

## Emerging Topics in Biological Networks and Systems Biology

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

## **JEAN-PHILIPPE VERT**, École Normale Supérieure and MINES Paris-Tech, France Graph Wavelets to Analyze Genomic Data with Biological Networks

## Abstract:

Biological networks are a common way of describing information on relationships between genes that are accumulated from many years of biomedical research, and they are thus potentially valuable when incorporated as prior knowledge to guide gene selection in genomic data analysis. In this study, we focus on network-based regularization methods through a predictive frame-work with linear models, and propose to use a class of methods based on wavelet smoothing over general graphs that directly detect subnetworks composing of collaboratively functional gene modules. We perform breast cancer survival analysis using a large gene expression dataset and a protein-protein interaction network obtained from public database, and demonstrate that the proposed methods are able to improve the efficacy of gene selection in terms of stability, connectivity and interpretability while achieving competitive performance of survival risk prediction. This is joint work with Yunlong Jiao.

## About:

Jean-Philippe Vert is Professor at the Department of Mathematics and Applications of the Ecole Normale Supérieure, Paris, and Senior Researcher at Mines ParisTech and at the Curie Institute, in Paris, where he heads a laboratory focusing on machine learning and computational biology. He holds a degree from Ecole Polytechnique and a PhD in mathematics prepared at the Ecole Normale Supérieure in Paris. He works in particular in the field of kernel methods and structured sparsity, and is interested in the development of predictive models for drug discovery and precision medicine in cancer research.