	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

נושא השיעור ותכני השיעור (מטלות, רשימת קריאה, משימות וכיו"ב)	תאריך / מס' שיעור
Introduction to NGS – sequencing technologies, basic terminology: reads, paired-end sequencing, coverage, depth, sequencing errors.	7.3.21
Linux operating system – file system navigation, working with text files, CLI software, piping and redirection	14.3.21
NGS data QA and preprocessing - Fasta and Fastq formats, Phred scores, various QA metrics, quality trimming, merging PE reads, deduplication	21.3.21
Sequence mapping I – the BLAST algorithm and CLI	23.3.21
Sequence mapping II – short read mapping, working with SAM/BAM files	11.4.21
Variant calling – short and structural variant calling, working with VCF/BCF files	18.4.21
Genome assembly – de novo assembly from short reads, De-Bruijn graph assembly, assembly quality measures	25.4.21
Gene and variant annotation – structural and functional annotation of genes and prediction of variant effects, the GFF format	2.5.21
Transcriptomics I – RNA-seq data, spliced read mapping, read counting and biases	9.5.21
R programming for genomics – R basics, vectors, data frames, plotting, loading genomic data, Bioconductor	23.5.21
Transcriptomics II – differential gene expression analysis	30.5.21
3rd generation sequencing – long read technologies (PacBio, ONT), linked reads (10X genomics), detecting structural variants with long reads	6.6.21
TBD – genomics DBs / phylogenomics / guest lecture	13.6.21

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.

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