

Seminar Series in Statistics and Biostatistics

28.09.2018, 09:15 @ Seminar Room 819, Niels Henrik Abels hus, 8th floor

Rebecka Jörsten Network modeling of large-scale genomic data

Abstract: Genome-wide network models of multi 'omics cancer data are popular tools for studying and revealing both unique and shared mechanisms across malignancies. In this talk we will discuss some "pan-can" (multi-cancer) models based on SICS (sparse inverse covariance selection). We will present some statistical methods for selecting network complexities and how one can use concepts of data depth to produce robust network estimates. Time permitting we will present some recent results on multiresolution network models (MR-SICS). While our SICS model is a highly useful tool for network modeling, there are important questions that warrant further study. First, the large number of co-linear vari- ables creates instability of network estimation. Secondly, while model estimation is based on highly optimized solvers, improvements of scalability are needed to handle future data sets. Our multi-resolution method, MR-SICS, builds on a nested latent model formulation of network components. At each level of resolution of the model, the parameters for comparative inference are relatively small, substantially improving estimation stability and interpretabil- ity over standard SICS models.



Rebecka Jörsten

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Rebecka is professor of Biostatistics and Applied Statistics at the University of Gothenburg/Chalmers, division of Applied Mathematics and Statistics.

Her research focuses on the development of new statistical methodology for network modeling, clustering and model selection, with applications to high-dimensional biological data. Rebecka is particularly interested in integrating techniques from information theory into new tools for statistical model selection and high-dimensional data exploration.

Next seminar

01.10.2018 @ 14:15 Ingrid van Keilegom (Leuven)

Contact Information

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