BIOL510/480/630: Bioinformatics · Winter 2017
Lecture: Monday 10:15-11:30 in CC-405
Lab: Tuesday 9:30-11:30 in CC-203

Instructor
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Course Summary and Objectives: Modern biology is increasingly employing genome-scale and high throughput data-generation approaches to address questions on human health, the environment and biotechnology. This trend has given rise to the discipline of bioinformatics: the use of algorithms, statistics and computing to analyze and interpret biological sequence data. In this course, students will become familiar with the theory and methodologies of bioinformatics. The course is comprised of three general themes each supported by lectures and hands on computer-based learning. These themes include (1) biological sequence data and evolutionary analysis, (2) structural and functional analysis of genes and genomes and (3) comparative genomics. Lecture material is supplemented by in-class activities, assignments and a bioinformatics project where students have the opportunity to apply their skills and knowledge to a self-generated research question.
Please note: a strong understanding of molecular biology and genetics is essential for this course.

Class Schedule (subject to change)

Week	Topic	Chapter	Example tools
01	Introduction and biological databases	Ch. 1-3	NCBI,
02	Sequence alignment	Ch. 4-5	Pairwise BLAST
03	Searching sequence databases	Ch. 4-5	BLAST searching
04	Multiple sequence alignments	Ch. 6	CLUSTAL, MUSCLE
05	Molecular phylogenetics I	Ch. 7	MEGA
06	Molecular phylogenetics II	Ch. 8	
07	Gene prediction and genome annotation	Ch 9-10	GLIMMER
08	**Midterm exam** *(covers weeks 1-6)*		
09	Predicting secondary structure	Ch 11	
10	Modeling 3D protein structure	Ch 13	Cn3D
11	Functional annotation of proteins	Ch 14	InterproScan
12	Inferring metabolic pathways	Ch 17	KEGG, MetaCyc
13	Proteomics and gene expression	Ch 15	GEO, Mascot

Suggested Course Textbook: Zvelebil and Baum (2008), *Understanding Bioinformatics* is available at the bookstore. The textbook is not mandatory, but will be very helpful as a study tool and as a general bioinformatics reference.

Office Hours: Office hours are held in TBA on TBA.

Student Evaluation

20%	Laboratory assignments	20%	Midterm exam
20%	Bioinformatics project	40%	Final exam

Please Note:

1. No food or drink in the computer lab.
2. The username and password are the same as your Concordia Portal Login.
3. Any information saved on the computers may get deleted upon reboot. If you want to keep a copy of your work safe, you should eg place it on Google Drive.

Guidelines for Bioinformatics Project (due TBA).

Goal: The purpose of this assignment is two-fold. First, it will give you practice in using some of the bioinformatics tools that you have learned in the course and, secondly, it will provide you with experience in writing a paper in a format that would be acceptable for a scientific journal.

Choice of topic: The main topic of your paper will be the bioinformatics analysis of a particular gene or genome.

Choice of gene: The gene can be one of your own choice. You may choose a gene that is of personal interest to you, or is related to your research. You should not, however, choose a gene that has already been used in the worked examples or homework assignments.

Choice of Analyses: You do not have to perform every analysis that was described in the course. You should, however, do at least three different analyses, such as Blast search, multiple alignment, phylogeny building, finding genome location, etc. Rather than just doing a list of analyses, however, you should use the results of the analyses to describe the new information that you have discovered about this gene.

Format: Your paper should be no longer than ten pages in length (double spaced typing). This includes figures and references. Please write as clearly and concisely as you can, and use complete sentences (not point form). In order to give you practice writing scientific papers, we will follow the format required by the journal, ***Molecular Systems Biology (Nature Publishing Group)*** (see http://www.nature.com/msb/authors/index.html#a3.1). Follow the instructions for preparing "Preparation of Research Articles". You will see that many of the instructions are not relevant for your paper (e.g., online submission procedures, etc).

Supplementary material: As you will see, almost any bioinformatics analysis can generate large amounts of results. You should not simply "cut and paste" these results into your paper. You can, however, save them as "supplementary material", refer to them in your main text, and submit them by e-mail. The figures and tables in your main text should only contain the information that you feel is most important; generally, this would correspond to a summary of the results from the bioinformatics analyses.