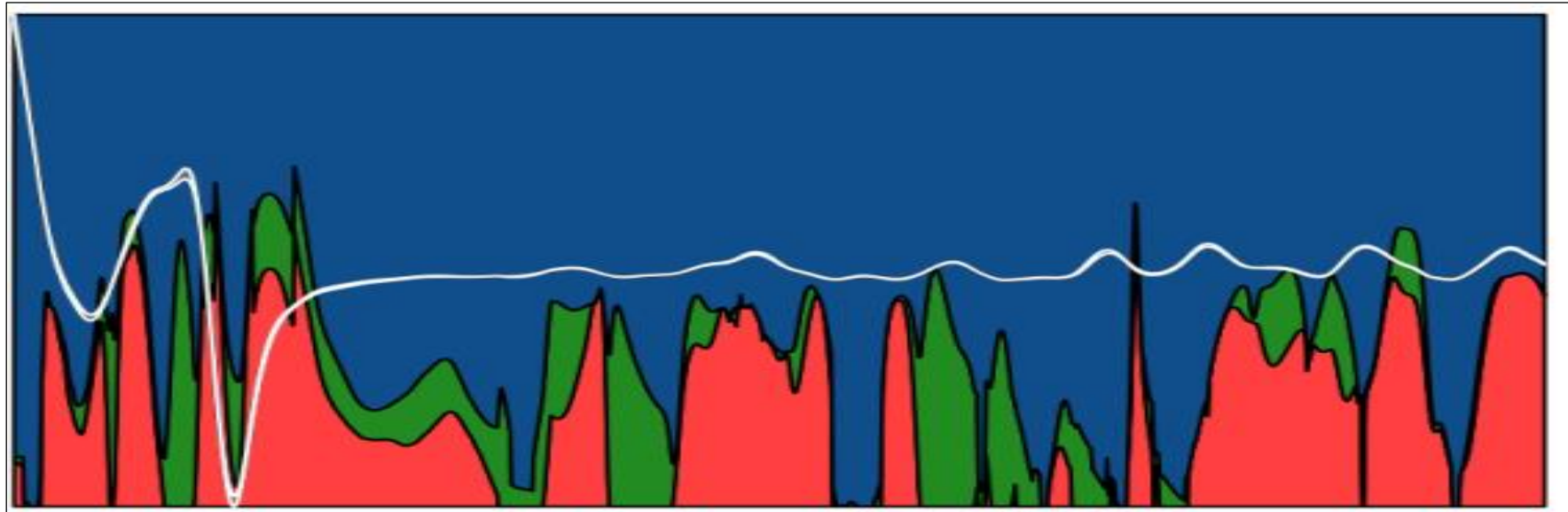


Phenomic selection workshop - Practicals -

V. Segura, R. Rincent

Practical based on the wheat dataset and analysis from Rincent et al. (2018) *Phenomic Selection Is a Low-Cost and High-Throughput Method Based on Indirect Predictions: Proof of Concept on Wheat and Poplar.*



Objectives

Run genomic and phenomic predictions in R

- Pre-treatment of the NIRS data (normalisation, detrend, derivatives)
- Estimation of the covariance matrices (kinship for GBLUP, hyperspectral similarity matrix for HBLUP)
- Estimation of the genomic heritability along the spectra
- Applying genomic and phenomic predictions in the reference environment and the other environments using cross-validations.

Materials – Proof of concept

Panel of 224 French elite varieties of winter wheat (Rincent et al. 2018 + few lines):

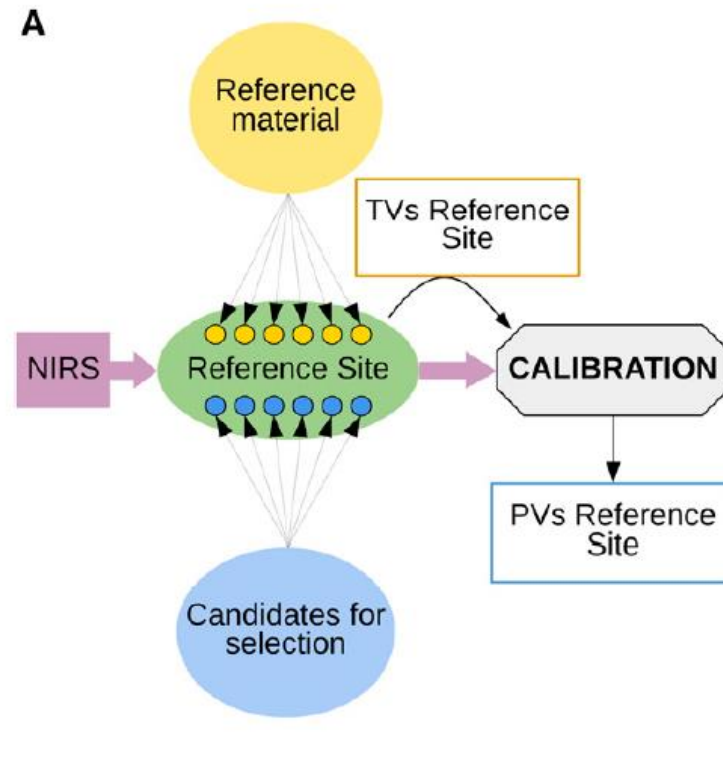
Genotyping: A subset of TaBW280K genotyping array (Rimbert *et al.* 2018), yielding 10,533 SNP.

NIRS: Measured on grains harvested in Clermont-Ferrand 2016 under drought (= reference environment)

Phenotyping: Grain Yield in the reference environment, 1 irrigated trial next to the reference environment, and 3 independent trials with 2 N treatments (no NIRS for these 7 environments).

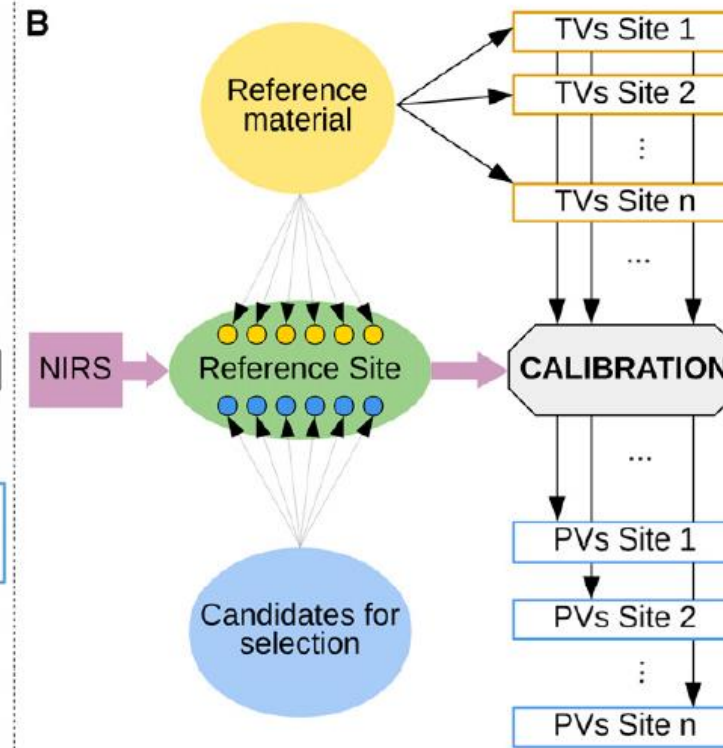
Prediction scenarios

Scenario S1



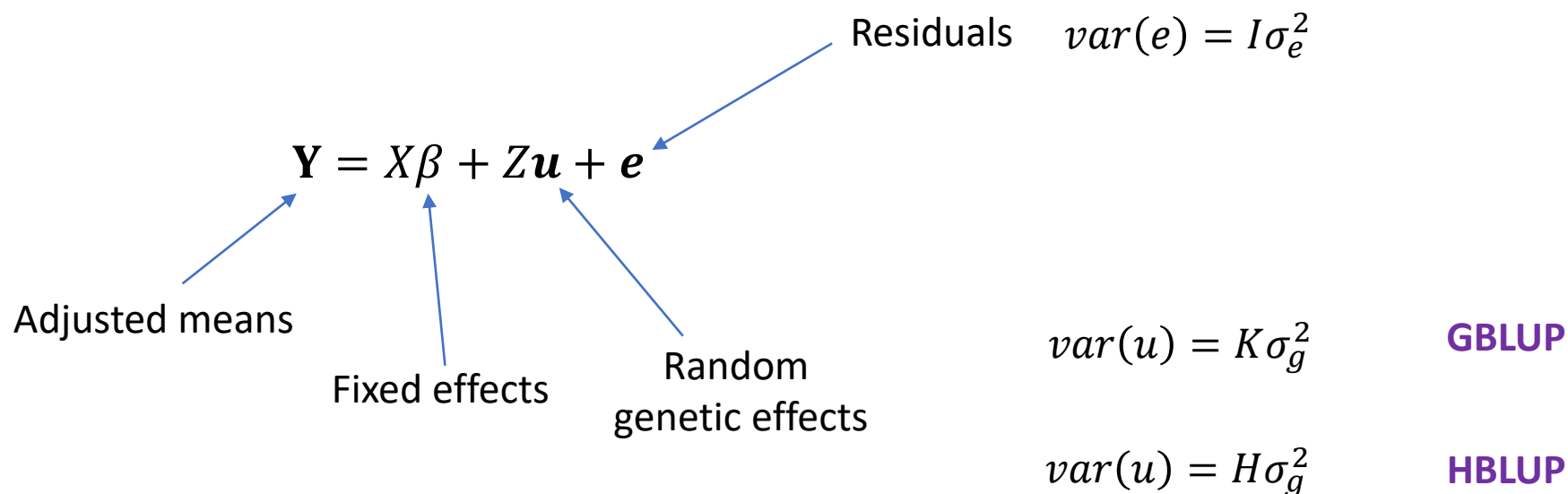
Scenario S2

= GLOB (Genomic-Like Omics Based predictions)



- **In Scenario S1**, all varieties (calibration + test set) are NIRSED in the environment in which the calibration set is phenotyped. The test set is predicted in the reference environment.
- **In Scenario S2**, all varieties (calibration + test set) are NIRSED in the reference environment, and the calibration set is phenotyped in an independent multi-environment trial (MET). The phenomic selection model is used to predict the test set in the MET. The test set is completely absent from the MET. (This scenario could also include situations in which all individuals are NIRSED in nursery, and the calibration set is phenotyped the next year in a MET).

Prediction models : GBLUP and HBLUP



K is the kinship matrix estimated with the genetic markers.

H is the hyperspectral similarity matrix estimated with the (pre-treated) spectra.

Remark: most GS models can be used for phenomic predictions (ridge, lasso, Bayesian alphabet, machine learning...)

I/ Load packages and data

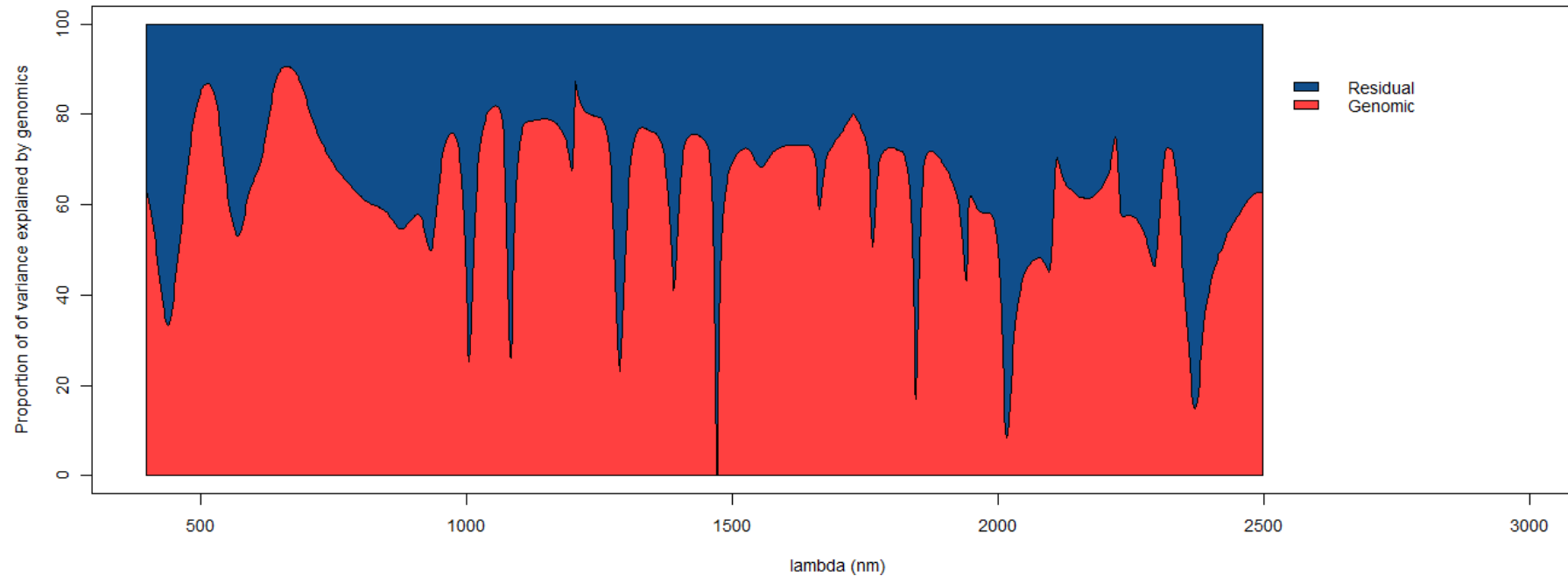
II/ Filters on genomic data and computation of kinship matrix

III/ Statistical preprocessing of the spectra

IV/ Are the spectra under genetic control ?

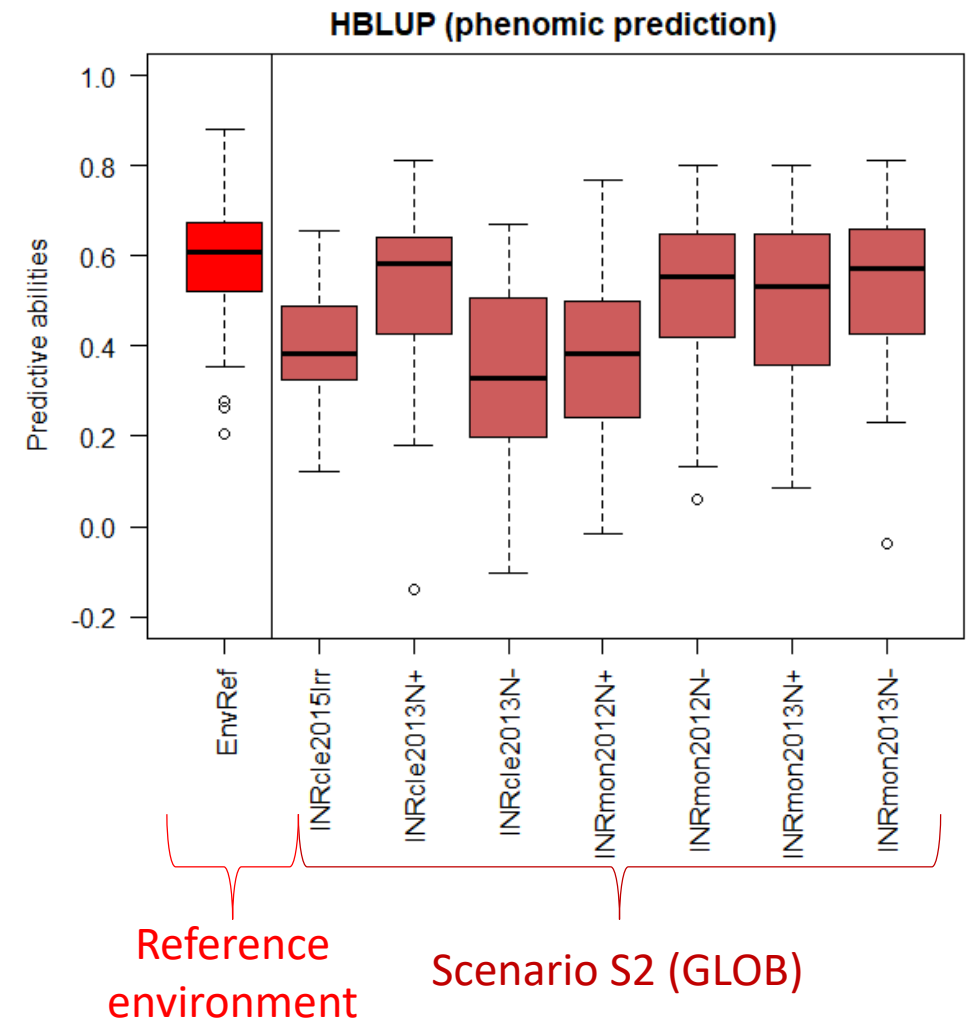
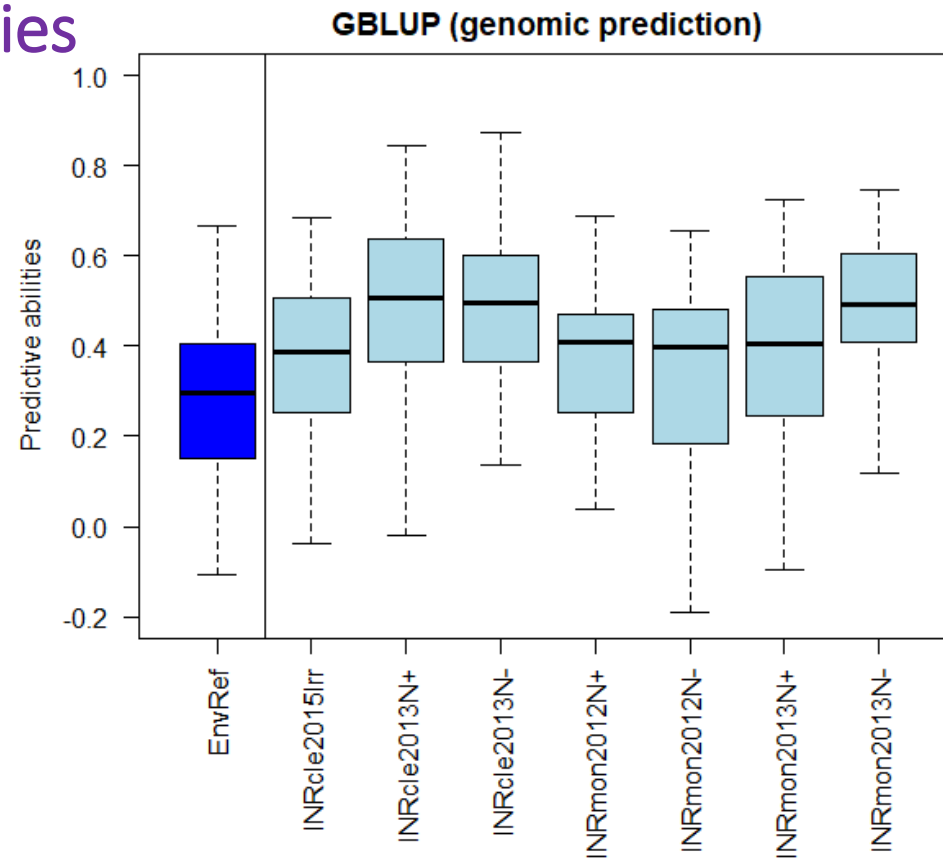
V/ Genomic and Phenomic predictions (within environment cross-validations)

Results : part of variance spectra explained by genomics



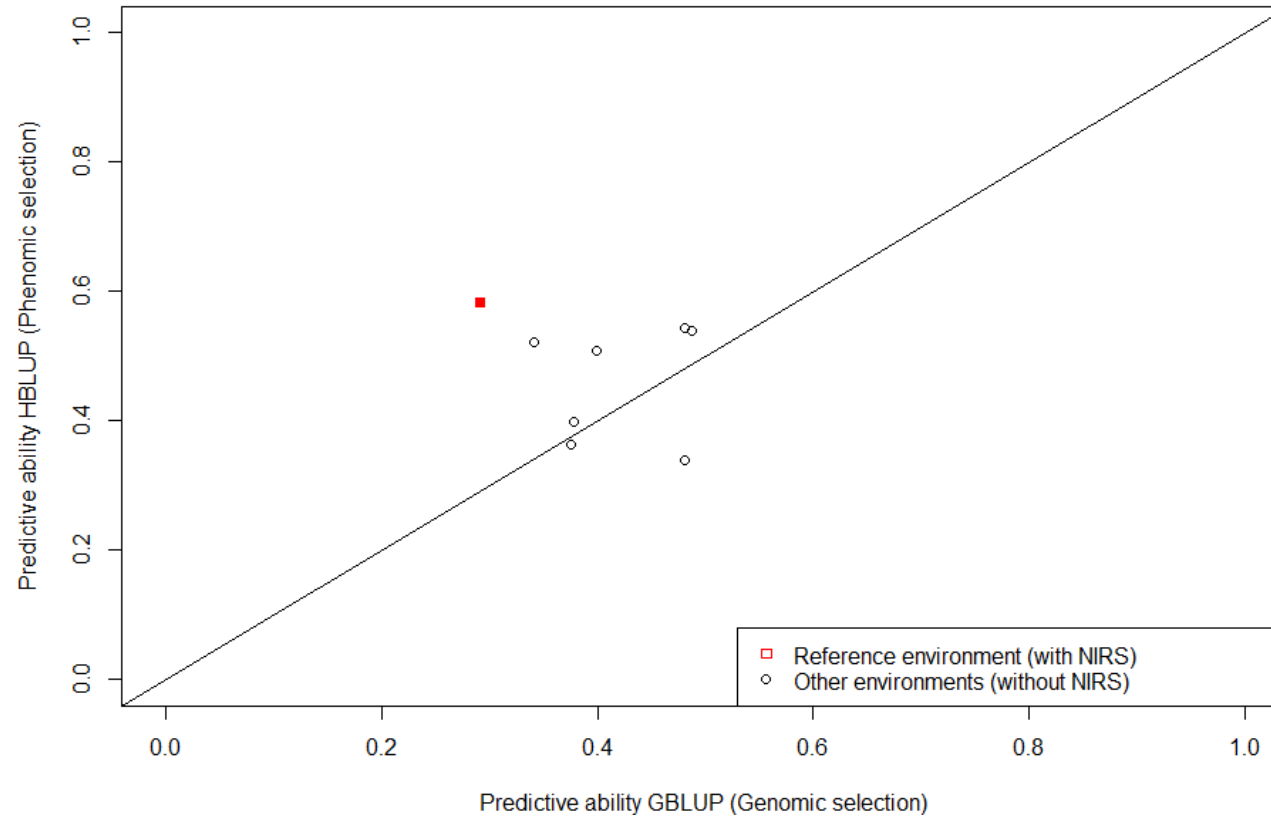
Genomic heritability is high for most wavelengths, so absorbance can be considered as a polygenic trait. Spectra are mainly driven by genetics (and GxE). Can we use it for predictions ?

Predictive abilities



- Predictive abilities are intermediate for GS and PS.
- Predictive abilities are higher in the reference environment than in the other environments (probably because NIRS capture GxE interactions).

Comparing GS and PS predictive abilities



- On average PS is more accurate than GS
- The gain is higher for the reference environment (GxE captured by the spectra ?)

Conclusions

- Phenomic prediction is **easy** to implement !
- It is **worth pre-treating** the spectra (and doing some **spatial adjustments for each wavelength** if possible is strongly recommended).
- Phenomic predictions are **accurate for polygenic traits** (but not for oligogenic traits, see Zhu et al. 2021, TAG).
- On this dataset, PS is more accurate than GS in the reference environments **and in the environments without any NIRS data** (scenario S2, GLOB).
- The gain in comparison to GS is higher in the reference environment, probably because of **GxE interactions captured by the spectra** (see Robert et al. 2022b TAG for an analysis on GxE).
- **It is not necessary to grow the test set** to apply phenomic selection, as it can be applied with NIRS collected on seeds (or the previous year in nurseries).