

Course syllabus: Phenotyping Technologies in Plant-environment Interactions – Common Data Standards and Omics Technologies in Phenotyping

Number of credits: 3 ECTS

Subject: Biology

Language of education: English

Entry requirements: MSc degree in a relevant field is required. Relevant fields: agriculture, biological and environmental sciences.

Learning outcomes:

Participation in lectures and daily learning diaries (1.5 ECTS)

- knowledge about the whole range of analysis sensors available for plant phenotyping
- gaining understanding of the opportunities and challenges in experimental design in plant phenotyping
- using R and similar tools for analysis of plant phenotyping data
- using common standards for data handling, metadata generation using ontologies and data storage

Participation in the workshops (0.5 ECTS)

- gaining hands on experience of image-based data acquisition, and handling and processing of –omics and phenotype data.

Literature study, presentation and a research plan as post assignments (1 ECTS)

- gaining deeper understanding of the chosen biological process and chosen technology through own study
- making a presentation introducing the chosen biological process or technology and describing the goal of the research plan
- application of gained knowledge in the research plan

Objective and Content:

The changing climate demands the development of faster breeding methods to provide effective solutions for the future agriculture. Plant phenotyping is used for plant-environment interactions in a number of settings, from highly controlled environments to field conditions. This course series aims to introduce the emerging research fields of high throughput plant phenotyping and omics technologies (including bioinformatics). This core focus of the course is on computational solutions for handling and analyzing plant phenotyping data.

The course is part of a NOVA course series of four courses. This course introduces the emerging technologies related to i) automated and image based plant phenotyping technologies that are intended to remove bottlenecks between genotype and phenotype screens, ii) high throughput field phenotyping technologies and iii) use of analysis tools including R to analyze plant phenotype and -omics data iv) use of common standards for data handling, metadata generation using ontologies and data storage.

The objective of the course series is to provide the participating students with the basic knowledge and understanding of the emerging fields of plant phenomics and data processing that can serve breeding efforts as well as precision agriculture for current and future climate conditions.

Pedagogical form:

Student activation by access to pre-course literature, in depth scientific lectures, hands-on experience during workshops and post-course assignment in the form of a research plan that allows for application of the gained knowledge.

Examination: For passing the course, the students are required to participate in the discussions during the workshops and to make a presentation as described above. The learning diaries describing their daily progress during the course and post-assignment (research plan) must be approved by the course NOVA teacher team. Estimated workload: 15 hours workshops, 15 hours lectures, and 50 hours independent work

Technical requirements: Own laptop.

Course leader: Erik Alexandersson (erik.alexandersson@slu.se)

Teachers: TBD