according to the rich get richer rule while some others are allocated totally at random. This yields a very accurate model that is governed by merely three easily interpretable parameters: productivity, total impact, and *rho*.

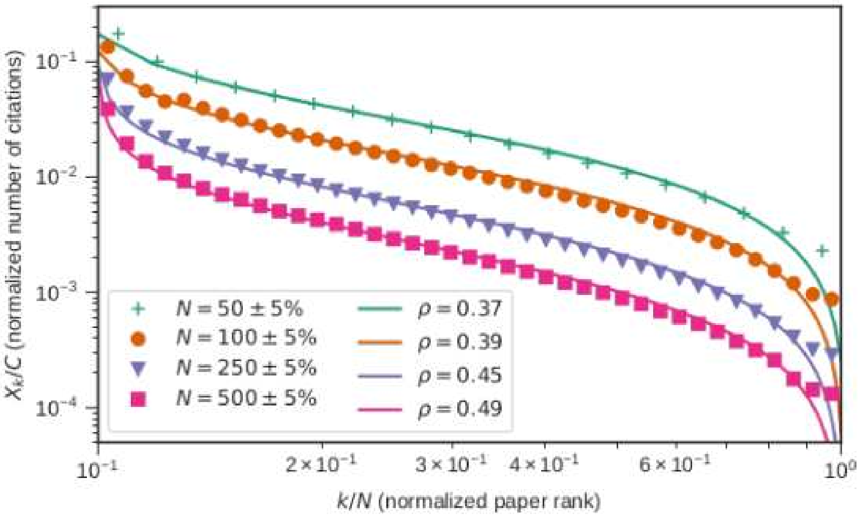

Figure 1. Three parameters can accurately describe citations vectors [1]

Acknowledgements

The project was funded by POB Research Centre Cybersecurity and Data Science of Warsaw University of Technology within the Excellence Initiative Program - Research University (ID-UB).

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Modelling the Coronavirus Second Wave
in Presence of the Lockdown and Quarantine Measures

SONNINO Giorgio, PEETERS Philippe, and NARDONE Pasquale

ABSTRACT

After successfully tamping down the first surge of infection and death, Europe is now in the middle of a second coronavirus wave as it moves into winter [1]. We propose a realistic model for the evolution of the COVID-19 pandemic subject to the lockdown and quarantine measures. The dynamic equations for the entire process are derived by adopting a "*kinetic-type reactions*" approach. More specifically, the lockdown and the quarantine measures are modeled by some kind of inhibitor reactions where susceptible and infected individuals can be "*trapped*" into inactive states. The dynamics for the recovered people is obtained by accounting people who are only traced back to hospitalized infected people. To get the evolution equation we take inspiration from the *Michaelis- Menten's enzyme-substrate reaction model* (the MM reactions-model) [2] where the *enzyme* is associated to the *available hospital beds*, the *substrate* to the *infected people*, and the *products* to the *recovered people*, respectively. In other words, everything happens as if the hospitals beds act as a "*catalyzer*" in the hospital recovery process. Of course, in our case the reverse MM reaction has no sense in our case and, consequently, the kinetic constant is equal to zero. Finally, the O.D.E.s for people tested positive to COVID-19 is simply modeled by the following kinetic scheme **S+I => 2I** with **I => R** or **I => D**, where **S**, **I**, **R**, and **D** denote the compartments Susceptible, Infected, Recovered, and Deceased people, respectively [3]. The resulting "*kinetic-type equations*" provide the O.D.E.s, for elementary "*reaction steps*", describing the number of the infected people, the total number of the recovered people previously hospitalized, subject to the lockdown and the quarantine measure, and the total number of deaths.

We show that our model is able to produce predictions not only on the first but also on the second or even the third waves of COVID-19 infections. The theoretical predictions are in agreement with the official number of cases with minimal parameter fitting. We discuss the strengths and limitations of the proposed model regarding the long-term predictions and, above all, the duration of how long the lockdown and the quarantine measures should be taken in force in order to limit as much as possible the intensities of subsequent SARS-CoV-2 infection waves. This task has been carried out by taking into account the theoretical results recently appeared in literature [4].

We are currently incorporating real data into a stochastic model in order to obtain a comparative analysis against the deterministic one and for using the new theoretical results to predict the number of new cases of infected people and to propose possible changes to the measures of isolation.

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DOI: http://dx.doi.org/10.47829/ACMCR.2020.4902

A State Feedback Vaccination Law for an Age-Dependent SIR Epidemic Model

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Epidemic models aim to describe the evolution of diseases in order to have a better understanding of these processes. Those models allow the comparison, planification and implementation of some prevention, therapy or control programs. Here, we are interested in vaccination as control policy. In our work, an adaptated version of the well-known SIR model of Kermack and McKendrick is used. The particularity of this work is to take into account the importance of the ages of the individuals in the model. It is motivated by the fact that several factors in diseases propagation depend on the age of the individuals, vaccination being one of them. Up to our knowledge of the literature, a specific feature of this research is the design of an age-dependent control law.

The dynamics of the disease propagation are based on the model described in [1, pp. 40-43]. The dynamics are given by the following set of integro-partial differential equations, for $t > 0$ (time variable) and $a \in [0, L]$ (age variable),

$$\begin{cases} (\partial_t + \partial_a)S(t,a) = -\mu(a)S(t,a) - \beta(a)S(t,a)\displaystyle\int_0^L I(t,b)db - \vartheta(t,a), \\ (\partial_t + \partial_a)I(t,a) = -\big(\gamma(a) + \mu(a)\big)I(t,a) + \beta(a)S(t,a)\displaystyle\int_0^L I(t,b)db, \\ (\partial_t + \partial_a)R(t,a) = \gamma(a)I(t,a) - \mu(a)R(t,a) + \vartheta(t,a) \end{cases} \quad \text{with} \quad \begin{array}{c} S(0,a) = S_0(a), \\ I(0,a) = I_0(a), \\ R(0,a) = R_0(a), \\ S(t,0) = B, \\ I(t,0) = 0, \\ R(t,0) = 0. \end{array} \tag{1}$$

The parameter $\vartheta(t,a)$ denotes the density of vaccinated individuals by unit of time, which is the control variable that needs to be designed.

First, it is shown that, under the basic reproduction number, there is only one stable equilibrium corresponding to the disease-free case. Above the treshold, there are two equilibria, the disease-free one, which is locally unstable and an endemic stable one. In view of this result, it seems natural to try to find an appropriate vaccination policy in order to stabilize the system around the disease-free equilibrium. That is done, like in Tudor's article [2], via the discretisation of System (1) by dividing the population into n classes of ages $[0, a_1[, \ldots, [a_{n-1}, L[$ to obtain a set of nonlinear ordinary differential equations

$$\begin{cases} \dfrac{di_k(t)}{dt} = T_k i_{k-1}(t) - \big(T_k + \gamma_k\big)i_k(t) + \beta_k s_k(t)\displaystyle\sum_{j=1}^{n} N_j(t)i_j(t), \\ \dfrac{ds_k(t)}{dt} = T_k s_{k-1}(t) - T_k s_k(t) - \beta_k s_k(t)\displaystyle\sum_{j=1}^{n} N_j(t)i_j(t) - \vartheta_k(t), \end{cases} \tag{2}$$

for $k = 1 \ldots n$ with $T_k = \rho_k + \mu_k$ where $T_0 = 0$ and $s_0 = 0$.
The design of a nonlinear feedback control law is based on differential geometry, see Isidori's book [3]. By applying an appropriate change of coordinates to System (2), it is shown that this state feedback control law exponentially stabilizes the closed-loop system and implies the asymptotic convergence of the infected population towards the disease-free equilibrium, under specific conditions on the control tuning parameters. Numerical simulations complete this analysis and illustrate the theoretical results.

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Multistability in an Ensemble of Coupled Duffing Oscillators

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We analyze the collective dynamics of an ensemble of identical, globally coupled, externally forced, mechanical oscillators with cubic nonlinearity. Focus is put on solutions where the ensemble splits into two internally synchronized clusters, as a consequence of the bistability of individual oscillators. The multiplicity of these solutions, induced by the many possible ways of distributing the oscillators between the two clusters, implies that the ensemble can exhibit multistability. As the strength of coupling grows, however, the two-cluster solutions are replaced by a state of full synchronization. By a combination of analytical and numerical techniques, we study the existence and stability of two-cluster solutions. The role of the distribution of oscillators between the clusters and the relative prevalence of the two stable solutions are disclosed.

The emergence of segregation driven by mobility and homophily

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Socio-economic segregation shapes the dynamics of the population distribution in urban areas, so a good understanding of the elementary mechanisms driving this phenomenon is essential to develop public policies that increase interaction among groups in the society and bring equal access to facilities and resources. In this work, we extend the idea behind the Schelling's model, i.e., that segregation emerges as a consequence of homophily and clustering, by including a more realistic mobility model.

We consider a synthetic society as a graph $G(V, E)$ of niches or neighbourhoods, represented by the weighted adjacency matrix $W = \{w_{ij}\}$, and we assume that a number of agents belonging to C classes diffuse on G through a random walk with diffusion probability μ. Upon leaving its current node i, an agent of class α jumps to one of the neighbours of i following a biased transition rule, so that a given destination node j is chosen proportionally to the abundance of other agents of class α already sitting at j. In particular, each of the $m_i^\alpha(t)$ agents of class α sitting on node i at time t move to node j with probability proportional to $\mu w_{ij} f_j^\alpha(t)$, where $f_j^\alpha(t) = (m_j^\alpha(t)/m_j(t))^\beta$, and β encodes the effect of homophily, i.e., the preference for nodes where the abundance of agents of class α is higher.

Thus, for $\beta \approx 0$ the system behaves similarly to a uniform random walk, with stationary distribution determined by the degree distribution of G. Instead, for $\beta \gg 0$, local fluctuations in the distribution of agents of class α could cause the concentration of agents on nodes where the class α is already predominant.

Numerical simulations confirm that the steady-state distribution of classes across nodes depends in a non-trivial way on both mobility (μ) and homophily (β). As an example, in Fig. 1**a** we show the phase diagram of the system as a function of the two control parameters on a 20×20 lattice with $C = 7$ distinct classes. The order parameter here is the average difference on the abundance of a class across neighbouring nodes:

$$\rho = \frac{1}{K} \sum_{\alpha} \sum_{i,j} a_{ij} |m_i^\alpha - m_j^\alpha|$$

where K is an appropriate normalisation constant. When $\rho \approx 0$ the distribution of classes is close to uniform, while $\rho \approx 1$ when the system is segregated.

Interestingly, segregated regimes are dominant for a wide range of combinations of the control parameters. In particular, when μ is small and $\beta \gtrsim 0.5$ the majority of solutions converge to a segregated state where agents diffusing across G and move to a site in which their class is predominant. Conversely, when $\mu \gtrsim 0.7$ the steady-state solutions are heterogeneous combinations of the classes, but the system converges gradually to segregated regimes as β gets larger. Interestingly, the values of ρ obtained for real cities are confined in the small region where $\beta \gtrsim 0.5$ and $\mu \gtrsim 0.7$ (See Fig. 1**b**) where the transition between regimes of segregation changes abruptly.

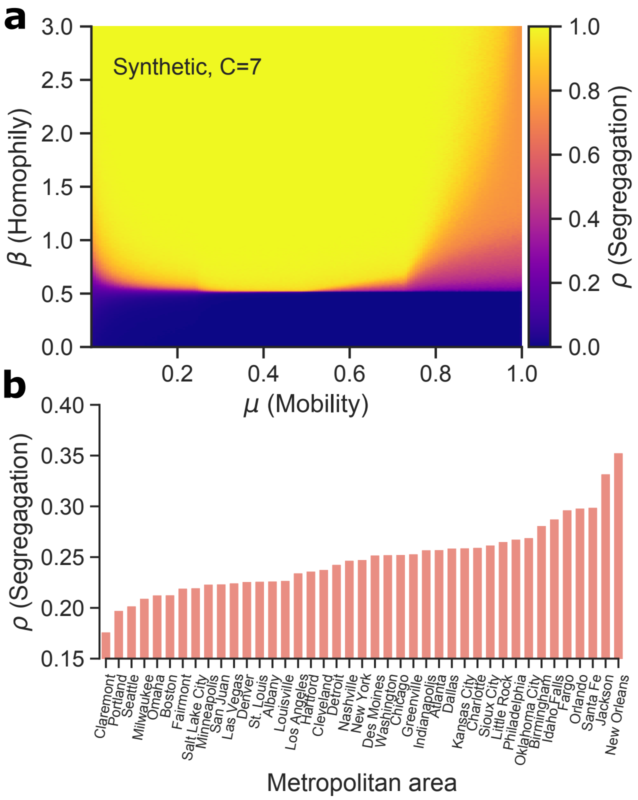

FIG. 1. **(a)** Phase diagram of the segregation model as a function of mobility (μ) and homophily (β). The order parameter ρ consists on the difference of the fraction of agents of the same class living in neighbouring nodes. Regimes where $\rho \to 1$ indicates segregated states. The estimates correspond to 5000 iterations on a periodic lattice of 400 cells and 7 distinct classes. **(b)** Metropolitan areas in the US ranked by ρ where the population distribution (7 classes) is obtained from Census.

These results confirm quantitatively that homophily is dominant for the emergence of segregation, while mobility can indeed favour the attainment of non-segregated regimes.

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A Zika model with sexual transmission and vertical vector transmission

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The main objective of the study of Zika transmission is to determine the best approach to reduce human mortality and morbidity caused by the disease. Therefore, it is essential to identify the relative importance of the different factors that contribute to the transmission and prevalence of the disease. Although many mathematical models have been formulated to study zika transmission dynamics in the presence of vertical transmission [1] and human-to-human transmission [2], they did not take into account the combination of both types of transmission. The question raised is does the combination of both transmission types results in a higher number of infection cases? To answer this question, a deterministic model of Zika with vertical transmission in vector population and human-to human transmission is developed (see figure). It includes the immature phase of mosquitoes (eggs), adult mosquitoes (susceptible, exposed and infectious) and human hosts (susceptible, exposed, infectious and recovered). Using the homogeneous mean-field approach the dynamics of the epidemic spreading is analyzed. Results show that neglecting the vertical transmission in the vector population leads to an underestimation of the proportion of the infected population. Furthermore, it reduces the speed of the disease spreading. The same effect is observed if one does not consider the sexual transmission. A sensitivity analysis of the reproductive number R_0 is performed in order to gain a better understanding on the main parameters driving the dynamics of the disease. It appears that the most sensitive parameters by decreasing order are: the adult mosquito mortality rate (μ_v), the mosquito bite rate (a), the transmission probability mosquito to human (β_{vh}) and the transmission probability human to mosquito (β_{hv}). Furthermore, the proportion at equilibrium of infected humans is very sensitive to the rate of transition from the immature vector stage to the adult stage (ϕ), the human to human transmission rate (β_{hh}) and the human recovery rate (γh). These results confirm that Zika control policies that target the vector population and the recovery rate of individuals are quite effective control solutions. Future work will incorporate environmental conditions [3].

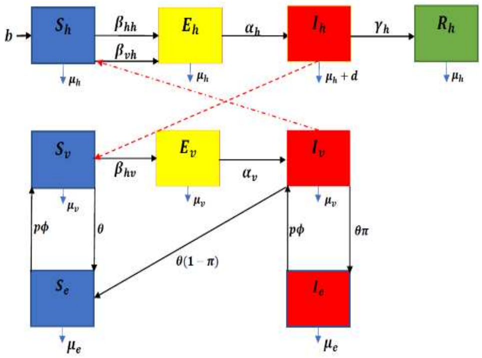

Figure. The flow chart represents the interactions and transfer of a vector-borne disease in both human and vector populations. The host population is split into states: Susceptible S_h, Exposed E_h, Infectious I_h, and recovered R_h. The vector population is split into 3 states: Susceptible S_v, Exposed E_v and Infectious I_v .The eggs population is split into 2 states: Susceptible S_e, Exposed and Infectious I_e. Relevant parameters are transmission probability human to mosquito (β_{hv}), the transmission probability human to mosquito (β_{hv}), the human to human transmission rate (β_{hh}), the immature vector stage to the adult stage (ϕ), the mosquito bite rate (a), the adult mosquito mortality rate (μ_v), the human recovery rate (γ_h), Number of Aedes eggs laid per day (θ), Vertical transmission rate(π), Daily human recruitment rate(b), incubation rate of an vector(α_v).

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Network-based Phase Space Analysis of the El Farol Bar Problem

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The El Farol Bar problem is a game theory problem where actors must decide whether or not to go to a bar with limited information. We recently proposed to study this problem as a dynamical system of strategy distribution space and revealed its dynamics and attractors in this phase space [1]. However, the previous research was limited in that the phase space required *N-1* dimensions to fully visualize where *N* is the number of decision strategies. To address this issue, here we propose a novel phase space visualization and analysis method that converts the dynamics of the strategy distribution with any number of decision strategies into a weighted directed network. Each node represents a unique distribution of strategies and each edge represents an observed state change from one distribution to another (Fig. 1a). The edge weight indicates the number of times the transition occurred in all simulations. This network-based representation of the strategy dynamics lets us identify an attractor in the strategy phase space as a strongly connected component with no outgoing edges. The entire phase space topology can also be systematically investigated using various other network analysis tools. We found power law relationships in the node degree (strength) distribution (Fig. 1b) and the edge weight distribution, which manifest more when the number of strategies increases. Furthermore, this approach not only provides a generalized analysis of the El Farol Bar Problem as a dynamical system but is problem-agnostic and can be applied to any high-dimensional discretized dynamical systems.

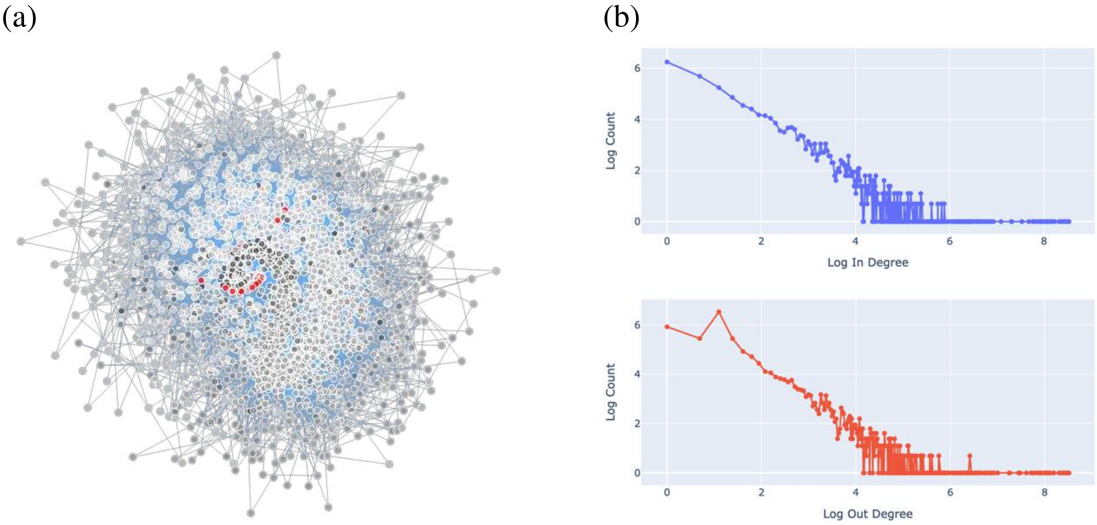

Figure 1: Example of network-based phase space of the El Farol Bar Problem and its properties. (a) Visualization of the network-based phase space. Red nodes form the attractor. Colors of other nodes represent the distance from the attractor (darker: closer). (b) Degree (strength) distributions of the network (top: in-degree, bottom: out-degree).

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APPLICATION OF DEEP LEARNING AND CHAOS THEORY FOR LOAD FOREACTING IN GREECE

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The decision making and operation of the power grid are directly related to the electrical load and consequently, its accurate prediction is of major importance. However, electric load, due to the non-linear and stochastic behavior of consumers, is considered a complex signal. Despite the research that has been implemented in this area, accurate forecasting models are still needed. In this article, a novel technique that combines deep learning and chaos theory is proposed for short-term electric load forecasting in Greece. The proposed model is a Recurrent, Long Short Term Memory (LSTM), Neural Network, and combined with maximum Lyapunov exponent produces predictions of high accuracy. The historical data we used has been taken from ADMIE (Independent Electricity Transmission Operator) in Greece and the meteorological data from Acharnes Meteorological Station in Athens. We focused our predictions on periods with smooth variation and abrupt variation by applying neural network models and chaos theory trying not only to predict values within these time ranges with high accuracy but also to establish a safe forecasting horizon. The deep learning model that has been applied is a univariate LSTM neural network with multiple layers and it is validated by comparing it with a univariate single layer Feed Forward Neural Network (FFNN) and a multivariate single layer LSTM. From our results, the proposed Deep Learning model outperforms the other two in terms of accuracy. Moreover, the estimation of the safe horizon is under the prediction of the maximum Lyapunov exponent.

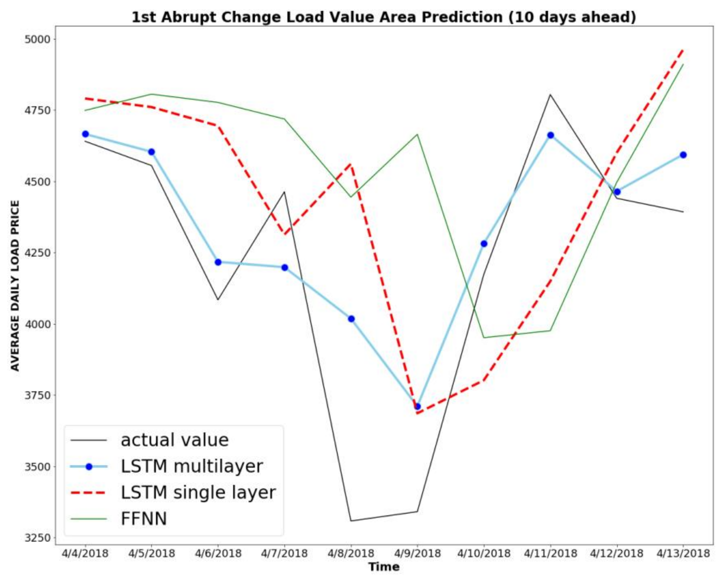

Figure 1: Predictions for the 1st Abrupt Change Load Area, for 10 days ahead

The cost of coordination can exceed the benefit of collaboration in performing complex tasks

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Collective decision-making is ubiquitous when observing the behavior of intelligent agents, including humans. However, there are inconsistencies in our theoretical understanding of whether there is a collective advantage from interacting with group members of varying levels of competence in solving problems of varying complexity. Moreover, most existing experiments have relied on highly stylized tasks, reducing the generality of their results. The present study narrows the gap between experimental control and realistic settings, reporting the results from an analysis of collective problem-solving in the context of a real-world citizen science task environment in which individuals with manipulated differences in task-relevant training collaborated on the Wildcam Gorongosa task, hosted by The Zooniverse.

First we train the participants for the task and by randomly allocating them in two different conditions, we generate a difference in their level of competence. Then in the second phase of the experiment, we build dyads of participants with different combinations of their training conditions ("targeted" and "general") and compare their performance among the dyads as well as with the individuals.

We find that dyads gradually improve in performance but do not experience a collective benefit compared to individuals in most situations (Figure 1); rather, the cost of team coordination to efficiency and speed is consistently larger than the leverage of having a partner, even if they are expertly trained. It is only in terms of accuracy in the most complex tasks that having an additional expert significantly improves performance upon that of non-experts.

Our findings have important theoretical and applied implications for collective problem-solving: to improve efficiency, one could prioritize providing task-relevant training and relying on trained experts working alone over interaction and to improve accuracy, one could target the expertise of selectively trained individuals.

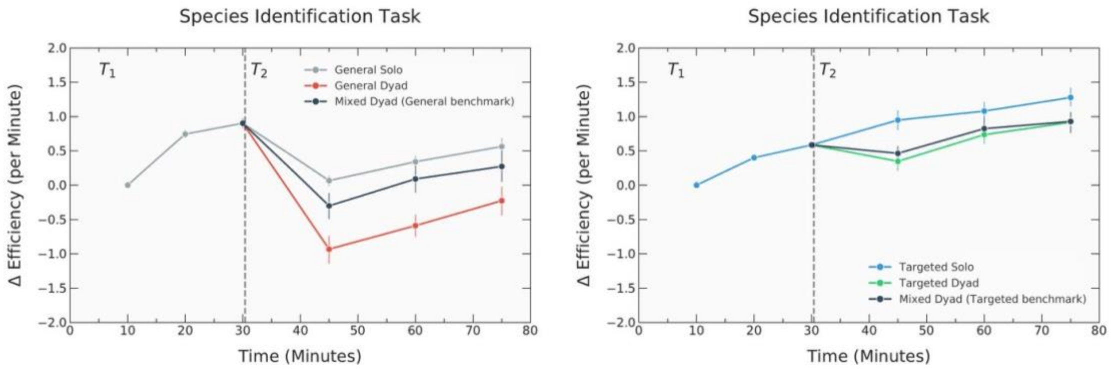

Figure 1: Performance differences between individuals and dyads over the course of training (T1) and testing (T2) phases in terms of efficiency: number of correct classifications per time unit, for the species identification task.

A Growth Model for Water Distribution Networks with Loops

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Water distribution networks (WDNs) evolve in time. Specifically, WDNs expand their service areas from one or more root nodes which act as sources. One facet of WDNs is that they have loops in general, and closing loops may be a functionally important process in the entire growth process. So far, most existing models for spatial networks rely on global optimization and neglect mechanistic processes, and evolution of spatial networks is poorly understood.

Here we propose a novel growth model for WDNs. The proposed model is classified as a greedy model where edges are added one by one based on a local optimization. Our model generates networks with loops, and it can be applicable to networks with multiple root nodes. The model requires only a few inputs (i.e., the numbers of nodes and edges, the two-dimensional coordinates of the nodes, and ID of the root node(s)) and only has one parameter γ that controls the trade-off between the Euclidean length of new edges and the Euclidean length of loops closed by the new edges. We applied the model to four data sets of empirical WDNs. We show the results for the Colorado Springs WDN in Figure 1, which indicates that the model produces networks similar to the empirical WDN at $\gamma \approx 0.4$ in several structural properties (e.g., average degree, maximum degree, cost, route factor, and robustness). We obtained similar results in the other three data sets. These results imply that our model may offer an explanation of the growth mechanisms of the WDNs. It may also be applicable to other spatially distributed physical transport networks such as gas pipelines and railway networks.

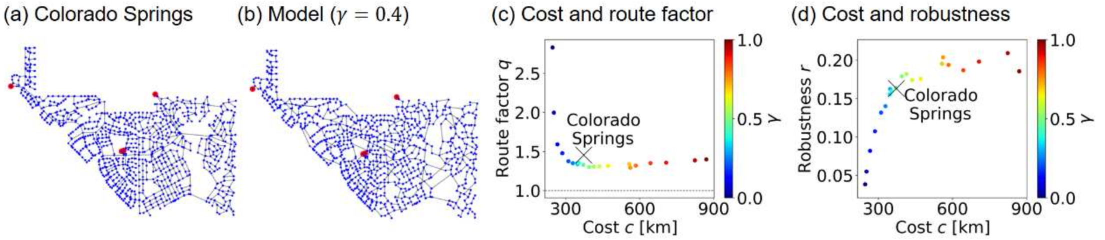
(a) Colorado Springs
(b) Model ($\gamma = 0.4$)
(c) Cost and route factor
(d) Cost and robustness

Figure 1: Comparison between the empirical and synthetic network. (a) The Colorado Springs WDN. Red-colored nodes represent root nodes. (b) A network generated by our model with $\gamma \approx 0.4$. (c) Cost and route factor of the empirical and synthetic networks with different values of γ. We define the cost c by the total length of all edges [km]. We define the route factor q by $q = \frac{1}{N-1}\sum_{i=1}^{N-1}\frac{l_{i0}}{d_{i0}}$, where N is the number of nodes, d_{i0} is the literal Euclidean distance between the root node v_0 and node v_i, and l_{i0} is the Euclidean length of the shortest path in the network (i.e., shortest in terms of the Euclidean distance) between nodes v_0 and v_i. We define the route factor for networks with multiple root nodes by the average of the route factor over the root nodes. (d) Cost and robustness of the empirical and synthetic networks with different values of γ. We define the robustness r by $r = \frac{1}{M}\sum_{Q=1}^{M} s(Q)$, where $s(Q)$ is the fraction of demand nodes (i.e., nodes except for the root nodes) that are connected to any of the root nodes after one removes Q edges. In every step of edge removal, we choose an edge uniformly at random and remove it from the network.

Dynamic metabolic adaptation can promote species coexistence in competitive microbial communities

Samir Suweis, Leonardo Pacciani-Mori, Andrea Giometto, Amos Maritan

Since a celebrated experiment by Monod in 1949, we know that microbes can adapt their metabolic strategies in response to their environment, thus uptaking different nutrients at different rates depending on their relative quality and availability. It is currently unclear whether this physiological plasticity of microbes contributes to maintaining the high degree of diversity found in natural microbial communities, even in the presence of very few resources. By introducing dynamic and optimal metabolic strategies in consumer- resource models, we show that we can correctly reproduce the experimental growth of Saccharomyces cerevisiae on two different resources and we show that dynamic metabolic strategies allow the community to self-organize and to ensure the coexistence of multiple species competing for few resources.

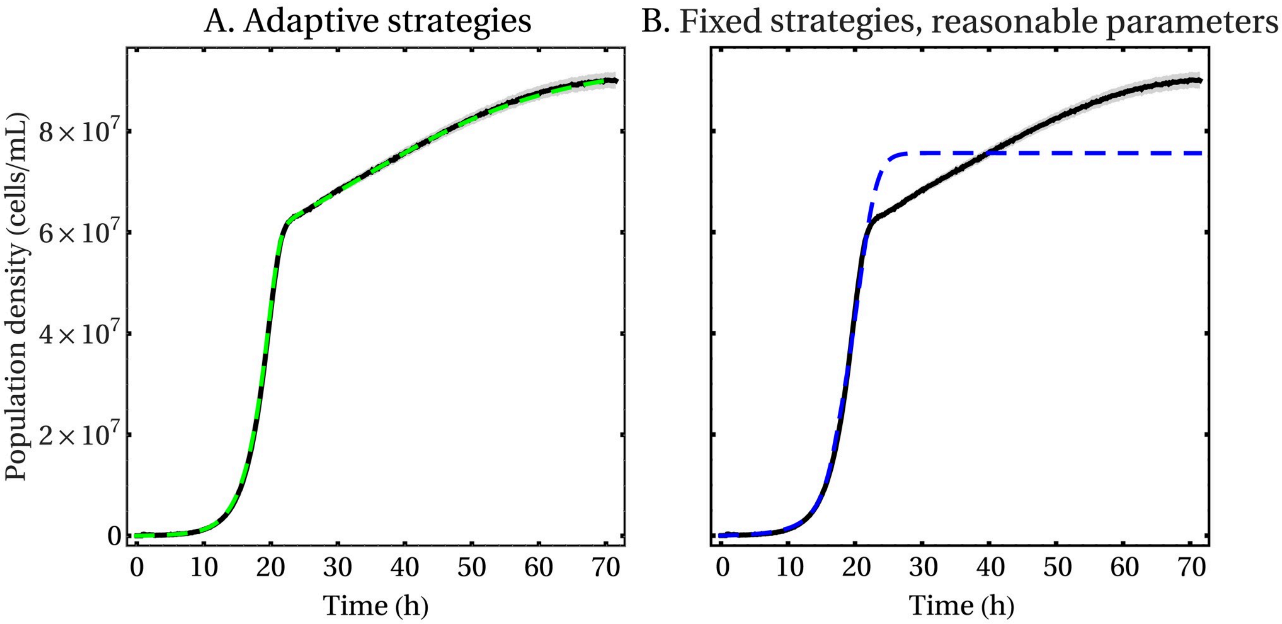

Fig 1. Comparison between the best fits of MacArthur's consumer-resource model (dashed lines) and experimental measures of the growth of *S. cerevisiae* on galactose as the primary carbon source and ethanol as a byproduct of fermentation, in the case of adaptive (A) and fixed (B) metabolic strategies.

From metagenomes to species: the need of a novel approach to learn from microbiomes

Samir Suweis

Characterizing species diversity and composition of bacteria hosted by biota is revolutionizing our understanding of the role of symbiotic interactions in ecosystems. Determining microbiomes diversity implies the assignment of individual reads to taxa by comparison to reference databases. Although computational methods aimed at identifying the microbe(s) taxa are available, it is well known that inferences using different methods can vary widely depending on various biases. In this study, we first apply and compare different bioinformatics methods based on 16S ribosomal RNA gene and shotgun sequencing to three mock communities of bacteria, of which the compositions are known. In this ignite talk we will share our view on the need of a novel approach to learn from microbiomes data. In particular, we will propose a taxonomic classification method, named Core-Kaiju, which combines the power of shotgun metagenomics data with a more focused marker gene classification method similar to 16S, but based on emergent statistics of core protein domain families. We have tested [1] the proposed method on various mock communities and we have shown that Core-Kaiju reliably predicts both number of taxa and abundances [1].We have also applied our method on human gut samples [1], showing how Core-Kaiju may give more accurate ecological characterization and a fresh view on real microbiomes.

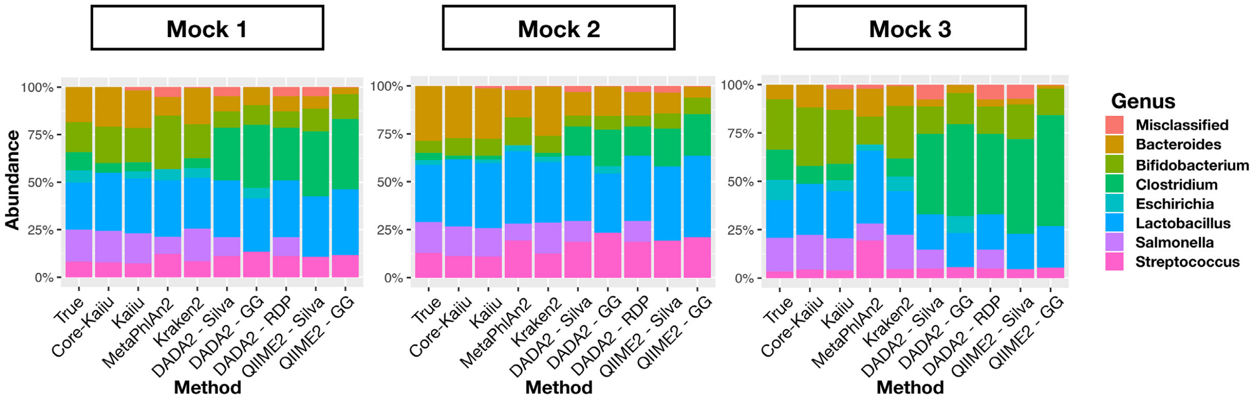

Figure: Comparison between theoretical and predicted relative abundances in small mock communities via different taxonomic classification methods. Our proposed approach, Core-Kajiu, outperfoms the other methods.

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Impact of the Latent Infection Transmissions on SARS-CoV-2 Epidemics: Agent-Based Modelling Framework

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We have developed an agent-based modeling framework for simulations of bio-social stochastic processes underlying SARS-CoV-2 epidemics. The individual features of the agents that affect the process at elementary interaction scale incorporate their susceptibility to the virus, which helps to differentiate between the symptomatic and asymptomatic cases, and exposure time of each actor, as well as the virus survival time and potential mutations. The process is visualized by a growing bipartite graph of the infected host and viruses that they produce, see Fig.1. A large number of asymptomatic individuals, as well as the secondary transmission due to the virus survival outside the human host, comprises the latent infection transmission, contributing to the widespread epidemics. We demonstrate [1] how the infection curves depend on the social participation activity, which is the driving force of the dynamics, and the exposure time of each participant. Our simulations reveal the mechanisms through which the social lock-down becomes effective and how the second wave raises when it is lifted. Moreover, by tracing the virus transmission paths on the graph, we can study a potential mutation of the virus. For example, assuming that its transmissibility reduces with the number of different hosts along the infection path, we show that the infection curves slow down as compared with the no-mutation case. The advantage of this mathematical framework is that it reveals the genesis of the collective phenomenon across the scales starting from individual actors. It allows for implementing different intervention scenarios that can affect the social participation level as well as the individual behaviour of each actor.

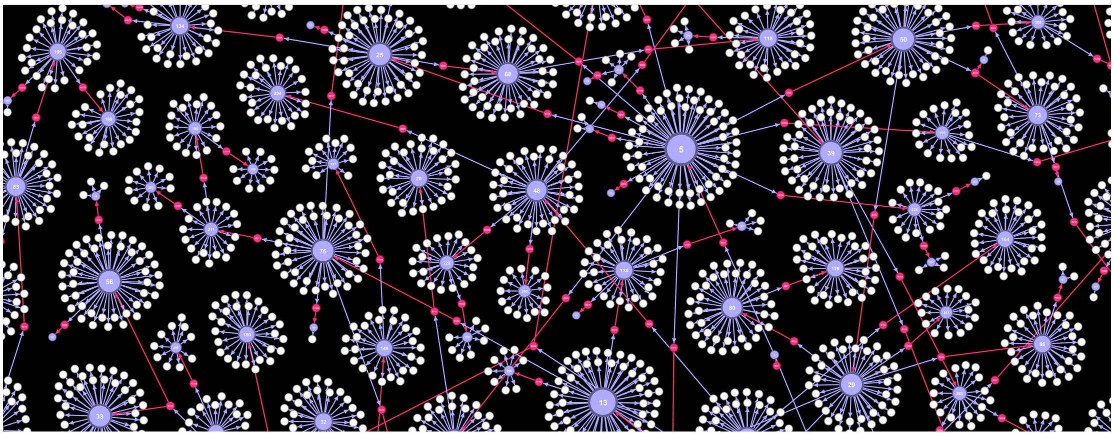

Figure 1: Directed bipartite graph of the infection transmissions with Host and Virus nodes

Acknowledgements

Work supported by The Research Agency of the Republic of Slovenia through the Program P1-0044 and The NSERC and the Program CRC of Canada.

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Burstiness in the Physical Activities of Children and Adults

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Burstiness in human behavior has been observed at various levels, from individual behavior to collective social phenomena [1]. Identifying the non-trivial mechanisms that cause burstiness is a crucial issue for understanding the universality of human behavior. Many studies on human behavior use web-based data and show burstiness in various contexts [2]. In such cases, the state and attributes (e.g., demographic information) of the individuals are often unknown. On the other hand, there are still few studies on human behavior using physical activity data, where the individual's state and attributes are clear. Previous research on human physical behavior has shown that the shape of the distribution of inter-event times (IETs) changes with mental illness. The burstiness of the activity may depend on the various states of the individual [3]. Thus, investigating how burstiness is affected by an individual's state and attributes will help to clarify the mechanism of the universality of human behavior and has possible medical implications.

Therefore, in this study, we measured human physical activities using accelerometers, along with recording the subjects' states (e.g. active or resting) and investigated those burstiness and temporal correlation. Here, subjects are infant (2-month-old), children (3-year-old), and adults.

We find that children showed the lower scaling exponent in cumulative distribution of IETs (Fig. 1). Also, some of the physical activity data show 1/*f* noise, which has also been identified in the brain activities [4]. Finally, we also discuss the point processes that may generate our observed features.

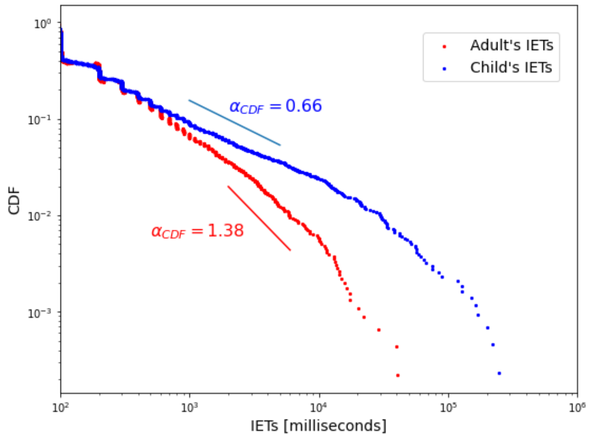

Figure 1: CDF of IETs for adult and child. α is scaling exponent of CDF.

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Simple discrete model emulating properties of hyperbolic geometrical graphs

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Experimentally observed complex networks often simultaneously exhibit scale-free degree distribution, small-world property and high clusterization. Classical textbook models of network theory (Erdos-Renyi, Barabasi-Albert, Watts-Strogatz, geometrical random graphs in Euclidean space, etc.) cannot simultaneously reproduce all three of these properties. It has been known at least since [1] that geometrical random graphs on a hyperbolic disk can reproduce all three and are therefore a good candidate model for understanding the structure of experimentally observed datasets. This idea gained significant traction in the last years, but its widespread application, especially in multidisciplinary research, is suppressed by heavy reliance on cumbersome formulae of hyperbolic geometry.

Here we suggest a simple discrete model which reproduces the main properties of hyperbolic geometrical random graphs. Namely, consider a regular tree with degree p and n generations, and add a bond between any two vertices if the shortest path connecting them on the tree is not longer than $m \leq n$. It is easy to show that for $m = n$ such a regular graph has a log-periodic discrete power-law degree distribution with scaling exponent -2, diameter 2, and clustering coefficient of order 1. However, it is, strictly speaking, a dense graph: the average degree diverges for $n \to \infty$ proportionally to the square root of the number of vertices. There are two possible ways to rectify that.

First, consider a limit when n tends to infinity while m stays finite. In this case the graph has a distinct core-periphery structure, with core consisting of vertices of generations smaller than (n-m), which all have the same degree. However, in the periphery the power-law degree distribution is preserved, while the fraction of monomers in the core is finite and exponentially small for large m. As a result, the degree distribution converges to a curtailed power law, while diameter of the network diverges as n/m, i.e. logarithmically with the number of bonds.

Second possible generalization implies that each node can be either filled or empty, and the probability of filling the node is a function of, generally speaking, the generation k to which a node belongs, and the total number of generations n. If this probability is k-independent and decays with growing p in a way that average degree of a node remains n-independent, the resulting limiting degree distribution is continuous and, for several orders of magnitude, almost exactly power law with scaling exponent -3, similar to the random geometrical graphs on a continuous hyperbolic disk [1]. By changing the k dependence of filling probability one can reproduce power law scaling with different exponents.

Moreover, one can reduce clustering coefficient to fit experimental values by introducing temperature in the system in a way similar to [1].

Thus, the suggested simple model reproduces the main properties of continuous hyperbolic graphs without relying on overcomplicated calculations. It seems that such a simple formulation of a hyperbolic geometrical graph can lead to further insights into their structure and be a good for promotion of their application for data analysis.

This work is partially supported by RFBR grant 18-29-03167.

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Complexity and Entropy Reduction in Systems with Multiple Delays

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Delayed differential equations (DDEs) are class of dynamical systems in which the current states strongly depend on their previous states. They received considerable attention due to their rich dynamical properties such as hyperchaotic attractors. One of the most useful models is the Lang-Kobayashi (LK) equations for a semiconductor laser with optical feedback. The chaotic dynamics of semiconductor laser have been exploited for applications such as random bit generation [1]. The performance of this time delayed system can be improved by destroying the time delay signature, a feature which can be extracted from the time series by various methods such as autocorrelation function. It has been shown experimentally and numerically that using multiple delays in this model makes the signature vanish [2]. However, we have found out that increasing the number of delays up to a very large number may result in much simpler dynamics [3]. This is due to the increased averaging of the feedback fluctuations as the number of delays increases, thus simpler dynamics can be observed. This complexity collapse in multi-delayed LK model is similar to distributed delay systems with an infinite number of delays. It has been shown for different dynamical models with distributed delays that broadening the delay kernel simplifies the dynamics, and that consequently, limit cycle and stable fixed point behavior can be expected. We found that this transition from hyperchaotic behavior to stable oscillatory and fixed point behavior occurs in other nonlinear delayed differential equations as well, such as the Mackey-Glass system, when the number of delays increases.

Here we studied the complexity of these nonlinear DDE models with multiple delays by estimation of dynamical invariants, namely Kolmogorov-Sinai entropy (KS entropy) and Permutation entropy. We approximated KS entropy for a multi-delayed system by extending a recent method introduced in [4] for estimation of Lyapunov exponent in nonlinear DDEs from single delay to multiple delays. We found that the complexity, as measured through KS entropy and permutation entropy, decreases for a large number of delays.

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Revealing the Semantic and Emotional Structures of Suicide Notes with Cognitive Network Science

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Understanding the perceptions of people who commit suicide is a sensitive and crucial scientific challenge. There are circumstances where people feel the need to leave something written, a note where they express and register their last thoughts. Our work investigates 139 genuine suicide notes, reconstructing the cognitive and emotional states of people who committed suicide. Our cognitive network approach enables a quantitative analysis of the language of suicide notes through structural balance theory, semantic frame theory and emotional profiling. Our results indicate that connections between positive and negative concepts give rise to a degree of structural balance that is significantly higher than in a null model where the affective structure is randomized. Hence, suicide notes are affectively compartmentalized and positive concepts tend to cluster together. Positive words are also central in the overall network structure (see Figure 1, left). A key positive concept is "love", which integrates information relating self to others in ways that are semantically prominent across suicide notes. The emotions populating the semantic frame of "love" combine joy and trust with anticipation and sadness (see Figure 1, right), which can be linked to psychological theories of meaning-making as well as narrative psychology. Our results open new ways for understanding perceptual shifts in suicide ideation and inform future research on suicide prevention.

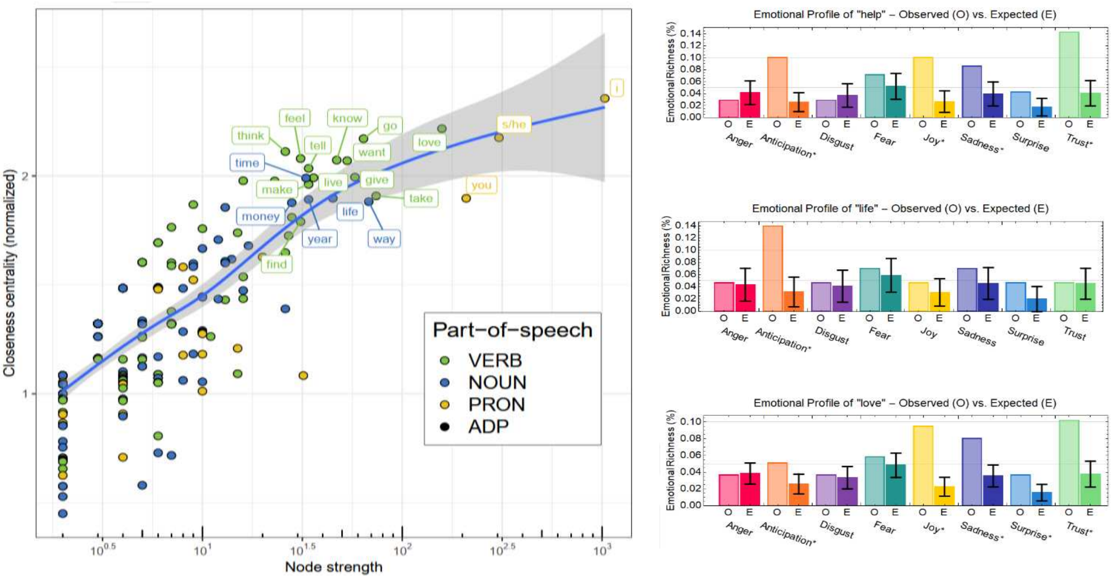

Figure 1: Left: Scatter plot of node strength (frequency of co-occurrence) and closeness centrality in a network of word-word co-occurrences. Right: Number of network neighbours around "help", "life" and "love" eliciting a given emotion (emotional intensity) against samples extracted uniformly at random.

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Fairness in multiplayer ultimatum games through degree-based role assignment

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From social contracts to climate agreements, individuals engage in groups that must collectively reach decisions with varying levels of equality and fairness. These dilemmas also pervade Distributed Artificial Intelligence, in domains such as automated negotiation, conflict resolution or resource allocation. As evidenced by the well-known Ultimatum Game – where a Proposer has to divide a resource with a Responder – payoff-maximizing outcomes are frequently at odds with fairness. Eliciting equality in populations of self-regarding agents requires judicious interventions. Here we use knowledge about agents' social networks to assess the impact of a novel fairness mechanism, in the context of Multiplayer Ultimatum Games. We focus on network-based role assignment and show that preferentially attributing the role of Proposer to low-connected nodes increases the fairness levels in a population. The probability that a node j is selected as Proposer is given by $p_j = \frac{e^{\alpha k_j}}{\sum_i e^{\alpha k_i}}$, where α controls the dependence on the degree (see Fig. 1 **a)**). We evaluate the effectiveness of low-degree Proposer assignment considering networks with different average connectivity (using the Barabási-Albert algorithm (BA) of growth and preferential attachment and Dorogotsev-Mendes-Samukhin (DMS) duplication model), group sizes, and group voting rules - (***M***) - when accepting proposals (e.g. majority or unanimity) (see Fig. 1**b)**). We further show that low-degree Proposer assignment is efficient, not only optimizing fairness, but also the average payoff level in the population (see Fig. 1 **c)**). Finally, we show that stricter voting rules (i.e., imposing an accepting consensus as requirement for collectives to accept a proposal) attenuates the unfairness that results from situations where hubs are the natural candidates to play as Proposers (see Fig. 1 **d)**). Our results suggest new routes to use role assignment and voting mechanisms to prevent unfair behaviors from spreading on complex networks.

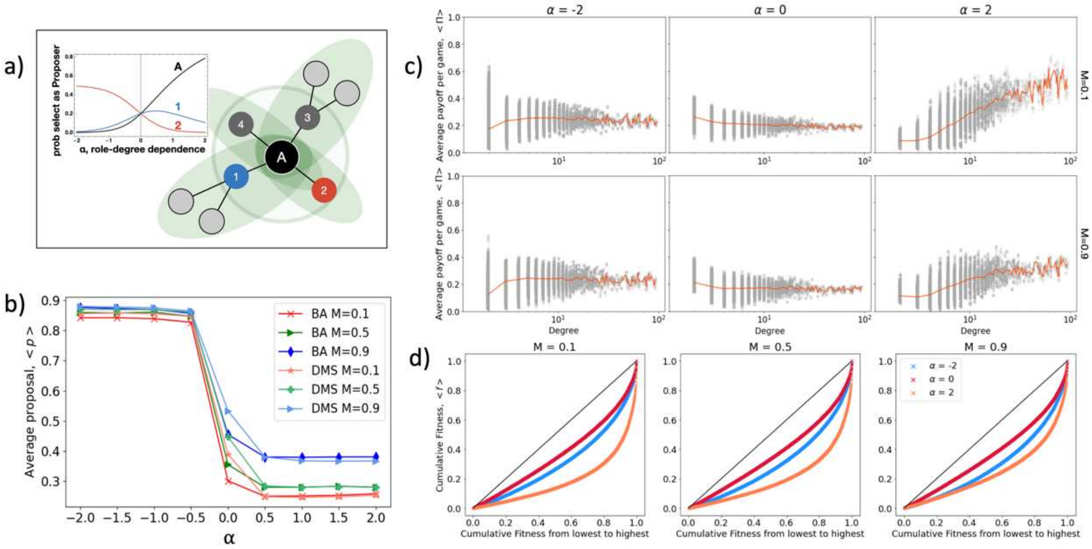

Figure 1: Panel a): Example of probability distribution of degree-based assignment of the role of the proposer. Panel b): Average proposal for different networks, different values of α (low (high) α means that nodes with low (high) degree are more likely to be the proposers) and different group voting rules (M stands for the minimum group fraction of acceptance necessary for the proposal to be accepted). Panel c): Distributions of average fitness for different values of α and group voting rules. Panel d): Lorenz curves for different values of α and group voting rules.

Building Foundations for Complex Thinking: A call for inter/transdisciplinary collaborations

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We briefly present the main goals, activities and underlying assumptions of the Building Foundations for Complex Thinking project. This interdisciplinary project rests upon the assumption that the understanding and management of the complexity and the world, along with its most complex challenges, are dependent upon the congruence of our own modes of coupling with it, namely our modes of thinking i.e. our capacity to affect and manage positive change is constrained by the complexity of our thinking. The study of complex systems has led to the development of theories and approaches more attuned to critical features and expressions of the underlying complexity of the world, namely its relational organisation. This attunement and sensitivity is associated with what might be called *complexity thinking*, a form of thinking informed by the concepts of complexity theories, which act as lenses, shaped to attend to particular processes and more or less guided by them [1,2]. The project is grounded in a wider notion of *Complex Thinking,* conceived both as a mode and process of coupling with the world, and as an outcome [1]. In both of these dimensions - process and outcome - the complexity of the thinking is associated with its ability not only to attend to but to actually perform or enact the same organising principles attributed to the so called complex systems. A recent theoretical framework [1] opens terrain for the pragmatic realisation of complex thinking through a set of properties that mimic the organisation of the complexity of the world. These properties, when realised at the level of the organisation of our thinking are more likely to increase its (relative) complexity (differentiation, integration, emergence) and inform actions which may result in more positive outcomes. The project aims to operationalise these properties of complex thinking through particular strategies and to identify, in different domains of intervention with complex systems, existing tools and resources that support their enactment. It aims to identify tools and resources used across different domains and those more specific to particular domains, exploring possibilities for inter/transdisciplinary interaction. Additionally, it aims to determine the more neglected dimensions and properties and to develop meta, process-focused tools for the management of the complexity of the thinking, targeting the understanding and management of change in complex systems. This communication is a call for inter and transdisciplinary collaborations, to assemble and build a suite of resources to advance the practice of complex thinking. We aim to deepen our knowledge of the processes that may bring us closer to building the necessary complexity to build positive change in the context of 'real-world' interventions.

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Managing complexity through the complexity of our thinking: Key research questions and challenges to the development of a meta-heuristic

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Recently, a new theoretical framework conceptualises complex thinking both as a mode and process and as an outcome of our coupling with the world, closely connected with our actions in it [1]. This framework rests on the assumption that if we organise our thinking according to properties similar to those organising the complexity of the world - those attributed to the complex systems - we will be more likely to make contributions to that coupling relationship which are congruent with its complexity. Likewise, the realisation of such properties may lead to forms of 'second order complex thinking' where emergence takes place in the form of abductive leaps which may further contribute to the congruence of the coupling relationship. As a new, higher order and coherent emergent dimension, that coupling relationship may present the requisite variety [2] to guide our actions in the world, contributing to and managing its complexity towards outcomes, where different critical observers can coordinate and co-evolve in more positive and sustainable ways. This new framework lists a series of dimensions and properties aiming to operationalise complex thinking with a focus on the management of 'real-world' complexity through the management of the complexity of our thinking - in terms of the complexity of its processes and outcomes (differentiation, integration, emergence).

In this presentation, we reflect upon the next major theoretical challenges for the further development of the framework and the practice of complex thinking in terms of understanding the structural and dynamical complexity associated with the relational organisation of those properties. Additionally, we reflect upon the challenges of managing the complexity of our thinking, throughout the process of coupling with a (constructed) target system of interest, in order to increase its congruence, thereby developing a more complex relationship capable of guiding and affecting us in ways that may expand our possibilities for action. Additionally, we reflect on the challenges of building a meta-heuristic for managing the complexity of the thinking through the management of its properties. The meta-heuristic may be critical in allowing a better use and selection of a variety of available tools (and leading to new ones) supporting both a mapping of its complexity as well as contributing to the complexity of the thinking.

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Methodological Insights Into the Validation of Agent-Based Models in Macroeconomics

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Agent-based modeling is a promising new route in macroeconomics research. Questions have been raised, however, regarding the validity of such models. A deeper understanding of the validation methodology in MABM is required. In order to provide this, I connect three frameworks. The first framework regards the foundations of model validation in general. In this framework, I will give a definition of model validation and relate this to the concept of model domain. The second framework regards a classification of models, dependent on how a model is validated. An important distinction in the framework is the difference between mechanism and target validation. The third framework revolves around the relationship between the structure of models of complex systems with emergent properties and validation in practice. Important in this framework is to consider MABMs as modeling multiple non-trivial levels that are subject to distinct forms of validation. By connecting these three frameworks, I will come to several conclusions regarding how we should characterize MABMs. First, it is important to pinpoint what the mechanisms of MABMs are constituted by. I will argue that the mechanisms at a lower level are distinct from, but provide input to, higher levels of mechanisms. Since mechanisms at different levels are validated in different ways, I come to a specific characterization of MABMs within the model classification framework, that is, in some ways, distinct from other types of models in macroeconomics. Second, I will show that because the mechanisms of MABMs are validated in a direct way at the level of the agent, MABMs can be seen as a move towards a more realist approach to modeling compared to the neoclassical approach.

Sensing Network Dynamics of Weakly Coupled Rössler Units

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Real-world complex systems are composed of many interacting units. We are able to collect data from these units for most of the systems such as climate dynamics, neuronal activity etc. Predicting critical transitions in network behavior from data is important to avert the disastrous consequences of major disruptions however having only well sampled data is not enough. To reconstruct network, one first needs to discover the governing equations of the system of interest. This is not a straightforward process for weakly interacting chaotic systems over a heterogeneous network. In this study, we approach this reconstruction problem by blending sparse regression techniques with dynamical systems' theory to reveal rules which govern the local dynamics of each node and determine the topology of networks. As an application, we illustrate this approach by reconstructing the dynamics and structure of weakly coupled Rössler model on different networked systems.

Node Immunization with Non-backtracking Eigenvalues and X-Centrality

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The *non-backtracking matrix* (or *NB-matrix* for short) has many applications in network science, in particular in node centrality and epidemic thresholds. Let λ be its leading eigenvalue. In epidemiology, $1/\lambda$ is a good approximation for the epidemic threshold of certain network dynamics. In this work, we introduce efficient ways of identifying which nodes have the largest impact on λ. We do so by studying the spectrum of the NB-matrix after a node is removed from the graph. From this analysis we derive two new centrality measures: *X-degree* and *X-non-backtracking centrality*.

Given a graph G, the *NB-matrix* B is indexed in the rows and columns by directed edges, and it is defined by $B_{k\to l,i\to j} = \delta_{jk}\left(1-\delta_{il}\right)$, where δ is the Kronecker delta. Consider a node c, and let λ_c be the leading eigenvalue of the NB-matrix of the graph after c has been removed. We call $\lambda - \lambda_c$ the *eigen-drop* induced by c. Computing the eigen-drop is computationally expensive. Our spectral analysis naturally yields two new measures that are highly correlated with the eigen-drop (see Fig. 1) and faster to compute.

First, the *X-degree* centrality of node c is defined as $\left(\sum_i a_{ci}\left(k_i-1\right)\right)^2 - \sum_i a_{ci}\left(k_i-1\right)^2$, where (a_{ij}) is the adjacency matrix of G and k_i is the degree of i. Second, the *X-non-backtracking centrality* of c is defined as $\left(\sum_i a_{ci}\mathbf{v}_i\right)^2 - \sum_i a_{ci}\left(\mathbf{v}_i\right)^2$, where $\mathbf{v}_i$ is the *non-backtracking* centrality of i [1]. Note the similarity of these expressions: they are both defined as a function of the second moment of the distribution of a node's neighbors' (degree or non-backtracking) centralities. Note also the similarity between *X-degree* and the Collective Influence measure [2]. We think of *X-degree* as a second-order aggregation of the excess degree values (k_i-1), whereas CI is a first-order aggregation. Importantly, our two measures are derived from first principles in ways entirely different from the derivation of CI, based on a novel spectral perturbation analysis. These similarities will be explored in future lines of research.

We perform extensive experimentation with targeted immunization strategies derived from these centrality measures, whose objective is to reduce λ as much as possible. Our algorithms have average time complexity that is linear in the number of nodes in G. Additionally, we further explore the implications of the X-centrality framework, whose formulae indicate that nodes whose neighbors' centralities have small variance (i.e. large second moment) will have a large influence on λ. For more details, see [3].

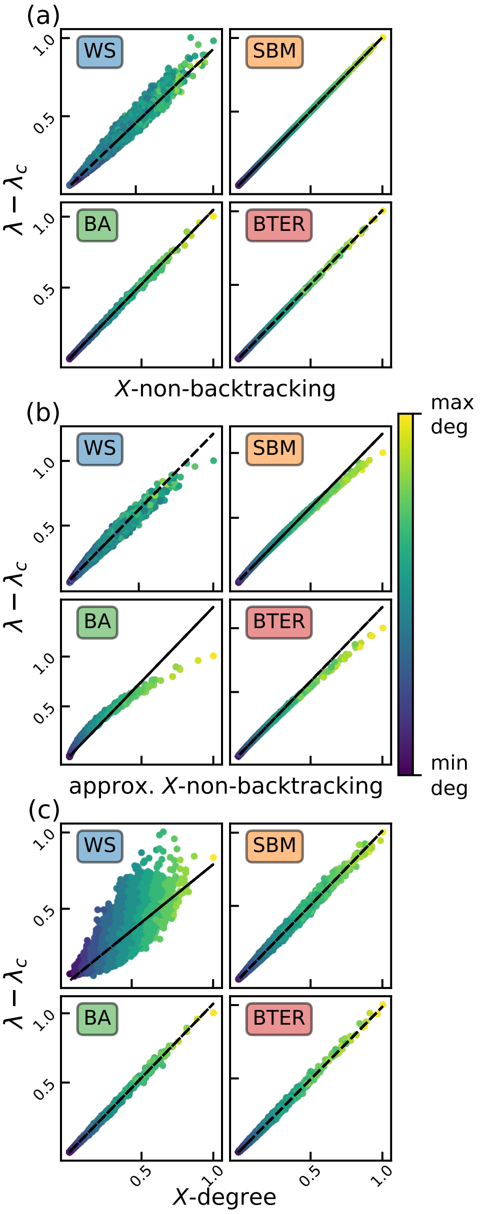

Fig. 1. **Eigen-drop and X-Centrality are highly correlated.** Each marker represents one node randomly sampled from a graph. WS: Watts-Strogatz, SBM: Stochastic-Block Model, BA: Barabási-Albert, BTER: Block Two–Level Erdős-Rényi. We sampled 100 graphs per model, each with 10^5 nodes. Dashed black lines are linear regression lines.

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Structural analysis of semiconductor a-SiC:H thin-films alloys based on statistical physics

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The use of a-SiC:H thin-films alloys in p-i-n (a-SiC:H(**p**)/a-Si:H(**i**)/a-Si:H(**n**)) photovoltaic components has widely attracted the research interest, especially towards the direction of optimizing the optoelectronic attributes of a-SiC:H that aim to the exploitation of a wider range of the solar spectrum. A major effort towards this direction concerns the increase of the carbon concentration in the a-SiC:H thin-films alloys, which causes a consequent increase of their optical energy-band gap up to a critical ceiling value, while afterwards the energy-band gap decreases. However, the increase of carbon concentration induces to the alloys structural disordering that is related to subsequent downgrade of their optoelectronic attributes. Therefore, another direction for the photovoltaic performance optimization regards the control of the hydrogen concentration to the a-SiC:H thin-films alloys composition, which results to better structures in comparison with the carbon-control techniques. Aiming at promoting the multidisciplinary demand of modern material physics, this paper broadens the conceptualization of complex network analysis of time-series by applying the visibility graph algorithm (NVG) to a DC activation-energy instead of time-series data, to study the performance of a-SiC:H thin-films alloys, as a function of temperature and hydrogen flow. Laboratory experiments are conducted to measure the dependence of structural, optical, and electrical properties of a-SiC:H thin films, which are deposited by using the RF-sputtering process on the substrate temperature, for different hydrogen flow rates, so that to gain the optimum material quality. The available data of the study regard measurements of the DC activation-energy (E_a) of a-SiC:H thin-films alloys, which were extracted from four distinct temperature flows referring to 0, 9, 14, and 20sccm (standard cubic centimeters per minute), each configuring a temperature curve calibrated at 30, 100, 120, 140, 160, 180, 220, 250, 270, 290, 300, and 320°C.

The methodological framework is composed by a multilevel analysis consisting of three steps; the first is based on statistical inference analysis, the second on pattern recognition, and the third on network analysis. The statistical inference analysis revealed that at zero hydrogen-flow levels, the dc activation-energy is statistically indifferent to the temperature, whereas, for non-zero hydrogen-flows temperature affects the semiconductor's structure. Also, the application of non-zero hydrogen-flows can statistically change the levels of DC activation-energy, but variations amongst DC activation-energy levels cannot be considered as statistically significant. In a pattern recognition approach, the supply of hydrogen-flow to the semiconductor body led to better semiconductor structures at lower temperatures, where a zone of 17-20sccm appeared with the better activation energy levels. The network analysis of the visibility graphs revealed a rich-club configuration at a temperature range [120,180]°C and three distinct DC activation-energy states, which correspond to different structural (semiconductor) behaviors of the a-SiC:H thin-films alloys. The overall analysis provided insights of dealing with multivariate structural analysis, within the context of insufficient information.

Keywords: structural optimization; complex network analysis of time-series; community detection

NASDAQ Composite analysis using Principal Component Analysis, Multiple Linear Regression and Cluster Analysis for the period between 5/2019 and 5/2020

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In this study, a system consisting of NASDAQ Composite and selected stock prices has been created and analyzed using various techniques. Principal components analysis (PCA) is a reduction method of dimensionality on a data set consisting of many variables correlated to each other, while retaining the variation present in the dataset, up to the maximum extent. Using the aforementioned technique alongside with Multiple Linear Regression and Cluster analysis, description of the studied system has been made possible, by extracting the largest amount of data, which maximizes the information available provided by the system. Finally, an attempt to analyze the financial influence of COVID-19 pandemic outbreak, has been made, in order to approach the answer to the question, of a systemic risk causing a system disorder.

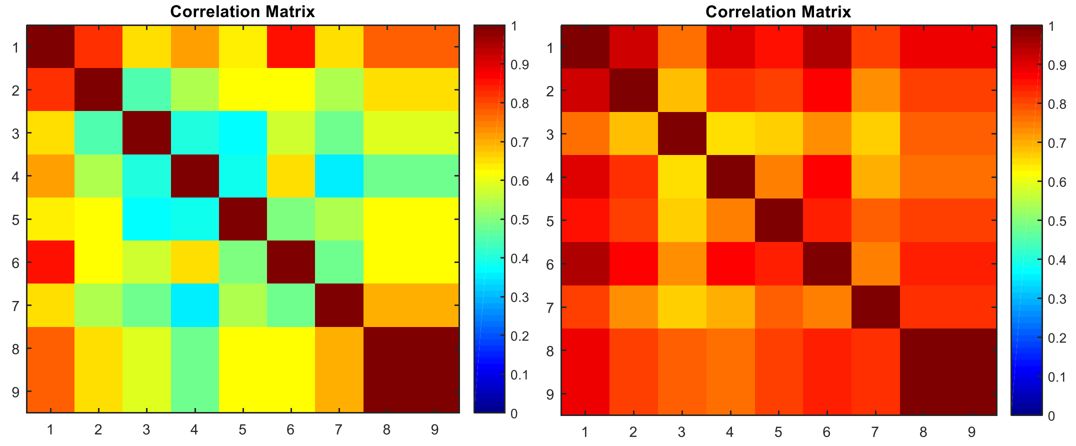

Figure 1: (Left) Correlation Matrix of the system studied for the period from 9/5/2019 to 19/2/2020 (Right) Correlation Matrix of the system studied for the period from 9/5/2019 to 12/5/2020 including the financial influence of the COVID-19 pandemic outbreak to the system.

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Simplicial persistence of financial markets: filtering, generative processes and portfolio risk

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We introduce simplicial persistence, a measure of time evolution of network motifs in subsequent temporal layers [1]. We observe long memory in the evolution of structures from correlation filtering, with a two regime power law decay in the number of persistent simplicial complexes. Null models of the underlying time series are tested to investigate properties of the generative process and its evolutional constraints. Networks are generated with both TMFG filtering technique and thresholding showing that embedding-based filtering methods (TMFG) are able to identify higher order structures through-out the market sample, where thresholding methods fail [2]. The decay exponents of these long memory processes are used to characterize financial markets based on their stage of development and liquidity. We find that more liquid markets tend to have a slower persistence decay. This is in contrast with the common understanding that developed markets are more random. We find that they are indeed less predictable for what concerns the dynamics of each single variable but they are more predictable for what concerns the collective evolution of the variables. This could imply higher fragility to systemic shocks.

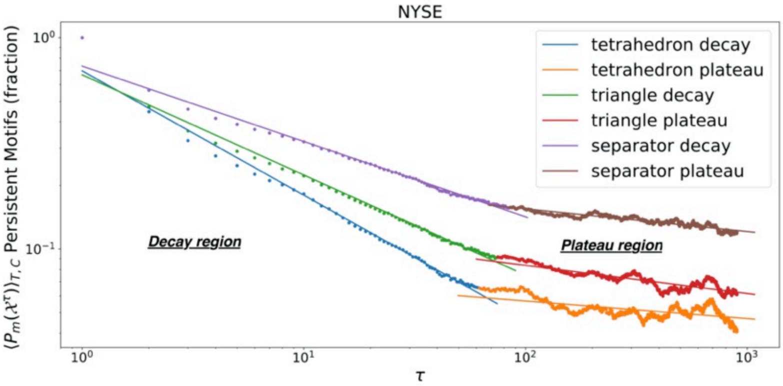

Figure 1: **Persistence Decay.** Decay of triangular clique faces, separators and clique motifs persistence for 100 NYSE stocks, as a function of time interval δt=[0,900] (average over 200 starting points). The two power-law regimes are identified by the minimum MSE sum of the fits.

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The key player problem in complex oscillator networks

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Identifying key players in coupled individual systems is a fundamental problem in network theory. We investigate synchronizable network-coupled dynamical systems such as high-voltage electric power grids and coupled oscillators on complex networks. We define key players as nodes that, once perturbed, generate the largest excursion away from synchrony. A spectral decomposition of the coupling matrix gives an elegant solution to this identification problem. We show that, when the coupling matrix is Laplacian, key players are peripheral in the sense of a centrality measure defined from effective resistance distances. For linearly coupled systems, the ranking is efficiently obtained through a single Laplacian matrix inversion, regardless of the operational synchronous state. The resulting ranking index is termed LRank. When nonlinearities are present, a weighted Laplacian matrix inversion gives another ranking index, WLRank. LRank provides a faithful ranking even for well-developed nonlinearities, corresponding to oscillator angle differences up to approximately $\Delta\theta \lesssim 40°$

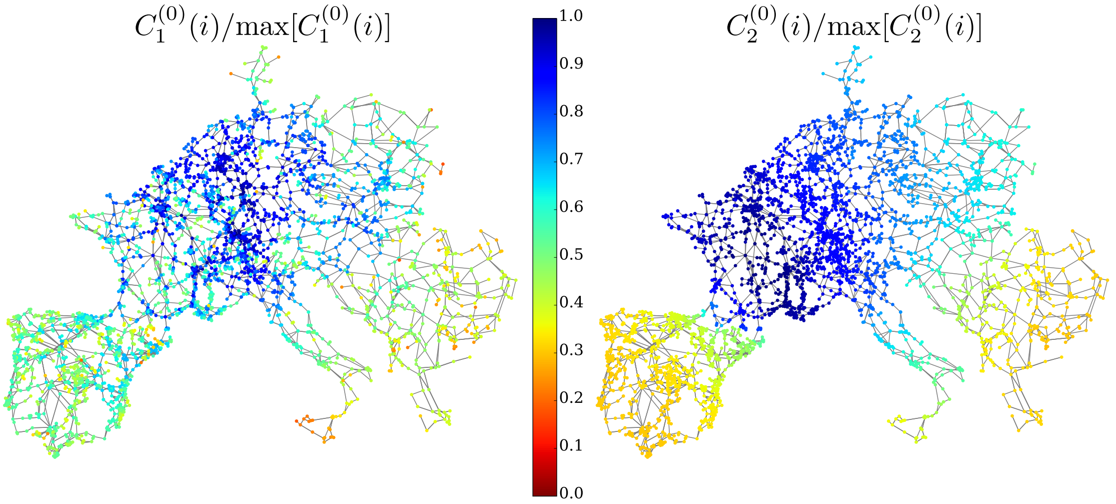

Figure 1: Maps of resistance centralities for a model of the European transmission power network.

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Uncovering the Relative Effects of Modifiable Risk Factors in Alzheimer's Disease Prevention: a Systems Modelling Approach

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Alzheimer's Disease (AD) is the most common type of dementia and a tremendous source of suffering worldwide. Since available treatments exclusively address symptoms but not the disease course, preventive interventions are of vital importance. And due to the multicausality of AD, computational systems models will likely be crucial for informing the design of prevention trials.

Using group model building, we have developed a causal loop diagram (CLD) together with domain experts [1]. This CLD graphically describes the relationships between (modifiable) risk factors and other causal mechanisms in non-familial AD. We applied centrality analysis to the CLD and then developed a proof-of-concept system dynamics model from it to assess the relative effects of modifiable risk factors on cognitive decline.

In this way, we elucidate possible leverage points and demonstrate the potential of systems-oriented approaches for unravelling AD.

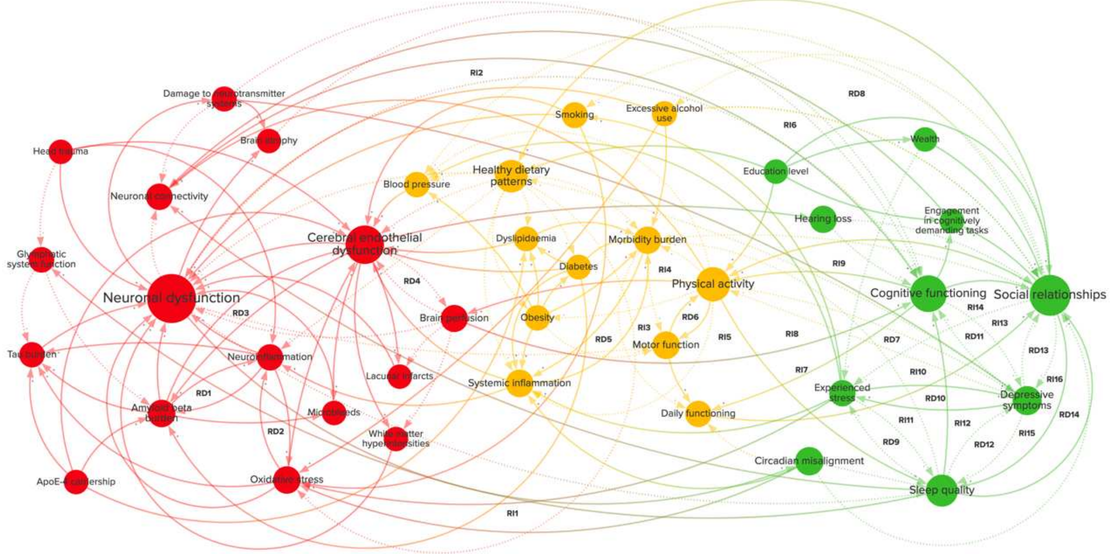

Figure 1: Causal loop diagram for Alzheimer's Disease [1]

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The emergence of social structure: deconstructing the myths of preferential attachment and triadic closure

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I propose a theory of social structure that challenges the widely accepted role of preferential attachment and triadic closure as primary mechanisms of network formation. For this, I build upon Feld's concept of social circles (1), Breiger's concept of the duality of actors and groups (2), and Hinde's concept of interactions and relationships (3). The theory emphasizes that ties between actors arise and evolve according to social circles and social situations in which they participate, a notion straightforwardly modeled through two-mode and projected networks. Using recent results (4) aided by analyses of empirical and artificial networks, I argue that structural properties such as tie strength, heterogeneity of popularity and strength among actors, clustering, community formation, and segregation emerge from homophily, jointly with overlap and social activity—mechanisms introduced in this study. The mechanisms form the two-mode network, and these structural properties naturally arise in the one-mode projection. The results show that social circle and social situation size distributions modulate network structures by interweaving with social activity distributions, and that overlap increases segregation from a network viewpoint. This theory's implications are broad, affecting several social processes ranging from social cohesion, tolerance, and child development to the spread of infectious diseases.

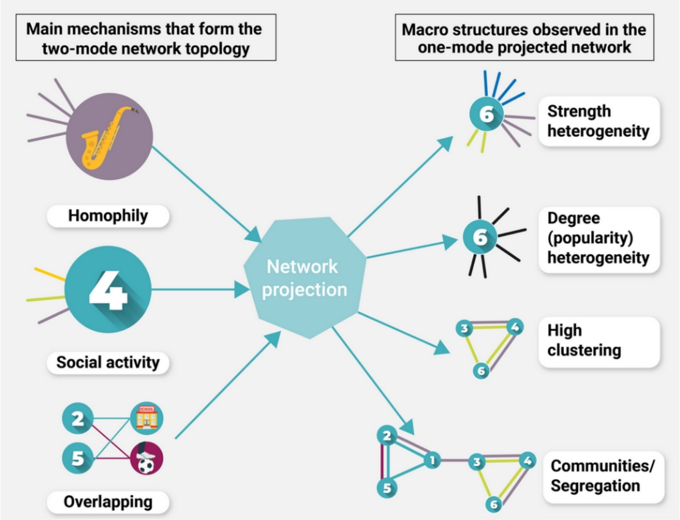

Figure 1: Diagram illustrating that mechanisms generate a two-mode network. Its projection displays structural properties observed in general population social networks.

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Analysis of Human Mitochondrial Genome Co-occurrence Networks of Asian Population at Varying Altitudes

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Networks have been established as an extremely powerful framework to understand and predict the behaviour of many large-scale complex systems. We have studied network motifs, the basic structural elements of networks, to describe the possible role of co-occurrence of genomic variations behind high altitude adaptation in the Asian human population. Mitochondrial DNA (mt-DNA) variations have been acclaimed as one of the key players in understanding the biological mechanisms behind adaptation to extreme conditions. To explore the cumulative effects and variations in the mitochondrial genome with the variation in the altitude, we investigated human mt-DNA sequences from the NCBI database at different altitudes under the co-occurrence motifs framework. Analysis of the co-occurrence motifs using similarity clustering revealed a clear distinction between lower and higher altitude regions. In addition, the previously known high altitude markers 3394 and 7697 (which are definitive sites of haplogroup M9a1a1c1b) were found to co-occur within their own gene complexes indicating the impact of intra-genic constraint on co-evolution of nucleotides. Furthermore, an ancestral 'RSRS50' variant 10398 was found to co-occur only at higher altitudes supporting the fact that a separate route of colonization at these altitudes might have taken place. Overall, our analysis revealed the presence of co-occurrence interactions specific to high altitude at a whole mitochondrial genome level. This study, combined with the classical haplogroups analysis is useful in understanding the role of co-occurrence of mitochondrial variations in high altitude adaptation.

Optimal assignment of buses to bus stops in a loop by reinforcement learning

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Bus systems involve complex bus-bus and bus-passengers interactions. In this paper we study the problem of assigning buses to bus stops to minimise the waiting time of passengers.

We formulate an analytical theory for two specific cases of interactions: all the buses interact with each other via the boarding/alighting of passengers (regular buses) and disjoint subsets of non-interacting buses. The second case is a novel configuration where disjoint subsets of buses serve disjoint subsets of bus stops and we call it “express bus”. Our formulation allows for the exact calculation of the average waiting time for general bus loops in the two cases examined. Compared with regular buses, we show scenarios where “express buses” show an improvement in terms of average waiting time. From the theory we can obtain simple insights: there is a minimum number of buses needed to serve a bus loop, splitting a crowded bus stop into two less crowded ones always increases the average waiting time for regular buses, changing the destination of passengers and displacement of bus stops does not influence the average waiting time.

In the second part, we introduce a platform based on reinforcement learning that can overcome the limitations of our analytical method to search for better allocations of buses to bus stops that minimise the average waiting time. Compared to the previous cases, any possible interaction between buses is allowed, unlocking novel emergent strategies. We apply this tool to a simple toy model and three empirically-motivated bus loops, based on data collected from the NTU shuttle bus system. In the simplified model, we observe an unexpected strategy emerging that could not be analysed with our mathematical formulation and displays chaotic behaviour. The possible configurations in the three empirically-motivated cases are approximately 10^8, 10^{10} and 10^{17}, so a brute-force approach is impossible. Our algorithm can reduce the average waiting time by 12% to 32% compared to regular buses and significantly outperforms express buses. This tool can have practical applications because it works independently of the specific characteristics of a bus loop.

Big Data Analytics: A New Methodology For Discovering Complexity?

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With the development of information and communication technologies, such as Big Data analytics, the process of scientific discovery has faced a growing process of automation. The extensive use of Big Data analytics brought about by statistics and artificial intelligence has impacted the methodology of data-driven sciences such as genomics, astronomy, and earth sciences [1]. The possibility of mining and analyzing massive amounts of a wide variety of data, from different sources, generated and processed in high speed brings new possibilities and new challenges to the sciences of complexity. According to Pietsch [2][3], the advent of Big Data analytics allowed a new method of modelling – horizontal modelling - which brings to the fore 'the new science of complexity'. The author advocates that big data analytics, along with the method of eliminative induction, provide the detection of causal relevance between variables hidden in high-dimensional data with no need of idealized modelling. We challenge this approach by inquiring to which extent methods that rely on eliminative induction and big data analytics provide sound explanation of complex phenomena that encompasses characteristics such as non-linearity, circular causality, emergence, and context dependency. Moreover, the discuss the concept of data in order to investigate the scope and limits of the automation of the process of scientific investigation. We propose an empirically informed research by focusing on attempts to automate scientific discovery using natural language processing algorithms in the context of the sciences of complexity. As a case study, the research on drug repositioning is investigated aiming at the development of a software that searches for unexpected effects of known drug usage by applying natural language processing algorithms in texts of social media [4]. In short, this paper discusses methodological implications of big data analytics for the sciences of complexity exploring the impact of the automation of the process of scientific discovery for science and society.

Acknowledgements

This research is supported by the State University of São Paulo and FAPESP Grant No. 2020/03134-1. For important comments and criticism we thank Mariana Claudia Broens, Maria Eunice Quilici Gonzalez and Ettore Bresciani Filho.

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Correlation networks of air particulate matter (PM2.5): A comparative study

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Over the last decades, severe haze pollution constitutes a major source of far-reaching environmental and human health problems. The formation, accumulation and diffusion of pollution particles occurs under complex temporal scales and expands throughout a wide spatial coverage. To comprehensively understand the transport patterns of haze pollutants, we develop a sequence of time-evolving directed and weighted air quality correlation networks exploiting hourly $PM_{2.5}$ concentration data. The study domain includes monitoring stations' time-series data from China and California, to test the framework's sensitivity in region size, climate and pollution magnitude across multiple years (2014-2020). In both areas, the probability distributions of correlations are separated into distinct positive and negative parts. The PDFs of time lag exhibit a 12hr periodicity and reveal the longer time lag, and therefore the larger distance, behavior of negative correlations. We implement two methods of network formulation: i) the maximal value of cross-correlation function method and ii) the standardization of the correlation function method. We evaluate the dispersion of a severe haze event at the North China Plain, spreading southeast within a few days, and a wildfire event in California during December 2017, occurring simultaneously with the long-lasting offshore Santa Ana winds. The function of our networks is also confirmed at the beginning of COVID-19 outbreak in China. We observe a significant drop in the magnitude of the assigned weights, indicating the improved air quality and the slowed transport of $PM_{2.5}$ due to the lockdown. Finally, we detect communities in our dynamic networks and track their evolution over time, identifying regions in China where pollution transport is more persistent.

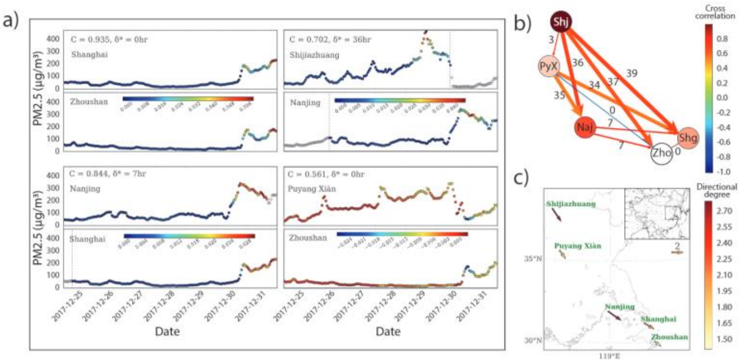

Figure 1: Illustration of network definition method based on the maximal value of cross-correlation function during haze event in eastern China during December of 2017. a) Time series of PM2.5 concentrations colored by contribution to the generated correlation among pairs of cities (three highest positively correlated pairs and the one negative are displayed). b) Network visualization (nodes colored by out degree). c) Distribution of directional degrees in the positive correlations network.

What Are Group Level Traits?

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Abstract

The intent in this paper is to explore ways that group level traits are conceived, make distinctions that will help to clarify their nature, and illustrate problems that need to be addressed. Three theoretical approaches to cultural evolution are reviewed: *culture-gene coevolution* (CGC), *cultural attractor theory* (CAT), and *culture-worldview coevolution* (CWC). In CGC the prime emphasis is on means for accurate transmission of cultural traits. CAT is based on the assumption that cultural traits are reconstructed in the minds of each succeeding generation. Transmission is not accurate, but cultural traits remain relatively stable because of *cultural attractors* that bias the reconstruction process. In both of these cases cultural group selection is modelled on Darwinian variation and selection. CWC takes a different view, emphasizing that the biological analogy is faulty because there is no phenotype/genotype distinction in culture. In CWC, individual worldviews and cultural traits (cultural idea systems) coevolve through a non-Darwinian process of communal exchange. While cultural group selection plays a major role in all three theories, questions arise with respect to how group level traits are defined. In CGC and CAT, group level traits are often conceptualized as weighted averages over individual traits. Group level selection acting on this sort of group trait can be dealt with by inclusive fitness. This is not the case with CWC and cultural idea systems. Thus, two types of group level traits are distinguished, *synthetic traits* which exist at the group level as a result of synthesis over individual traits in the group population and *intrinsic traits*, which exist at the group level but cannot be reduced to averages or summations over individual traits. With intrinsic traits the group trait indicates socially acceptable situation dependent behavior choices, prescribing how individuals are expected to behave if they are to remain group members. One aspect of this distinction is the direction of benefit. With synthetic traits, the group benefits by virtue of genetic traits of individual group members. With intrinsic traits, it is the group members who benefit by adherence to prescribed behavioral constraints. Finally, a mathematical model illustrates a simple case of selection on a situation dependent cultural option that is not reducible to selection on individual traits.

Search behaviour in agent-based models on complex decision problems: Hill-climbing or satisficing?

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Human decision-makers show various cognitive limitations in terms of “bounded rationality” [1]. Among these limitations is that decision-makers usually do not know the entire solution space in advance but have to search stepwise for new options in the hope to identify superior solutions. For capturing this kind of search behavior and to represent experiential learning, models in the domains of economics and managerial science often employ greedy algorithms and, in particular, hill-climbing algorithms [2]. However, based on experimental evidence, it has been argued that hill-climbing algorithms may be inappropriate representations of managerial search behavior for decision problems of any complexity [3]. With this, also the question arises in how far results of models relying on hill-climbing algorithms may hold if other and possibly more realistic representations of search behavior are implemented.

Against this background, the paper suggests to capture managerial behavior in agent-based models following Herbert A. Simon's concept of satificing [3] which was found to be a relevant representation of human search behavior (e.g., [4]): Satisficing means a process of sequential search for options until a satisfactory level of utility is achieved; what is regarded satisfactory is captured in the aspiration level which – shaped by the difficulty of the decision problem – may be subject to adaptation over time as well as the maximum number of options searched. In particular, a satisficing algorithm is proposed and contrasted to hill-climbing algorithms via the example of an agent-based simulation model based on the framework of NK fitness landscapes [5] which allows to conveniently control for the complexity of the decision-problem. In the model, decision-makers collaboratively search for superior performance to a multi-dimensional binary decision problem.

The results suggest that the models' behavior may remarkably differ depending on whether search behavior is captured by a hill-climbing or a satisficing algorithm in combination with the complexity of the decision problem. Hence, one may infer that further research is required to assess the effects of the representation of managerial behavior on the results of agent-based models in managerial science.

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Loop-erased Random Walks, Charge-Density Waves, φ^4-Theory and the Abelian Sandpile Model

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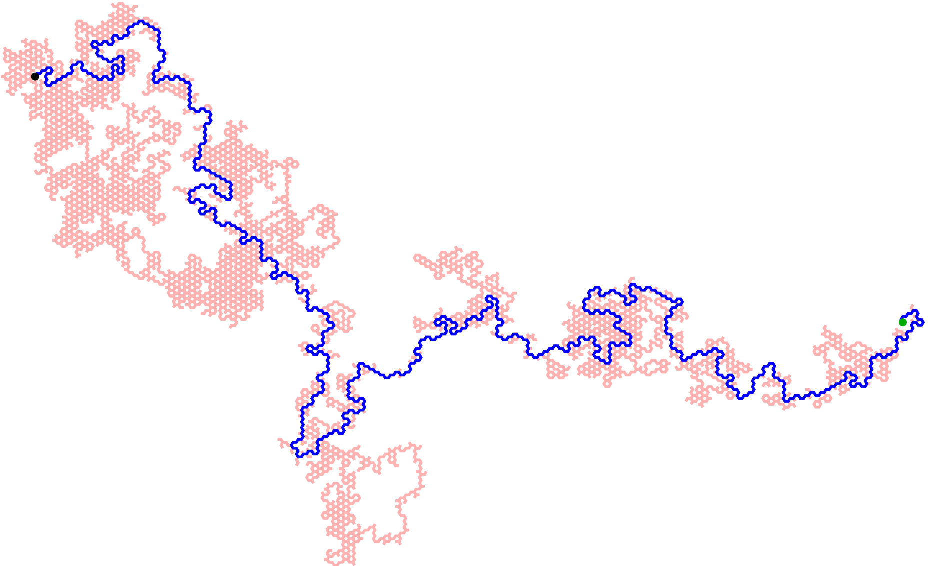

Figure: Loop-erased random walk (blue) and trace of the underlying random walk (red)

Imagine an ant starting at its nest (black dot to the left), walking around randomly (trace detectable by smell, in red) until it finds food (green dot to the right). A second ant may follow efficiently: Instead of walking randomly on the red trace, whenever it encounters a crossing, it follows the youngest trace (strongest smell), effectively *erasing* the superfluous loops. Mathematicians call the resulting object (blue) a loop-erased random walk (LERW). By construction, it is non-self-intersecting.

While ants probably use only an approximation to this trick, we have been able to prove mathematically that the theory behind is equivalent to an interacting theory with two fermions and one boson, or the N-vector model in the unusual limit of N=-2 components. These models are themselves equivalent to charge-density waves at depinning, Laplacian growth (describing electric discharges), Abelian sandpiles (the key model of self-organised criticality), uniform spanning trees, and the Potts model with q=0 states. The talk will discuss some of the key relations.

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Periodic Motion in the Chaotic Phase of an Unstirred Ferroin-catalyzed Belousov Zhabotinsky Reaction

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The Belousov Zhabotinsky reaction, a self-organized oscillatory color-changing reaction, can show complex behavior when left unstirred in a closed cuvette environment. The most intriguing behavior is the transition from periodicity to chaos and back to periodicity as the system evolves in time. It was discovered that this complex behavior is due to the decoupling of reaction, diffusion and convection [1]. We have recently discovered that, as the so-called chaotic transient takes place, periodic bulk motions like convective rolls are visible in the reaction solution.

In this work we investigated this phenomenon experimentally by changing cuvette size and dimension to allow different types of convection patterns to appear. So far, we have observed single and double convection rolls in the system. The above-described experimental observations are supported by a numerical investigation of the underlying reaction-convection-diffusion equations that govern the behavior of the system. The connection between the periodic bulk motion and the local chaotic color change is still under investigation.

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Analysis and modeling of flight delays in air traffic systems

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Keywords: Delay distribution, Lognormal distribution, Multiplicative process, Cascade effect.

The increase of flight delays in recent years which resulted from the rapid development of the civil aviation industry have become a worldwide challenge in recent years. Thus, it is of great importance to understand the origin and mechanism of flight delays in the complex socio-technical air traffic systems, a problem that attracted much attention recently [1,2,3]. Here, we apply a comprehensive analysis of the delay distributions and propose a mathematical model that could help to improve the understanding of delay cascades and the accuracy of flight delay predictions.

Our analysis is based on the collection of flight information of departure and arrival delay in both China and USA from [4,5]. We analyzed the probability density distribution of times of flight delays. While earlier studies conducted a decade ago suggested a Normal distribution for the flight delays [2], our study suggests that a lognormal distribution is best fitted as seen in **Figure 1**(a) and (b).

We also find a strong memory effect between successive departure delays, using a lagged conditional PDF method as shown in **Figure 1**(c). This memory effect indicates that the lognormal distribution is a result of a multiplicative process of delays causing further delay. Thus, we develop a multiplicative process model with a multiplication factor from one step delay to the next delay in aircraft itinerary. The model simulations fit the data well as shown in **Figure 1**(d) and could explain the empirical lognormal distribution found here for flight delays.

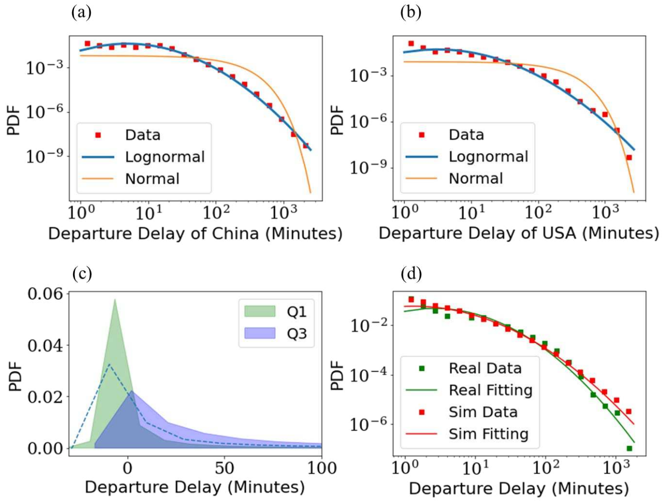

Figure 1 : **Probability density distributions fitting of departure delay** in (a) China and (b) USA. The red squares represent the empirical histograms, while the colored lines represent the best fitted distribution according to least-square method. The departure delay is best fitted with a lognormal distribution for both China and USA. **Correlation between successive departure delays**. (c) Conditional PDF of successive departure delays of August flights in USA. The dashed curves indicate the PDFs for all delays. We first sort all departure delays in ascending order and divide them into three equal quantiles. The conditional PDF of departure delays is defined as $P(d' | d)$, where d belongs to the first quantile Q1 or the third quantile Q3 and d' is the successive departure delay that follows d. A larger common area indicates less correlation. The common area between Q1 and Q3 is 0.51, which shows a strong correlation between two successive departure delays. **Model simulation**. (d) Simulation results compared to real data. We construct 1000 flight routes with multiplicative process in simulation. The initial delay of each route is randomly choose from the real data. The change factors of the next delay are generated according to the conditional PDF of successive departure delays. It indicates that the multiplicative process can well reproduce the distribution of flight delays.

In-silico Modelling of Cell Aggregation Dynamics of Annual Killifish Embryogenesis

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Embryonic development generates a variety of complex organisms using diverse and contrasting developmental strategies. For instance, adaptation to seasonal drought by annual killifish leads to a unique developmental pattern in which embryogenesis occurs only after undifferentiated embryonic cells have completed epiboly and dispersed at low density on the egg surface (Fig 1A). Hence, the first stage of embryogenesis requires congregation of embryonic cells to form a single aggregate that gives rise to the embryo proper. How embryonic cells do this is currently unknown. To address this question, we developed a biophysical model of the aggregation dynamics of early killifish embryogenesis. Dispersed cells that initially move by random walk form a circular cell aggregate at a pole of the embryo. However, directed cell motion and changes in migration persistence - suggestive of chemotaxis – are not experimentally observed. Hence, we propose that cell aggregation is driven by self-organizing processes due to the intrinsic motility and polarity of the cells and the interplay between cell adhesion and contact inhibition of locomotion (Fig 1). Our numerical simulations demonstrated that aggregation can indeed spontaneously emerge under a limited set of conditions (Fig 1C). However, the dynamics of aggregation as well as the resulting morphology depart from the experimental data (Fig 1B). This suggests a role for other factors either intrinsic to the self-organizing system or provided by external cues. We are currently exploring these mechanisms. The aggregation phase of annual Killifish is unique among vertebrates and presents the opportunity to dissect the self-organizing principles involved in early organization of embryonic stem cells.

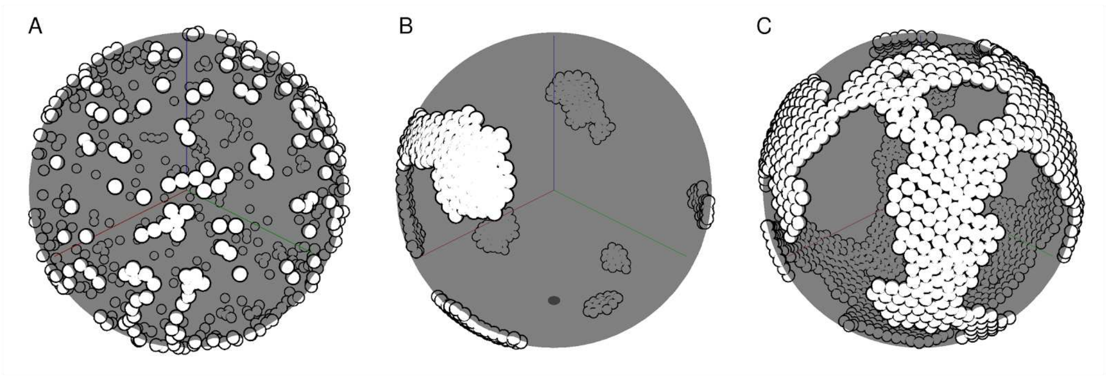

Figure 1: Simulations of aggregation dynamics of annual killifish embryogenesis show (A) dispersion phase, and multiple (B) and single (C) cell aggregations.

Emergence of Traveling Waves from a Synthetic Oscillatory Gene Network

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Multicellularity and collective cell behavior exemplify the emergence of complex patterns and structures across scales in living systems. When cells interact they can generate higher order patterns of gene expression or patterns of mechanical stresses and strains. There are a wide range of phenomena in which a key element to a developmental process is the appearance of a traveling wave of chemical concentration, mechanical deformation, electrical or other type of signal. Thus, studying traveling waves is relevant to our understanding of fundamental mechanisms underlying pattern formation. We have developed a study of the coupling between a synthetic genetic oscillator and constraints on cell growth in colonies via protein dilution [1]. Our theory predicts that these mechanical constraints generate characteristic patterns of growth rate inhomogeneity in growing cell colonies, inducing the emergence of traveling waves of gene expression. The dynamics of these traveling waves are determined by two parameters feasible to control experimentally: protein degradation rate and maximal protein synthesis rate. This work demonstrates that mechanical constraints give rise to higher order gene expression patterns in cell colonies, and provide a simple system for their design and analysis. The understanding of complex multicellular behaviors at multiple scales in order to control how these patterns are generated and maintained will enable applications in natural phenomena such as embryonic development, tumor formation, wound healing and tissue engineering. Supporting our predictions, we have preliminary experimental evidence that colonies of bacterial cells carrying the synthetic oscillatory circuit do indeed form traveling waves (figure 1).

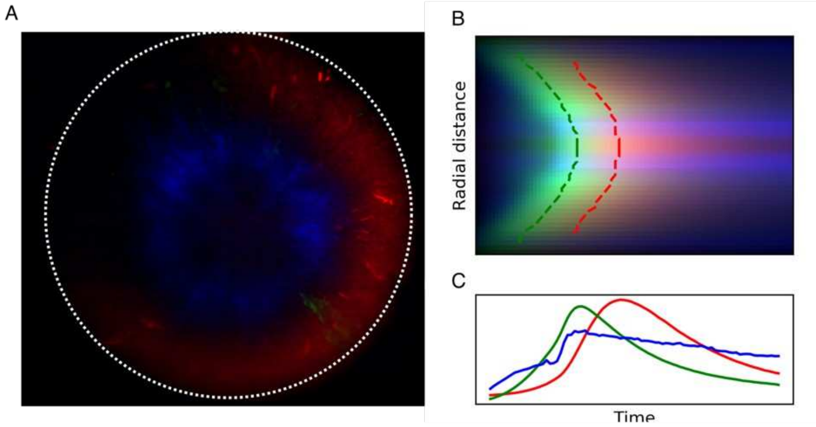

Figure 1: Time-lapse fluorescence microscopy of repressilator colonies show ring patterns (A) that form traveling waves, seen in kymograph (B) due to phase offsets (C).

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Who Is to Thank for the Rhythms of My Tail? – A Mathematical Study of Circadian Rhythmicity in Poly(A) Tail Length

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The biological circadian clock aligns our bodily functions to the day-and-night cycle and is important for our health. These bodily rhythms ultimately derive from rhythmic gene expression in individual cells. Because the core clock machinery includes several transcription factors, studies of circadian gene expression have long focused on rhythmic transcriptional control. However, recent studies suggest the importance of rhythmic post-transcriptional controls as well. One of such rhythmic controls occurs to the poly-adenosine (poly(A)) tail of mRNAs, a nearly universal feature of mRNAs which controls mRNA stability and translation. Specifically, the length of poly(A) tail in many mRNAs are found to cycle over the day. In this work [1] we constructed a parsimonious differential equation model (Figure 1) to investigate how the length of poly(A) tail is rhythmically controlled. Because the dynamics of mRNA expression and poly(A) regulation can vary significantly among different genes, to understand the general properties of the modeled system we performed a variance-based global parameter sensitivity analysis on the model. Our analysis reveals that the rhythmicity of poly(A) tail length and mRNA translatability are most strongly affected by the rhythmicity of deadenylation, the process that shortens the poly(A) tail. Particularly, the phases of poly(A) tail length and mRNA translatability are strongly dominated by the phase of deadenylation, through which deadenylation could potentially serve to synchronize the rhythms of target gene expression. Our findings highlight the critical role of rhythmic deadenylation in regulating poly(A) rhythms and circadian gene expression.

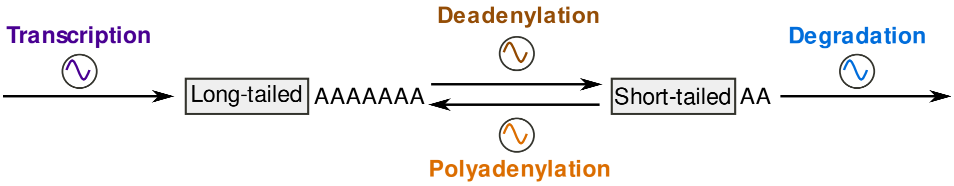

Figure 1: Model for coupled mRNA expression, degradation and poly(A) length regulation.

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On the Divergences of Nonextensive Statistics and How to Solve Them

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After more than 140 years of impressive success there is no doubt that the Boltzmann-Gibbs (BG) entropy is the correct one to be used for a wide and important class of physical systems, basically those are mixing and ergodic. However, a plethora of physical complex systems exists for which such simplifying dynamical hypotheses are violated. Corresponding anomalies are found in a variety of quantum systems as well. In order to statistically describe the dynamics of such systems, various generalized forms of statistical mechanics have been proposed such as those using the non-additive entropies [1], kappa distributions, superstatistical approaches, among various others. In the last decades, these new generalized statistical mechanical formalisms have found a large variety of very successful applications in complex systems, even beyond the realm of physics.

It was found in [2] that classical Tsallis' theory exhibits poles in the partition function and the mean energy. This occurs at a countable set of the q-line (see, for example, figure 1). I give a mathematical account of them. Further, by focusing attention upon the pole, one encounters interesting effects.

Divergences are an important topic in theoretical physics. Indeed, the study and elimination of divergences of a physical theory is perhaps one of the most important aspects of theoretical physics.

I propose two different approaches to solve those divergences: i- a perturbative approximation [3], useful for the weak non-additive limit, and ii- dimensional regularization [4].

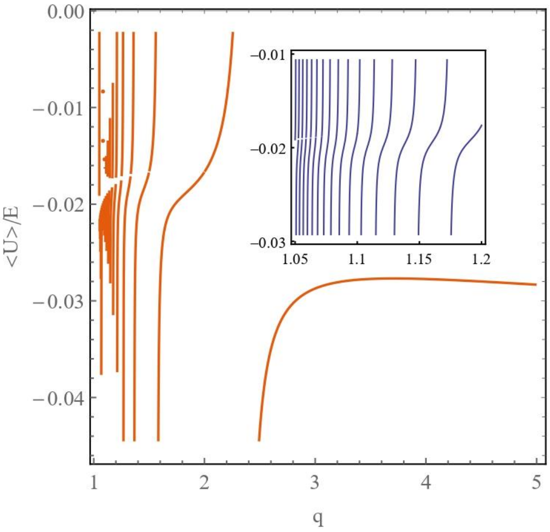

Figure 1: Divergences of the dimensionless mean energy of a self-gravitational system in non-extensive framework. q>1 regime.

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Ensemble nonequivalence in system with local constraints

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The equivalence between canonical and microcanonical ensembles (describing systems with soft and hard constraints respectively) is a basic assumption in statistical physics, traditionally verified through the vanishing of the relative fluctuations of the constraints in the thermodynamic limit. However, evidence has accumulated that, in presence of phase transitions or long-range interactions, this property will break down, a phenomenon known as *ensemble nonequivalence*. Normally, ensemble nonequivalence is ‘restricted’ to a certain region of parameter space, where the difference between canonical and microcanonical entropies is ‘strong’, i.e. of the same order as the entropies themselves. However, recent research on networks has shown that the presence of an extensive number of local constraints can also lead to ensemble nonequivalence, even in the absence of phase transitions. This new form of ensemble nonequivalence appears in the whole parameter space and is therefore ‘unrestricted’. One the other hand it is ‘weak’, i.e. it is characterized by a sub-leading entropy difference.

In this work, we focus on more general complex systems with local constraints (represented as generic matrices with constraints on their margins) and find that, surprisingly, ensemble nonequivalence can manifest itself in the whole parameter space. At the same time, when the degrees of freedom for each unit of the system remain finite in the thermodynamic limit, the entity of ensemble nonequivalence is of the strong type. This novel, simultaneously ‘strong and unrestricted’ form of ensemble nonequivalence is of the most robust type observed so far and imposes a principled choice of the ensemble in all real-world applications.

We also compare the traditional criterion for ensemble equivalence, based on vanishing relative fluctuations, with the more recent criterion based on the vanishing relative entropy density between microcanonical and canonical probabilities. In particular we consider weighted core-periphery networks with local constraints, for which the phenomenon of Bose-Einstein condensation can occur when a finite fraction of the link weights concentrates in the core. We find that the relative entropy density does not vanish, both in the condensed and in the non-condensed phase. By contrast, the relative fluctuations of the constraints do not vanish in the condensed phase, while they vanish in the non-condensed phase. To our knowledge, this model is the first one where local constraints coexist with a phase transition. Our results show that, in presence of local constraints, the traditional criterion based on vanishing relative fluctuations becomes misleading, while the one based on a vanishing relative entropy density remains correct.

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How Gamers Navigate the Information Network

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To study how humans navigate in the information space such as the internet, we carried out an online experiment where 460 participants play 9 rounds of navigation games on Wikipedia and fill out a survey with questions about the players' age, gender, ethnical background, etc. In each game, the players were given 2 Wikipedia articles as the source and target point and they try to go from the source article to the target article through the Wikipedia article hyperlinks on the page. Applying the DeepWalk [1] method, we trained a 64 dimension word embedding for Wikipedia articles. The successful game paths of the players are then clustered by the agglomerative clustering method, where the distance between two paths is calculated by the Frechet distance measure. We found that the successful game paths show clustering patterns for all 9 games, which indicates that despite the large number of choices at each step in the navigation process, we seem to follow only a small number of 'winning strategies'.

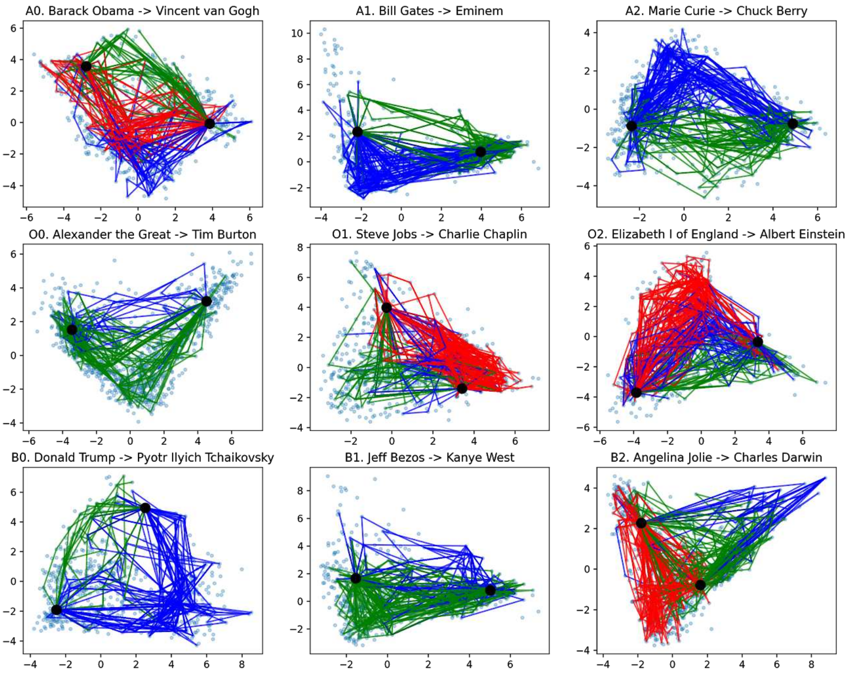

Figure 1: Visualization of the successful navigation paths of the 9 games. The x and y axis are the first and second principle components of the vector representation of Wikipedia articles after dimension reduction of PCA. The blue data points are the articles visited by the players.

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Modelling flood risk change in space and time – a complexity perspective

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Since 1714 AD, the rivers in Switzerland have been transformed from natural rivers to engineered river systems. The main human interventions were river deviations, river engineering projects, flood protection measures and the construction of hydropower facilities. The earliest human intervention was the river deviation of the Kander River (Switzerland). The river was deviated to the Lake Thun with the intention of making use of the retention effect of the lake and reducing the flood peaks for the city of Bern, located downstream. The river deviation got out of control within a few days by unintended river incision and made a spontaneously decided restoration impossible. This pioneer geoengineering measure triggered a cascade of unintended effects on water resources and flood risk management. The city of Bern located downstream transferred their flood risks to the city of Thun. The catchment area contributing to the Lake Thun doubled and the lake level raised. At the lake outflow in the city of Thun, all hydropower facilities and bridges collapsed, and the castle moat had to be opened in the following years as a second river course to enhance the lake outflow capacity. The downstream reaches of the Aare River lost their sediment supply and changed their morphology. After 1815, the rivers in the Aare River basin were straightened by lateral levees. This led to river incision that is still posing problems for bridges and groundwater extraction facilities nowadays. The problem of the increased flood risk of the city of Thun was finally resolved in 2009 by a relief tunnel that allows pre-emptive lowering of the lake level before an expected flood event.

The case study shows how human interventions in a natural system (river basin) trigger a cascade of unintended consequences for the socio-economic system and how the socio-ecologic system adapted to the disturbances. As human interventions in river systems are still massively going on in the Anthropocene, modelling approaches are needed to foresee their consequences on socio-ecological systems. We re-modelled the effects of the Kander river deviation on flood risks and evaluated the prediction capabilities of the developed model chain [1,2]. The retro-model experiments showed that a coupled model chain of regional climate models, hydrological models, inundation models and flood impact models [3] partly enables the simulation of the complex adaptive behaviour of the coupled human and natural system. However, the shaping of the land surface by human interventions following the first intervention could not have been predicted. This opens research questions on how to incorporate models for simulating societal adaptation to climatic changes into the existing model chains.

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Event Based Coupled Dynamics in Soccer: Attack-defense Interaction Networks

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In Soccer two teams are constantly interacting between each other, changing and adapting continuously accordingly to the rival's actions and environmental changes. As such, soccer is an excellent example of a complex adaptative system which, thanks to the recent growth of available data, allows to make novel approaches to study and describe its dynamics.

One of such approaches is that of complex networks, which has already been used mainly to study passing networks and to characterize player and team-centered dynamics. Nonetheless, in most of the literature, the analysis and description takes into account each team separately and the intertwined interaction dynamics of the two teams has just started to be explored recently. In this work we attempt to include the inherent coupled dynamics of the two teams involved in a soccer match, and to describe it on the basis of the notion of *events*.

Unlike other team sports as Football and Baseball in which the game develops in discrete sequences of events or turns, in Soccer the game develops in a continuous fashion and is only interrupted by certain events. When these particular events occur, the possession of the ball switches from team to team and a new sequence of events is started. Nonetheless, changes of ball possession are not necessarily triggered by this specific set of events and events such as interceptions or unsuccessful passing attempts can switch the team in possession of the ball without interrupting the flow of the game. We will refer to the set of events that can trigger a change of possession of the ball as *inter-team events* and to those which don't involve the loss of control of the ball as *intra-team events*.

During inter-team events, teams adapt and modify the players' interactions to respond to the current situation at each moment of the game, constantly switching from an attacking to a defensive behavior and vice versa. We consider that these events are the binding elements between team dynamics and the building blocks of the description of the game we propose.

Based on these observations, using a publicly available dataset from different european leagues and tournaments, we build mono and multi-layer networks of events (Fig. 1) which summarize the teams dynamics and behavior occurring during a match. By a statistical analysis of their topology we identify recurring patterns of sequences of events which more often lead to desired outcomes such as the occurrence of goals. This approach can also be used as a coarse grain assessing tool of team performance, as it is able to identify sequences of actions which lead to both desired and undesired game configurations.

We consider that event-based descriptions of the coupled dynamics of soccer matches like the one we propose, can shed light for the development of a holistic description of the game which takes into account its collective nature.

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