

Bio 4342: General Course Information (spring '05)

| <u>Instructors</u> | <u>Office</u> | <u>Telephone</u> | <u>e-Mail</u> |
|--------------------|--------------------------|------------------|---------------------------|
| Sarah C.R. Elgin | McDonnell 131 (Hilltop) | 935-5348 | selgin@biology.wustl.edu |
| Elaine Mardis | Genome Sequencing Center | 286-1805 | emardis@watson.wustl.edu |
| Darren O'Brien | Genome Sequencing Center | 286-1835 | daobrien@watson.wustl.edu |
| Chris Shaffer | McDonnell 155 (Hilltop) | 935-6837 | shaffer@biology.wustl.edu |
| Jeremy Buhler | Jolley Hall 530 | 935-6180 | jbuhler@cse.wustl.edu |
| Michael Brent | Jolley Hall 532 | 935-6621 | brent@cse.wustl.edu |

Teaching Assistants

| | | | |
|---------------|----------------------------|----------|-----------------------|
| Libby Slawson | McDonnell 155 (Hilltop) | 935-6837 | |
| | lslawson@biology.wustl.edu | | |
| Yue Yun | 4444 Forest Park, Rm4184 | 362-1715 | yyun@artsci.wustl.edu |

Class Schedule

Lecture and lab will be interspersed. The class will meet from 1:30 to 5:00 PM on Monday and Wednesday, and from 1:30 to 2:30 PM on Friday. A writing-intensive version of the course (Bio 432W) has just been approved; students who elect this option will have 4-5 additional hour-long meetings to focus on writing, scheduled for Friday 2:30-3:30 PM. Attendance is required.

Because this is a laboratory course, true make-up sessions are often not possible. Students who must miss a class due to ill health, a death in the family, or a required interview should inform Dr. Elgin prior to the class session to obtain a bye. If you miss a class, you are responsible for obtaining notes and information from your lab partner, and consulting the instructor and/or TA as necessary to gain an understanding of the material covered.

Meeting Sites

During the first half of the semester, class will meet at the WU Genome Sequencing Center, 4444 Forest Park Parkway. The Center is one short block from the corner of the Forest Park Parkway and Taylor; the shuttle bus will drop you off at the corner on request. Please sign in at the front desk. Class will meet in the Large Conference Room, 4th floor. During the second half of the semester, class will meet in the Biology Department, Life Sciences 202.

Texts

There are no required texts. The following may be useful, depending on your background.

“Bioinformatics and Functional Genomics” by R. Pevsner, J. Wiley & Sons, NJ (recommended for Bio majors if you would like more introduction to the computer tools we use).

“Gene Cloning: An Introduction” by Terence A. Brown, 3rd ed, Trans-Atlantic Publications (recommended if no equivalent book, such as the texts for Bio 2970, are in hand).

“Exploring Genomes: Web-based Bioinformatics Tutorials,” by Paul G. Young, Freeman & Co., NY (recommended if you have no prior experience with BLAST etc.).

Web Site

All course information, announcements, reading assignments, etc. will be posted on the Bio 4323 web site, maintained by the Biology Department through the NSLC. If lectures are presented

using PowerPoint, copies of the presentation materials will be posted if possible. The latter portion of the web site is password protected.

Student Responsibilities, Grading

Grades will be assigned based on the following components: attendance, 10%; participation in discussions, 10%; quality of wet lab notebook, 5%; five graded computer-based problem sets, 25%; report on finishing *Drosophila* fosmid clone, 20%; report on genes/pseudogenes, 10%; final report on individual *Drosophila* fosmid (analysis and annotation) (written and oral), 20%. Students who elect the Writing Intensive version of the course will have an introductory writing assignment that constitutes 5% of the grade.

Lab Overview: Sequencing / Finishing

We anticipate either 1) demonstrating or 2) having students perform hands-on, the following types of activities during the first half of the semester:

1. Library making process for fosmid clones (demo)
2. Clone picking, archiving and inoculation for prepping growth (demo)
3. Magnetic bead prep of plasmid DNA—both manual and automated (demo)
4. Agarose gel analysis of DNA preps (demo)
5. DNA sequencing reaction assembly and post-reaction processing
6. Loading of ABI Instruments/data transfer (demo)
7. QC procedures—how/when they are performed and why this is important
8. Looking at DNA sequence data—trace viewing and generating graphical representations of large data sets/comparative graphical views
9. Prefinishing process, including re-arraying of subclones, growth, prep and sequencing, addition of data to database, and reassembly/assessment of joins
10. Finishing process—calling primers for PCR, PCR amplification from BAC or genomic DNA, making joins and editing, methods for assessing quality of finished sequence

Lab Overview: Analysis / Annotation

We anticipate that students will become familiar with the use of Phred/Phrap/Consed to assemble and evaluate sequence reads (see above); Repeat Masker; commonly used DNA data bases; BLAST, FASTA searches for homology; Genscan, Twinscan and other search tools; Clustal for comparative analysis. If time permits, we may explore databases and tools for analysis of microarrays, and data bases for proteomics.