

Title: From data analysis to network modeling, with applications in systems biology

Author: Fabian J. Theis, Computational Modeling in Biology, Institute of Bioinformatics and Systems Biology, Helmholtz Zentrum München

fabian.theis@helmholtz-muenchen.de (<http://cmb.helmholtz-muenchen.de>)

Abstract:

Analyzing patterns in data sets is a challenging problem in statistics, with demanding applications in fields as varied as biomedicine, telecommunication or financial markets. Here we show how we iteratively refine initial analysis methods by including additional knowledge about the domain in order to arrive at detailed models of the system of interest. Our application focus are biological networks, namely gene regulatory networks.

Initially we demonstrate how statistical tools such as clustering and independent component analysis can be used to extract information from large data sets such as microarrays. The resulting model is of qualitative nature. We then proceed to include information about the network structure into the analysis and arrive at a more detailed small-scale model that may predict regulation in a quantitative fashion. However, detailed information about many parameters of the dynamical system is necessary; for this we describe a Bayesian framework for parameter estimation.

We will finish with an outlook towards building a small-scale model responsible for lineage differentiation of hematopoietic cells. In order to generate data for such models, the above data analysis techniques are then needed again for both microscopic image analysis, tree clustering and parameter quantification.