

# Gene expression analysis and modeling

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## **Abstract**

Recent progress in large-scale sequencing and comparative mapping have made available a flood of new genomic data. As whole genome sequences become complete, the focus is shifting from structural genomics to functional genomics. Microarrays with their massively parallel capabilities for measuring gene expression have become an attractive tool for the better understanding of biological processes. In this talk, we will review supervised and unsupervised statistical techniques for microarray analysis such as k-means and hierarchical clustering, PCA (principal component analysis), SVD (singular value decomposition), SVM (support vector machines). We will also describe the various discrete and continuous models that can be used for the analysis of gene networks. This include: boolean networks, qualitative and piece-wise linear models, differential equations and bayesian models.