TEL AVIV UNIVERSITY אוניברסיטת תל אביב

סילבוס

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	
Weekly 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)
23.10.22	Introduction to NGS – sequencing technologies, basic terminology: reads, paired-end sequencing, coverage, depth, sequencing errors.
30.10.22	Linux operating system – file system navigation, working with text files, CLI software, piping and redirection
6.11.22	NGS data QA and preprocessing - Fasta and Fastq formats, Phred scores, various QA metrics, quality trimming, merging PE reads, deduplication
13.11.22	Sequence mapping I – the BLAST algorithm and CLI
20.11.22	Sequence mapping II – short read mapping, working with SAM/BAM files
27.11.22	Variant calling – short and structural variant calling, working with VCF/BCF files
4.12.22	Genome assembly – de novo assembly from short reads, De-Bruijn graph assembly, assembly quality measures
11.12.22	Gene annotation and genomic DBs – BED and GFF formats, Bedtools, structural and functional annotation of genes, the SRA/ENA data base, Ensembl
18.12.22	Transcriptomics I – RNA-seq data, spliced read mapping, read counting and biases
1.1.23	R programming for genomics – R basics, vectors, data frames, plotting, loading genomic data, Bioconductor
8.1.23	Transcriptomics II – differential gene expression analysis
15.1.23	3rd generation sequencing – long read technologies (PacBio, ONT), linked reads (10X genomics), detecting structural variants with long reads
22.1.23	Course wrap-up + guest lecture
קריאת חובה	
קריאת רשות	

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