1 Recommendations Good for Teaching New Finding +1 more

Learning causal networks with latent variables from multivariate information in genomic data.

Verny L Sella N Affeldt S Singh PP Isambert H Author affiliations

ARTICLE PUBLISHED: 2017 Oct CITE AS: PLoS Comput Biol. 2017 Oct; 13(10):e1005662 https://doi.org/10.1371/journal.pcbi.1005662

Rated ★★ Very Good 28 Nov 2017

Denis Thieffry F1000 Faculty Member

Bioinformatics, Biomedical Informatics & Computational Biology / Systems & Network Biology

IBENS
Paris
France

Classified as

Good for Teaching New Finding Technical Advance

This manuscript describes a novel computational approach enabling the inference of interaction/regulation networks from observational data. Starting from a completely connected graph, the proposed algorithm first iteratively discards dispensable edges, uncovering significant information contribution from alternative (in)direct paths. Edge orientations are then derived based on causal signatures computed on subsets of connected vertices. Furthermore, a confidence score is computed, which enables a ranking of the inferred interactions before experimental validations. The resulting graphs combine non-directed, directed and bi-directional edges, but exclude cyclic directed paths (potentially revealed by non-directed cycles). Finally, the approach can predict non measured (latent) variables.

The authors have assessed the performance of their method with artificial datasets of increasing complexity, demonstrating that it delivers robust predictions, with reduced computing time compared to existing methods. Furthermore, the authors have tested their algorithm with real datasets on single-cell gene expression during embryonic haematopoiesis, on genomic alteration in breast tumours, as well as on massive gene duplications in the course of vertebrate evolution. In each case, the authors could make sense of the resulting graphs and emphasise promising novel connections.

The information-theoretic background and the algorithm are well explained in the core of the manuscript and in the Material and methods section, and the software is publicly available as an R package.

This manuscript should be a great interest to the many groups currently performing single-cell gene expression analyses and aiming to decode the underlying regulatory networks.

Disclosures
None declared

Cite this Recommendation: Copy to clipboard

Thieffry D: F1000Prime Recommendation of [Verny L et al., PLoS Comput Biol 2017 13(10):e1005662]. In F1000Prime, 28 Nov 2017; 10.3410/f.731602681.793539352

Related articles

Published on: 2016 Apr

Inferring causal molecular networks: empirical assessment through a community-based effort.

Hill SM. et al.

More like this › SmartSearch

Relevant Sections

Bioinformatics, Biomedical Informatics & Computational Biology

Computational Genomics & Genetic Analysis
Systems & Network Biology