

Preliminary work schedule ForBio course 'High Throughput Sequencing – data manipulation and analysis '. Morning lectures from 8:30-12:00 with coffee breaks. Lunch break from 12:00-13:00. Afternoon practical work from 13:00-16:30 with breaks.

	Monday 09.05.	Tuesday 10.05.	Wednesday 11.05.	Thursday 12.05.	Friday 13.05.
Morning lectures 8:30-12:00	<ul style="list-style-type: none"> - Introduction - Introduction course members <p>COFFEE BREAK</p> <ul style="list-style-type: none"> - Lecture: HTS methods, differences in datasets, application & usage in biology 	<ul style="list-style-type: none"> - Lecture: DNA libraries-sample prerequisites, laboratory work steps, qPCR, indexing & sequencing (Steffi) <p>COFFEE BREAK</p> <ul style="list-style-type: none"> - Lecture: Online resources, data handling and downstream analysis 	<ul style="list-style-type: none"> - Lecture: Whole genome sequencing and transcriptomics (Leon) <p>COFFEE BREAK</p> <ul style="list-style-type: none"> - Lecture: targeting specific genomic data using HTS 	<ul style="list-style-type: none"> - Lecture: RNA from the lab to transcriptomics – Why sequencing RNA? Sample preparation & quality assessment (Leon) <p>COFFEE BREAK</p> <ul style="list-style-type: none"> - Lecture: Systematic application of transcriptomes 	<ul style="list-style-type: none"> - Lecture: Applications of HTS in Research and future perspectives <p>COFFEE BREAK</p> <ul style="list-style-type: none"> - Open session to answer questions, discuss approaches and - Open session with student mini project presentations by those needing credits
12:00-13:00	LUNCH	LUNCH	LUNCH	LUNCH	LUNCH
Afternoon practical work 13:00-16:30	<ul style="list-style-type: none"> - Setting up student laptops for work with Unix - Hands-on introduction to Unix - Software download and installation in Unix - Illumina reads quality control and adapter trimming - Mini project group set-up 	<ul style="list-style-type: none"> - BLASTing sequences, MEGAN taxonomic evaluation of read composition - Reference genome download with Introduction to file structure etc. 	<ul style="list-style-type: none"> - read mapping - reconstruction of mitochondrial genome - mitochondrial genome annotation 	<ul style="list-style-type: none"> - Catch up - Mitochondrial genome alignments - Phylogenetic analysis <p>SOCIAL EVENT</p>	