The Hebrew University of Jerusalem

Syllabus

Introduction to genomics and bioinformatics - 71255

Last update 23-08-2021

<u>*HU Credits:*</u> *3*

<u>*Degree/Cycle:*</u> *1st degree (Bachelor)*

<u>*Responsible Department:*</u> *agro informatics*

<u>*Academic year:*</u> *0*

<u>*Semester:*</u> *2nd Semester*

<u>*Teaching Languages:*</u> *Hebrew*

<u>*Campus:*</u> *Rehovot*

<u>*Course/Module Coordinator:*</u> *Asaf Levy*

<u>*Coordinator Email:*</u> alevy@mail.huji.ac.il

<u>*Coordinator Office Hours:*</u>

<u>*Teaching Staff:*</u>

Dr. Assaf Levy,
Mr. alexander geller

Course/Module description:
The students will be exposed to the genomics research field: the study of the genomics of different organisms (eukaryotes and prokaryotes) from structure, organization, function, and evolution context. The students will learn and will gain experience in modern techniques to study genomes, gene function and expression.

Course/Module aims:
Gaining knowledge and experience in the fields of comparative genomics, functional genomics, metagenomics, transcriptomics, and bioinformatics.

Learning outcomes - On successful completion of this module, students should be able to:
The students will familiarize with terms from the genomics field, they will get to know and gain experience with methods and databases in the field, they will read a scientific paper in the field. They will design, implement, and present a research project based on what was learned in the course. They will gain experience in Python programming.

Attendance requirements(%):
80%

Teaching arrangement and method of instruction: Frontal teaching. The course might be recorded to allow access from other HUJI campuses.

Course/Module Content:
1. Background. Why is genomics important? The technological progress in the field.
2. Structure and function of a eukaryotic genome. The human genome project.
3. Structure and function of a prokaryotic genome.
4. Comparative genomics
5. Functional genomics
6. Metagenomics and single cell genomics
7. Basic computational methods in microbial ecology.
8. Transcriptomics, differential gene expression, functional enrichment
9. Reading, writing, and editing genomes.
10. Analysis of non-coding DNA (RNA genes, and regulatory sequences)
11. Phylogenomics

12. Methods for comparing and clustering sequences. Methods to detect mutations and genomics alterations.
13. Epigenomics.

<u>Required Reading:</u>
 not required

 <u>Additional Reading Material:</u>
  Will be given during the course.

 <u>Course/Module evaluation:</u>
  End of year written/oral examination 0 %
  Presentation 0 %
  Participation in Tutorials 0 %
  Project work 0 %
  Assignments 40 %
  Reports 0 %
  Research project 60 %
  Quizzes 0 %
  Other 0 %

<u>Additional information:</u>
  Important requirements: programming in Python, a genetics course.