



Seminar Series in Statistics and Data Science

26.03.2019, 14:15 @ Erling Sverdrups plass, Niels H. Abels hus, 8th floor

Andrea Cremaschi: Hierarchical Normalized Completely Random Measures for Robust Graphical Modeling

Abstract: Useful tools to express multivariate network structures in gene expression studies are graphical models. However, alternative models are needed when data are strongly overdispersed. An interesting proposal has been introduced by Finegold and Drton (2014) who used a Dirichlet process to cluster data components and accommodate for overdispersion. In this work, we consider a more general class of nonparametric distributions, namely the class of normalised completely random measures (NormCRM's), which yields a more flexible component clustering. Moreover, in order to borrow information across the data, we model the dependence among the NormCRM's through a nonparametric hierarchical structure. At data level, each NormCRM is centred on the same base measure, which is a NormCRM itself. The discreteness of the shared base measure implies that the processes at data level share the same atoms. This desired feature allows to cluster together components of different data. We compare the performances of the proposed model with competitors via a simulation study. Moreover, we explore genomic expression patterns in a *Saccharomyces cerevisiae* yeast microarray dataset, with the aim of identifying the multivariate network structure of the data, while clustering components according their degree of over-dispersion.



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Next seminar

09.04.2019 @ 14:15 **Aldo Solari**
Bicocca University of Milano (ITA)

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