

CMPE 549

Bioinformatics

Fall 2022

This course will provide an introduction to bioinformatics and the associated main algorithms.

Course Objectives:

- Understand the fundamentals of the field of bioinformatics.
- Learn the main bioinformatics problems and algorithms proposed to solve them.
- Design and apply computational methods to biological data.
- Read/present/review papers on state-of-the-art research in bioinformatics.
- Prepare for original research in bioinformatics.

Prerequisites: Medium level programming skills in the Python programming language, background on data structures and algorithms.

Course Format:

The lectures will take place on Thursdays between 12:00-15:00 at BM B3 (in-class). You are encouraged to attend and actively participate in the lectures.

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Course Web Site:

We will use the Moodle Course Management System for lecture notes, announcements, grades, as well as assignment and project submissions: <http://moodle.boun.edu.tr/>. You are expected to check the course web site for announcements regularly.

Textbook (Optional):

- P. Compeau, P. Pevzner. Bioinformatics Algorithms: An Active Learning Approach, 3rd Edition. 2018. (Volume 1 and 2 of the Second Edition is also fine.)
- Supplementary website: <http://bioinformaticsalgorithms.com>.
- First five chapters of the book and complimentary video lectures for all chapters from the textbook authors are available in the supplementary website, free of charge.

Tentative List of Topics:

- Review of relevant background material from molecular biology
- Dynamic Programming and Sequence Alignment
- Heuristic Sequence Similarity Search Algorithms (FASTA and BLAST)
- Phylogenetic Trees
- Gene expression analysis, Clustering and Classification Algorithms
- Graph algorithms and genome assembly
- Motif finding and Randomized Algorithms
- Combinatorial Pattern Matching and Suffix Trees
- Text mining for biology

Course Requirements

Programming assignments: There will be 2-3 programming assignments, involving intermediate-level programming in Python where you will implement and test some of the techniques that we cover in class. If you are unsure whether your existing proficiency will be sufficient, we will be discussing this more concretely in the first lecture; you might participate in the first lecture and then decide. The assignments will be completed individually.

Tool/Resource presentation: Presentation teams will consist of 1-2 *people* (you can form your own teams, or ask us to assign you to a team). Each team will give a 20min talk about a certain practical aspect of bioinformatics. For example, you can describe an available commonly used tool (e.g., Cytoscape for network analysis), a common pipeline (using the available tools) in bioinformatics to solve a certain problem (e.g., pipeline for processing sequence data and identifying mutations), a commonly used library (e.g., BioConductor, BioPython), resources for a certain type of data or problem (e.g. databases for protein sequence and structure) and how to use these resources to obtain the data, the format of the data, etc.

Term Project: The project teams will consist of 2-3 *people* (these teams do *not* have to be the same with the teams in the tool/resource presentation). Each team will choose a project topic by selecting a recent scientific paper from a Bioinformatics conference or journal. The project will involve addressing the limitations of the existing work, and extending or replicating it in some way. The teams will give short project progress and project final presentations in front of the class describing the addressed problem, the existing work and its limitations, the proposed/developed methods in the scope of the project, the results obtained, as well as the limitations and future work.

Exam: There will be one in-class exam.

Grading:

- Assignments: 30%
- Tool/Resource presentation: 15%
- Exam: 20%
- Term Project: 35%