

Bio 4342/434W: General Course Information (Spring 2018)

<u>Instructors</u>	<u>Office</u>	<u>Telephone</u>	<u>Email</u>
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<u>Teaching Assistants</u>			
Wilson Leung	McDonnell 112 (Danforth)	935-6837	wleung@wustl.edu
Sequence improvement:	Lee Trani	WU McDonnell Genome Institute	
Annotation:	Mary Richardson		m.richardson@wustl.edu
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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.

Office Hours

Office hours are available on request with Dr. Shaffer, Mr. Leung or Dr. Elgin. If there is interest, we will set up a Sunday afternoon office hour with a TA.

Meeting Sites

Class will meet in the Biology Department, Life Sciences 311, on the Danforth Campus. On Friday January 19 we will meet at the WU McDonnell 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 1:34 pm train at Skinker; tour starts at 2 pm).

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.

“Bioinformatics and Functional Genomics” by R. Pevsner, 2015 (3rd ed.), J. Wiley & Sons, NJ, (ISBN: 978-0-470-08585-1; WU QH441.2 .P48). Recommended for Bio majors if you would like more introduction to the computer tools we use.

“BLAST” by I. Korf, M. Yandell, J. Bedell, 2003, O’Reilly (ISBN 0596002998) (recommended for in-depth use of BLAST and interpretation of results). Available on-line from Olin Library at http://libproxy.wustl.edu/login?url=http://proquest.safaribooksonline.com/?uiCode=was_humo&xmlId=0-596-00299-8

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 also 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 under Curriculum → Student Work → Washington University.

Student Responsibilities, Grading

Grades will be assigned based on the following components: participation; four summary papers on readings (“Reading Reflections”), 12%; six graded computer-based problem sets, 18%; final report on finishing a ~100 kb *Drosophila* project (written 15% and oral 2%); report on first annotated gene (written 10%, oral 2%); first TSS report (written 10%, oral 2%); final report on individual *Drosophila* annotation and analysis projects (written 25% and oral 4%). (Note homeworks and reading reflections are graded on a scale of 1 - 10.) Students who elect the Writing Intensive version of the course will critique and rewrite four papers (Reading Reflection #1, finishing report, first gene report, first TSS report); the quality of all critiques and revisions will constitute 5% of the final grade.

Lab Overview: Sequencing / Finishing

During the first three 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; methods for assessing quality of finished sequence.

Lab Overview: Analysis / Annotation

We anticipate that students will become familiar with commonly used genomic databases; model organism websites; genome browsers; RepeatMasker; Genscan and other gene prediction tools; BLAST, BLAT searches for similarity; Clustal for comparative analysis of sequence; protein structure visualization; 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 three weeks of the course), as Consed (the key software) is available only for macOS and Linux. (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 recommend that you back up your work using WUSTL Box. We will also provide a portable hard-drive for the class, but you are responsible for backing up your work at the end of each session!

Revised 12/10/2017.