



JOHNS HOPKINS
BLOOMBERG
SCHOOL of PUBLIC HEALTH

Department of Biostatistics

BIOSTATISTICS SEMINAR

Statistical Genetics of Gene Expression

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Abstract

With the increasing availability of genomics technologies, it is becoming common to integrate two or more levels of genomic information in a given study. In this talk, I will consider several statistical problems arising from the joint analysis of genome-wide genetic variation and gene expression, including: (1) obtaining informative and unbiased tests of associations between genetic loci and gene expression variation and (2) building causal models connecting genetic variation to transcriptional regulation, and ultimately to complex traits. I will also make connections to more general statistical challenges emerging from integrative genomics studies.

**The Johns Hopkins Bloomberg School of Public Health
Department of Biostatistics, Wednesday, November 4, 2009
Room W2030 School of Public Health, 4:00-5:00pm (Refreshments: 3:30)**