Genomic prediction associated with citizen science for early selection and improvement in durum wheat

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# Research questions:

* Does farmers’ evaluations associated with genes provide better predictions on varietal performance then station-only data?
* Can the GxE estimates be improved by farmers’ evaluations associated to SNP markers?
* Can the combination of genomic and citizen science provide new insights in which traits farmers prioritise or which areas of the genome play a role?

# Methods

## Genomic prediction

RBlup to genomic prediction with SNP markers. Farmers’ evaluation from citizen science trials are connected to this approach by adding the probability of winning from Plackett-Luce as explanatory variables. Other explanatory variables include the metric traits from station experiments.

## GxE interactions

Split varieties from citizen science trails by groups from their origin (cold tolerants vs others). This can also be used in the genomic prediction.

Run a number of scenarios from varieties selection using the citizen science and station data to determine whether the genetic information provides any gain or not.

**Scenario 1**

Baseline: tricot without genomic prediction, blocked cross-validation with seasons as blocks

* Plackett-Luce model
* Bradley-Terry model. Improvement: same exercise, but adding genomic data as explanatory data
* Plackett-Luce model with covariance matrix derived from genomic data
* Bradley-Terry model with genomic random variables in a GLM framework(?)

**Scenario 2**

Baseline: farmer preferences from station rating exercise, predicting field performance in tricot perhaps stratifying by environment and using the two station sites separately for their respective most similar environments (to circumvent GxE).

Predict rating data with an appropriate GLM model for ordinal data (the rates should not be assumed to be equidistant, the difference between rates 1 and 2 may be different from the rates between 4 and 5).

Improvement: same farmer preferences + genomic data, letting the ordering be influenced by genomic relatedness The exercise could use rank correlation, Kendall´s tau as criterion, but could also make a real “selection” (say top 50%) of the accessions and determine the gain as the % that indeed falls in the top 50% in the tricot trial. A p value for this exercise could be determined by doing 10,000 random selections of 50% to get a null distribution.

# Topics for discussion (or keep in mind)

* GxE driven by under-representative samples or farm management.
* Is data missingness non-random? Can data missingness be predicted from farmer preferences?
* Can we say something about which genomic regions play a role?

# References