Next Generation Sequencing workshop, Tel Hai, August 2017

Where	Tel Hai College, Western Campus, Building 3, room 3426
Instructors	Sariel Hübner, Itai Sharon, Aia Oz
Wifi	Students (no password required)
Computer access	Username: sadna password: Sadna2017
Contact	bioinfodude@gmail.com

Agenda

Sunday, 13/8

10:30-11:00	**Registration, coffee**
11:00-12:00	**Welcome, Introduction to next generation sequencing technologies (Sariel Hübner)** Overview of NGS technologies, challenges
12:00-13:30	**Introduction to Linux, part I (Itai Sharon)** Operating systems, Linux history, the Linux file system, hello world, setting up accounts, class exercise
13:30-14:30	Lunch
14:30-16:00	**Introduction to Linux, part II (Itai Sharon)** manipulating directories and files, searching for patterns in files, generating file statistics, class exercise
16:00-16:15	Coffee break
16:15-18:00	**Introduction to Linux, part III (Itai Sharon)** Scripts, sed, downloading programs and scripts from the internet, good practices in working with computers, class exercise

Monday, 14/8

08:30-10:00	**Cleaning and trimming raw data, part I (Itai Sharon)** fasta/fastq file formats, quality scores for NGS data, adaptors, class exercise (fastx)
10:00-10:30	Coffee break
10:30-12:00	**Cleaning and trimming raw data, part II (Itai Sharon)** Trimming low quality data, class exercise (trimmomatic)
12:00-13:00	Lunch
13:00-14:30	**Introduction to alignment algorithms and tools, part I (Sariel Hübner)** What is sequence alignment, pairwise alignments, alignments to database and reference genomes
14:30-15:00	Coffee break
15:00-17:00	**Introduction to alignment algorithms and tools, part II (Sariel Hübner)** Mapping algorithms, viewing alignments, class exercise (bowtie2, bwa, samtools)

Tuesday, 15/8

08:30-10:00   **Transcriptomics and genomics assembly, part I (Itai Sharon)**
Genome assembly, what could go wrong, quality control, class exercise (spades)

10:00-10:30   Coffee break

10:30-12:00   **Transcriptomics and genomics assembly, part II (Itai Sharon)**
RNASeq experiments, transcriptomic data assembly, class exercise (trinity)

12:00-13:00   Lunch

13:00-14:30   **Expression profiling and statistics, part I (Sariel Hübner)**
Working with RNASeq data for quantifying expression, from experiment design to candidate genes

14:30-15:00   Coffee break

15:00-17:00   **Expression profiling and statistics, part II (Sariel Hübner)**
class exercise: A full RNASeq data analysis workflow, from alignments to genes and pathways

Wednesday, 16/8

08:30-10:00   **Phylogenetic analysis and inference, part I (Aia Oz)**
Multiple sequence alignment, class exercise (blast, clustal)

10:00-10:30   Coffee break

10:30-12:00   **Phylogenetic analysis and inference, part II (Aia Oz)**
Strategies and algorithms for constructing phylogenetic trees, class
exercise (fasttree, itol)

12:00-13:00   Lunch

13:00-15:00   Break

15:00-19:00   **Archaeological excursion and dinner (instructor: Gonen Sharon)**

Thursday, 17/8

08:30-10:00   **Variant calling and genome-wide association mapping, part I (Sariel Hübner)**
Identifying variants (mostly SNPs) from NGS data, filtering. What is GWAS and how to identify the genetic basis of traits of interest.

10:00-10:30   Coffee break

10:30-12:00   **Variant calling and genome-wide association mapping, part II (Sariel Hübner)**
Processing NGS data for variant calling, identifying variants and filtering bad calls. Performing GWAS to identify candidate genes, class exercise

12:00-13:00   Lunch

13:00-15:00   **Gene annotation (Itai Sharon)**
predicting genes, databases for gene annotation, class exercise (prodigal, prokka)

15:00-15:30   Coffee break

15:30-16:30   **Concluding remarks**