# Analysis and Application of DNA Microarrays

Todd Lowe

Bio 210

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# Class Information WWW

http://www.soe.ucsc.edu/~lowe/courses/MicroarrayW03/
(corrected)

Also, will be a link from my lab website:

http://lowelab.ucsc.edu/

Syllabus & reading list posted by monday

Lectures will be posted by morning of lecture

# Structure of Course

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  - Mondays: Lecture
  - Wednesdays: Guest speakers in Microarray Club
  - Friday: Lab

# Survey

- For lab, who has a conflict 11-12:30 Fridays?

# (Supplementary) Textbook for Course

- "A Biologist's Guide to Analysis of DNA Microarray Data" by Steen Knudsen, Wiley 2002

- Reading: Chapter 1

# Introductory Review

- "Genomics, gene expression and DNA arrays", Lockhart DJ, Winzeler EA, Nature 2000 Jun 15; 405:827-36

(link posted on class website)

# Teams

- Groups of 2-3 for “for-credit” students assigned by me next week for labs & problem sets

# Grading

Project Course:

- 50% Problem sets
- 50% Final project write-up (analysis of your own dataset)

# Getting more background…

- If a method or algorithm is cited & you need to know more about it, look it up at PubMed:

  www3.ncbi.nlm.nih.gov/Entrez/

- search "PubMed" database (not "protein" or "nucleic acid"), use AND / OR / NOT between keywords

  (will put a link from class web page)

Example: "cluster AND analysis AND microarray" gives 180 references – you can read abstracts, and usually get full text on-line from .ucsc.edu domain

# Molecular Biology Reference

- Current Protocols in Molecular Biology – a good reference if you are new to experimental genetics:

  www.wiley.com/legacy/cp/cpmb/
- Follow link "Click here for access to current protocols online"
- Select "Current Protocols in Molecular Biology"
- Read "Introduction" sections, and go from there (will put a link from class web page)

# The Goal

"Big Picture" Cell biology –

- What are *all* the components & processes taking place in a cell?
- How do these components & processes interact to sustain life?

- Functional Genomics – figuring out cellular functions & relationships between all genes in a genome

# Genome Sequence Flood

- Typical results from initial analysis of a new genome by the best computational methods:

  For 1/3 of the genes we have a *"good" idea* what they are doing (high similarity to exp. studied genes)

  For 1/3 of the genes, we have a *guess* at what they are doing (some similarity to previously seen genes)

  For 1/3 of genes, we have *no idea* what they are doing (no similarity to studied genes)

# Large Scale Approaches

- Geneticists used to study only one (or a few) genes at a time
- Now, thousands of identified genes to assign biological function to
- Microarrays allow massively parallel measurements in one experiment

# Microarrays Becoming Mainstream

- A “PubMed” search of keyword “microarray”
  - One year ago: 1177 references
  - Today: 2701 references

- variable *quality*, huge *quantity* and *complexity* of the data makes correct interpretation non-trivial
- An understanding of the technology will allow you to:
  - Be critical of published work
  - Recognize opportunities to employ the technology yourself