Bio 4342/434W: General Course Information (Spring 2017)

**Instructors**

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**Teaching Assistants**

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**Sequence improvement:**

- Lee Trani
  - WU Genome Institute

**Annotation:**

- Kailong Mao

- Emily Chi

**Writing Instructor:**

- April Bednarski
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**Class Schedule**

Lecture and lab will function together. 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; occasionally the Friday session will extend to 3:30 or 4:30 (see schedule). Students who elect the writing-intensive option (Bio 434W) will have ca. 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 med school/grad school 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 the instructor; consulting with the instructor and/or a TA as necessary to gain an understanding of the material covered; and catching up on your work as needed.

**Meeting Sites**

Class will meet in the Biology Department, Life Sciences 311, on the Danforth Campus.

On Friday January 20 we will meet at the WU Genome Institute, Fourth Floor Lobby, 4444 Forest Park Parkway, for a tour. The Institute is ca. 2 blocks from the West End Metro stop (catch the 1:14 pm train at Skinker).

**Texts**

There are no required texts. The texts used in Bio 2960/2970 (or any molecular genetics course) will cover the basic biology knowledge needed. The following books in bioinformatics may be useful, depending on your background.


**Web Site**

All course information, announcements, reading assignments, etc. will be posted on BlackBoard. Basic information and reading will also be posted on the Bio 4342 web site.
http://www.nslc.wustl.edu/courses/Bio4342/bio4342.html maintained by the Biology Department through the NSLC. The latter portion of the web site is password protected. This has copies of all of the recommended and required reading. Most of the teaching materials used in the course can be found at the Genomics Education Partnership web page (http://gep.wustl.edu) under Curriculum. Examples of student papers from previous years are also found on the GEP site.

**Student Responsibilities, Grading**

Grades will be assigned based on the following components: participation in discussions, four summary papers on reading, 12%; six graded computer-based problem sets, 18%; final report on finishing a ~100 kb Drosophila project (written 15% and oral 5%); report on first annotated gene (10%); TSS report (10%); final report on individual Drosophila fosmid (analysis and annotation) (written 25% and oral 5%). (Note homeworks and reading summaries are graded with a check = 8 pts, check plus = 10 pts, or check minus = 6 pt.) Students who elect the Writing Intensive version of the course will have an introductory writing assignment, and will critique and rewrite the other reports mentioned; quality of all critiques and revisions will constitute 5% of the final grade.

**Lab Overview: Sequencing / Finishing**

During the first 2½ weeks of the semester, we will be engaged in sequence improvement and genome assembly, covering the following:
- Direct sequencing techniques for DNA—both manual and automated (videos);
- Use of Phred/Phrap/Consed to assemble and evaluate sequence reads;
- Finishing process—scanning for errors in mononucleotide runs, sorting reads, searching for additional project data in the original data set, calling sequencing primers from the genomic DNA template, adding additional data; methods for assessing quality of finished sequence.

**Lab Overview: Analysis / Annotation**

We anticipate that students will become familiar with commonly used DNA databases; model organism websites; genome browsers; RepeatMasker; Genscan and other gene prediction tools; BLAST, BLAT searches for similarity; Clustal for comparative analysis; techniques for annotating transcription start sites; techniques for motif searching. As time permits and the research dictates, we may explore other databases and comparative tools.

**Computers**

We will have large-screen Macs available for your work in class, and/or we can provide Mac laptops for your use during the course. If you check out a laptop, you will be responsible for returning it in good condition at the end of the semester. If you prefer, you can use your own portable computer. However, we recommend that only Macs be used during our work on sequence improvement (first 2½ weeks of the course), as Consed (the key software) is available only in a Mac version. (It can only be used on a PC in a virtual machine.) Either a Mac or a PC can be used when we are working on annotation (remaining weeks of the course). We will provide a portable hard-drive for the class, but you are responsible for backing up your work at the end of each session!