The Hebrew University of Jerusalem

Syllabus

Computer Analysis of Genomic Data - 81808

Last update 06-10-2021

HU Credits: *6*

Degree/Cycle: *2nd degree (Master)*

Responsible Department: *Bio-Medical Sciences*

Academic year: *0*

Semester: *2nd Semester*

Teaching Languages: *English and Hebrew*

Campus: *Ein Karem*

Course/Module Coordinator: *Itamar Simon*

Coordinator Email: *itamarsi@ekmd.huji.ac.il*

Coordinator Office Hours: *No office hours, the student can call the teacher*

Teaching Staff:

Prof Ben Berman,
Dr. Yotam Drier,
Prof Itamar Simon

Course/Module description:

During the course we will learn to analyze deep sequencing data of RNA and DNA with R programing. We will learn to filter good quality data, to map to the desired genome, preform statistical analysis and provide annotations to the obtained genes. In addition we will learn to use basic commands in Linux and learn to use important tools through the terminal.

Course/Module aims:

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

- *Analyze RNA-seq data*
- *Analyze ChIP-seq data*
- *Analyze ATAC-seq data*
- *Analize Bisulfite sequencing (BS-Seq) data.*
- *Analyze HiC data*
- *Analyze genomic data using R.*
- *Work on a Linux cluster*
- *Retrieve data from huge datasets (like ENCODE) and integrate it with their results.*

Attendance requirements(%):

Mendatory attendance

Teaching arrangement and method of instruction: Computer lab hands on teaching

Course/Module Content:

1.Using the terminal
2.Deep sequencing: Fastqc, data filtering ,cutadapt ,Mapping and igv
3.ChIP seq analysis
4. Introduction to R and Markdown
5.R: graphs and Statistical analysis
6.htseq-count and DEseq2
7.Clustering

8.GO analysis – DAVID & annotation in R
9. ChIP-seq continued: IDR peak calling, Q/C metrics, aggregation plots
10. ChIP-seq cell type atlases: accessing large datasets, cell-type specificity, plotting multi-sample ChIP-seq data
11. Interpreting ChIP-seq peaks: TF binding motifs, linking to peaks to gene targets, GREAT
12. Associating ChIP-seq peaks with RNA-seq genes based on tissue-specificity
13. High throughput bisulfite sequencing (BS-seq) analysis.
14. HiC data analysis

Required Reading:

No

Additional Reading Material:

Course/Module evaluation:

End of year written/oral examination 0 %
Presentation 0 %
Participation in Tutorials 0 %
Project work 20 %
Assignments 10 %
Reports 0 %
Research project 70 %
Quizzes 0 %
Other 0 %

Additional information:

Mendatory exrecises
Prerequisite - a basic R programing course.