

Computation and **I**nformatics in **B**iology and **M**edicine
Training Program

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***A Unified Approach to Discovery and
Classification of Tumor Types using Gene
Expression Data***

Abstract:

DNA microarray technology has been increasingly used in cancer research. In the literature, discovery of putative classes and classification to known classes based on gene expression data have been largely treated as separate problems. We offer a unified approach to class discovery and classification, which has greater applicability in practical situations. The method we propose is based on modeling the distribution of the gene expression profile of a tumor sample as a mixture of an unknown number of distributions, each characterizing the gene expression levels in a class. We demonstrate an application to a leukemia dataset. With appropriate choices of genes and preprocessing method, the number of leukemia types is correctly inferred, and all the tumor samples are correctly classified into their respective types. Further evaluation of the method is carried out on other variants of the leukemia data and a colon cancer dataset.

**Tuesday, October 11th, 2005
4:00 p.m.**

Genetics/Biotechnology Center Auditorium
425 Henry Mall