The Hebrew University of Jerusalem

Syllabus

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

Last update 22-03-2020

<u>HU Credits:</u> 2

<u>Degree/Cycle:</u> 2nd degree (Master)

<u>Responsible Department:</u> Biotechnology

<u>Academic year:</u> 0

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

<u>Teaching Languages:</u> Hebrew

<u>Campus:</u> Rehovot

<u>Course/Module Coordinator:</u> Dr. Ido Carmel

<u>Coordinator Email:</u> ido.carmel@mail.huji.ac.il

<u>Coordinator Office Hours:</u> By Appointment

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

<u>*Course/Module description:*</u>
  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 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.

<u>*Course/Module aims:*</u>
  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.

<u>*Learning outcomes - On successful completion of this module, students should be able to:*</u>
  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_

Required Reading:
 To be announced

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

Introduction to Genomics/ Arthur Lesk

 Course/Module evaluation:
 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