Analysis of Microarray Data
May 14, 16 and 18
1:30pm - 3:30pm in the 7th Floor Classroom

The massive amount of data generated from microarray experiments requires knowledge of analytical and statistical methods in order to make sense of the data. Here we explore some of these methods to make biological discovery.

Day 1:
Experimental Design and Data Normalization
Effective design is crucial for any large-scale experiment, so we'll look briefly at some issues to consider before performing a microarray experiment. After data collection, effectively analyzing expression data requires some initial data normalization and transformation. We will discuss methods to remove unwanted variation within and between chips.

Day 2:
Differential Expression, Filtering and Clustering
We will discuss methods to identify genes exhibiting differential expression and ways to filter all the genes on a chip to some manageable number for further analysis. We will also review the specifics of some common clustering and segmentation methods used to find genes with similar expression patterns.

Day 3:
Functional Analysis and Visualization
Once you have a list of genes with "interesting" expression patterns, what do you do next? We will discuss ways to take advantage of gene annotation to further analyze expression data. We will also survey some ways of visualizing large amounts of expression data.

**Registration is free for the Whitehead community.
To register, please send mail to barc_courses@wi.mit.edu**

Please don't be a "no show".

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