BIOL 525L: Analysis and Interpretation of Sequence-based Functional Genomics
Department of Biology, University of North Carolina at Chapel Hill
Spring 2017

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Teaching Assistant: Ben Keith
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Computer Lab Meeting Time: Tues 2:00-2:50pm, GSB 1378
Final Exam: None
Concurrent enrollment in lecture class required

Description
This computer lab aims to provide students with experience using computational analysis software for genomics applications in a linux environment. The focus will be on applications for analysis of high-throughput sequence data. The labs will be designed to complement topics in the accompanying lecture class and provide more practical instructions on specific genomics resources such as the UCSC Genome Browser. Additional instruction to help complete class assignments will also be provided.

Goals
The goals of this class are to

(i) provide practical experience using computational biology software, and using web-based tools and resources for the analysis of genomics data;
(ii) provide understanding strengths and limitations of analysis software.

Prerequisites
This course is intended for upper-level undergraduate and beginning graduate students in life sciences. Basic knowledge of molecular biology, beginning level programming skills, and familiarity with basic statistical concepts are expected, such as those learned in the following UNC classes or their equivalents:

BIOL 202 – Molecular Biology and Genetics
COMP 116 – Introduction to Scientific Programming, COMP 110 – Introduction to Programming, or equivalent
STOR 155 – Introduction to Statistics, or equivalent

Students may also request a waiver from the instructor.
Weekly Topics

**Week 1 - no lab**

**Week 2 (1/16):** Becoming familiar with the virtual computing lab (VCL) at UNC, linux operating system

**Week 3 (1/23):** FastQC – assessing DNA sequence quality

**Week 4 (1/30):** Aligning short read sequences

**Week 5 (2/6):** RNA-seq analysis

**Week 6 (2/13):** Differential RNA-seq analysis

**Week 7 (2/20):** GO enrichment analysis

**Week 8 (2/20):** Transcription factor binding site (TFBS) peak calling

**Week 9 (2/27):** Differential ChIP-seq analysis

**Spring Break (3/12-3/16)**

**Week 10 (3/20):** Creating and using a MySQL database

**Week 11 (3/27):** The UCSC Genome Browser and database

**Week 12 (4/3):** Motif finding

**Week 13 (4/10):** micro-RNA analysis

**Week 14 (4/17):** Chromatin and transcription factor binding

**SAKAI**
The Sakai system at UNC ([http://sakai.unc.edu](http://sakai.unc.edu)) will be used extensively to provide instructional material, assignments including student submission and grading of assignments.

**Grading**
Grades for this course will reflect the ability of the student to master practical aspects of computational genomics analysis. This will be assessed through graded computer-based assignments. Late homework assignments will be penalized 10% a day, cumulatively. This means that an assignment three days late will be penalized 30%. Exceptions will be made by prior approval by instructor. Final grades for the lab portion of this course will be based on in-class assignments, and will be factored in with grades from the lecture portion of the course to assign a single combined grade (see syllabus for BIOL525 lecture).
A 10% grading scale will be used, meaning:

A  90% - 100%
B  80% - 89%
C  70% - 79%
D  60% - 69%
F  <60%

**Honor Code**
Computational genomic research is, in general, highly collaborative and open. That being said, students need to learn to independently perform the work assigned in this class. Students are encouraged to help classmates understand general concepts and techniques learned in class, even related to homework assignments, but under no circumstances should complete answers, computer code, or the like for homework be shared. Specific questions about individual homework assignments should be discussed with the professor.

**Syllabus Changes**
The professor reserves to right to make changes to the syllabus, including project due dates and test dates. These changes will be announced as early as possible.