Cancer Diagnosis using Microarray based Bayesian Models

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Date: Friday, April 21, 2006
Time: 10 am - 12 noon
Venue: CReWMaN Lab (WH 413)

Abstract:

Precise classification of tumors is critical for cancer diagnosis and treatment. Diagnostic pathology has traditionally relied on macro and microscopic histology and tumor morphology as the basis for tumor classification. Current classification frameworks, however, are unable to discriminate among tumors with similar histopathologic features, which vary in clinical course and in response to treatment. In recent years, there has been a move towards the use of cDNA microarrays for tumor classification. These high-throughput assays provide relative mRNA expression measurements simultaneously for thousands of genes. A key statistical task is to perform classification via different expression patterns. Gene expression profiles may offer more information than classical morphology and may provide an alternative to classical tumor diagnosis schemes.

In this research, we tackle the problem of gene expression based cancer classification using Bayesian hierarchical models. We develop full probabilistic model-based approaches like gene selection models as well as regularization methods like probabilistic relevance vector machines (RVM) and support vector machines for classification. It is shown through simulation and examples that SVM models with multiple shrinkage parameters produce fewer misclassification errors than several existing classical methods as well as Bayesian methods based on the logistic likelihood.

Biography:

Dr Bani Mallick is a Professor and the Director of the Bayesian Bioinformatics Lab at the Department of Statistics, Texas A&M University. His research group works in the fields

of Bayesian hierarchical modeling, classification, regression and spatial inferences with application in Bioinformatics. Dr. Mallick is an elected fellow of the American Statistical Association, Royal Statistical Society and International Statistical Institute. He has also received the 2006 Texas A & M Distinguished Achievement Award in Research.