**Genome Informatics I (56:121:552:01)**

Instructor: Professor Andrey Grigoriev

Office: Rm 205, Science Building

Phone: 856 225 2960

Email: andrey.grigoriev@rutgers.edu

Office hours: by arrangement

Preferred communication: by email

This course teaches common principles, concepts and methodologies for genome-scale data analysis driven by biological questions. It explains the application of typical analytical approaches to such data and the reasoning to infer biological meaning from the results.

This is a graduate course that usually gathers students with very different backgrounds. It consists of lectures, intense practical homework, active joint discussions of topics and journal club-like student presentations of recent scientific literature (individually and in teams), as well as analysis/programming projects. Many of these activities are assigned individually based on the student’s background in biology, math and programming (which are assessed in the first weeks during student presentations of their own prior research experiences). Advanced undergraduate students may be allowed to take this course at the sole discretion of the instructor.

Typical Schedule of Topics

Week 1, 2 and 3 (may vary depending on the number of students and their presentations): Introduction, genes and genomes, scientific disciplines in genomics. Sequences, alignments, motifs, information content. May include students’ brief presentations of their own prior research experiences.

Weeks 4 and 5: Concepts and practices in genome mapping and sequencing.

Week 6 and 7: Sequence analysis and links between sequence and genome features.

Week 8 and 9: Generation of genome-scale data beyond sequencing (expression, interactions, etc) for functional analysis.

Week 10 and 11: Integration of diverse genome-scale datasets.

Weeks 12 and 13: Journal club and projects.

Week 14: Programming project summaries/demonstrations.

Homework will include practical exercises and quizzes on using genomic resources, understanding their meaning, value and limitations.

Learning goals

Students will develop a strong understanding of common principles, concepts and methodologies for genome-scale data analysis driven by biological questions. By the end of the course, students will be exposed to typical approaches for broad classes of computational genomics problems (including some common numeric, statistical, graph-theoretic and data integration approaches). They will learn how to reason logically about specific properties of genome-scale datasets and related problems that lead to the development of correct and efficient analytical approaches.

Attendance, Grading and Exams

Attendance required. Points will accumulate from all the above activities, according to their score, which will be available in Canvas. No exam.

Grade boundaries

Graduate students: A: >93%; B+: >87%; B: >80%; C+: >73%; C: >66%

Undergraduate students: A: >92%; B+: >84%; B: >76%; C+: >68%; C: >60%

Other

For student-related policies, regulations and services at Rutgers University, please see

https://policies.rutgers.edu/view-policies/academic-%E2%80%93-section-10#2 and #3