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 section of Bioinformatics at MD Anderson, in the Dept of Biostatistics and Applied Mathematics. We've been working with microarray data for about 5 years, 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: Reviewing initial analyses. Introduction to R.

Week 4: Sample analysis using R/Bioconductor; Affymetrix and Bioconductor.

Weeks 5 and 6: Reviewing R basics, quantification and normalization of Affymetrix data, Latin Square studies.

Week 7: Measures of differential expression (DE); R and DE.

What are we going to tell you about, and when?

Week 8: Reviewing DE assessments, introducing glass arrays.

Week 9: Quantification and normalization of glass arrays; annotations for glass arrays.

Week 10: R and glass arrays. Putting it together for glass.

Week 11: Experimental design for array studies.

Week 12: Clustering microarray data, diagnostics, validation.

Week 13: Classification.

Week 14: Predicting clinical outcome.

Week 15: Meta-analysis, and 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.

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

Textbooks

Required: Simon RM, et al. *Design and Analysis of DNA Microarray Investigations.* Springer-Verlag, New York, 2003.

Optional: Dalgaard P. *Introductory Statistics with R.* Springer-Verlag, New York, 2002.

Optional: Speed T (ed). *Statistical Analysis of Gene Expression Microarray Data.* Chapman and Hall, New York, 2003.

Optional: Parmigiani G, et al (eds). *The Analysis of Gene Expression Data.* Springer-Verlag, New York, 2003.

Optional: Gentleman R, et al (eds). *Bioinformatics and Computational Biology Solutions Using R and Bioconductor.* Springer-Verlag, New York, 2005.

Where can you find ???

- Course web site
  http://bioinformatics.mdanderson.org/MicroarrayCourse
- Office hours: T, Th, 3:30-4:30, Faculty Center
  - Dr. Baggerly: FC2.2060
  - Dr. Coombes: FC2.3014

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.