



Development plan when funded by an external scholarship

Project:

The project is to learn and develop new methods in bioinformatics and write two papers on adaptation to changing environments.

Background:

The Arctic is changing more than any other ecosystem on Earth. For example, temperatures have warmed nearly four times faster than the globe since 1979. For this project, we have hundreds of samples of *Oxyria digyna* collected from nearly 100 natural populations distributed across the Arctic tundra in order to understand plant adaptation to changing environments. To determine climate adaptation, we focus on genomic response and vulnerability and therefore strong capacity for bioinformatics and an understanding of plant genomics are required.

Purpose:

To assemble the genome of *Oxyria digyna* and review the literature on genomic adaptation to climate change.

Method:

Merge HiC data from a single genomic library with ca. 15Gb from one SMRT cell of PacBio HiFi with a metagenome assembler such as hifiasm.

Work plan/Schedule:

Both papers will be written on in tandem, since the genomic data is already in house. The literature review can be used as a break from learning new bioinformatics tools, and allows for a wide collaboration with our network of collaborators. The genome should be assembled within the first year of the position, and a draft manuscript should be finished within 18 months of the start date. The literature review should be compiled over the first 18 months, with the last six months dedicated to the development of a first draft of the review paper.

Learning outcomes:

- Improve coding ability with command line tools within a unix environment
- Improve communication skills, both written and spoken
- Gain experience in plants, adaptation, the Arctic region, and climate change
- Gain experience with long-read DNA sequencing data
- Gain experience in writing a systematic review