



	Sunday 21/2/2015	Monday 22/2/2015	Tuesday 23/2/2015	Wednesday 24/2/2015	Thursday 25/2/2015
08:30-10:30	Getting the data: experimental planning, library prep, other sequencing platforms, FASTQ, estimated costs (Noa Sher)	Starting simple - bacterial transcriptomics: bacterial RNA-seq, mapping to a reference genome, quantifying expression, pathway enrichment (Daniel)	Eukaryotic transcriptomics: Eukaryotic RNA-seq, mapping spliced RNA to exons, alternative splicing, quantifying expression of alternative isoforms (Eyal)	9:00-10:30 <i>Guest lecturer:</i> Adi Stern, Department of Microbiology, Tel Aviv University	Environmental gene expression: Mapping vs searching (BLAST), normalization, inferring community structure and activity, web-based tools (Daniel)
10:30-11:00	Coffee break				
11:00-13:00	Illumina library prep and sequencing platforms, Roe Vidavski, Daniel Biotech	<i>Guest lecturer:</i> Gil Ast, Department of Human Molecular Genetics, Tel Aviv University	<i>Guest lecturer:</i> Tamir Tuller, Department of Biomedical Engineering, Tel Aviv University	De novo transcriptome assembly: Assembly of RNA-seq data, alternative splice isoforms (Eyal)	<i>Guest lecturer:</i> Erez Levanon, Faculty of Life Sciences, Bar Ilan University
13:00-14:00	Lunch (on your own)				
14:00-16:00	Tutorial: opening steps FASTQC, Bowtie, IGV (Yotam)	Tutorial: Intro to R - importing data and working with it (Ilia)	Tutorial: eukaryotic RNA-seq -I Tuxedo suit: Bowtie, Tophat, Cufflinks (Yotam)	Tutorial: eukaryotic RNA-seq III Tuxedo suit: Cuffdiff, CummeRbund (Yotam)	Tutorial: Transcriptomic databases, command-line BLAST (Ilia)
16:00-16:30	Coffee break				
16:30-18:30 Extra tutorials	Beer and one-minute presentations	Tutorial: Statistics and plotting in R (Ilia)	Tutorial: eukaryotic RNA-seq II Tuxedo suit: Bowtie, Tophat, Cufflinks (Yotam)	Tutorial: working with the output of Trinity (Yotam)	