

Cologne Evolution Colloquium

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Learning causal and non-causal networks from large scale genomic and clinical data

Network reconstruction aims at disentangling direct from indirect dependences in information-rich data and has become ubiquitous to analyze the rapidly expanding resources of genomic and clinical data. However, most network inference methods are restricted to specific types of data and assume either causal or non-causal graphical models a priori. We have developed an information-based approach, which reconstructs causal, non-causal or mixed networks from large scale genomic or clinical data, without the need for an a priori choice on the causal or non-causal nature of reconstructed networks. Starting from a fully connected graph, it first removes dispensable edges by iteratively subtracting the most significant information contributions from indirect paths between each pair of nodes. The remaining edges are then filtered based on their confidence assessment or oriented based on the signature of causality in observational data. This computational approach outperforms or matches state-of-the-art methods for either causal (eg regulatory interaction) or non-causal (eg protein contact map) network reconstruction. In the talk, I will present different applications on a broad range of biological and clinical data, from single-cell transcriptomics and genomic alterations in tumor progression to long term evolution of vertebrates through whole genome duplication.

Wednesday, November 21, 2018, 17:00

University of Cologne

Institute for Biological Physics

Zùlpicher Str. 77a

Seminar Room 0.03, Ground Floor

Hosted by Michael Lässig