האוניברסיטה העברית בירושלים THE HEBREW UNIVERSITY OF JERUSALEM



The Hebrew University of Jerusalem

Syllabus

High Throughput Biology - Methods and Bioinformatic Analysis of the Data - 94709

Last update 22-03-2020

HU Credits: 2

Degree/Cycle: 2nd degree (Master)

Responsible Department: Biotechnology

Academic year: 0

Semester: 2nd Semester

Teaching Languages: Hebrew

Campus: Rehovot

Course/Module Coordinator: Dr. Ido Carmel

Coordinator Email: ido.carmel@mail.huji.ac.il

Coordinator Office Hours: By Appointment

<u>Teaching Staff:</u> Dr. Ido Carmel

Course/Module description:

A significant portion of the new technologies in experimental biology are "highthroughput" 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 introduce these technologies, software tools used for analyzing their results and relevant databases. The course combines frontal lectures and hands-on sessions .

Students will present their research questions and a discussion will be held regards the appropriate methods to address these questions.

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:

To list the key technologies for high-throughput experiments, their advantages and limitations, the principle methods of data analysis and the biological insights that are produced.

To choose the method/technology that best suited to answer a specific biological question and at the same time, adjust the biological question to match the limitations of the chosen method.

<u>Attendance requirements(%):</u> 100

Teaching arrangement and method of instruction: Frontal Lectures and Practical Sessions

Course/Module Content:

- The Systems Biology Era
- Introduction to Genomics
- UCSC Genome Browser
- Introduction to Microarrays
- Next Generation Sequencing (NGS)
- The Galaxy suite of bioinformatics software
- SNP genotyping
- Introduction to Proteomics
- Introduction to Biological Networks

<u>Required Reading:</u> To be announced

<u>Additional Reading Material:</u> A primer to genome science/ Gibson & Muse Third Edition, (2009)

Introduction to Genomics/ Arthur Lesk

<u>Course/Module evaluation:</u> End of year written/oral examination 0 % Presentation 45 % Participation in Tutorials 5 % Project work 0 % Assignments 50 % Reports 0 % Research project 0 % Quizzes 0 % Other 0 %

Additional information:

A previous study of "Introduction to bioinformatics" is recommended Limited to 20 students