**Landscape transcriptomics Project**

Apart from gene sequence variation, gene expression variation can also have a large effect on the onset of important fitness traits in various environments. In this project, we are going to develop ideas to analyze how the environment pressures are reflected on traits and how these relate to gene expression variation. We will be analyzing a real data set composed of a common garden trait data of South African *Protea repens*, associated environmental variables from 19 source populations and RNA-seq sequence data. Main goal of the project is to gain insights on RNA-seq experimental design, data collection and processing. Some familiarity with R and command line applications might be useful in data analysis.

*Monday (1 hr)*

We will be discussing 1-2 related papers and construct ideas about landscape transcriptomics.

*Tuesday (3 hrs)*

- We will discuss and design a project for detecting signatures of local adaptations in gene expression. This will be done in groups of 2-3 people. We will focus on common garden experiments, sampling and sequencing strategies (2 hr).

- Each group will give a short presentation about their proposed projects and there will be discussions afterwards (1 hr).

*Wednesday (3 hrs)*

- A real data set composed of a common garden trait data, associated environmental variables from 19 source populations and RNA-seq sequence data will be given to students and a data analysis pipeline will be constructed (2 hrs).

- Assembly and annotation strategies such as blast, orthomcl etc. will be discussed (1 hr) and I will present what kind of results you could get from these type of analyses

*Friday (3 hrs)*

- Differential gene expression analysis will be discussed and using the given dataset analyses will be done in R using edgeR package. These analyses will include;

- Multi dimensional scaling (1 hr)

- Environmental variables vs. MDS axes correlations (1 hr)

- ANOVA-like analyses will be done to detect differentially expressed genes between populations (1 hr)

*Saturday (7 hrs)*

- GO analysis will be discussed and performed to reveal what the differentially regulated genes are, which pathways, processes and functional groups (2 hrs).

- WGCNA will be discussed and since the analysis is memory demanding, the type of results we can get will be presented by me (1 hr)

- Preparing presentation (2 hrs)

- 2 hrs buffer for uncompleted tasks