

## **Bioinformatics for Microbiology**

**SPRING SEMESTER 2023**

Theory

**Time and location:** Mondays, 9-11 AM. Building B

**Instructional Mode:** The mode of instruction for this course is face-to-face

**Professor:** Fakher Rahim, Assistant professor, Medical Biotechnology, Building B, third floor

**Course Description:** This course will provide a practical and fundamental introduction to sequence-based analysis focused on microbial systems. No prior knowledge of computational biology is required. Emphasis on gaining a basic understanding of the principles of both classical and newer algorithms useful for bioinformatics analysis. Students will spend a significant portion of the class on the computer learning a number of skills including, but not limited to, Unix command line, installation of bioinformatics programs (e.g. BLAST), databases, and introductory programming in Perl. Evaluation will include a midterm exam and a project geared towards solving a bioinformatics problem. Topics to be covered include: BLAST; RNA-seq analysis; transcriptional binding prediction; genome sequence assembly, analysis and annotation; and comparative genomics. Other topics may be covered, as time permits. This course requires that each student have access to a laptop that runs a Linux/Unix Operating System such as a Mac or a ChromeBook. PCs running a VM are also acceptable.

**Prerequisites:** This course is open to both graduate and undergraduate students with consent of the instructor. All undergraduates are expect to have taken one of MICROBIO, BIOCHEM, GENETICS, or GENETICS.

Learning At the conclusion of this course, both undergraduate and graduate students Outcomes: will gain the following skills and concepts:

- Students will gain familiarity with Unix/Linux-based platforms and how to interact with an operating system using command line
- Students will be familiar with basic sequence data formats and how to access publicly available datasets
- Students will be able to download and install sequence analysis programs locally on their own computers
- Students will conceptually understand key sequence analysis algorithms, including BLAST, genome assembly and annotation, RNA-seq analysis, and metagenomic analysis
- Students will gain familiarity with programming in the language python
- Students will be able to construct pipelines of programs that start with raw sequence data and build in more complex analysis tools.
- Students will be able to evaluate the outcomes of sequence data analysis and determine if an analysis is statistically relevant and robust.

In addition, graduate students in the course will also gain the following skills and concepts:

- Apply sequence data analysis to projects ongoing in their research labs.
- Learn to utilize advanced parameters in BLAST, genome assembly and annotation, RNA-seq analysis, and metagenomic analysis and further understand how to tailor these programs for comparative analyses.
- Code complex and advanced programs in python that not only facilitate pipeline construction, but also more in-depth parsing of tool output.
- Utilize bioinformatics tools to enable comparative genomics analysis that extend the standard use of those tools.
- Evaluate primary literature and determine what available tools are most appropriate for a specific problem in their field, as assessed by the term project.

**Grading:** The grade will be based on the following elements totaling 100% based on if you are an undergraduate or graduate student, as described below.

**Textbook:** There are NO required textbooks for this course. All material discussed in class and tested on exams will be provided to you on Canvas. Readings will include primary literature on relevant topics. A sample reading list is attached to the end of this syllabus.

**Midterm Exam:** The midterm exam will be administered halfway through the course and will be worth 30% of the final grade, based on if you are an undergraduate or graduate student, respectively. The exam itself will be a practicum that will be administered in class and will cover all material up to the midterm exam date. The exam will be open book/computer.