

The Hebrew University of Jerusalem

Syllabus

Introduction to Bioinformatics - 94510

Last update 19-10-2022

<u>HU Credits:</u> 5

Degree/Cycle: 1st degree (Bachelor)

Responsible Department: Bio-Medical Sciences

<u>Academic year:</u> 0

<u>Semester:</u> 1st Semester

<u>Teaching Languages:</u> Hebrew

<u>Campus:</u> Ein Karem

Course/Module Coordinator: Dr. Yotam Drier

Coordinator Email: yotam.drier@mail.huji.ac.il

<u>Coordinator Office Hours:</u> by appointment via email

Teaching Staff:

Dr. Yotam Drier, Mr. Elad Sharon, Ms. Rachel Rapoport, Ms. Shira Fisher

Course/Module description:

The course focuses on understanding the information encoded in nucleic acids and protein sequences, using bioinformatic approaches. We will learn basic and advanced approaches for computational sequence analysis, such as sequence alignment, identification of common motifs, protein structure prediction, characterization of protein families and analysis of sequencing based data. These approaches will be applied to specific biological questions, such as characterization of new species and cancer research. The lectures will provide the basis for these approaches while demonstrating their application to specific biological questions. Practicing these approaches will be carried out in the accompanying exercise class. The course advances gradually from basic sequence comparison approaches to advanced analysis of genomic data.

Course/Module aims:

The genomic revolution and high throughput technologies developed following it have turned bioinformatics to be an integral part of biological research. Modern biological studies produce vast amounts of data that necessitate computational analysis by appropriate algorithms and tools. Likewise, there is a vast amount of biological information of various types in electronic databases, which requires computational tools for its processing and interpretation. Knowledge of computational approaches for analyzing biological data is essential in modern biological research. The aim of the course is to introduce these computational approaches, while demonstrating their application to specific biological questions. The lecture will present the basis of these approaches, and special attention will be paid to critical assessment of the results, and understanding the challenges of developing and applying bioinformatic methods. The practicing of these approaches will be done in the accompanying exercise class. The main aim of the course is to enable the students to exploit the relevant computational tools and to integrate them skillfully in their biological research.

Learning outcomes - On successful completion of this module, students should be able to:

To apply suitable bioinformatic tools to the biological question they study and to skillfully interpret the results. Specifically, the students will be able to extract data from various data sources (genomic, epigenomic, gene expression, etc.); to annotate protein sequences, compare and align DNA and protein sequences; to identify gene that are altered in a given cancer type, identifying cancer subtypes and compare them, link genomic alterations and clinical attributes, etc.; analyze results of high throughput experiments (such as RNA-seq and ChIP-seq); to identify common motifs in DNA and protein sequences, and find these motifs in other sequences; to characterize transcription factor binding sites and predict gene targets; to compare gene expression profiles between two conditions; to find functional enrichment in a set of genes; to analyze evolutionary conservation between proteins, characterize protein families, and protein predict the structure; and more.

Attendance requirements(%):

Attendance required in project presentation lessons. Mandatory submission of class exercises (not graded).

Teaching arrangement and method of instruction: Lecture and exercises

Course/Module Content:

High throughput sequencing, genomic databases and the "omics" revolution. Sequence assembly, alignment, and BLAST. Analysing gene expression and splicing with RNA-seq.

Characterizing the epigenetic landscape.

Using bioinformatic analysis and databases for cancer research and precision medicine.

Protein function and domains, protein structure prediction. Molecular evolution and conservation.

<u>Required Reading:</u> None

<u>Additional Reading Material:</u> Bioinformatics and Functional Genomics / Jonathan Pevsner

<u>Course/Module evaluation:</u> End of year written/oral examination 0 % Presentation 10 % Participation in Tutorials 10 % Project work 0 % Assignments 40 % Reports 0 % Research project 40 % Ouizzes 0 % Other 0 %

Additional information: