GS01 0163
Analysis of Microarray Data

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Lecture 0: Outline and Details

Welcome!

• Why are we here?
• Who are we?
• What are we going to tell you about, and when?
• What do we assume you’re familiar with?
• Where and when can you find ???
• What are we going to ask of you?
So, why are we here?

We want to learn about microarrays.

Microarrays have caught on as high-throughput assays for understanding molecular biology – they let us measure expression levels for thousands of genes in a single sample all at once.

This means new biology, and new data analysis.

We want to

- Understand how microarrays work and how they are analyzed.
- Perform some basic analyses of microarrays.

We’re going to dive in here; we hope to have you analyzing data this week or next.
Who are we?

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We’re faculty in the department of Bioinformatics and Computational Biology at MD Anderson. We’ve been working with microarray data for about 8 years now. We think we’ve done pretty well with it, and we’re going to trade off in telling you about it.
What are we going to tell you about, and when?

**Week 1:** How microarrays work, and Affymetrix file structures. The basics of dChip.

**Week 2:** Using dChip. Connecting numbers to biology – the basics of annotation and databases.

**Week 3:** Documentation. Reviewing initial analyses. Introduction to R.

**Week 4:** Sample analysis using R/Bioconductor for Affymetrix.

**Week 5:** Reviewing R basics, quantification and normalization of Affymetrix data, Latin Square studies.

**Week 6:** Measures of differential expression (DE); R and DE.
What are we going to tell you about, and when?

**Week 7:** Reviewing DE assessments, introducing glass arrays.

**Week 8:** Case Study in R, start to finish

**Weeks 9-10:** Glass arrays. R and glass arrays. Putting it together for glass.

**Week 11:** Clustering microarray data, diagnostics, validation.

**Week 12:** Classification.

**Week 13:** Experimental design, proteomics.

**Week 14:** Meta-analysis

**Week 15:** Pathways, other arrays, open questions.
What do we assume you’re familiar with?

Some biology.

Some programming.

Some statistics.
Computing

Microarray datasets are large. One of our initial data sets will involve 100 Affy gene chips; the files take up 1.5G of disk space when uncompressed. Another dataset takes 4G.

The image files from some of the newest arrays (e.g., Affymetrix exon arrays) are 1.5G per array, so data summarization is a real issue.

We will be using lots of freeware, including dChip (Windows-based), R, and the Bioconductor repository.
Textbooks


Where can you find ???

- Course web site
  http://bioinformatics.mdanderson.org/MicroarrayCourse

- Office hours: T, Th, 4:30-5:30, HMB
  - Dr. Baggerly: HMB 13.336
  - Dr. Coombes: HMB 13.402
What are we going to ask of you?

Grading: Homeworks (roughly every two weeks)

1. Homeworks can be worked on jointly.

2. Assignments submitted electronically, in a single file (zipped is fine), by midnight on the assigned due date.

3. Submissions should include figures, R code, and text.

We’re very interesting in getting good documentation for how analyses were performed. Thus, as we move into R we’ll also be talking about Sweave, which helps us track things better.