TEL AVIV UNIVERSITY אוניברסיטת תל אביב

סילבוס מפורט

With Next Generation Sequencing (NGS) costs constantly dropping, genomic data is becoming more and more available and are now commonly used across multiple scientific disciplines. Nevertheless, the analysis of such data is a non-trivial task, requiring computational skills and knowledge of the relevant theory.

The course is an introductory, hands-on computational lab covering a range of topics related to NGS and genomics data processing and analysis. The course will include both theoretical and hands-on modules. At the end of the course students will be able to perform basic NGS data analysis tasks relevant to their field of research.

The first part of the course will focus on basic topics related to NGS data, such as sequencing data generation and pre-processing, NGS reads mapping to a reference genome, variant-calling, genome assembly, transcriptome assembly, structural and functional gene annotation, gene expression analysis based on RNA-Seq data. In the second part of the course, some advanced topics will be discussed including 3rd generation sequencing and other.

In each session, students will practice the various methods by following structured exercises entailing running relevant software and analysing the results.

Grade: 70% - final project, 30% - homework assignments.

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שם הקורס

מעבדה חישובית - ניתוח נתוני ריצוף עמוק בעידן הגנומי

מרצה

ליאור גליק

סמסטר

ב

דרישות הקורס

Homework assignments + Final project

הרכב הציון הסופי

70% Final project, 30% homework assignments

מבנה הקורס

תאריך / מס' שיעור	נושא השיעור ותכני השיעור (מטלות, רשימת קריאה, משימות וכיו"ב)
10.10.21	Introduction to NGS – sequencing technologies, basic terminology: reads, paired-end sequencing, coverage, depth, sequencing errors.
17.10.21	Linux operating system – file system navigation, working with text files, CLI software, piping and redirection
24.10.21	NGS data QA and preprocessing - Fasta and Fastq formats, Phred scores, various QA metrics, quality trimming, merging PE reads, deduplication
31.10.21	Sequence mapping I – the BLAST algorithm and CLI
7.11.21	Sequence mapping II – short read mapping, working with SAM/BAM files
14.11.21	Variant calling – short and structural variant calling, working with VCF/BCF files
21.11.21	Genome assembly – de novo assembly from short reads, De-Bruijn graph assembly, assembly quality measures
28.11.21	Gene and variant annotation – structural and functional annotation of genes and prediction of variant effects, the GFF format
12.12.21	Transcriptomics I – RNA-seq data, spliced read mapping, read counting and biases
19.12.21	R programming for genomics – R basics, vectors, data frames, plotting, loading genomic data, Bioconductor
26.12.21	Transcriptomics II – differential gene expression analysis
2.1.22	3rd generation sequencing – long read technologies (PacBio, ONT), linked reads (10X genomics), detecting structural variants with long reads
9.1.22	TBD – genomics DBs / phylogenomics / guest lecture

קריאת חובה

קריאת רשות

הערות

Each lesson (except the first and last) will consist of a lecture and a hands-on exercise session in which students will analyze genomic and NGS data (mostly eukaryotic) using a variety of software tools.
In the final project, students will apply everything they learned to answer a scientific question.

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No prior technical or programming experience is required, but basic biological knowledge is expected.