



CABILDO DE LANZAROTE

3-6 June 2019

Outline

Handouts will be provided at the start of the course and will include the material presented in R. This outline is provisional, small changes may occur.

DAY 1. *Introduction to R / Quantitative Genetics* R is a powerful language and environment for statistical computing and graphics. It is a public domain and the main advantages of R are the fact that R is freeware and that there is a lot of help available online. R is a versatile, open source programming language that was specially designed for data analysis. As such R is extremely useful both for statistics and data science. In this workshop, we will start by learning about:

- R and R studio
- Understanding basic data types in R. Loop and functions in R
- Graphics
- Basic statistical operations in R.
- Linear and multiple regressions in R

We will focus on quantitative traits, especially on:

- Sources of quantitative trait variation
- Variation in population
- Breeding Values and Heritabilities
- Response from selection
- Resemblance among relatives.
- Linear models/ANOVA/GLM
- Big picture of GS/Populations in GS

DAY 2. *Genomic Selection in R.*

- Factors affecting Genomic Selection.
- Optimization of GS.
- Fixed-Random Effects
- Best Linear Unbiased Estimator
- Best Linear Unbiased Predictor

DAY 3. *Statistical concepts for Genomic Selection analysis in R*

- Pedigree vs. Kinship matrix.

- Imputation.
- Statistical Models.
- GxE.
- Multi-trait analysis.

DAY 4. *Statistical Analysis in Genomic Selection: Genomic Mating*

- One-step model.
- Two-Step models.
- Cross-Validations.
- Parental proportion and genomic mating.

Suggested reading

- Breeding for Quantitative Traits in Plants. Chapter 11. <http://stemmapress.com>.
- DS Falconer and TFC Mackay. Introduction to quantitative genetics. Longman, 19(8):1, 1996.
- Crossa, José, et al. "Genomic selection in plant breeding: methods, models, and perspectives." *Trends in plant science* 22.11 (2017): 961-975.
- Rincent, Renaud, et al. "Maximizing the reliability of genomic selection by optimizing the calibration set of reference individuals: comparison of methods in two diverse groups of maize inbreds (*Zea mays* L.)." *Genetics* 192.2 (2012): 715-728.
- Akdemir, Deniz, Julio I. Sanchez, and Jean-Luc Jannink. "Optimization of genomic selection training populations with a genetic algorithm." *Genetics Selection Evolution* 47.1 (2015): 1.
- Isidro, Julio, et al. "Training set optimization under population structure in genomic selection." *Theoretical and applied genetics* 128.1 (2015): 145-158.
- Isidro, J., Akdemir, D., and Burke, J. (2016). "Genomic selection," in *The World Wheat Book: A History of Wheat Breeding*, Chap. 32, Vol. 3, eds A. William, B. Alain, and V. G. Maarten (Lavoisier), 1001–1023
- Akdemir, Deniz, and Julio I. Sánchez. "Efficient breeding by genomic mating." *Frontiers in genetics* 7 (2016).