TEL AVIV UNIVERSITY אוניברסיטת תל אביב

סילבוס

Course Description
This course offers an introduction to Next-Generation Sequencing (NGS) and genomics data analysis, tailored for students with biology background and eagerness to learn basic bioinformatics skills for genomic analysis. Through a blend of theoretical and hands-on assignments, students will gain the computational skills required to analyze NGS data relevant to their research.
No computational background is required.

Course Objectives
By the end of this course, students will be able to:

- Basic understanding and navigation of Linux OS
- Generate and preprocess sequencing data
- Map NGS reads to a reference genome
- Perform variant calling and genome assembly
- Conduct transcriptome assembly
- Annotate genes both structurally and functionally
- Analyze gene expression of RNA-Seq data
- Will be given background more advanced 3rd generation sequencing techniques

Course Structure
Part I:

- Foundations of NGS Data Analysis
- Basic Linux skills and navigation
- Sequencing Data Generation and Preprocessing

Part II:

- NGS Reads Mapping to a Reference Genome
- Variant Calling and Genome Assembly
- Transcriptome Assembly
- Structural and Functional Gene Annotation
- RNA-Seq-based Gene Expression Analysis

Part II:

- Advanced Topics
- 3rd Generation Sequencing

Course Format
In each session, students will engage in structured exercises that involve running relevant software and interpreting the results.

Grading Scheme
70% Final Project
30% Homework Assignments

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מעבדה חישובית - ניתוח נתוני ריצוף עמוק בעידן הגנומי	
מרצה	
הדס וולקוב	
סמסטר	
א	
דרישות הקורס	
Weekly homework assignments + Final project	
הרכב הציון הסופי	
70% Final project, 30% homework assignments	
מבנה הקורס	
מס' שיעור	נושא השיעור ותכני השיעור (מטלות, רשימת קריאה, משימות וכיו"ב)
1	Introduction to NGS – sequencing technologies, basic terminology: reads, paired-end sequencing, coverage, depth, sequencing errors.
2	Linux operating system – file system navigation, working with text files, CLI software, piping and redirection
3	NGS data QA and preprocessing - Fasta and Fastq formats, Phred scores, various QA metrics, quality trimming, merging PE reads, deduplication
4	Sequence mapping I – the BLAST algorithm and CLI
5	Sequence mapping II – short read mapping, working with SAM/BAM files
6	Variant calling – short and structural variant calling, working with VCF/BCF files
7	Genome assembly – de novo assembly from short reads, De-Bruijn graph assembly, assembly quality measures
8	Gene annotation and genomic DBs – BED and GFF formats, Bedtools, structural and functional annotation of genes, the SRA/ENA data base, Ensembl
9	Transcriptomics I – RNA-seq data, spliced read mapping, read counting and biases
10	R programming for genomics – R basics, vectors, data frames, plotting, loading genomic data, Bioconductor
11	Transcriptomics II – differential gene expression analysis
12	3rd generation sequencing – long read technologies (PacBio, ONT), linked reads (10X genomics), detecting structural variants with long reads
13	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.