



Emerging Topics in Biological Networks and Systems Biology

Symposium at the Swedish Collegium for Advanced Study (SCAS), Uppsala
9-11 October, 2017

GEORGE MICHAILIDIS, University of Florida, USA

An Integrative Statistical Framework for Multi-Modal Omics Data

Abstract:

It is becoming increasingly common for patients to be profiled across multiple molecular compartments -genomic, transcriptomic, proteomic, metabolomic, etc. A big challenge confronting biomedical researchers is to link alterations in expression level to biological processes that can inform the underlying onset and progression of disease. This process moves biomarker identification to the realm of mechanistic insights. Exploiting the hierarchy of gene to mRNA to protein to metabolite can be a first step. To that end, we develop a framework that leverages recent developments in the estimation of high-dimensional multi-layered graphical models that provide insights on interactions across molecular compartments (layers), as well as on molecular interactions within each layer and are also capable of accommodating outcome variables such as disease risk, or patient survival times. We discuss algorithmic issues and theoretical properties of the estimates and apply them to real data from a hyperurecimia study.

About:

George Michailidis is the Director of the University of Florida Informatics Institute and a Professor of Statistics and Computer Science. He holds a Ph.D. in Mathematics from UCLA. His research interests are in the modeling, optimization issues and analysis of high-dimensional data and networks with applications to Omics studies.