Genome-wide predictions in breeding: genotype-phenotype associations and genomic selection (5 credits)

This course has been designed by the SLU breeding network and the the Organismal Biology Research School. Experts in the plant and animal breeding areas at our university collaborate to answer common questions: (1) how to associate phenotypes and genotypes and (2) how to accelerate marker-assisted selection in the era of high throughput genome sequencing. While plant and animal populations are intrinsically different, quantitative genetics principles and association mapping methods rely on the same theoretical basis. Along this course, students will be able to review basic principles of association mapping, study in detail the bioinformatic methods today available, and do extensive hands-on work both on pre-designed examples or using their own data sets.

The course will take place in SLU campus Ultuna and is divided in three weeks of full-time work:

Week 1, Oct 16th-20th : Theoretical background in breeding (hybrid sessions).

Week 2, November 13th-17th : Genomic selection, theory and in silico laboratories (on campus).

Week 3, December 4th-8th : GWAS, theory and in silico laboratories (on campus).

Course coordinators: Martha Rendón (martha.rendon@slu.se) and Sreten Andonov (sreten.andonov@slu.se)

Application: send an email to martha.rendon@slu.se no later than **September 15th**.

The course can accommodate 15 students; priority will be given to SLU PhD students.