

# Department Seminars

## Design of Microarray Experiments for Genetical Genomics Studies with Outbred Populations

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### Abstract:

Genetic analysis of transcriptional profiling experiments has emerged as a promising approach for unraveling genes and pathways that underlie variation of complex biological traits. The design of such experiments, nevertheless, is currently challenged by the high cost of microarrays, which limits the sample size for global genetic mapping of transcript abundance. Conversely, as genotyping costs are generally smaller, the number of genotyped individuals available can be substantially larger than that used for gene expression profiling. In this context, several selective phenotyping strategies have been proposed to determine optimal subsets of individuals for microarray experiments, including methods based on the maximization of genotypic dissimilarity, or the maximization of balance and number of crossover events, or the information on a correlated economically relevant trait (ERT) for which a QTL has been identified. However, most of these methods were developed in the context of crosses between inbred lines, e.g. with plant and animal model organisms. In this seminar, we will discuss extensions of such selective phenotyping strategies for mapping populations derived from crosses between outbred populations, typical in livestock studies. Through a simulation study we compare the performance of different selective profiling strategies in terms of sensitivity and specificity of QTL detection and the precision of inference on the corresponding QTL location and effect. Moreover, we compare alternative statistical modeling approaches to analyze selectively profiled expression data that vary in the manner in which they utilize information on a correlated ERT. It is shown that selective phenotyping strategies are usually more efficient than a random sub-set selection of individuals, especially when the proportion of samples selected for gene expression profiling is small.

Professor Rosa develops research programs at the interface between statistical/theoretical and molecular genetics, focusing on applications to animal models in domestic/managed and natural populations and teaches courses in animal breeding, statistical genetics and statistical genomics.

**Friday,**

**October 2, 2009**

**G5/113 CSC  
140 Bardeen  
(note location change)**

**12:00-1:00 p.m.**