



GEA-R: suite of R programs for Genotype \times Environment Analyses

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Abstract

Appropriate use of statistical methods for selecting a genotype's best performance under different environmental conditions is essential for breeding programs. Sets of genotypes evaluated in single or multiple environments (locations, years, etc.) under different management conditions such as water stress or low nitrogen are known as multi-environment trials (METs). These trials can detect and explain whether there are repeatability or interaction mechanisms between genotypes and environments. The GEA-R is a suite of R codes for analyzing and interpreting the genotype \times environment interaction (GEI) from METs. The models calculated by the GEA-R are: The well-known Additive Main Effects and Multiplicative Interaction (AMMI or GE model), Sites Regression (SREG or GGE model), and when external environmental or genotypic covariates (molecular markers) is available, it is possible to use Partial Least Squares (PLS) regression and/or Factorial Regression (FR) models. Also are available several parametric and non-parametric methods for Stability Analyses. GEA-R can adjust the models for sets of genotypes evaluated in different environments using complete and/or incomplete blocks designs, or using only the adjusted means. To make GEA-R more accessible and easy to use, it runs through a graphic interface created in JAVA software. This interface generates graphics statistics (biplots), as well as numerical summaries of results in comma-delimited files. Additionally, other important contribution of this suite of R programs resides in the fact that is based on free software.

Keywords: GE and GGE models; Partial Least Squares regression; Factorial Regression; Free Software.