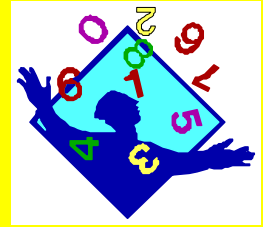


# STATISTICS SEMINAR



## Identifying gene regulatory sequences by hidden Markov model and integrative analysis of gene expression

Jun Xie

Purdue University

DATE: November 10, 2005

TIME: 4:00 PM

PLACE: Dickens 106

REFRESHMENTS: 3:30 pm - Dickens 108

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Identification of gene regulatory sequences is a first step toward deciphering gene regulatory networks. In our study, gene regulatory sequences are referred to as transcription factor binding sites, which often occur in close proximity. Despite the acceleration of algorithm developments in this area, current methods are not ready for serious applications because of the poor predictive specificity. We propose to improve predictions by adding extra information and underlying properties to the model of regulatory sequences. Specifically, we have developed a hidden Markov model that describe a cluster of transcription factor binding sites, also called cis-regulatory module. In addition, genome-wide expression data are integrated into a multivariate regression model to validate binding site predictions. This integrative analysis will help the understanding of temporal and spatial structure of transcription factor binding in gene regulation.

\*\* Upcoming seminars may also be found on the web at <http://www.ksu.edu/stats/current.seminars/nav.currentseminars.html>.