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1   **Title**

2   Patterns and consequences of age-linked change in local relatedness in animal societies

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Patterns and consequences of age-linked change in local relatedness in animal societies

39 **Abstract**

40 The ultimate payoff of behaviours depends not only on their direct impact on an individual but also on
41 the impact on their relatives. Local relatedness – the average relatedness of an individual to their
42 social environment – therefore has profound impacts on social and life history evolution. Recent work
43 has begun to show that local relatedness has the potential to change systematically over an
44 individual's lifetime, a process called kinship dynamics. However, it is unclear how general these
45 kinship dynamics are, whether they are predictable in real systems and their impacts on behaviour and
46 life history evolution. In this study, we combine modelling with data from real systems to explore the
47 extent and impact of kinship dynamics. We use data from seven group-living mammals with diverse
48 social and mating systems to demonstrate not only that kinship dynamics occur in animal systems, but
49 also that the direction and magnitude of kinship dynamics can be accurately predicted using a simple
50 model. We use a theoretical model to demonstrate that kinship dynamics can profoundly impact
51 lifetime patterns of behaviour and can drive sex differences in helping and harming behaviour across
52 the lifespan in social species. Taken together this work demonstrates that kinship dynamics are likely
53 to be a fundamental dimension of social evolution, especially when considering age-linked changes
54 and sex differences in behaviour and life history.

55

56

57 **Main text**

58 <u>Introduction</u>

59 The behavioural decisions and life history strategies of group-living animals are influenced both by
60 their direct impact on an individual's own survival and reproduction and their impact on the fitness of
61 group-mates and relatives[1–4]. The inclusive fitness consequences of interacting with related group-
62 mates represent a balance between the benefits of helping relatives and the costs of competition with
63 those same relatives[5–7]. The average relatedness of an individual to their social group – their local
64 relatedness – therefore sets the foundations for selection on helping and harming behaviour.
65 Reflecting this, local relatedness is a key predictor of social behaviours and social organisation in
66 group-living species[8–13].

67 Until recently, local relatedness has tended to be treated as a static property of a group or species.
68 However, there has been an increasing appreciation that in some social species, each individual's
69 local relatedness can change systematically with age – a process we refer to as kinship dynamics[14–19].
70 Kinship dynamics concepts and models were initially developed to explain the taxonomically rare
71 phenomenon of extended female post-reproductive lifespans (menopause)[14,20]. The models
72 demonstrated that, under some patterns of sex-specific dispersal and rates of local mating, female
73 local relatedness can increase with age and that this will lead to selection for older females to decrease
74 the harm they cause to the reproductive success of other, increasingly related, group members by
75 ceasing their own reproduction[14,20]. Subsequent empirical work in killer whales (*Orcinus orca*) and
76 humans has demonstrated that the cessation of reproduction by older females is indeed linked to the
77 increasing local relatedness of females to their group as they age[21–23]. Kinship dynamics can change
78 selective landscapes and shape behaviour and life history evolution, and treating local relatedness as
79 static may miss fundamental drivers of evolution in social species[19]. Currently, however, the presence
80 and causes of kinship dynamics have not been investigated outside of species exhibiting menopause.

81 There is no reason why the influence of kinship dynamics should be limited to the evolution of post-
82 reproductive lifespans, indeed it would be a surprise if they were. Local relatedness influences many
83 aspects of behaviour. For example, in spotted hyenas (*Crocuta crocuta*) local relatedness predicts the
84 amount of social support an individual will receive which in turn predicts their probability of winning
85 an agonistic interaction and, ultimately, their social rank[24]. Differences in local relatedness can also
86 translate into direct fitness outcomes. For example, in red howler monkeys (*Alouatta seniculus*)
87 females in groups with high local relatedness have greater reproductive success than females in
88 groups with low local relatedness, potentially as a result of increased cooperation and decreased
89 competition amongst females[25]. Where behaviours are contingent on local relatedness, a change in
90 local relatedness with age may lead to corresponding changes in behaviour. Further, while kinship
91 dynamics research thus far has focused on females, similar processes should lead to changes in male
92 local relatedness with age. Moreover, because kinship dynamics are driven by patterns of mating and
93 dispersal - and males and females of the same species often differ in their dispersal and mating
94 strategies - they are likely to differ between males and females in the same system. Sex differences in
95 kinship dynamics could lead to sex differences in behaviour, particularly in relation to the trajectories
96 of behavioural change with age. Despite the potential importance of kinship dynamics, its general role
97 in social evolution, and the conditions under which age-linked relatedness trajectories differ between
98 the sexes, remains largely overlooked.

99 In this study, we combine theoretical modelling with long term individual-based data from several
100 species of group-living mammals to investigate the predictability and consequences of sex differences
101 in kinship dynamics in animals. Specifically, we: (1) develop a theoretical model to predict male and
102 female kinship dynamics under different rates of dispersal and local mating; (2) compare these
103 predicted kinship dynamics with empirical data from seven mammal systems with contrasting social

104   and mating systems; (3) use a model to demonstrate that these patterns of kinship dynamics can select
105   for age-linked behavioural change and that these changes can differ by sex.

106 <u>Results and Discussion</u>

107 *Sex differences in kinship dynamics*

108 To explore and predict patterns of kinship dynamics in both sexes, we extended a previous model that
109 focused explicitly on female kinship dynamics[14], to also include the kinship dynamics of males
110 (supplementary 1). Our analytical model predicts the kinship dynamics of a population parameterised
111 by: the rates of male and female dispersal (d_m, d_f; proportion of each sex who permanently leave their
112 natal group at sexual maturity), rate of local mating (m; proportion of offspring fathered by in-group
113 males), group size (n, number of adults) and probability of mortality (μ). For simplicity here we focus
114 on the three dispersal and local mating scenarios most commonly exhibited in mammals (for all: $n = $
115 10, $\mu = 0.1$; see Supplementary Figure 2 for other combinations): (i) male-biased dispersal with
116 predominantly local mating ($d_f = 0.15$, $d_m = 0.85$, $m = 0.82$), (ii) female-biased dispersal with
117 predominantly local mating ($d_f = 0.85$, $d_m = 0.15$, $m = 0.82$) and (iii) bisexual philopatry with out-
118 group mating ($d_f = 0.15$, $d_m = 0.15$, $m = 0$). In each of these scenarios, our model predicts that the
119 sexes will differ in their patterns of kinship dynamics (figure 1). Under male-biased dispersal, male
120 local relatedness increases with age whereas female local relatedness decreases (figure 1). The
121 opposite pattern occurs under female-biased dispersal (figure 1). In both cases, these patterns occur
122 because a dispersing individual joins a group containing no relatives, but over time these non-kin are
123 replaced with that individual's offspring and grandoffspring of the opposite (philopatric) sex. For
124 example, under male-biased dispersal with local mating males join a group containing no relatives
125 and, over time, their own philopatric daughters and granddaughters replace the unrelated females in
126 the group, while their sons disperse. The philopatric sex, on the other hand, shows a decrease in local
127 relatedness with age as close kin of both sexes die and are only replaced by their philopatric-sex
128 offspring. Under bisexual philopatry with out-group mating female local relatedness increases
129 because offspring of both sexes join their group, replacing more distant relatives, but male local
130 relatedness decreases because their offspring are not recruited to their group and their close relatives
131 at birth are replaced by more distant relatives as they age.

132

133

134

135   *Kinship dynamics in mammals*

136   We tested whether our simple model could predict patterns of kinship dynamics in real systems using
137   detailed empirical data from long-term individual-based studies of seven mammal systems with
138   differing dispersal and mating rates (table 1): banded mongooses (*Mungos mungo*), chimpanzees (*Pan*
139   *troglodytes*), European badgers (*Meles meles*), killer whales (resident-ecotype), rhesus macaques
140   (*Macaca mulatta*), spotted hyenas and yellow baboons (*Papio cynocephalus*). To generate predicted
141   kinship dynamics specific for each species, we first develop an agent-based formulation of our kinship
142   dynamic model (hereafter simulation model). This approach allowed us to more closely represent the
143   biology of our example species, particularly by including a non-breeding juvenile phase and a realistic
144   representation of time. We then compared these predicted patterns of kinship dynamics with observed
145   kinship dynamics derived from each study population.

146   Kinship dynamics in both the simulated and observed data are modelled in a Bayesian hierarchical
147   framework, which accounts for error in estimates of local relatedness. All results presented here
148   (simulated and observed) represent relatedness among adults (individuals older than the age of sexual
149   maturity; see Supplementary Figure 3 for an alternative approach including juveniles). We report
150   modelled change in local relatedness as the proportional change per year of adulthood: posterior mean
151   β [95% credible interval]. In examples where the 95% credible interval of slope-coefficient (β) did not
152   overlap 0, we also use the posterior mean to calculate Δr: the percentage expected change in local
153   relatedness between an individual of age-at-maturity and an individual reaching the sex-specific
154   expected adult lifespan. For example, if the average male in a population were predicted to double
155   their local relatedness from age-at-maturity to age of expected lifespan then Δr would equal +100%.

156   In six of our seven study species (exception: European badgers) at least one sex showed a change in
157   observed local relatedness with age (95% credible intervals of β slope parameter do not overlap 0;
158   figure 2H; Supplementary Table 1; see Supplementary Table 2 for a detailed breakdown of the β slope
159   parameter). In five of the seven species (exceptions: European badgers, yellow baboons) the observed
160   sexes show different local relatedness trajectories (95% credible intervals of β slope parameter do not
161   overlap; figure 2H; Supplementary Table 1). In addition, our simulation model correctly predicted the
162   direction of change (positive, negative, no change) in local relatedness with age in 10 of the 14
163   species-sexes (exceptions: female yellow baboons, male rhesus macaques, both sexes of European
164   badgers), and magnitude of change (95% credible intervals of β slope parameter overlap; complete
165   posterior overlap in Supplementary Table 2) in 9 of 14 species-sexes (figure 2; Supplementary Table
166   1; Supplementary Table 2; Supplementary Table 3; Supplementary Figure 4). The good match
167   between our simulated and observed kinship dynamics demonstrate that kinship dynamics are driven,
168   at least in part, by the parameters captured by our model, the most important of which are sex-
169   specific patterns of dispersal and rate of local mating.

170   Chimpanzees show strongly female-biased dispersal and rare extra-group mating[26–31] (table 1). This
171   female-biased dispersal is reflected in their kinship dynamics: females increase their local relatedness
172   as they age (β = 0.074 [0.051 – 0.098], Δr = +33%) while male relatedness does not change with age
173   (β = -0.009 [-0.067 – 0.049]). These observed results match our predictions in both sexes (figure 2B).

174   Rhesus macaques, spotted hyenas and yellow baboons all have strongly male-biased dispersal, very
175   rare female dispersal and high rates of local mating[32–38]. In both spotted hyenas and yellow baboons,
176   male local relatedness increased with age (spotted hyenas: β = 0.12 [0.105 – 0.135], Δr = +72%;
177   yellow baboons: β = 0.033 [0.009 – 0.058], Δr = +23%) as predicted by our simulation models
178   (figures 2F, 2G). In yellow baboons, this increase is more pronounced after age 14 when their own
179   adult offspring begin joining the reproductive pool of the group (β = 2.18 [1.398 – 2.96]). While our
180   modelling predicts that rhesus macaque males will show a modest increase in local relatedness with
181   age (figure 2E), this is not reflected in the observed data where male rhesus macaques showed an age-
182   linked decrease in local relatedness (β = -0.143 [-0.149 – -0.137], Δr = -40%). There is, however, a

183 positive relationship between the number of years a male has been in their group (their group-tenure)
184 and their local relatedness (β = 0.85 [0.79 – 0.92]). This suggests that the common secondary
185 dispersal in rhesus macaques[36,37] is nullifying age-linked kinship dynamics, but that local relatedness
186 is still dynamic in this species.

187 In female rhesus macaques, spotted hyenas and yellow baboons our simulations predict a slight
188 decrease in local relatedness with age (figures 2E, 2F 2G). In the observed data this decrease is found
189 in the rhesus macaques (β = -0.034 [-0.039 – -0.030], Δr = -37%) and the spotted hyenas (β = -0.021
190 [-0.03 – -0.012], Δr = -12%) but not in the yellow baboons. In the yellow baboons, observed female
191 local relatedness increases with age (β = 0.011 [0.005 – 0.016], Δr = +10%), potentially as a result of
192 the occasional group-fissioning which occurs in this population[39].

193 In both the banded mongooses and killer whales, neither males nor females disperse from their natal
194 group at sexual maturity[40,41]. In both of these species female local relatedness increases with age as
195 more distant relatives are replaced by the female's own offspring (banded mongoose: β = 0.025
196 [0.008 – 0.043], Δr = +7.5% ; killer whales: β = 0.011 [0.000 – 0.023], Δr = +42%). We predicted
197 that local relatedness of banded mongoose males would show no change with age because mating is
198 usually local, whereas male killer whale local relatedness would decrease because mating is non-local
199 [42,43]. Our predictions were matched in male killer whales but not in banded mongooses where male
200 local relatedness also decreased with age (killer whales: β = -0.017 [-0.037 – 0.000], Δr = -14%;
201 banded mongooses β = -0.033 [-0.045 - -0.021], Δr = -13%).

202 European badgers do not show strongly sex-biased dispersal, with 45% of males and 23% of females
203 dispersing at adulthood (table 1; Supplementary Table 6). In addition, 52% of offspring are fathered
204 by out-group males (table 1; Supplementary Table 6). This pattern of incomplete dispersal and local
205 mating results in a very shallow increase in local relatedness for both sexes in our simulations but no
206 detectable change in local relatedness in the observed data (figure 2C). The badgers represent an
207 interesting contrast to the other systems represented here because their groups are defined by shared
208 territory. Each group-territory contains at least one large breeding sett as well as multiple satellite
209 setts. Although we find no evidence of kinship dynamics at the group-territory level future work
210 investigating dynamics at a finer scale, within-sett or within-part-of-sett may find evidence of more
211 consistent changes in local relatedness. Supplementary Table

212 Supplementary Table

213 *The consequences of kinship dynamics*

214 Our models and empirical data demonstrate profound differences between the sexes in their changes
215 in local relatedness with age. Next, we explore the potential consequences of these sex differences in
216 kinship dynamics for behaviour and life history evolution. We extend our analytical model (see *Sex*
217 *differences in kinship dynamics* section) by using an inclusive fitness approach to determine the
218 strength of selection on helping and harming given age[6,7], under different rates of male and female
219 dispersal and local mating[14]. In this model, individuals can incur a cost (c) to their own fitness to
220 change the fitness of their group mates (b). The effect on group mates can be positive ($b > 0$; hereafter
221 help) – increasing their group-mates fitness – or negative decreasing their group-mates fitness ($b < 0$;
222 hereafter harm). We consider fitness in terms of survival and fecundity. In terms of survival,
223 individuals incur a decrease in their own survival to increase or decrease the survival of their group
224 mates. Similarly, females incur a cost to their own fecundity to increase or decrease the number of
225 offspring produced by their group mates. In both scenarios, while the cost is incurred by the
226 individual, the help or harm is undirected, applying to all their group mates (see Supplementary
227 Figures 5 & 6 for sex-directed behaviours).

228 Selection on helping and harming changes with age, differs with demographic pattern and is different
229 for males and females (figure 3). As in the *Sex differences in kinship dynamics* section (above), while
230 our model makes general predictions, we focus here on three demographic scenarios as examples -
231 male-biased dispersal with local mating, female-biased dispersal with local mating and bisexual
232 philopatry with non-local mating - which span the diversity of social systems in mammals.

233 The magnitude and direction of selection are determined primarily by the inclusive fitness outcomes
234 of the behaviours, while changes with age are driven by kinship dynamics (figure 3). Under selection
235 for survival (figure 3A), for example, harming decreases the survival probability of group mates,
236 decreasing within-group competition. Individuals will harm when, overall, reduced within-group
237 competition allows the recruitment of a more closely related individual than their current group mates.
238 Conversely, they will help when any newly recruited individuals are likely to be less closely related
239 than their current group mates. For example, under female-biased dispersal, females are always
240 predicted to harm because they are decreasing the survival of, mostly, non-relatives who will
241 potentially be replaced in the group by their own sons (figure 3Aii). On the other hand, under male-
242 biased dispersal, females will always help because by doing so they increase the survival of their
243 mother, father and daughters while any replacement has only a $1/n_f$ probability (ignoring fitness
244 differences) of being their offspring (figure 3Ai). However, as individuals age, the magnitude of
245 selection for helping or harming changes in line with changes in kinship dynamics: less harm or more
246 help is selected for with increasing relatedness, and more harm or less help with decreasing
247 relatedness. These changes can be dramatic, for example, under bisexual philopatry females are under
248 strong selection to harm the survival of group mates when young, but by the time their grandchildren
249 are born (generation 2) there is almost no selection for harming (figure 3Aiii). In contrast, males in the
250 same bisexual philopatry system are strongly selected to help when young, but by the time their
251 grandoffspring are born (in other groups) there is much lower selection to help (figure 3Avi). Similar
252 sex differences in helping and harming trajectories are found under other demographic scenarios.

253 In our model, as in most mammals, groups are characterised by female demographic dominance:
254 females compete for the number of offspring they produce, males compete to father those
255 offspring[46,47]. This has important implications for selection on fecundity behaviours (figure 3B).
256 Under female demographic dominance, males can increase their fitness both by increasing the
257 fecundity of in-group females and by increasing the fecundity of their male and female relatives
258 (figures 3Biv, 3Bv & 3Bvi). When mating is local, males can increase their direct fitness by
259 increasing the fecundity of within-group females. Therefore, in situations with local mating, males
260 have a strong selection for helping their group because that help is averaged over both sexes (figures

261   3Biv & 3Bv; see figure S5B for selection on sex-specific helping and harming). Males can
262   additionally increase their indirect fitness if the females or males they are helping are close relatives,
263   and it is these indirect benefits that are affected by kinship dynamics. For example, older males under
264   male-biased dispersal (figure 3Biv) or younger males under female-biased dispersal and bisexual
265   philopatry (figures 3Bv & 3Bvi) tend to inhabit groups with their close relatives and can therefore
266   increase the inclusive fitness by increasing their relatives' fecundity, whereas males of other ages in
267   these systems are less related to their group and therefore under weaker selection to help. These
268   indirect fitness benefits are particularly highlighted under bisexual philopatry where mating is outside
269   the group so males cannot gain direct benefits by helping or harming other group members, so all
270   changes are due to the indirect fitness benefits of helping relatives (figure 3Bvi).

271   In contrast to males, under female-demographic dominance, females are in direct reproductive
272   competition with other females in their group. In general, females are selected to help when their
273   female group mates are close kin - for example, all females under male-biased dispersal (figure 3Bi)
274   and older females under female-biased dispersal and bisexual philopatry (figures 3Bii & Biii)– and
275   are selected to harm when they are unrelated (e.g. young females under female-biased dispersal) or
276   under particularly intense reproductive competition (e.g. young females under bisexual philopatry).
277   Kinship dynamics play an important role in female fecundity because the change with local
278   relatedness changes the relative importance of kin cooperation and kin competition with age. This is
279   particularly highlighted for females under female-biased dispersal and bisexual philopatry where
280   selection switches from harm to help at around the age of generation one when females begin sharing
281   the group with their own adult offspring (figures 3Bii and 3Biii).

282

283

284   *General Discussion*

285   We have shown that kinship dynamics are widespread, can show meaningful differences between the
286   sexes and can be predicted from simple demographic parameters. Further, our modelling predicts that
287   kinship dynamics can drive sex differences in selection in age-related patterns of helping and harming
288   in social species, which will have profound implications for the evolution of social behaviours and life
289   history.

290   In both the modelled and real populations, we found strong sex differences in kinship dynamics under
291   male-biased dispersal with local mating, female-biased dispersal with local mating and bisexual
292   philopatry with out-group mating. The modelling results demonstrate that the patterns of kinship
293   dynamics are driven, at least in part, by dispersal and mating patterns. Under male and female-biased
294   dispersal, the dispersing sex shows an increase in local relatedness with age (after maturity), as
295   unrelated group members are replaced with their own philopatric offspring. The philopatric sex, under
296   these scenarios, shows less pronounced changes in relatedness with age because offspring are
297   replacing close kin. If neither sex disperses, female relatedness increases with age, while male local
298   relatedness can increase or decrease depending on mating patterns. Our models of kinship dynamics
299   are relatively simple and yet can accurately reproduce patterns of age-linked changes in local
300   relatedness observed in complex biological systems. This is particularly striking given the number of
301   important biological processes that can affect individual reproductive success not represented in the
302   model such as dominance, senescence and social support. Notably, although secondary dispersal did
303   affect the observed kinship dynamics of male rhesus macaques, in other species exhibiting this
304   behaviour -such as spotted hyenas and yellow baboons[34,38]- our model was still able to predict changes
305   in local relatedness with age. Dispersal as a driver of kinship dynamics is supported by recent cross-
306   cultural ethnographic comparisons of human societies which have shown that, in general, the local
307   relatedness of dispersing individuals increases with age, while that of philopatric individuals does not
308   change[17]. More generally, our results support previous results highlighting an important role of
309   dispersal rates in determining within-group local relatedness[48–50].

310   Kinship dynamics provide a framework to understand age-linked changes in social behaviours which
311   have been found in a variety of species and contexts (Table 2). As well as selection on helping and
312   harming *per se* predictable changes in local relatedness have the potential to contribute to other age-
313   linked changes in behaviour such as social selectivity, extra-group mating and intergroup conflict
314   (Table 2). In addition to behavioural effects, kinship dynamics can also have life history
315   consequences. This is clearly illustrated by research in humans and killer whales demonstrating that
316   kinship dynamics and their resultant relatedness asymmetries can lead to selection for prolonged
317   female post-reproductive lifespans[14,21,51]. By creating relatedness asymmetries and by influencing life
318   history trade-offs, kinship dynamics are likely to be an important influence on selection for other life
319   history traits such as reproductive schedules, age at maturity and rates of senescence. The influence of
320   kinship dynamics on life history traits is an exciting area for future research.

321   We have also shown here that kinship dynamics can and do differ between the sexes. Although they
322   are not widely studied, sex differences in the age-linked trajectories of social behaviours have been
323   documented in some systems. For example, in Hadza hunter-gatherer societies, females increase their
324   time spent foraging for shared resources as they age, whereas male foraging activity peaks in late
325   adolescence and declines thereafter[52]. However, age-linked changes in behaviour have rarely been
326   linked to changes in local relatedness. The results from the Hadza study, for example, would fit the
327   predictions of investment in helping behaviours under kinship dynamics of increasing female
328   relatedness and decreasing male relatedness with age. This pattern would result from female-biased
329   dispersal which is the norm in chimpanzees[27,29,31] and bonobos (*Pan paniscus*)[53,54]. However, there
330   remains considerable debate over ancestral human dispersal patterns[55–61], and female-biased dispersal
331   is not the case for all contemporary hunter-gatherer groups[17,50,62,63] or the Hadza in particular[64,65].

332 Kinship dynamics represent a framework under which to investigate and evaluate these sex
333 differences in trajectories of social behaviour.

334 Kinship dynamics represent a step forward in the development of a theory of social life history.
335 Classical life history theory describes how selection acts on fecundity and mortality over an
336 individual's lifespan[66–69]. Because it deals with events across the lifespan, life history theory is
337 explicitly dynamic. However, classic life history theory is also asocial, with models usually
338 optimising population-level fitness traits without a social component[67]. Kin selection theory in
339 contrast is explicitly social but static, with demographic change across the lifespan rarely included in
340 the framework[1,70 but see16,71–73]. Moreover, kin selection based 'social ageing' theories remain largely
341 distinct from life history theories of ageing[74]. Kinship dynamics represent an important bridge
342 between these traditions. This bridging is important because recent work has begun to explore the
343 links between group-living and life history evolution, particularly the role of sociality in the evolution
344 of senescence[75–77].

345 Here we have shown that in real animal systems relatedness – the r in Hamilton's rule – can change
346 systematically with age, changing selection on patterns of helping and harming across the lifespan.
347 However, it is not just relatedness that is likely to change with age. Both the benefits and costs –
348 Hamilton's b and c – of a behaviour may also change systematically with age. Theoretical work has
349 shown that the state of the actor can dynamically influence the payoff of (in terms of b and c) and
350 subsequent selection for behaviours[78]. As an individual's state can vary systematically with age, the
351 payoffs from behaviour will also vary with age[e.g. 79]. Further, both reproductive value and knowledge
352 can change systematically with age which will also feed into the costs and benefits of a behaviour. For
353 example, older and more experienced individuals may be important as repositories of ecological
354 knowledge- and therefore more able to benefit their relatives in times of ecological hardship[e.g. 80,81]. A
355 greater understanding of how payoffs change with age and integrating these findings with the kinship
356 dynamics results presented here would represent an important next step towards understanding the
357 social dimensions of life history evolution.

358 Although in this study we focus on age-linked kinship dynamics, other axes of kinship dynamics
359 could also have important implications for social evolution. We show that tenure – the length of time
360 an individual has been present in a group – can be an important driver of kinship dynamics. We found
361 that for male rhesus macaques group tenure, but not age, predicted local relatedness change.
362 Similarly, the amount of social support received by immigrant male spotted hyenas during intragroup
363 agonistic interactions is positively correlated with their group tenure[24]. In many systems, tenure and
364 age are likely to be closely correlated but in some systems, notably those where animals may disperse
365 multiple times over their lifetime, they may not be. The action of selection on tenure-length, and the
366 interaction between tenure length and changes in local relatedness are exciting areas for further
367 research.

368 Our examples in this study demonstrate the impact of kinship dynamics in group-living species with
369 pluralistic or partly pluralistic breeding, where all mature individuals have the potential to reproduce.
370 However, in many species, including some mammals, breeding is monopolised by one or a few
371 individuals within the group[82]. While the mechanisms of kinship dynamics presented here may not
372 apply to non-pluralistic breeders, age-related changes in relatedness have been found in several
373 cooperatively breeding vertebrates. In African wild dogs (*Lycaon pictus*), dwarf mongooses (*Helogale*
374 *parvula*) and Lake Tanganyika cichlids (*Neolamprologus pulcher*) the relatedness of helpers to the
375 dominant breeders is higher in younger than in older helpers[83–85]. These patterns are driven by turn-
376 over of the dominant individuals in the philopatric sex and dispersal by groups, rather than by
377 individuals, in the dispersing sex[84]. Interestingly, male banded mongooses also have a strict
378 reproductive dominance hierarchy[41], and rather than showing no change in local relatedness with age
379 as our pluralistic breeding model predicted, male banded mongoose local relatedness decreased with

380 age. Dominance may be playing a role in modulating male banded mongoose kinship dynamics.
381 Overall, these reproductive-dominance linked patterns demonstrate that kinship dynamics, perhaps
382 achieved by different mechanisms, are likely to be widespread beyond the examples of group-living
383 pluralistic breeding mammals presented here.

384 In conclusion, predictable age-linked changes in local relatedness can and do occur in social species,
385 and have the potential to profoundly affect behaviour and life history evolution. Kinship dynamics
386 have the potential to be an important but underappreciated force in social evolution.

387 **Methods**

388 *Analytical kinship dynamics model*

389 This model explores a sexually reproducing diploid population with an arbitrarily large number of
390 discrete groups. Each group contains a fixed number of males and females (n_m, n_f). At each discrete
391 time step, individuals: reproduce, disperse, experience mortality and compete for reproduction (in
392 order). During *reproduction,* females produce an arbitrarily large number of offspring with an even
393 sex ratio creating an offspring pool for the group. A proportion m of these offspring are fathered by
394 the males in the group, the rest are fathered by males randomly chosen from other groups. Male and
395 female offspring *disperse* from the pool at rate d_m and d_f respectively and immigrate into other groups
396 in the population at random. In turn, offspring dispersing from other groups will disperse into the
397 offspring pool of the focal group. After dispersal, each adult male and female have a probability of
398 *mortality* μ_m and μ_f. Offspring in the offspring pool then *compete* equally to fill the empty male and
399 female slots and restore sex-specific group sizes to n_m and n_f respectively. The remaining offspring in
400 the group then die. More details about the implementation and derivation of this model can be found
401 in the supplementary material (supplementary 1; Supplementary Figure 1).

402 Throughout the manuscript we focus on three illustrative scenarios (but see Supplementary Figure 2
403 for other dispersal scenarios): male-biased dispersal with local mating ($d_f = 0.15$, $d_m = 0.85$, $m =$
404 0.82), female-biased dispersal with local mating ($d_f = 0.85$, $d_m = 0.15$, $m = 0.82$) and bisexual
405 philopatry with out-group mating ($d_f = 0.15$, $d_m = 0.15$, $m = 0$). Male-biased dispersal is the most
406 common dispersal pattern in mammals[98–100]. Female-biased dispersal is relatively rare in mammals but
407 is common in the great apes[57]. Bisexual philopatry is also relatively rare in mammals and is illustrated
408 here with reference to the dispersal pattern found at the matriline level in the multi-level society of
409 resident killer whales[40]. Dispersal rates are chosen to match those illustrated in Johnstone and Cant's
410 (2010)[14] study, representing high but not complete dispersal or philopatry. For the case studies with
411 local mating, we model $m = 0.82$ because this is the mean local mating rate reported for 26 species of
412 group-living mammal[101]. Group size ($n_m + n_f = n$) determines the absolute local relatedness values but
413 does not affect patterns of kinship dynamics while $n_m \approx n_f$. For these case studies we set $n_m = n_f = 5$.

414 We use this model to predict selection on helping and harming given age under different patterns of
415 male and female dispersal. An actor can choose to pay a cost c to change the fitness by b of their
416 group members. b is undirected and applies to all group members at once, or (to put it another way) a
417 randomly chosen group member. We explore the cost-benefit ratio (c/b) of actions selected for under
418 different patterns of male and female dispersal. If $b>0$ individuals are considered to be helping their
419 group by sacrificing their own fitness to increase the fitness of group members. If $b<0$ actors are
420 harming group members, paying a cost to decrease the fitness of group mates. We then use an
421 inclusive fitness approach[6,7] to determine the strength of selection for helping and harming at different
422 ages given rates of male and female dispersal. We explore two measures of fitness: survival and
423 fecundity. Both c and b are considered in terms of the same measure of fitness.

424 Two other approaches have recently been used to model age-linked changes in local relatedness.
425 Caswell (2019)[15] takes a demographic approach to model the number of various classes of kin a focal
426 individual is likely to have given their age and the demographic parameters of the population. This
427 approach considers the population as a whole, rather than social groups, so is less suited to
428 understanding the role of kinship dynamics in social evolution, as we aim to do here. Rodrigues
429 (2018)[16] uses an inclusive fitness approach, like that used here, to investigate patterns of helping and
430 harming across the lifespan under different patterns of survival and mortality, while dispersal is
431 allowed to evolve independently. This approach gives valuable insights into the coevolution of
432 demography, life history and age-dependent behaviour. However, because the modelled populations
433 are asexually reproducing and haploid, and because dispersal is an evolving rather than imposed trait,
434 it is not suited to predicting patterns of kinship dynamics in real animal populations.

Kinship dynamics in mammals

435

436   We calculated patterns of change in relatedness with age in seven mammal populations. Each
437   population has been the subject of a long-term research project, from which the data for this study are
438   derived. The populations are: banded mongooses in Queen Elizabeth National Park, Uganda;
439   chimpanzees in Taï National Park, Ivory Coast; European badgers in Woodchester Park, UK; southern
440   resident-ecotype killer whales in the north-east Pacific ocean; rhesus macaques on Cayo Santiago
441   Island, Puerto Rico, USA; spotted hyenas in the Ngorongoro crater, Tanzania; and yellow baboons in
442   Amboseli National Park, Kenya (further details including data collection and maternity and paternity
443   assignment in each system are in supplementary 2; for sample sizes see Supplementary Table 4).

444   In each system, we calculated the pairwise relatedness of all adults of known age to all adult members
445   of their group in a given year. We focus on adults and consider offspring to be extensions of their
446   parents' fecundity until they reach adulthood and begin reproducing (see Supplementary Figure 3 for
447   relatedness including juveniles). The analysis is annual, with ages and group composition considered
448   to be stable for one calendar year. In all populations, the ages of most individuals are derived from
449   known birth years. For some individuals of unknown age, researchers have been able to infer age
450   based on biological characteristics (see supplementary 2). Pairwise relatedness was calculated by
451   creating pedigrees based on known parents (supplementary 2; see *Calculating relatedness* section). To
452   be consistent with the other systems, for female resident killer whales we only calculate kinship
453   dynamics over their reproductive lifespan (i.e. we do not calculate kinship dynamics for females
454   during their long post-reproductive lifespan) but females of all ages are included in calculations of
455   local relatedness.

456   Local relatedness is defined between group members. We consider a social group to be a set of
457   individuals who mostly interact with each other and rarely with other similar sets of individuals[102,103].
458   With the exception of killer whales, all the species studied here inhabit closed groups and defining
459   group boundaries is relatively straightforward (supplementary 2). Resident killer whales, on the other
460   hand, inhabit a multi-level society with pronounced fission-fusion dynamics[40]. We used binomial
461   mixture modelling to define an individual's local social environment based on their patterns of
462   association[104]. We used the mixture models and 40 years of association data to categorise every
463   pairwise social association in the population into four components[104] (supplementary 2). We consider
464   an individual's local social environment to be the partners with whom they share the strongest
465   category of social bond. These local social environments approximately correspond to matrilines as
466   defined in other studies of this population[40]. For the purposes of this study, these local social
467   environments are equivalent to the groups in the other study populations because they represent the
468   partners who are the main recipients of helping or harming behaviour performed by the focal whale.

Kinship dynamics simulation model

469

470   To facilitate comparison with the empirical data, we reformulated our analytical model (see *analytical*
471   *kinship dynamics* model section) as an agent-based simulation model. For each of the seven mammal
472   examples, we used the simulation model to predict the expected pattern of kinship dynamics. The
473   simulation model requires 6 input parameters: male and female dispersal rates, adult group size,
474   juvenile group size, local mating rate, expected adult female lifespan, expected adult male lifespan
475   and age at maturity (see Supplementary Table 5 for detailed definitions). For each species, we defined
476   these six parameters based on the published literature and by deriving them directly from the
477   empirical data (Supplementary Table 6).

478   The agents in the model are adult individuals. Each model iteration is considered to be a year, and
479   agents increase their age each iteration. The agents inhabit groups of fixed size and even sex ratio. At
480   each time step, the agents have a fixed probability of mortality, determined by sex-specific expected
481   lifespan. Dead agents are replaced by either a philopatric or immigrant of the same sex. All agents

482   join a group at a fixed age input as 'age at maturity'. The probability that individuals are philopatric or
483   immigrants is determined by the sex-specific rates of dispersal. Philopatric individuals have a mother
484   chosen from within the group, and the rate of in-group mating determines the probability that the
485   father is also from within the group. Immigrants are unrelated to the other members of their group.
486   The model is run until 2000 individuals have lived in the group- for some species due to
487   computational limitations the target of 2000 was reached by running the model 4 times to 500
488   individuals. Patterns of kinship dynamics from the simulation model are robust and qualitatively
489   identical for 500 and 2000 individuals. If juveniles are being included in the analysis, after the model
490   of adults has run, non-breeding juveniles are added to each group-year *post-hoc*. Juvenile group size is
491   an inputted model parameter and is filled by maturing philopatric individuals and other offspring who
492   are considered to die or disperse before reaching maturity. More details about the formulation of the
493   simulation model can be found in supplementary 3. The model outputs the age and pedigree of all
494   individuals in the group in each model-year. We use this information to calculate kinship dynamics
495   (see *calculating relatedness* and *statistically modelling* sections).

496   *Calculating relatedness*

497   We calculate the pairwise relatedness of an individual to all other members of their group in both the
498   simulated and real data from pedigrees. We developed and applied a novel method to calculate
499   relatedness from pedigrees to overcome two problems that would preclude accurate assessment of
500   relatedness and comparison between species and between real and simulated populations: (1)
501   pedigrees are of different depth (i.e. number of known ancestral generations), (2) pedigrees are
502   sometimes incomplete. More classes of relative can be distinguished in deeper pedigrees which will
503   increase observed local relatedness. Incomplete pedigrees - pedigrees where some individuals have
504   missing parents – can result in an underestimation of local relatedness. For example, if two
505   individuals have no known common ancestors but one has an unknown parent, they could be siblings.
506   Distinguishing individuals of unknown relatedness from true non-relatives is important to properly
507   estimate relatedness in the empirical data where unknown pairwise relatedness is common. For this
508   study, we developed a methodological pipeline in R to (1) limit all pedigrees in all species and
509   simulations to a depth of 2 and (2) identify individuals of unknown pairwise relatedness. This pipeline
510   was developed in R using the igraph and kinship2 packages[105,106] and is incorporated into a new
511   package: comparekin (github.com/samellisq/comparekin).

512   Local relatedness is the mean pairwise relatedness between an individual and other members of the
513   group. In the simulations, this can be calculated directly because all pedigrees are complete. However,
514   logistical limitations in real data mean that pedigrees are often incomplete, and taking a mean of an
515   individual's known pairwise relatedness's $\bar{r}$ will misrepresent the true local relatedness (r). We,
516   therefore, calculate an estimated local relatedness ($\hat{r}$) – and the error around that estimate (σ_r) - for
517   each individual, given the number of other group members to whom their relatedness is unknown (u).

518   The estimated local relatedness is calculated as a weighted mean of the potential local relatednesses
519   (R). R_j is the conditional true local relatedness if j of the u unknown pairwise relatednesses are kin
520   (equation 1).

521   equation 1.

$$R_j = \frac{\Sigma\bar{r} + (j)(\bar{r}_{>0}) + (u - j)(0)}{g - 1}$$

523   Where $\bar{r}_{>0}$ is the mean of all pairwise relatedness's in the population that are known and not 0, $\Sigma\bar{r}$ is
524   the total known local relatedness, and g is the number of individuals in the group. Weights are
525   calculated by using binomial theorem to determine (given $p = 0.2$) the probability that j of the n
526   unknown relatednesses are kin (equation 2).

527   equation 2

528
$$w_j = \binom{u}{j} \cdot 0.2^j \cdot 0.8^{u-j}$$

535
529   *p*=0.2 is likely to overestimate the number of relatives, and therefore lead to an overestimate of local
530   relatedness because it is likely that most unknown relatedness pairs are non-relatives. However, in the
531   absence of any information, we use $p = 0.2$ as a simple assumption. Changing this assumption
532   rescales local relatedness but does not change the observed patterns of kinship dynamics. We use the
533   true value of local relatedness and weights to calculate the estimated local relatedness as a weighted
534   mean (equation 3).

536   equation 3.

538
$$\hat{r} = \frac{\sum_{j=0}^{u} w_j R_j}{\sum_{j=0}^{u} w_j}$$

537

539

540   We also calculate the weighted standard deviation σ_r using the same inputs implemented in the Hmsic
541   package in R[107]. We use this pipeline to calculate an estimated local relatedness ($\hat{r}$) and the error
542   around that estimate (σ_r) for every individual in each year. If all relatednesses are known to all of an
543   individuals group mates $\sigma_r = 0$, however, to facilitate statistical modelling this error is assumed to be
544   an arbitrarily small non-zero number. Individuals who have no known pairwise relatednesses (i.e. all
545   their pairwise relatedness' are unknown) are not included in the analysis.

546   *Statistical modelling*

547   We use a hierarchical Bayesian framework to model change in local relatedness with age in both the
548   real and simulated data. For the real data, because the error is generated by an additive process we
549   model the estimated local relatedness ($\hat{r}$) as a sample from a normally distributed function centred on
550   the true local relatedness (r) with standard deviation of σ_r. The true local relatedness (r) is considered
551   to be drawn from a beta distribution with a mean of $\bar{p}$ and variance θ. Mean local relatedness at
552   datapoint *i* ($\bar{p}_i$) is modelled as a function group size (G_i) and sex-specific age (A_i), with an intercept
553   for sex ($s_{sid[i]}$) and an individual-level intercept for individual id ($\alpha_{id[i]}$; equation 4; supplementary 4).
554   All parameters have weakly informative priors (supplementary 4). The same framework is used to
555   model the simulated data but without the estimated relatedness step or the group size term because
556   pedigrees are complete and the group size is constant (supplementary 4).

557   equation 4

564
$$\hat{r} \sim Normal(r, \sigma_r)$$
565
$$r \sim Beta(\bar{p}, \theta)$$
566
$$logit(\bar{p}_i) = \alpha_{id[i]} + s_{sid[i]} + \beta_{sid[i]}A_i + \gamma G_i$$
558
$$\alpha_j \sim Normal(\bar{\alpha}, \sigma_a) \ for \ j = 1..n$$

559
560   Where *n* is the number of individuals (*id*), $\bar{\alpha}$ is a shared population-level intercept for individual and
561   *sid* is a numeric index for sex. We fit models using Hamiltonian Monte Carlo with 4 chains
562   implemented in R via the RStan package with additional functionality from the rethinking
563   package[108,109].Supplementary Figure

Author contributions

SE, RAJ, MAC, DWF, MNW and DPC conceived and designed the study programme. SE designed and implemented the analysis, made the figures and wrote the first draft of the manuscript with input from RAJ, MAC, DWF, MNW and DPC. RAJ designed and implemented the analytical model with MAC and with input from SE, DWF, MNW and DPC. Data from long-term research projects were contributed, collected and managed by: MAC, MM, HJN, FJT (banded mongoose data); CC, LV, RMW (chimpanzee data); CHB, RJD, RAM (European badger data); KCB, DKE, MNW (killer whale data); LJNB (rhesus macaque data); ED, OPH (spotted hyena data) and SCA (yellow baboon data). All authors contributed to later drafts of the manuscript and approved the manuscript for publication.

Data availability

Data to reproduce these analyses are available at: osf.io/pzfex. Anonymised data to derive kinship dynamics are included for: banded mongooses, chimpanzees, killer whales and spotted hyena. Data sharing agreements mean that for the remaining species, anonymised data to reproduce the analysis needs to be requested from the corresponding author, all other forms of data request should be addressed to the manager of the system in question.

Code availability

Code to reproduce these analyses are available at: osf.io/pzfex. The repository includes: a Mathematica file to run and reproduce the mathematical model; R code to implement the kinship dynamics simulation model; and R code to analyse both the simulation and observed kinship dynamics data. A simplified version of the simulation model can be explored at samellisq.shinyapps.io/kinship_dynamics_shinyapp_basic/ or downloaded from github.com/samellisq/kinship_dynamics_shinyapp. In addition, an R package, comparekin, created as part of this study, can be accessed at github.com/samellisq/comparekin.

612 **Competing interests**

613 The authors declare no competing interests.

614

615

616 **Tables**

617 Table 1. Species-specific dispersal and local mating input parameters for the simulation model and used to
618 generate predicted kinship dynamics. References and other input parameters can be found in Supplementary
619 Table 6.

Species	Female dispersal rate	Male dispersal rate	Local mating rate
Banded mongoose	0.12	0.12	0.64
Chimpanzee	0.89	0	0.93
European badger	0.23	0.45	0.52
Killer whale	0	0	0.02
Rhesus macaques	0.05	0.79	0.13
Spotted hyena	0	0.91	0.96
Yellow baboon	0	0.8	1

620

621 Table 2. Examples of behaviours that could be affected by kinship dynamics. The 'examples of age-linked change in the behaviour' highlights empirical
622 examples of these types of behaviour changing with age. These empirical examples demonstrate that the behaviour example in question can change with age-
623 further work is required to establish if the changes fit the patterns expected under kinship dynamics. Only in two studies (†) have the changes been explicitly
624 linked to kinship dynamics.

BEHAVIOUR EXAMPLES	POTENTIAL ROLE OF KINSHIP DYNAMICS	EXAMPLES OF AGE-LINKED CHANGE IN THE BEHAVIOUR
COOPERATION/HELPING	The maintenance of cooperation depends on the costs and benefits of the behaviour and the relatedness between the partners[1]. Helping can involve both directed cooperation with a particular partner or undirected help, such as investment in common goods. Kinship dynamics allow selection for investment in helping to change with age.	- In Hadza hunter-gatherers, females increase time spent foraging with age whereas male foraging activity peaks in late adolescence[52]. - Younger male meerkats (*Suricata suricatta*) spend more time mobbing potential predators than older male meerkats[86]. - Banded mongooses, of both sexes, in good condition, decrease their probability of providing cooperative offspring care with increasing age[87]. - Older female killer whales are more likely to share food than younger female killer whales[88]. - Male spotted hyenas with longer group tenures have higher local relatedness and receive more social support during intragroup conflict[24].
AGGRESSION/HARMING	The payoff of aggression towards or harm inflicted on social partners depends in part on the relatedness between the partners[1]. Kinship dynamics change the payoff from aggression with age and allows selection for systematic change with age.	- Prime-aged female Columbian ground squirrels (*Urocitellus columbianus*) show more aggression to more partners than younger females (some evidence of a decreased aggression in older females relative to prime-age)[89]. - Older meerkats have higher pairwise rates of aggressive interactions than younger meerkats[90].
REPRODUCTION	Reproduction is a form of generalised harm. By reproducing into a group, an individual increases competition for group resources at the expense of other group members[6,7]. Kinship dynamics allow for selection on the payoff of inflicting this generalised harm with age.	- In humans and killer whales, females reproducing at the same time as their daughters suffer increased infant mortality risk[21†, 51†].
KIN DISCRIMINATION/ BEHAVIOURAL SPECIFICITY	Exhibited social behaviours are linked to within-group relatedness[11,13]. Specifically, high local relatedness is linked to generalised helping behaviours, while low local relatedness is linked to increased kin discrimination in social partners[11]. Kinship dynamics allows selection for behavioural specificity to change systematically with age.	- Male chimpanzees become more socially selective (spend time with a smaller circle of social partners) as they become older[91]. - Barbary macaques (*Macaca sylvanus*), of both sexes, decrease their rate of social affiliation as they age[92].
EVICTION & SECONDARY DISPERSAL	Inbreeding risk[93] and competition with relatives[11,13] can be resolved by dispersing ('voluntarily' leaving a group) or eviction (being ejected from a group). Kinship dynamics change the payoff from dispersing predictably with age or group tenure.	- Male secondary dispersal in black-tailed prairie dogs (*Cynomys ludovicianus*) and yellow baboons coincides with their philopatric daughters reaching reproductive maturity[34,94]. - Eviction probability in banded mongooses of both sexes peaks at age 2-3 before declining. For males, there is an increased eviction risk in very old males[41].
EXTRA-GROUP MATING	Inclusive fitness gains can be an important part of the payoff from extra-group mating. For example, when local relatedness is high the risks of inbreeding will be high. Kinship dynamics can change the risk of inbreeding predictably with age. The payoff from extra-group mating may, therefore, also change with age selecting for different mating decisions in animals of different ages.	- Female banded mongooses demonstrate an increased probability of mating outside their group as they age[95].
INTERGROUP CONFLICT	Local relatedness can regulate the costs and benefits of engaging in risky intergroup aggressive interactions[96]. Kinship dynamics will modulate this payoff from engaging in intergroup conflict with age.	- The probability of male grey wolves (*Canis lupus*) engaging in aggressive chases during intergroup encounters increases with age[97].

625

626 **Figure legends**

627 Figure 1. Modelled sex differences in kinship dynamics under three scenarios: male-biased dispersal with local
628 mating (d_f = 0.15, d_m = 0.85, m = 0.82, n = *10*, μ = 0.1), female-biased dispersal with local mating (d_f = 0.85, d_m
629 = 0.15, m = 0.82, n = *10*, μ = 0.1) and bisexual philopatry with out-group mating (d_f = 0.15, d_m = 0.15, m = 0, n
630 = *10*, μ = 0.1). Local relatedness is the mean relatedness of an individual of that sex-age to all other individuals
631 in their group (of both sexes). Age is scaled relative to mean generation time, where age 0 is the age of maturity
632 and dispersal. Only patterns up to the third generation are plotted. The model assumes an arbitrarily large
633 population (and therefore with no population-size effects) of social groups of size n with an even sex ratio. The
634 model iterates through fixed times steps. At each time step, individuals have a fixed probability of mortality (μ),
635 and vacated slots are filled by a new individual of the same sex. Replacements have a *1-d* probability of being
636 offspring of group females and have a *m* probability of being fathered by in-group males (see methods;
637 Supplementary Figure 1).

638

639 Figure 2. Predicted (left-hand panels, orange outline) and observed (right-hand panels, black outline) kinship
640 dynamics for males (green) and females (purple) in 7 species of group-living mammal: banded mongooses (A),
641 chimpanzees (B), European badgers (C), killer whales (D), rhesus macaques (E), spotted hyenas (F) and yellow
642 baboons (G). In all panels, line and ribbon show mean changes in local relatedness with age generated as the
643 posterior mean (+/- 95% credible interval) from a linear model, incorporating error around local relatedness
644 estimation. Predictions are generated from a simulation model calculating local relatedness change with age,
645 parametrised by rates of male and female dispersal and local mating. Plotted relationships result from a linear
646 model applied to the output of the simulation model. Observed data are derived from long term studies of the
647 species. In both the predicted and observed panels local relatedness is calculated as the mean pairwise
648 relatedness from an individual to all other members of their group. Accounting for unknown relatedness' results
649 in an estimated local relatedness with error (points and error) in the observed data. Different relatedness scales
650 in the simulated and observed axis are consequences of group size and relatedness assumptions, changing these
651 assumptions changes the y axis scales but does not change the patterns of kinship dynamics. For male
652 chimpanzees and male killer whales, maximum age represents an absence of older individuals in the data rather
653 than their maximum lifespan. For female killer whales, we only calculate female kinship dynamics over the
654 reproductive lifespan and not over their post-reproductive lifespan (see methods). For the rhesus macaque
655 observed data a number of outliers with relatedness above 0.06 are not included in the plot. Panel H compares
656 species and sexes and shows the expected percentage change in local relatedness for an adult from age at
657 maturity to the expected adult lifespan in the species-sex calculated from the distribution of β slope parameters
658 Bayesian hierarchical model fitted to the observed data. Distribution widths are scaled within species-sex for
659 visibility. All silhouette images except the killer whale are taken from PhyloPic[44] and are in the public domain,
660 the killer whale image is original.

661

662

663 Figure 3. Selection on group directed behaviours given kinship dynamics under three dispersal scenarios for a)
664 survival and, b) fecundity. Age is scaled relative to mean generation time, where age 0 is the age of maturity and
665 dispersal. In both a and b, the selective landscape for females is shown on the upper row (blue lines and areas)
666 and males are on the lower row (green lines and areas). The lines and areas on each panel show the absolute cost
667 (c) to benefit (b) ratio under which an outcome will be favoured by selection. c is borne by the individual while
668 b applies to the whole group. In panel A, c and b are in terms of survival (a cost to an individuals' own survival
669 to increase or decrease the survival of group mates), and in panel B c and b are considered in terms of fecundity
670 (a cost to an individuals' own fecundity to increase or decrease the fecundity of their group mates). c always
671 has a positive value, whereas b can be either positive – the behaviour helps their group mates – or negative – the
672 behaviour harms their group mates. Therefore, areas above 0 c/b ratio indicate selection for helping behaviours,
673 areas below 0 for harm. In each panel, behaviours with a cost/benefit outcome between the line and $c/b=0$ (filled
674 areas) are selected. Lines distant from $c/b=0$ indicate that behaviours resulting in a relatively smaller b for a
675 larger c will be selected. While lines close to $c/b=0$ indicate that behaviours will require either a relatively small
676 c or a large b to be selected. The direction a line trends, therefore, indicates how selection for behaviours will
677 change with age. Model parameters in all dispersal scenarios are the same as those used in figure 1.

678

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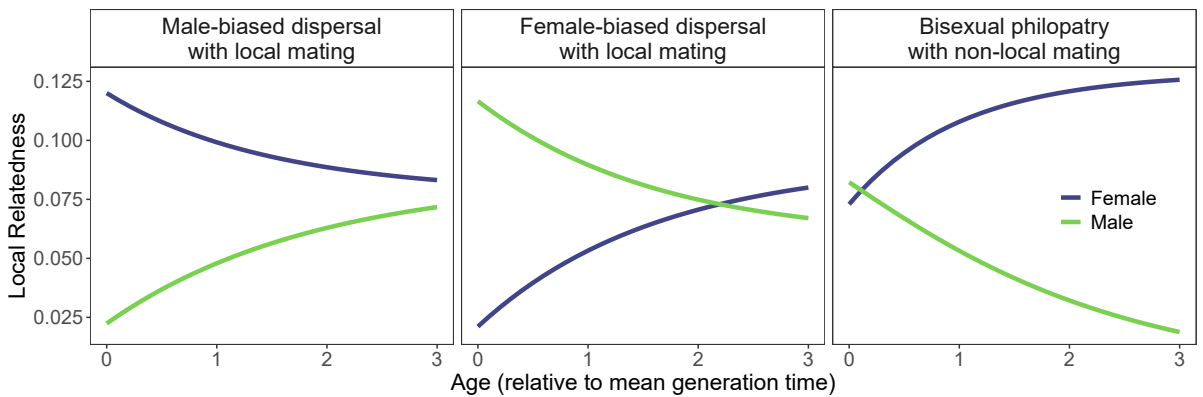914   109.   Stan Development Team. RStan: the R interface for Stan. (2020).

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918   Fig 1

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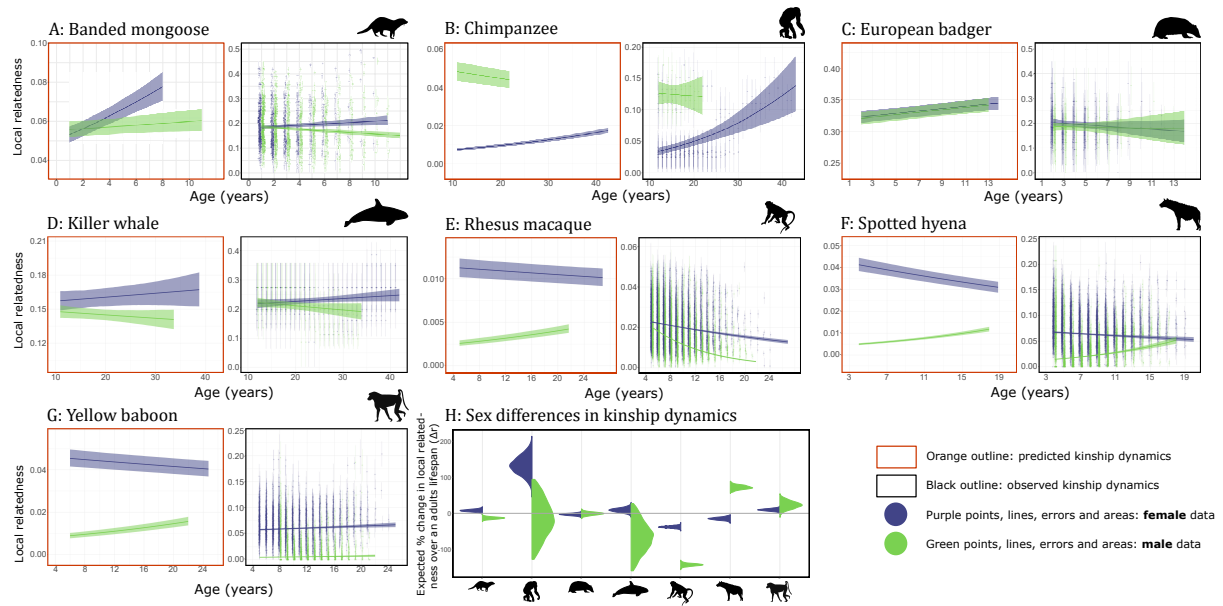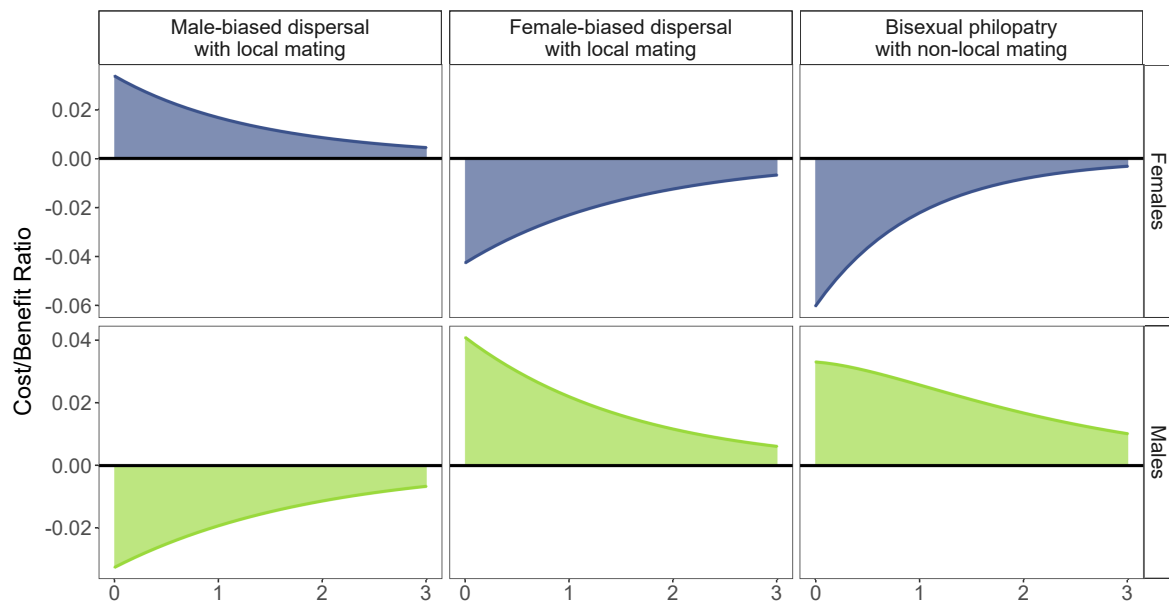# Patterns and consequences of age-linked change in local relatedness in animal societies

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921 Fig 2

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Patterns and consequences of age-linked change in local relatedness in animal societies
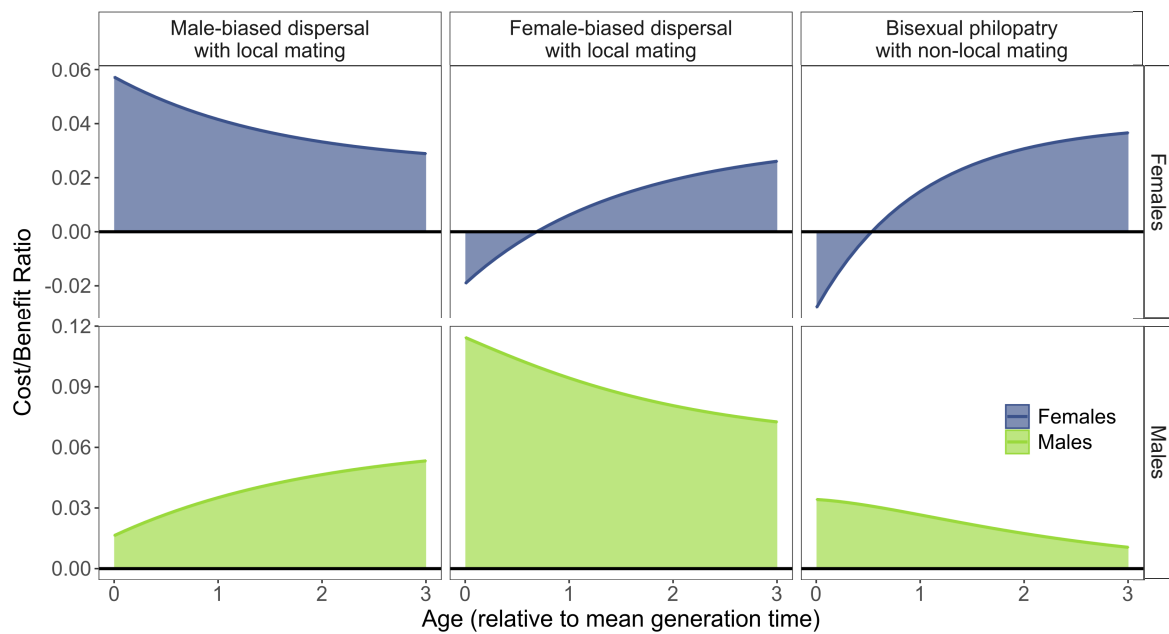
a) Survival

b) Fecundity

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924   Fig 3