

## Schedule

### Monday, Sept 24th - 'Introduction and Lab workflow'

09:00-10:00	Welcome, course overview, introduction	L	Tobias Andermann
10:00-10:30	Short personal introductions	D	
10:30-11:00	Coffee break		
11:00-12:30	Library preparation - workflow, protocols and useful tips	L	Logan Kistler
12:30-13:30	Lunch		
13:30-15:00	Target enrichment and Illumina sequencing - workflow, tips, alterations	L	Logan Kistler
15:00-15:15	Coffee break		
15:15-16:00	How to log into the cluster, how to submit jobs, bash command line refresher	P	Tobias Andermann, Vincent Manzanilla
16:00-17:00	Exercise how to plan and calculate target enrichment experiments (calculating read-coverage, multiplexing, etc.)	P	Vincent Manzanilla, Logan Kistler

--> Aim: Getting to know each other. Understanding the basic principle and procedure behind sequence capture and Illumina sequencing. All students have access to the cluster and basic bash (command line) knowledge.

### Tuesday, Sept 25th - 'Bait design and data cleaning'

09:00-10:00	Introducing different (popular) bait sets (universal set for angiosperms, UCEs, other examples)	L	Christine Bacon
10:00-10:30	How to design your own baits (1)	L	Vincent Manzanilla, Logan Kistler
10:30-11:00	Coffee break		
11:00-12:30	How to design your own baits (2)	L	Vincent Manzanilla, Logan Kistler
12:30-13:15	Lunch		
13:15-15:15	Joint walk around field station		
15:15-17:00	Overview of FASTQ format, quality scores, cleaning Illumina reads	L P	Tobias Andermann

--> Aim: Knowledge of different bait sets and ability to decide what is most suitable for a project (existing bait set or designing your own). Being familiar with FASTQ file format and knowing how to clean, trim and quality-check FASTQ files.

### Wednesday, Sept 26th - 'Assembly and data overview'

09:00-10:30	Introducing the SECAPR pipeline, explain workflow = overview of following steps	L	Tobias Andermann
10:30-11:00	Coffee break		
11:00-12:30	Working with <i>de novo</i> contigs and extracting target contigs, building alignments	P	Tobias Andermann
12:30-13:30	Lunch		
13:30-15:00	Reference-based assembly and choice of reference library	L P	Tobias Andermann

## ForBio Target enrichment workshop, Sept 24th-28th 2018

15:00-15:15	Coffee break		
15:15-17:00	Checking data coverage, plotting results, reviewing BAM-files, polyploidy assessment	P	Tobias Andermann

--> Aim: Overview of different assembly strategies, knowing basic workflow from sequencing reads to multiple sequence alignments. Being able to gauge data-coverage with various plotting functions.

### Thursday, Sept 27th - 'Heterozygosity information'

09:00-10:30	Allele phasing - theory and practical, building allele alignments	L P	Tobias Andermann
10:30-11:00	Coffee break		
11:00-12:30	SNP extraction - theory and practical	L P	Tobias Andermann, Vincent Manzanilla
12:30-13:30	Lunch		
13:00-15:30	Applications of SNPs in population genetics	P	Vincent Manzanilla, Logan Kistler, Christine Bacon
15:00-15:15	Coffee break		
16:00-17:00	Using allele sequences for species tree inference under the Multispecies Coalescent model with STACEY	P	Tobias Andermann

--> Aim: Learning how to extract the heterozygosity information by phasing allele sequences and extracting SNPs and how to apply both data types for population genetic and phylogenetic purposes.

### Friday, Sept 28th - 'Phylogenetics'

09:00-09:30	Phylogenetic inference with target enrichment data - advantages and challenges	L	Tobias Andermann
09:30-10:30	Species tree inference with summary coalescent models	P	Vincent Manzanilla
10:30-11:00	Coffee break		
11:00-12:30	Network analysis, identifying hybridization, introgression	P	Vincent Manzanilla, Logan Kistler
12:30-13:30	Lunch		
13:30-15:30	Reviewing species tree and population genetic results, discussion	D	Tobias Andermann, Vincent Manzanilla, Logan Kistler, Christine Bacon
15:00-15:15	Coffee break		
15:15-16:00	Wrap-up, final questions, course review	D	Tobias Andermann, Vincent Manzanilla, Logan Kistler, Christine Bacon

--> Aim: Knowing different options of phylogenetic inference with sequence capture data, understanding the challenges and limitations of different methods.

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