

Applied and Computational Mathematics and Statistics Colloquium

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Will give a lecture entitled:

*Incorporating Genomic Annotation in the Statistical
Analysis of DNA Methylation Tiling Array Data*

Monday, October 25th, 2010

4:00 PM

Location: 127 Hayes-Healy Hall

Abstract:

Epigenetic modifications are biological phenomena that enable change in genome function without change in DNA sequence. DNA methylation is an epigenetic modification that occurs when a methyl chemical group attaches to a cytosine base on the DNA molecule. It may play a role in the regulation of gene expression, silencing transposable elements in plants, and development of human cancer. To better understand this epigenetic mechanism, genome-wide profiles of DNA methylation are being developed by identifying all locations of DNA methylation in a genomic region for a variety of cell types and organisms. Large-scale studies of DNA methylation are supported by microarray technology known as tiling arrays. They provide high-density coverage of genomic regions through the unbiased, systematic selection of probes that are tiled across the regions. Hidden Markov models can be employed to estimate each tile's methylation status while accounting for dependency between tiles. Previous studies indicate that methylation patterns of some organisms may differ by genomic content (e.g., gene, transposon), suggesting that genomic annotation information may be useful in a statistical analysis. In this work, a Hidden Markov model, which incorporates genomic annotation information, is proposed to estimate DNA methylation status for all tiles in a DNA methylation tiling array experiment.