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***Temporal Discrimination of Microarray
Data for Toxicogenomics***

Abstract:

Analysis of microarray data may be able to help make assays for toxic chemicals faster, cheaper, and more accurate. We are investigating the task of learning models for classifying uncharacterized chemicals and for identifying chemicals that do not fit into previously defined classes (i.e., anomaly detection). Because the microarray data we are using is sparse in time and sampled at irregular intervals, our model incorporates splines to interpolate the missing data. We find that our models are able to make more accurate classifications when they use this representation for the temporal evolution of expression profiles.

**Tuesday, February 1st, 2005
4:00 p.m.**

Genetics/Biotechnology Center Auditorium
425 Henry Mall