

11th GENOMIC SELECTION IN BREEDING A HANDS-ON SHORT COURSE IN R

Date:
May 18–22
2026

Location:
Mádrid, SPAIN

Instructors:
Dr. Julio Isidro y Sánchez
Dr. Tiago Olivoto
Dr. Javier Fernández-González



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Register:
<https://bit.ly/gotoGS2026>

Genomic Selection Course 2026

📅 18–22 May 2026 | 🕒 09:00–17:00 (Mon–Thu), 09:00–13:00 (Fri)

📍 Technical University of Madrid (UPM), Agronomy School

<https://goo.gl/maps/F49jFi63iVM2tnHGA>

❗ **Who is this for?** Plant breeding scientists, graduate students, postdocs, and professionals interested in applying genomic selection (GS) with hands-on R practice.

Course Description: Why a Course in Genomic Selection?

The rapid decline in genotyping costs has fueled a surge of phenotype–genotype data (markers, sequence, expression, chromatin, metabolomics, microbiome, and more), enabling new tools that are transforming biology and breeding.

Genome-wide marker selection, *Genomic Selection (GS)*, uses genome-wide molecular markers to predict breeding values for polygenic quantitative traits and is now widely adopted across public and private programs.

This course provides the quantitative and statistical foundations to apply GS routinely, with a strong emphasis on plant breeding applications via practical exercises in R. We combine essential theory with hands-on labs and problem-based learning.

Learning outcomes:

- Build GS models from scratch and understand key statistical concepts.
 - Apply $G \times E$ models, multi-trait analysis, and hybrid prediction.
 - Use optimal parental contributions and mating designs for multi-criteria breeding.
- A certificate of attendance will be provided (equivalent to **2.5 ECTS**).

Target Audience and Prerequisites

Participants should be familiar with plant breeding and basic statistics. Tutorials use **R** and **RStudio**; prior R experience is recommended but not essential.

Program (Tentative)

Day 1 — Mon, May 11 (09:00–17:00): Quantitative Genetics / R Programming

- Review of quantitative genetics and QTL; sources of quantitative trait variation
- Breeding values, heritabilities, response to selection
- Resemblance among relatives; pedigree vs. kinship matrix

Day 2 — Tue, May 12 (09:00–17:00): GS Introduction / Linear Models

- Big picture of GS / machine learning approach; factors affecting GS; Training set optimization
- Linear models / ANOVA / GLM; Fixed and Random effects

Day 3 — Wed, May 13 (09:00–17:00): Statistical Concepts for GS

- BLUP / BLUE; Mixed models; statistical frameworks
- Imputation strategies

Day 4 — Thu, May 14 (09:00–17:00): GS Models and $G \times E$

- One-step and two-step GS models; cross-validation; hybrid prediction
- Modeling $G \times E$ interaction

Day 5 — Fri, May 15 (09:00–13:00): Future Directions

- $G \times E$ (continued); Genomic Mating plans; and future applications of GS

Costs

€ Regular fee €1199

€ Student fee €699

Fees include morning and afternoon breaks. **Accommodation is not included.**

Computers

Class materials will be shared via Dropbox/Google Drive. Please bring your own laptop with **R** and **RStudio** installed to run the analyses.

Location

📍 Technical University of Madrid (UPM), Agronomy School.

[Google Maps link](#)

Online Registration

👤 **Limited to 25 participants.** All information: <https://genomicselection.github.io/GSWebsite/>.

Registration is complete upon payment. **Deadline: April 20, 2026.**

Accommodations

Participants are responsible for their own accommodation. Nearby options:

[Hotels on Google Maps](#)

Instructors

Instructors have extensive experience in statistical genomics, quantitative genetics, and plant breeding.

- Julio Isidro y Sánchez — [Google Scholar](#)
- Tiago Olivoto — [Website](#) - [Google Scholar](#)
- Javier Fernández González — [ORCID](#)

Contact

For further information: ✉ genomicselectioncourse@gmail.com

Note: Organizers may cancel the course due to unforeseen circumstances or if the number of participants is fewer than 10 (it never happened).