



Emerging Topics in Biological Networks and Systems Biology

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Large-scale Network Modeling of Cancer: Validation, Feature Extraction and Comparative Modeling

Abstract:

High-dimensional modeling of genomic data can provide insights into subtypes of diseases, identify biomarkers that are potential candidates for therapeutic development, and reveal mechanistic hypotheses of genomic regulation.

In this talk, we will present an integrative and comparative network model for different types of cancer, focusing on the statistical tuning and validation of such models. We propose a new method, based on the statistical concept of data depth, geared at producing robustly estimated network components and to enable testing and comparisons of network components between disease subtypes or against pathway data bases.

Finally, we give a brief outline of our current research program into multi-layer/multi-resolution network modeling. This framework allows us to identify disease-driving components from sub-type specific network components. These network-derived biomarkers have been shown to correlate with clinical variables such as patient survival.

About:

Rebecka Jörnsten is Professor of Biostatistics and Applied Statistics at the division for Applied Mathematics and Statistics and the University of Gothenburg and Chalmers University of Technology. Jörnsten received her Ph.D. from the University of California at Berkeley in Mathematical Statistics under the supervision of Prof. Bin Yu in 2001. Her research centers on large-scale modeling and feature selection for biomedical data, information theory-based methods, clustering and network modeling.