

## *Application of mixed model analysis for crop improvement: prediction of genetic values with BLUP and Bayesian methods*

### **Abstract**

The selection of elite individuals among a population of candidates requires partitioning the observed phenotypic values (data records) into genetic and environmental effects. This can be done based on a linear mixed model where the genetic values are considered random. One of the major interests of the mixed model is its ability to exploit the genetic correlations arising from the relatedness between individuals. The mixed model can be analyzed with best linear unbiased predictor (BLUP) methodology and with Bayesian approaches. Until recently, the relatedness between individuals was estimated based on pedigree. However, this yields expected relationships, which can differ widely from the value of interest, ie the realized relationships. The traditional pedigree-based relationships are now being replaced by molecular relationships computed from a large number of markers covering the whole genome. This opened the way to genomic predictions of genetic values, which gives the possibility of predicting the genetic value of individuals without data records, providing they were genotyped with the same markers as the individuals used to calibrate the genomic model. This new approach is expected to revolutionize plant breeding.

This talk will first give basic information regarding the genome and SNP markers and will present the model of quantitative genetics, gene effects and the computation of pedigree-based and genomic relationships. In a second part, it will show how to predict genetic values by mixed model analysis and will present the genomic selection approach. The participants will then learn how to implement that with the R software.

**Keywords:** linear mixed model, BLUP, quantitative genetics, genomic predictions, breeding value.

**R packages for practical sessions: R synbreed —gplots — BGLR — pedantics**