

Schedule

Monday, Sept 4th- 'Introduction'

09:00-10:00	Introduction to target capture and enrichment	L	Tobias Hofmann
10:00-10:30	Coffee break		
10:30-11:10	Examples of NGS projects, project design	L	Christine Bacon
11:15-12:00	Bioinformatic best practices and infrastructure - Downloading data, disk space, Bioinformatic requirements, project planning, necessity to automate, large data sets	L	Mats Töpel
12:00-13:00	Lunch		
13:00-14:45	Personal presentations, 5 minutes with the following content: <ul style="list-style-type: none"> • Title of my NGS project, organism. • What I expect from Target capture techniques in terms of data and results. • Which data is already available from my target organism (genome, transcriptome, etc.) 	D	Tobias Hofmann, Vincent Manzanilla, Christine Bacon
14:45-15:00	Coffee break		
15:00-16:00	Continuation of personal presentations	D	Tobias Hofmann, Vincent Manzanilla, Christine Bacon
16:00-17:00	Optional: bash-lab - Short practical to command line tools and logging into the local computer cluster Albiorix	P	Tobias Hofmann

Tuesday, Sept 5th - 'Lab procedures, first data processing steps'

09:00-10:00	Preparing samples for libraries, overview of lab protocol, DNA extraction quality, different options and alterations in the lab protocol	L	Christine Bacon
10:00-10:30	Coffee break		
10:30-12:00	Sequence capture and sequencing	L	Christine Bacon
12:00-13:00	Lunch		
13:00-15:30	What do the results look like - Quality check, read counts, trimming, contaminants, FASTQ-format	P	Tobias Hofmann
15:30-16:00	Coffee break		
16:00-17:00	Continuation of practical	P	Tobias Hofmann

Wednesday, Sept 6th - 'Designing bait-sequences'

09:00-10:00	Developing nuclear markers for sequence capture of non-model organisms	L	Vincent Manzanilla
10:00-10:30	Coffee break		
10:30-12:00	Identifying and extracting single-copy nuclear markers	L	Vincent Manzanilla
12:00-13:00	Lunch		
13:00-15:30	Bait design	P	Vincent Manzanilla
15:30-16:00	Coffee break		
16:00-17:00	Departmental guest seminar about Sequence Capture	S	Brant Faircloth

Thursday, Sept 7th - 'From reads to alignments'

09:00-10:00	de novo assembly, identifying target regions	L	Tobias Hofmann
10:00-10:30	Coffee break		
10:30-12:00	mapping, BAM files, phasing, SNPs	L	Tobias Hofmann
12:00-13:00	Lunch		
13:00-15:30	from cleaned reads to alignments, using the Phyluce pipeline	P	Brant Faircloth
15:30-16:00	Coffee break		
16:00-17:00	Continuation of practical	P	Tobias Hofmann
Afterwork	Social event		

Friday, Sept 8th - 'Advanced processing'

09:00-10:00	Orthology assessment	P	Vincent Manzanilla
10:00-10:30	Coffee break		
10:30-12:00	reference-based assembly, inspecting BAM-files	P	Tobias Hofmann
12:00-13:00	Lunch		
13:00-15:30	from BAM files to allele alignments	P	Tobias Hofmann
15:30-16:00	Coffee break		
16:00-17:00	Wrap-up, discussion of results	D	Tobias Hofmann

L = Lecture, P = Practical, S = Seminar, D = Discussion