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Course Description

This course will introduce the principles of bioinformatics analysis of genes and proteins and provide a practical introduction to a variety of bioinformatics resources and tools. Course consist of lectures, tutorials, hands-on exercises, quizzes and a term project. This is an introductory course. You should have a vested interest in learning bioinformatics. A basic understanding of molecular biology concepts is required but no computer programming experience is required. As a reference, expect to allocate an average of 10 (ten) hours a week for working on this course.

To navigate this course successfully, you will need to:

- be familiar with reading scientific publications.
- feel comfortable with navigating the web, communicating in different virtual modalities, especially using Canvas and Zoom.
- familiarize with recording and posting a video in Canvas environment, as you may be asked to give a live or pre-recorded presentations to the instructors and/or a group.

Requirements

Completion of [Bioinformatics Program Orientation](#)

Completion of [Bioinformatics block](#)

Course Objectives

- To introduce the basic concepts of bioinformatics, including data retrieval and nucleic acid and protein sequence analysis.

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- To provide an understanding of web accessible bioinformatics resources, including the underlying computational approaches, how data is processed and how to interpret results. Some of the concepts, databases and tools include: literature databases, nucleotide and protein databases, sequence alignment and homology search, phylogenetic analysis, structure prediction and genome and protein annotation.
- To provide hands-on activities for real-world biological applications to bioinformatics approaches learned throughout the course.

Course instructor and class information

Instructor: Dr. Cecilia Arighi

Teaching assistant: Ms. Neha Sindhu

All communication with instructors should be done via Canvas email.

[Cyber Cafe](#) Course Question Forum. This is a discussion session for students.

Class meeting date/location:

This syllabus covers both hybrid (BINF644-010) and asynchronous (BINF644-194) course information. All modules and activities are accessible online and should be reviewed independently by the students.

For BINF644-10, We will meet on Wednesdays, **starting on February 8**, 11:15am-12.05pm in Sharp Lab, **room SHL 118**.

[Sharp Lab \(SHL\): 104 The Green](#)

Attendance is required.

Students from BINF644-194 are welcome to attend in person or via zoom (see Zoom info below).

Class recordings can be accessed in "My Media"

Course Content

Module Outline	
Module	Topic
Module 1	<p>Bio of Bioinformatics</p> <ul style="list-style-type: none"> • What is Bioinformatics • History of Bioinformatics • From Genome to Proteome • Bioinformatics applications
Module 2	<p>Bioinformatics Data and Biocuration</p> <ul style="list-style-type: none"> • Database elements and types • Biocuration • Data Management
Module 3	<p>Gene/Protein Knowledgebases</p> <ul style="list-style-type: none"> • NCBI Gene • Uniprot • Hands on exercises
Module 4	<p>Protein Diversity</p> <ul style="list-style-type: none"> • Alternative Splicing • Protein processing • Post-translational modifications • Proteoforms • Hands on exercises

Module 5	Bioinformatics Fundamentals <ul style="list-style-type: none">• Molecular Evolution: Domain, Structure and Function• Protein Sequence Analysis• Protein Structure Analysis and prediction• Hands on exercises
Module 6	Bioinformatics Fundamentals: Methods <ul style="list-style-type: none">• Pair-wise sequence alignment• Multiple sequence alignment• Sequence search
Module 7	Biomedical Ontologies <ul style="list-style-type: none">• What are ontologies?• Why are ontologies needed in biology/biomedical domain?• Gene Ontology• Protein Ontology• Hands on exercises• Semantic web and bioinformatics (Dr. Chen)
Module 8	Introduction to Final Project

Module 9	Biomedical Text Mining <ul style="list-style-type: none">• Source of free-text biomedical data• What is Text Mining?• Methods in text processing• Application• Hands on exercises
Module 10	Genome Annotation <ul style="list-style-type: none">• Gene organization and methods for gene finding• Genome annotation pipelines• Genome Browsers• Comparative Genomics
Module 11	Protein Functional Annotation <ul style="list-style-type: none">• Elements of an Annotation• Sequence and structure analyses for functional annotation• Automatic annotation• Hands on exercises
Module 12	Phylogenetic Trees <ul style="list-style-type: none">• Rooted vs unrooted trees• Parsimonious approaches: Fitch algorithm• Distance based approaches: Neighbor-Joining algorithm• Probabilistic approaches

Module 13	From Genotype to Phenotype and Beyond <ul style="list-style-type: none">• Genomic variation and their different types• Understand the difference between genotype and phenotype• Functional characterization of variants affecting protein coding genes
Module 14	Beyond protein coding genes <ul style="list-style-type: none">• non-coding RNAs• Complexes• Pathways
Module 15	Artificial intelligence/Machine learning in Bioinformatics <ul style="list-style-type: none">• What are AI and ML?• Main concepts• Applications in bioinformatics

Grade Scheme

Below is the make-up of your grade. The course contains modules that fall into two sections: application and methods. The former is about using resources and methods in practical setting, whereas the latter focuses on the underlying algorithms behind the methods.

Participation: 5 % of the grade

Application Assignments: 30 % of the grade

Methods Assignments: 30 % of the grade

Final Project : 35 % of the grade

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Letter grades will be assigned and recorded on student transcripts. The [university catalog](#) has detailed information on standard grading definitions and the impact of each grade on the calculation of the student's grade point average.

Policy regarding use of AI tools for assignments and projects

Use only with prior permission

Students are allowed to use advanced automated tools (artificial intelligence or machine learning tools such as ChatGPT or Dall-E 2) on assignments in this course **if instructor permission is obtained in advance or instructors explicitly indicates that these tools can be used**. Unless given permission to use those tools, each student is expected to complete each assignment without substantive assistance from others, including automated tools. The permission is needed per assignment.

If permission is granted to use advanced automated tools (artificial intelligence or machine learning tools such as ChatGPT or Dall-E 2), they must be properly documented and credited.

Any text generated using ChatGPT-3 should include a citation such as: "Chat-GPT-3. (YYYY, Month DD of query). "Text of your query." Generated using OpenAI. <https://chat.openai.com/>"

Students should also provide a copy of the raw output of the tool.

Material generated using other tools should follow a similar citation convention and directions.

Copyright information

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Academic policies

Each tab provides access to UD policies for your review:

- Academic Integrity
- Harassment and Discrimination
- Faculty Statement on Disclosures of Instances of Sexual Misconduct
- Accommodations for Students with Disabilities
- Non-discrimination
- General Academic Support
- Student Support