

Fall 2017 Course: 11:126:485 / 16:765:585

COURSE SYLLABUS

Location

LECTURE: Foran Hall, Room 191B, Tuesdays, 5:35pm-6:55pm

JOURNAL CLUB (grad section ONLY): to be determined

LAB: Foran Hall, Computer Lab, Room 124, Thursdays, 5:35pm - 8:35pm

CLASS E-mail: yanab@rci.rutgers.edu

Lecturer:

Dr. Yana Bromberg

Lipman Hall 218

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Office Hours: Tuesdays 4-5 or By Appointment

Lab Instructors:

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Office Hours: By Appointment

Brief Intro:

Bioinformatics as a field attempts to build computational models of the biological systems and mechanisms. More specifically, bioinformatics involves creating algorithms, databases, systems, and web applications to solve problems in molecular biology. Here, all computational advances are “fair game”. Bioinformatics tools use artificial intelligence, rely on “cloud” computing, and borrow concepts from signal processing and circuit theory. ALL these developments are necessary to deal with the inordinate amounts of data that is being produced by modern high-throughput experimental techniques. Due to the drop in sequencing costs we are awash in DNA, RNA, and protein sequences. Massive genomics and metagenomics efforts are opening new horizons in variation analysis. The past few years of structural genomics efforts have produced a crystal structure representative of almost every protein family. Microarray technologies allow simultaneous studies of expression of thousands of genes on a single chip. The improvements keep on coming – more information, higher resolution. Yet the unintended result of improved experimental techniques is a flood data that we have yet to make sense of. What does our genome encode? What about the soil metagenome? Can we decipher the mechanisms of disease? How are we different from other organisms? How are we different from each other? Bioinformatics attempts to answer all these questions... and give the statistical significance.

What this course IS:

This course is designed to introduce experimental biologists to bioinformatics concepts, principles, and techniques within the framework of basic shell scripting and web-based databases/tools. Prior to starting class, students are expected to know how to work in a command-line environment and have a basic understanding of programming/scripting. The course includes a brief introduction to working with UNIX/LINUX systems, writing Python scripts, and automating/using existing applications for the analysis of large datasets. All work will be done in a live development environment; *i.e.* students will have access to the same computational resources used by dedicated bioinformatics labs on campus. By the end of this course, students will possess a sufficient bioinformatics skill set, including an informed vocabulary and knowledge of basic script development, for productive collaboration within a multi-disciplined research team.

What this course IS NOT:

This is NOT an applied methods course; rather, this class is aimed at *understanding of underlying algorithms*. We will NOT attempt to list all available tools for every project or teach you how to use them. Method selection, along with the corresponding cutoffs, thresholds, and settings, is specific to each and every research project. If you keep up with the class material you will understand the method underpinnings and be able to able to optimize your project choices on your own.

COURSE OBJECTIVES

1. Introduce students to the current bioinformatics algorithms/concepts and their implementations.
2. Introduce students to the basics of working in a Linux environment, GridEngine submissions for parallel computing, and Python scripting.
3. Teach students to cast a molecular biology problem as a bioinformatic problem, provide them with the skills necessary to independently select relevant tools, optimize their settings, and build pipelines to solve the set problem.
4. Prepare students for more advanced bioinformatics courses involving method development.
5. Teach students a sufficient bioinformatics skill set, including an informed vocabulary and knowledge of basic script development, for productive collaboration within a multi-disciplined research team.

REQUIRED TEXT

There is **NO REQUIRED TEXT** for the lab or lecture.

Suggested textbooks are: **Bioinformatics Algorithms: An Active Learning Approach, 2nd Ed. Vol. 1 and 2**, by Philipp Compeau and Pavel Pevzner. Publisher: Active Learning Publishers; 2nd edition (2015); ISBN-13: 978-0990374619 and 978-0990374626

Suggested Online resource at: <http://rosalind.info>

LECTURES AND LECTURE SLIDES

Lectures will be taught as a combination of PowerPoints with blackboard and discussions. Slides will be posted, but will contain only an outline of the work done in class. They are intended to help you reconstruct the work from class, but are not intended as a substitute for taking notes. Slides will sometimes be posted before class, but this is not guaranteed. Additionally, these are meant to be drafts, provided as a “heads up” for anyone interested to do some online reading prior to coming to class. Students are not expected to look at them before lecture, and it is possible that corrections will be made to these slides before the final version is posted.

GRADING

Coursework will be weighted as follows:

Class Participation	10%
Lab Homework/Quizzes	30%
Midterm	20%
Final	40%
Journal Club (graduate component only)	No Credit

Attendance / Class Participation

Regular, on-time, attendance is expected of all students. If you are going to miss a class, please inform the instructor ahead of time.

Lecture: Attendance is not required, but missed lectures will be counted against your grade for class participation (10% of the total). Consistent minor lateness interrupts class flow and will reduce the percentage for assigned for class participation as well. Since there is no textbook for this course, *attendance* is necessary for understanding of the material. Please note that you are responsible for all material covered in class whether it is present in lecture PowerPoints or not. If you intend to miss classes, find a friend who takes good notes. Note that the entire class consists of 13 inter-dependent lectures. Missing three or more lectures (a quarter of the class) suggests that the information presented in the course was not learned.

Further, class participation is necessary for understanding of the material – your final grade will depend on you asking questions and/or participating in class discussions. Please note that if you do not participate voluntarily, you will be called upon. Class participation grade has nothing to do with being correct – it will only reflect your willingness to work towards a solution for the posed problem.

Lab: Missing any number of labs without a valid (WRITTEN and DOCUMENTED explanation) will result in a FAILING GRADE for the entire class. Since time is short relative to typical lab classes, late attendance is also not acceptable. Important information and quizzes will be typically given at the beginning of class without a make-up option.

Homework / Quizzes

Completed homework assignments are due at the beginning of lab or lecture class one week from the date they are assigned, unless otherwise specified. Late submissions will NOT be accepted. Assignments containing scripts (written code) must run properly in the standard development environment. No submission, empty submissions, or “fake” submissions (i.e. scripts that are clearly not expected to do the assignment) will receive 0% grades. Properly commented scripts that produce errors/warnings and/or fail to provide the correct, formatted output will receive no more than 50% of the grade. That being said, your programs will not be expected to handle user-input errors (unless otherwise specified) and will not be tested for such.

Quizzes will be given at the discretion of the lab/lecture instructor. Quizzes **may be** announced, but **do not have to be**. Quizzes may be written, coding, or both. They may cover lab and/or lecture material, but they will always relate to current topics. We are not looking to “burn” students with Linux questions in week 10, though you should get perfect scores if such a quiz was given. A quiz may be given at any time during any class period - immediately before or after a lecture, during a class, etc. There will be no make-up quizzes.

Midterm/Final

The **midterm** will have a written portion (taken in-class) **and** a take-home programming assignment. It will be based on material covered in lecture AND lab. This should underscore the importance of keeping up with the material. You will have one week to complete the take-home project, including the time in regularly scheduled lab. Your TA will be available during lab-time to discuss assignment problems (NOT to help you solve them). **Late projects will NOT be accepted.**

The final may (but not necessarily will) have both an in-class and a take-home component. The **in-class portion of the final** will be a multi-tool workflow/pipeline exercise (very flexible in implementation, but necessarily well explained and documented), focusing on all techniques learned throughout class.

The **take-home portion of the final** will include designing and running a computational analysis of some biological data, using techniques learned in class. The results will need to be described in scientific article format; *i.e.* introduction and background, results, materials and methods, and discussion. You will have at least a week to complete the take-home portion. **Late projects will NOT be accepted.**

Journal Club (Graduate Component Only)

Graduate students in the class will be **required** to attend journal club meetings. The number of sessions will be adjusted depending on the number of people in the class. In the span of the semester you will be required to read, analyze, and present at least one bioinformatics paper of your choice. The presentations will not be graded, but without a presenting you will be assigned a FAILING grade in the course. Undergraduates are encouraged to attend the journal club, read the papers, and potentially present. Note, however, that this will NOT count as extra credit.

ACADEMIC HONESTY:

Academic honesty is an absolute requirement for students taking Bioinformatics. Dishonesty, in any form, will NOT be tolerated. This includes cheating on homework, quizzes, projects, as well as any form of plagiarism. Please note that working together on homework assignments and submitting identical work is NOT THE SAME; same goes for searching the web for solutions to problems, text for your project written components, and/or ready-made code. ***VERY IMPORTANT:*** We read (and write!!) papers and Wikipedia entries too and know where certain texts come from. It's easy to tell when you've copied a sentence or two. It is even easier to tell if script code was copied – please keep this in mind. ALL CHEATING WILL BE REPORTED. The Rutgers University Academic Integrity Policy can be found at: <http://academicintegrity.rutgers.edu/integrity.shtml>. Students contemplating cheating should consider the severe repercussions of getting caught.

Group work policy: In order to facilitate learning, students are encouraged to discuss homework problems amongst themselves. Copying a solution is not, however, the same as “discussing”. According to one colleague, Dr. Iddo Friedberg, a good rule of thumb is the “cup of coffee” rule. After discussing a problem, you should not take away any written record or notes of the discussion. Go have a cup of coffee, and read the front page of the newspaper. If you can still re-create the problem solution afterward from memory, then you have learned something, and are not simply copying.

GROUP WORK ON MIDTERM AND FINAL PROJECTS IS NOT ALLOWED.

CLASSROOM RULES OF CONDUCT

1. No checking email, IM'ing, Texting, looking or catching Pokemon, or talking to friends during class time. Phones must be off, or set to quiet. Repeat offenders will be asked to leave the classroom and downgraded in class participation.
2. Food and beverages are not permitted in the classroom or lab, whether opened or not.
3. Lab time is to be spent on lab work. Lab time is not free time. If you finish early, you may start on the associated homework assignment.
4. Again, please be on time.

YOUR IDEAS, EVALUATIONS, ETC.

In general, your ideas, comments, suggestions, questions, grade challenges, etc. are welcome. Your discretion in these matters is expected, however. No part of your grade will be based on anything other than your coursework and attendance.

SUGGESTIONS FOR SUCCESS

Make sure you stay on top of your homework assignments. Waiting until the last minute to complete an assignment will not work in this course.

TENTATIVE SCHEDULE (subject to change)

5-Sep	Intro to Bioinformatics	7-Sep	Intro to Linux
12-Sep	Gene Finding	14-Sep	Intro to Python
19-Sep	Pairwise sequence alignment, deriving BLOSUM	21-Sep	Python II / EMBOSS / BLAST
26-Sep	BLAST, affine gap costs, database searches	28-Sep	Python III / PSI BLAST
3-Oct	MSAs and domain families	5-Oct	AmiGO and String
10-Oct	Sequence signatures and motifs	12-Oct	InterPro and Pfam
17-Oct	Structural Bioinformatics	19-Oct	Python IV, Chimera
24-Oct	<i>Midterm in-class and take-home portion assigned (collected Oct 27th)</i>		
31-Oct	Structure/Phylogenomics	2-Nov	MAFFT and R
7-Nov	Phylo/Meta -genomics	9-Nov	MG-RAST and mi-faser
14-Nov	Gene expression and Microarrays	16-Nov	Microarray and Plink
21-Nov	LAB SCHEDULE (SNAP, Weka I)	23-Nov	Thanksgiving Break, no class
28-Nov	Variation and molecular level natural selection	30-Nov	STRING, Weka II;
5-Dec	Disease gene prioritization	7-Dec	LECTURE starting at 5:35: Precision Medicine (<i>Take-home portion of final assigned, if any</i>)
12-Dec	In-class Final (if any); NOTE: Lab Space, 3 hours required; starting 5:35pm	14-Dec	<i>Take home portion of finals collected (if any)</i>

Official Final Date (8:00-11:00pm)

19-Dec

NO FINAL IF WE CHOOSE AN EARLIER DATE