SYSTEMS BIOLOGY AND NETWORKS USING MACHINE LEARNING APPROACHES"

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High-throughput technologies enable the study of biological processes at the systems level. However, analyzing the large amount of data generated by high-throughput techniques and translating these data into biological knowledge is currently a critical bottleneck in systems biology. In particular, network inference refers to the problem in which the biological evidence on the characteristics and the state of a system's elements is used to deduce associations or functional relationships among these elements and to construct the interaction graph underlying the system.

In order to infer such biological networks, different computational techniques and mathematical modeling strategies could become valuable tools. In this context, the data-mining methods configure suitable approaches for performing the reverse engineering of these relational structures and, in particular, these reconstruction strategies can be beneficed from the application of *association rule* (AR) extraction algorithms. Basically, an AR establishes a causal link between two or more variables, where the semantics and the interpretation of the rule depend of the input data and on the mechanisms employed for inferring the association. ARs have been extensively used for discovering interesting relationships between variables in large data sets and, in bioinformatics, these methods be able to reveal biologically relevant associations among genes, at diverse environmental conditions or time point observations, from different microarray samples. In this lecture we will focus on gene regulation and the ways that transcriptome data can be used to unravel the complex relationships between the genes and pathways. In particular, we will describes the main topics that must be considered in the field of AR mining for reverse engineering of biological networks and presents some techniques currently available in the literature.