

BCH364C/BCH394P Bioinformatics (course # 55120/55210)
Spring 2017 **Tues/Thurs** **11 – 12:30 PM** **GDC 4.302**

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Course web page: http://marcottelab.org/index.php/BCH364C_BCH394P_2017

Open to graduate students and upper division undergrads (with permission) in natural sciences and engineering.
Prerequisites: Basic familiarity with molecular biology, statistics & computing, but realistically, it is expected that students will have extremely varied backgrounds. UGs have additional prerequisites, as listed in the catalog.

An introduction to systems biology and bioinformatics, emphasizing quantitative analysis of high-throughput biological data, and covering typical data, data analysis, and computer algorithms. Topics will include introductory probability and statistics, basics of Python programming, protein and nucleic acid sequence analysis, genome sequencing and assembly, proteomics, synthetic biology, analysis of large-scale gene expression data, data clustering, biological pattern recognition, and gene and protein networks.

** Note that this is not a course on practical sequence analysis or using web-based tools (although we'll use a few), but rather on algorithms, exploratory data analyses and their applications in high-throughput biology. **

Most of the lectures will be from research articles and slides. For sequence analysis, there will be an **Optional text:** *Biological sequence analysis*, Durbin, Eddy, Krogh, Mitchison, Cambridge Univ. Press (available from Amazon, used from \$15.00)

For biologists rusty on their stats, *The Cartoon Guide to Statistics* (Gonick/Smith) is very good (really!).

We will also be learning some Python programming. The following is highly recommended:

Python programming for beginners: <http://www.codecademy.com/tracks/python>

Online homework will be assigned and evaluated using the free bioinformatics web resource Rosalind (<http://rosalind.info/faq/>). **Enroll here:** <http://rosalind.info/classes/enroll/b22533ccd7/>

No exams will be given. Grades will be based on online homework (counting 30% of the grade), **3 problem sets** (given every 2-3 weeks and counting 15% each towards the final grade) **and a course project** (25% of final grade), which can be collaborative (1-3 students/project). The course project will consist of a research project on a bioinformatics topic chosen by the student (with approval by the instructor) containing an element of independent computational biology research (e.g. calculation, programming, database analysis, etc.). This will be turned in as a link to a web page. **The final project is due by midnight, April 27, 2017. The last two classes will be spent presenting your projects to each other. (The presentation will account for 5% of the project.)**

All projects and homework will be turned in electronically and time-stamped. No makeup work will be given. Instead, all students have 5 days of free "late time" (for the entire semester, NOT per project, and counting weekends/holidays). For projects turned in late, days will be deducted from the 5 day total (or what remains of it) by the number of days late (in 1 day increments, rounding up, e.g. 10 minutes late = 1 day deducted). Once the full 5 days have been used up, assignments will be penalized 10 percent per day late (rounding up), e.g., a 50 point assignment turned in 1.5 days late would be penalized 20%, or 10 points.

Homework, problem sets, and the project total to a possible 100 points. There will be no curving of grades, nor will grades be rounded up. We'll use the plus/minus grading system: A= 92 and above, A-=90 to 91.99, etc. Here are the grade cutoffs: $92\% \leq A$, $90\% \leq A- < 92\%$, $88\% \leq B+ < 90\%$, $82\% \leq B < 88\%$, $80\% \leq B- < 82\%$, $78\% \leq C+ < 80\%$, $72\% \leq C < 78\%$, $70\% \leq C- < 72\%$, $68\% \leq D+ < 70\%$, $62\% \leq D < 68\%$, $60\% \leq D- < 62\%$, $F < 60\%$.

Students are welcome to discuss ideas and problems with each other, but **all programs, Rosalind homework, and written solutions should be performed independently** (except the final collaborative project). Students are expected to follow the UT honor code. Cheating, plagiarism, copying, & reuse of prior homework or programs from CourseHero, Github, or other sources are all strictly forbidden and constitute breaches of academic integrity (http://deanofstudents.utexas.edu/sjs/acint_student.php) and cause for dismissal with a failing grade.

We'll cover the following topics, approximately in this order:

BASICS OF PROGRAMMING

Introduction to Rosalind
A Python programming primer for non-programmers
Rosalind help & programming Q/A

BIOLOGICAL SEQUENCE ANALYSIS

Substitution matrices (BLOSSUM, PAM) & sequence alignment
Protein and nucleic acid sequence alignments, dynamic programming
Sequence profiles
Guest lecture: Homologs, orthologs, and paralogs
BLAST! (the algorithm)
Biological databases
Markov processes and Hidden Markov Models

GENOMES, PROTEOMES, & "BIG BIOLOGY"

Gene finding algorithms
Genome assembly & how the human genome was sequenced
Guest lecture: Next- (& next-next-) generation DNA and RNA sequencing
An introduction to large gene expression data sets
Promoter and motif finding, Gibbs sampling
Clustering algorithms, hierarchical, k-means, self-organizing maps, force-directed maps
Guest lecture: Overview of mass spectrometry shotgun proteomics
Guest lecture: Protein 3D structural modeling
Classifiers, k-nearest neighbors, Mahalanobis distance
Principal component analysis and data transformations

NETWORK & SYNTHETIC BIOLOGY

Biological networks: metabolic, signaling, graphs, regulatory
Network alignment and comparisons, network organization
Deep homology and the evolution of traits
Guest lecture: Genome engineering
Designing, simulating, and building gene circuits
Genome design and synthesis

***** THE FINAL COURSE PROJECT IS DUE by midnight, April 27, 2017 *****

The last two class days will be devoted to presenting your projects to the rest of the class.

Note that there is NO CLASS over spring break (March 14 & March 16).