



and



present Guest Speaker :

Eleazar Eskin

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Computer Science Department, UCLA

*Computational and Statistical Challenges in the
Design of Genetic Association Studies*

Variation in human DNA sequences account for a significant amount of genetic risk factors for common disease such as hypertension, diabetes, Alzheimer's disease, and cancer. Identifying the human sequence variation that makes up the genetic basis of common disease will have a tremendous impact on medicine in many ways. Recent efforts to identify these genetic factors through large scale association studies which compare information on variation between a set of healthy and diseased individuals have been remarkably successful. However, despite the success of these initial studies, many challenges and open questions remain on how to design and analyze the results of association studies. In this talk, I will formulate association study design as an optimization problem where the goal is to design a study which maximizes the statistical power to detect genetic risk factors given a fixed budget. I will demonstrate how we can leverage the inherent correlation structure of variation in the human genome to design efficient association studies.

Student Presentation (10 mins):

Sohrab Shah, Department of Computer Science

(Dr. Raymond Ng, Dr. Kevin Murphy)

Detection of structural abnormalities in tumour genomes using model based approaches: application to 107 patients with follicular lymphoma.

Thursday, November 8, 2007, 6:00 pm

Gordon and Leslie Diamond Family Theatre,
BC Cancer Research Centre, 675 West 10th Avenue



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