The Hebrew University of Jerusalem

Syllabus

ADVANCED ANALYSIS OF HIGH-THROUGHPUT EXPERIMENTS - 71216

Last update 06-09-2018

HU Credits: *2*

Degree/Cycle: *1st degree (Bachelor)*

Responsible Department: *Plant Sciences in Agriculture -Special in Biotec*

Academic year: *0*

Semester: *2nd Semester*

Teaching Languages: *Hebrew*

Campus: *Rehovot*

Course/Module Coordinator: *Inbar Plaschkes*

Coordinator Email: *inbar.p@mail.huji.ac.il*

Coordinator Office Hours: *By Appointment*

Teaching Staff:
Ms.

Course/Module description:

A significant portion of the new technologies in experimental biology are "high-throughput" i.e. produce huge amount of raw data as an output. This data is further processed using diverse inventory of software to produce biological insights and a large part of the data is available online. The course "Advanced Analyses" introduces these technologies, software tools used for analyzing their results and relevant databases. The course combines frontal lectures and hands-on sessions that will provide the students with a basic knowledge of experimental design and data analyses using the systems biology approach.

Course/Module aims:

1. *Introduction of the recent technologies for high-throughput experiments.*
2. *For each technology, introduction of software tools for data analysis, principles of analysis and relevant databases.*
3. *Introduction of the biological insights that are deduced from high-throughput experiments and their contribution to a comprehensive understanding of a biological system.*

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

1. *Knowledge of key technologies for high-throughput experiments, their advantages and limitations, the principle methods of data analysis and the biological insights that is produced.*
2. *Understanding the main principles in the systems biology approaches.*

Attendance requirements(%):
100

Teaching arrangement and method of instruction: frontal lectures, hands on sessions and home assignments

Course/Module Content:

1. *Stand alone BLAST installation and basic usage*

2. Introduction to NGS
3. Running bioinformatics tools using LINUX command line environment
4. RNA-seq primary analysis
5. Advanced analysis of gene lists
6. Resequencing and variant calling
7. De-Novo sequence assembly
8.Introduction to Networks approach
9. Bioinformatics public databases
10. Introduction to new sequencing technologies – student's 15 min. presentations

Required Reading:
None

Additional Reading Material:
A Primer of Genome Science/Gibson & Muse

Introduction to Genomics
Arthur Lesk

Course/Module evaluation:
End of year written/oral examination 0 %
Presentation 30 %
Participation in Tutorials 30 %
Project work 0 %
Assignments 40 %
Reports 0 %
Research project 0 %
Quizzes 0 %
Other 0 %

Additional information:
Students are advised to take before or at the same time, course 71437 "Introduction to Bioinformatics".
Limited to 20 students.