# Bioinformatics problem-solving

## NGS data processing

### ddRADseq 🡪 SNP calls and genotyping

#### Guide –generic information of what steps need to be taken

###### Removing adapters/barcodes and demultiplexing data

###### Quality filtering

###### De novo assembly

###### Read mapping

###### SNP calling

###### SNP filtering

###### Genotyping

###### Sequenom primer design

#### Analysis pipeline – easy to follow yet adjustable, with information about what is happening at each step

#### Install programs on ERSA nectar or shared Mac Pro

#### Train staff on using the pipeline

#### Compare with results from other workflows (e.g. pericopsis)

#### Share pipeline info with Australian museum forensics visitors

### Metagenomic barcoding

Work with Stefan on data processing for metabarcoding pipeline

### Transcriptomics and hybrid capture sequencing

Work with Matt on data processing for datasets focussing on signatures of selection

## Preliminary data analysis

### Generic

#### Tests for neutrality/selection

##### HWE, Fst outliers

#### Linkage disequilibrium

#### Population structure/clustering

##### PCA

##### Structure, DAPC

#### Diversity statistics

##### Ho, Fst, Fit etc.

#### Maximum likelihood tree