

Learning Graphical Models for DNA Chip Data Mining

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Abstract

The past few years have seen a dramatic increase in gene expression data on the basis of DNA microarrays or DNA chips. Going beyond a generic view on the genome, microarray data are able to distinguish between gene populations in different tissues of the same organism and in different states of cells belonging to the same tissue. This affords a cell-wide view of the metabolic and regulatory processes under different conditions, building an effective basis for new diagnoses and therapies of diseases.

In this talk we present machine learning techniques for effective mining of DNA microarray data. A brief introduction to the research field of machine learning from the computer science and artificial intelligence point of view is followed by a review of recently-developed learning algorithms applied to the analysis of DNA chip gene expression data. Emphasis is put on graphical models, such as Bayesian networks, latent variable models, and generative topographic mapping. Finally, we report on our own results of applying these learning methods to two important problems: the identification of cell cycle-regulated genes and the discovery of cancer classes by gene expression monitoring. The data sets are provided by the competition CAMDA-2000, the Critical Assessment of Techniques for Microarray Data Mining.

Curriculum Vitae

Byoung-Tak Zhang

I am interested in biointelligence which I understand as bio-inspired computer technologies for learning and inference. Currently, my research centers around Bayesian theory of evolutionary computation, learning and evolution of probabilistic neural networks, and their application to bioinformatics and biocomputing. I am serving as a Technical Co-Chair of *The 2001 Congress on Evolutionary Computation (CEC2001)*, an associate editor of the *IEEE Transactions on Evolutionary Computation*, and a member of the editorial boards of *Genetic Programming and Evolvable Machines* and *Evolutionary Optimization*. For further information, please click the links above or visit the SCAI Lab which I lead.