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**Seminar**

Speaker: **Professor Javier Cabrera**  
**Jie Liu PhD Candidate**  
**Department of Statistics**  
**Rutgers University**

Title: **Post GWAS analysis of SNP data with applications to systolic blood pressure sensitivity to weight and sodium change**

Time: **3:20 – 4:20pm, Wednesday, March 13, 2013**

Place: **552 Hill Center**

**Abstract**

Genome Wide Association Studies (GWAS) are epidemiological studies that identify genetic factors (1M Single Nucleotide Polymorphisms - SNP) that are related to a disease or health condition. Next Generation Sequencing attempts to observe a much larger number of SNP's (of the order of 30M). The result of GWAS is generally a short list of SNPs that are statistically significant under some model which compares two or more conditions. We developed methodology to analyze the data combining the list of important SNPs obtained by a literature search of GWAS together with clinical data from existing clinical trials. The objective of the methodology is to explore dependencies of deep combination of SNPs and the disease or health condition in the context of clinical trial data. The methodology includes several procedures: (i) greedy model search on the combination of SNPs, (ii) SNP tree models (iii) Handling multiplicity by FDR correction for p-values. The computations required for analyzing combinations of several SNP's are very large due to the combinatorial nature of the problem and seem unrealistic. However we consider only those genotype combinations that are present in the data and make the number of combinations smaller and we are able to produce some results. Our motivation in studying SNPs is derived from clinical trials, and in particular from the Trial of Nonpharmacologic Interventions in the Elderly (TONE), where we study the systolic blood pressure sensitivity to weight and sodium change among patients with hypertension.

Collaborators: Jerry Cheng, William Kostis, John Kostis.

**\*\* Refreshments will be served at @2:50pm in Room 502 Hill Center \*\***

