cng465-introduction-to-bioinformatics-syllabus-spring-2023-2024-20240219

March 5, 2024

1 CNG 465 – Introduction to Bioinformatics – Syllabus

Reference: https://catalog.metu.edu.tr/course.php?course_code=3550465

Course Code	**3550465**
METU Credit (theory-lab hours/week)	**3(3-0)**
ECTS Credit	**6.0**
Language of Instruction	**English**
Level of Study	**Undergraduate**
Prerequisite	—

1.1 Course Description (*tentative*)

This course covers computational techniques for mining the large amount of information produced by recent advances in biology, such as genome sequencing and microarray technologies. The main topics of the course include DNA and protein sequence alignment, phylogenetic trees, protein structure prediction, motif finding, microarray data analysis, and gene/protein networks.

The course will use the Python programming language and Python-based software libraries such as Pandas and BioPython. The course will programming intensive.

Interactive in-class discussions, homework, and project assignments are aimed to provide a solid basis for the student's grasp of the course material.

The student is expected to learn practical aspects of the course with self-study.

NOTE that additional topics will/may be added as the course progresses.

1.2 Learning Outcomes

On successful completion of this course, a student will

- Understand main computational problems in life sciences
- Understand the main terminology used in bioinformatics
- Apply statistical analyses on results of algorithms
- Understand key methods and tools used in bioinformatics
- Design and implement a computational solution to a molecular biology problem

1.3   Evaluation *(tentative)*

Type of Work	Percentage
Midterm Exam	**20%**
Final Exam	**30%**
Homework	**20%**
Projects/Presentations	**30%**

1.4   Policies

- Active class participation is key to hold discussions and learn from interactions with others

- The instructor will take attendance, but lack of attendance will not be penalized.

- Late assignment submissions will not be accepted.

1.5   Students with Disabilities

Students with disabilities should consult with the course instructor, ODTU Disability Support Office, and or the student advisor for students with disabilities for the department:

> http://engelsiz.metu.edu.tr/en/advisor-students-disabilities

For more information, please visit the Disability Support Office website:

> https://engelsiz.metu.edu.tr/en/

1.6   Academic Honesty

Please keep in mind that the METU Academic Code of Ethics applies at times:

> https://ncc.metu.edu.tr/res/academic-code-of-ethics

The instructor reserves the right to take any appropriate action according to University rules and regulations whenever a failure of compliance with this code occurs.

2   Textbook and Course Material

- Several textbooks and online materials will be used throughout the course. All such material will be provided on the course website

- Additional material will also be provided including websites, scientific papers, articles, or books

- See the ODTUClass page for the course for all lecture materials

3   Course Content (tentative)

- Introduction
- Cellular and Molecular Biology Fundamentals
- Basic Processing of Biological Sequences

- Finding Patterns in Sequences
- Pairwise Sequence Alignment
- Searching Similar Sequences in Databases
- Multiple Sequence Alignment
- Phylogenetic Analysis
- Motif Discovery Algorithms

NOTE: As time allows, other topics will be added.