



## *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](mailto:ido.carmel@mail.huji.ac.il)*

*Coordinator Office Hours: By Appointment*

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Teaching Staff:

Dr. Ido Carmel

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 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.

Attendance requirements(%):

100

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

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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*