

STATISTICS COLLOQUIUM

MONDAY, FEBRUARY 12, 2007

TALK: 4:00 PM — SCIENCE CENTER RM. 705

RECEPTION: 5:15 PM — SCIENCE CENTER, 7TH FLOOR

Detection of eQTL Modules Mediated By Activity Levels of Transcription Factors

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ABSTRACT

Studies of gene expression quantitative trait loci (eQTL) have shown the existence of eQTL hotspot: one small segment of DNA sequence that harbors large numbers of eQTLs. Two questions of great interest about eQTL hot-spots arise: (1) Which gene within the hotspot is biologically responsible for the linkages, i.e., which gene is the quantitative trait gene (QTG)? (2) How does a QTG affect expression levels of many genes linked to it? The first question can be answered by biological evidence or statistical methods. The second question is harder to address. One simple situation is that the QTG encodes a transcription factor (TF), which regulates the expression of genes linked to it. However, previous results have shown that TFs are not over-represented in the eQTL hotspots. We consider the scenario that the propagation of genetic perturbation from a QTG to other linked genes is mediated by the TF activity. We develop a statistical procedure to detect the eQTL modules (eQTL hot-spots together with linked genes) that are compatible with this scenario.