

This is a repository copy of *Bringing numerous methods for expression and promoter analysis to a public cloud computing service*.

White Rose Research Online URL for this paper:

<https://eprints.whiterose.ac.uk/123822/>

Version: Accepted Version

Article:

Polanski, Krzysztof, Gao, Bo, Mason, Sam A et al. (4 more authors) (2018) Bringing numerous methods for expression and promoter analysis to a public cloud computing service. *Bioinformatics*. 884–886. ISSN 1460-2059

<https://doi.org/10.1093/bioinformatics/btx692>

Reuse

Items deposited in White Rose Research Online are protected by copyright, with all rights reserved unless indicated otherwise. They may be downloaded and/or printed for private study, or other acts as permitted by national copyright laws. The publisher or other rights holders may allow further reproduction and re-use of the full text version. This is indicated by the licence information on the White Rose Research Online record for the item.

Takedown

If you consider content in White Rose Research Online to be in breach of UK law, please notify us by emailing eprints@whiterose.ac.uk including the URL of the record and the reason for the withdrawal request.

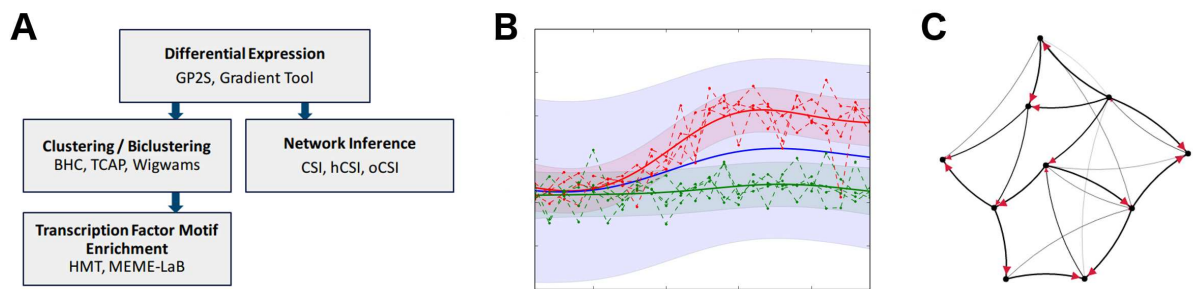


Figure 1: **A**: Workflow of a typical time course data analysis facilitated by some of the tools provided; **B**: a visualisation of GP2S model fits for expression data in two conditions (red, green) compared to an alternative, non-differential model (blue); **C**: a network visualisation in the CSI result webapp. Thickness of edges represents confidence in interactions.