

Reconstruction and interrogation of biological networks

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Inferring and using biological networks, guided by data from large-scale genomic experiments, is currently an active area of research with numerous applications in understanding biological systems. Machine learning with its large spectrum of techniques ranging from generative models to concept learning methods plays a major role in this endeavour, typically involving “case-by-case” development of methodologies.

In recent years, we have developed sets of tools that allow i) the reverse engineering of gene regulatory networks, including their cis-regulatory elements, ii) the identification of master regulators controlling the transition between phenotypes, and iii) the extraction of biologically relevant pathways connecting core proteins within protein-protein interaction networks.

In this talk we will focus on the reconstruction and the dissection of human gene regulatory and protein-protein interaction networks to understand biological process involved in tumor progression in bladder cancer.

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