

# **PNS0221**

## **From population to ecological functional genomics: Concepts, tools and applications, 2.5 Credits**

Syllabus approved

2021-03-08

### Subjects

Biology

### Grading scale

Pass / Failed The requirements for attaining different grades are described in the course assessment criteria which are contained in a supplement to the course syllabus. Current information on assessment criteria shall be made available at the start of the course.

### Language

English

### Prior knowledge

The course is primarily for SLU PhD within the Graduate School Organism Biology but is open for all interested SLU PhD students. Other SLU staff and PhD students from other universities are welcomed if space allows. Basic knowledge of the programming language R is preferable.

### Objectives

This course aims to enable the participants to analyze the partitioning of genetic variation across genomes and investigate natural populations' evolutionary trajectories. The participants will:

- be introduced to key concepts in population genetics and ecological genomics.
- become familiarized with methods to quantify genetic diversity and test concepts derived from population genetic theories.
- learn how to combine population genetics with ecology and quantitative genetics to unravel gene function in natural environments.
- gain the ability to critically reflect on the design and interpretations of population and ecological genomic studies.

### Content

The course will introduce fundamental concepts in population genetics and discuss how to apply these concepts to analyze population structure, infer demographic history and study the genomic basis of adaptive evolution. Basic knowledge will be provided as lectures, group discussions and

literature reviews. The participants will also be introduced to the command line (unix), data formats, data conversion and various tools for population genomics analyses. They will apply this practical knowledge through hands-on computer exercises. Note that the course will not cover pre-processing of Next Generation Sequencing data (NGS).

### Additional information

The course is organized by Adrien Sicard and Pär Ingvarsson (Department of Plant biology, NJ faculty) on behalf of the SLU Organism Biology research school. The entire course will be conducted remotely via Zoom. Participants are expected to use their laptop for practical computer exercises and have a good internet connection. Students will be provided data for all analyses in the practical parts, but are welcome to use personal data if possible. Maximum 15 students per course occasion.

### Responsible department

Department of Plant Biology