**Computational and Life Sciences Seminar**

*Integrated Genomics Approaches to Discovering the Genetic Basis of Complex Traits in Inbred Mouse Strains*

Eleazar Eskin  
University of California, Los Angeles

**Abstract:** Inbred mouse strains are a very powerful and well studied human disease and complex trait model. A tremendous amount of information is available for various inbred strains including phenotypic information stored in the Mouse Phenome Database (MPD) and high-throughput genomic data such as expression microarray data.

Recently, several high density SNP maps have also been developed for inbred mouse strains. These resources combined with what is already known about mouse genetics in terms of quantitative trait loci (QTLs) and known pathways, make inbred mouse strains an ideal model system.

We present results of our analyses which combines multiple types of data in order to understand the genetic basis of complex traits. We perform whole genome association analysis of the mouse SNP maps over the phenotypes in the MPD. We describe how we augment our association analysis results with information from expression data, known pathways and QTLs. We demonstrate the how our approach is able to discover many regions in the mouse genome associated with phenotypes and how many of our predictions are consistent with genes known to influence specific traits.

Friday, April 11, 2008, 3:00 pm  
Mathematics and Science Center: W201

Light refreshments will be served.