

COURSE ANNOUNCEMENT

DESIGN AND ANALYSIS OF MICROARRAY EXPERIMENTS IN AGRICULTURE

FALL SEMESTER 2007

COURSE SYNOPSIS

High-throughput technologies such as DNA microarray chips for gene expression profiling have been increasingly used in many areas of agricultural research. Microarray technology is used, for example, to evaluate and to compare the gene expression in different tissues, genetic backgrounds or environmental conditions. Such experiments, however, generate data sets of unprecedented complexity and dimensionality, such that specific statistical and computational methods are required for their successful data mining. Moreover, appropriate statistical design is essential to make the best use of the limited number of chips and samples that are generally available. In this course we will discuss the practical use of statistical methods for designing and analyzing microarray experiments, using a simple language accessible to biologists with some quantitative training. Some basic principles of biology, genetics and statistics will be reviewed, and the fundamentals of microarray technology will be introduced. Some aspects related to planning of microarray experiments in crop and livestock research will be discussed, with emphasis on the statistical design of such trials. In addition, statistical and computational techniques related to microarray data acquisition, data normalization, significance testing and clustering will be presented.

OUTLINE OF MAJOR TOPICS

- Central Dogma of Molecular Biology, Phenotypic Variation, Heritability
- Analysis of Variance; Introduction to Randomization Tests
- DNA Microarray Technology, Data Acquisition and Normalization
- Planning Microarray Essays; Choice of Microarray Platform, Tissue and Time Points, Sources of Variation in Microarrays
- Introduction to Statistical Design of Experiments; Incomplete Block Structures; Reference and Loop Designs
- Biological and Technical Replication, mRNA Pooling Strategies
- Fixed and Random Effects, Introduction to Mixed Linear Models
- Choosing Between Competing Experimental Designs
- Fundamental Power and Sample Size Determinations
- Modeling Ratios and Individual Channel Intensities
- Estimation of Gene-Specific Variances
- Multiple Testing Methods: Family-wise Error Rate (FWER), False Discovery Rate (FDR), False Positive Rate (FPR)
- Cluster Analysis of Microarray Data
- Identifying Differentially Expressed Gene Categories
- Analysis of Quantitative RT-PCR Data
- Combining Microarray Data with Molecular Marker Information

Interested students should register in Section 6 of DY SCI 875

Prerequisites: STAT 571 & 572 (or consult instructor); Date/Time to be decided with enrolled students

Please contact Dr. Guilherme Rosa (grosa@wisc.edu) for further information