

**PLGXXX:** Biometrical methods for analyzing plant breeding trial data in the omics era (3 ECTs)

**Location and Dates:** SLU, Alnarp; 18<sup>th</sup> – 22<sup>nd</sup> November 2019

**Guest Lecturers:** Prof. José Crossa (Centro Internacional de Mejoramiento de Maíz y Trigo, CIMMYT, Texcoco, México), Prof. Paulino Pérez (Colegio de Postgraduados, Montecillo, México)

**SLU Co-organizers:** Prof. Rodomiro Ortiz (Course Leader), Dr. Therese Bengtsson

**Marking scale:** Pass / Fail

### **Prerequisites**

Basic knowledge about genetics, quantitative genetics, linear regression models, analysis of variance and basic experience with R. At least a MSc degree in agronomy, biology, forestry, genetics, horticulture or enrolled as a PhD student

### **Target**

Post-graduate students and professional doing field research on plant breeding using trials across sites and over years or cropping seasons, particularly those working on the analysis of controlling the inheritance of complex traits

### **Objectives**

- To provide some basic biometrical and quantitative genetic concepts to be applied in designing and analyzing data from field trials, particularly variety testing
- To give some basic statistical models and methods for dissecting genotype-by-environment interaction in the omics era
- To show practical results on multi-environment trials across sites and over years (or seasons) in different breeding contexts.
- To demonstrate implementations of various stat methods using the R software package

- To discuss general concepts of genomic selection and prediction
- To learn the quantitative genetic basis of genomic selection
- To understand statistical models for genomic selection and prediction

## **Content**

### ***Theoretical sessions***

1. Revisiting field plot techniques for variety testing design and analysis: principles of good design, blocking, spatial analysis
2. Brief overview of mixed models (BLUE, BLUP, REML, variance components)
3. Linear and other models for analyzing genotype-by-environment (G×E) interactions
4. Association genetics (GWAS) and genomic estimated breeding values (GEBV) for genetic enhancement
5. G×E in association mapping (GWAS) and genomic prediction (GEBV). Genomic prediction models for G×E (reaction norm models)

### ***Practical Sessions***

1. A brief introduction to R
2. Spatial analysis, use of incomplete block ( $\alpha$ -lattice) and augmented design
3. Analysis of variance across sites and over years
4. Modeling multi-environment data under significant G×E
5. Including G×E in GWAS and GEBV

## **Examination**

Completion of all course assignments (pre-course readings, post-course practices-report), attendance and active participation in all theory lectures and computer practices, and oral exam to be taken with course leader

## **Additional information**

Pedagogical approach

Lectures, demonstrations and computer practices.

## **Technical requirements**

Own participant laptop with the last version of R installed (<http://www.r-project.org>)

## **Learning outcomes**

At the end of this intensive 1-week course, the participant will

- ➔ Refresh some basic ideas of Biometrical Methods for Plant Breeding Trial Data
- ➔ Understand the conceptual framework of experimental design, multi-environment testing, use of association genetics and genomic prediction for plant breeding.
- ➔ Know how to design, analyze and handling genotype-by-environment interactions
- ➔ Learn results that clearly show that biometrics works for plant breeding
- ➔ Tell how to prepare phenotypic and genotypic data for analyzing plant breeding data with R
- ➔ Run some R codes for analyzing plant breeding data involving different statistical models.
- ➔ Test if there are differences between breeding lines or populations, and cultivars

### **Course time**

8:30AM – 12:30AM Theory and Results from real data applications

1:30PM-5:30PM Practices – hands on for running R codes fitting a variety of stat models

### **Organizers**

Application to [Rodomiro.Ortiz@slu.se](mailto:Rodomiro.Ortiz@slu.se) cc. [Therese.Bengtsson@slu.se](mailto:Therese.Bengtsson@slu.se) no later than mid-August 2019.

Course organizer: Dept. of Plant Breeding, LTV.

### **Responsible department**

Faculty of Landscape Architecture, Horticulture and Agricultural Science, Dept. of Plant Breeding (VF)