

Target sequence capture workshop, Sept 28th-Oct 2nd 2020

## Program

### **Monday**

#### ***Theory:***

Welcome, course overview, introduction  
Library preparation - workflow, protocols and useful tips  
Target enrichment and Illumina sequencing - workflow, tips, alterations

#### ***Practical:***

Bash command line refresher  
Cluster login  
Software installation

### **Tuesday**

#### ***Theory:***

Popular bait sets  
Designing your own baits  
FASTQ format, quality scores  
Overview of bioinformatic workflow for processing FASTQ reads  
Computational pipeline solutions

#### ***Practical:***

Calculating read-coverage, multiplexing, etc.  
Cleaning Illumina reads  
Evaluating data quality

### **Wednesday**

#### ***Theory:***

From reads to full sequences  
Overview of de novo assembly approaches

#### ***Practical:***

Assembling reads into contigs  
Extracting target sequences  
Multi-sample processing with SECAPR

### **Thursday**

#### ***Theory:***

Reference-based assembly  
Allele phasing

#### ***Practical:***

Investigating BAM files  
Phylogenetics with contigs vs. allele sequences  
Gene trees vs. species trees

### **Friday**

#### ***Theory:***

SNP extraction  
Applications of SNPs in population genetics

#### ***Practical:***

Genomic likelihood trees  
Population genetics exercise with SNPs  
Reviewing species tree and population genetic results, wrap-up discussion