

NUMERICAL ANALYSIS AND SCIENTIFIC COMPUTING
SEMINAR

Inference of gene regulatory networks by feature selection

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Abstract: Gene Regulatory Networks (GRN) can be viewed as a gene interaction network where the level of expression of each gene is related to how vigorously that gene will be transcribed into RNA. The cell control is the result of a multivariate activity of genes, and the understanding of such activity is crucial for therapeutic purposes and development of new drugs. In this context, since the available data is usually noisy and scarce (only dozens of samples with thousands of gene expression values), the inference of GRNs is one of the big challenges in bioinformatics. GRNs can be modeled as graphs where the vertices represent genes and the edges represent dependencies between genes. There are many categories of GRN modeling, such as Bayesian Networks, Boolean Networks (and its stochastic version: Probabilistic Boolean Networks), differential equations and others. This presentation will give an overview of GRNs and some problems about inference by feature selection approaches. Works in progress on this topic will be briefly discussed.

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