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EXploring PhenOtypic SpacE for mining genotypes and alleles in Maize

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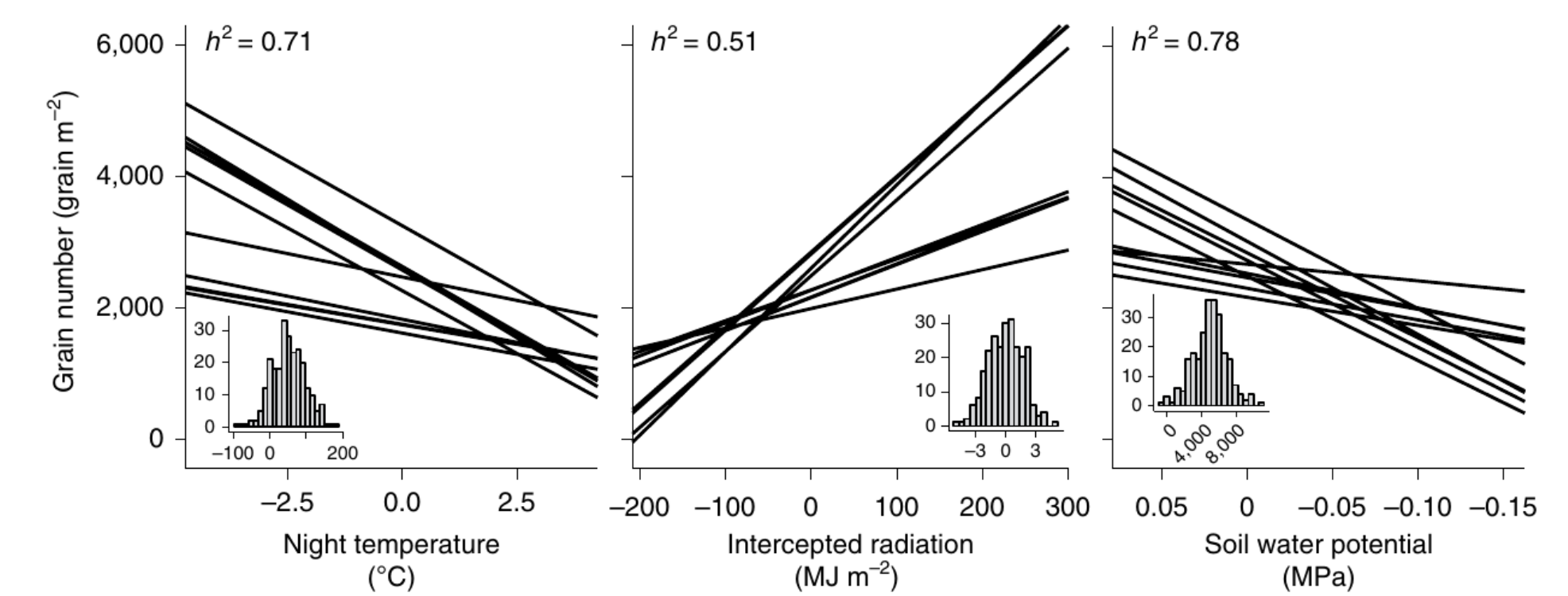
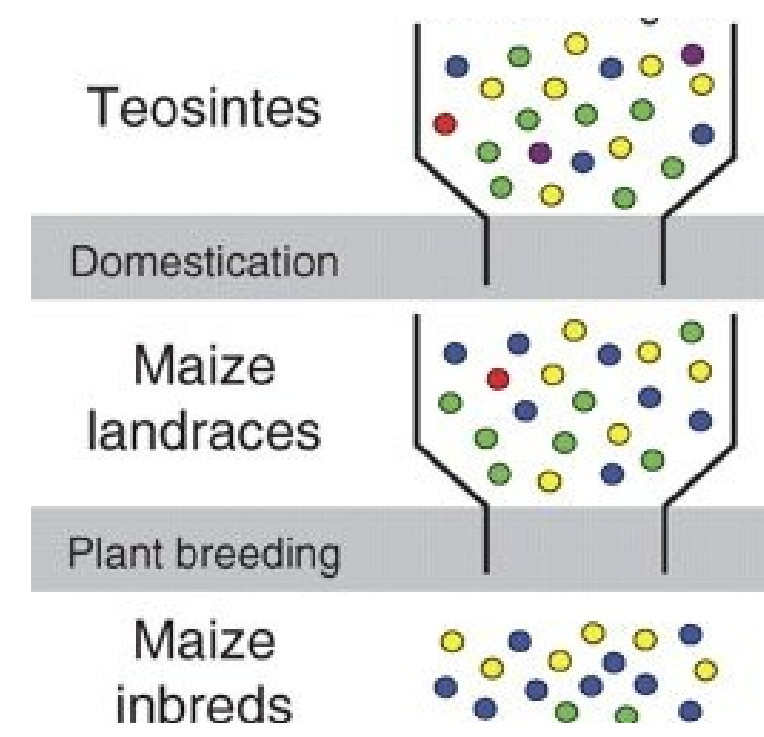
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Background

- Climate change: more frequent episodes of drought and/or heat (extreme events) ⇒ Impacting negatively the crop yield
- Maize is a major crop worldwide with large diversity ⇒ can be used for identification of novel alleles for tolerance to drought and heat
- Phenotypic response can differ for different varieties $P = G + E + G \times E$
Detection of genomic regions will depend on the environment ⇒ environment dependent effects



Which genotypes and alleles across the exotic gene pool are favorable under different drought or heat conditions?
How to navigate the vast space of genotype-by-environment (G×E) interactions to discover climate adaptations?

Progress in phenomics and modelling makes it possible to predict G×E from a multitude of physiological traits measured on a phenotyping platform



High-throughput Phenotyping platforms:
→ multiple scales and with a high dimensionality



Multi-environment field trials:
→ environmental scenarios in wide ranges, target traits and their components



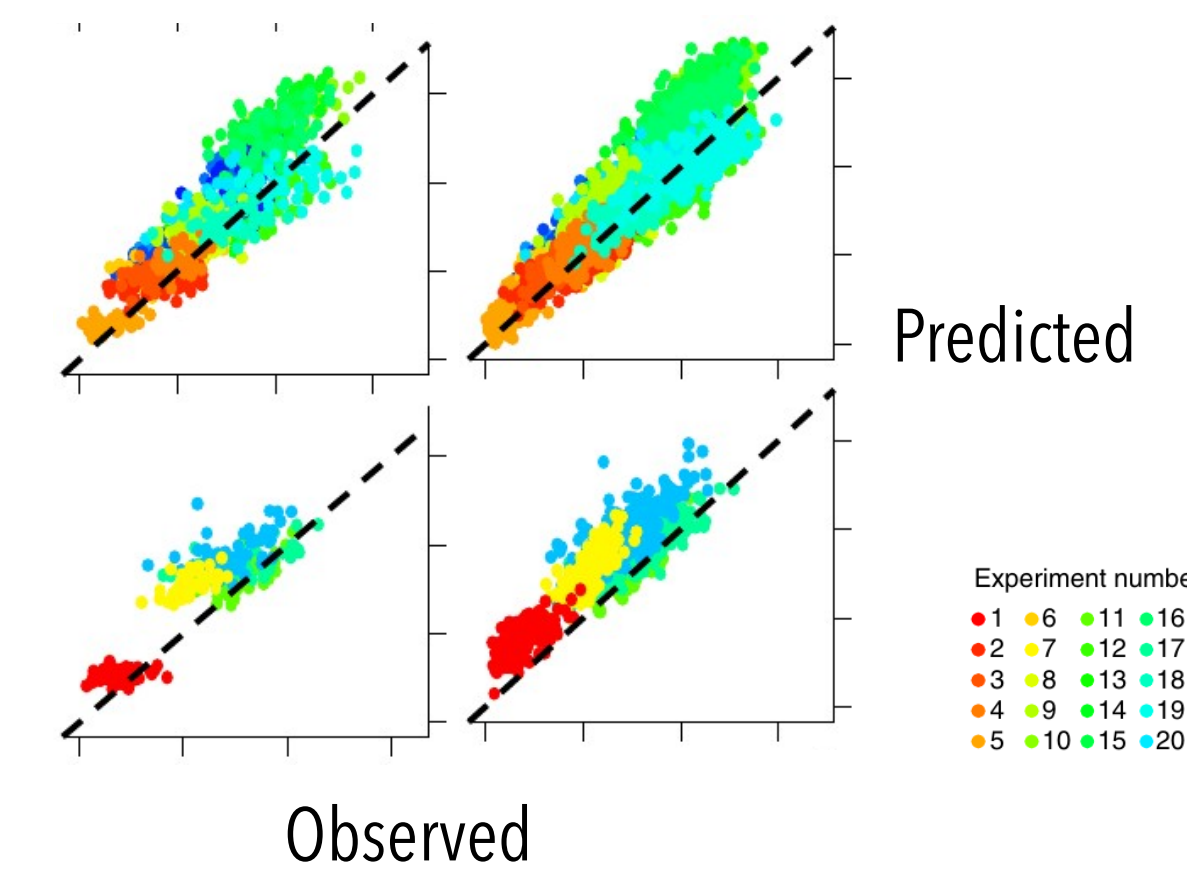
Model

Diversity of modelling techniques:

Statistics: penalized regression, Bayesian, Deep Learning, etc.

Crop models: APSIM, Sirius Quality, etc.

Prediction/Simulation across environmental conditions:

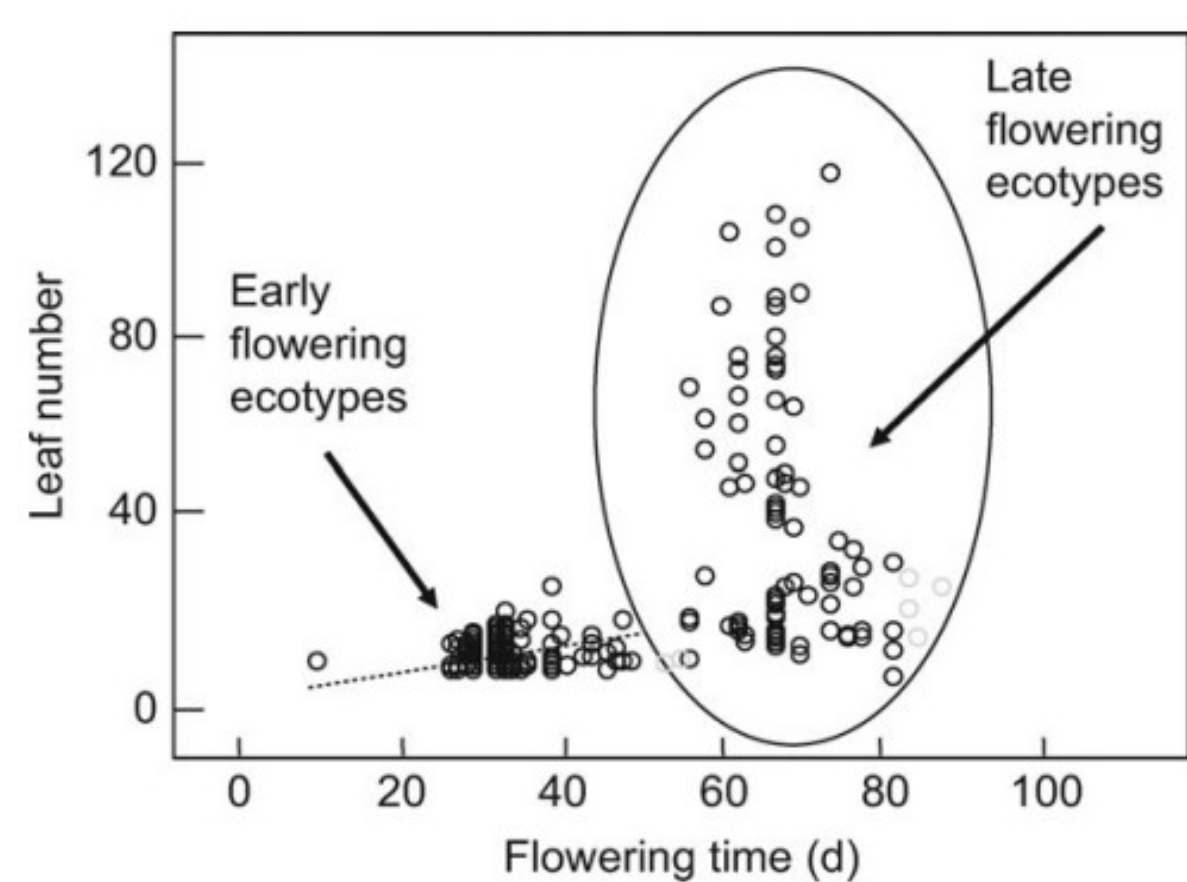


→ However, a considerable effort still needs to be dedicated to understanding the distribution/structure/shape for combinations of correlated traits - phenotypic space.

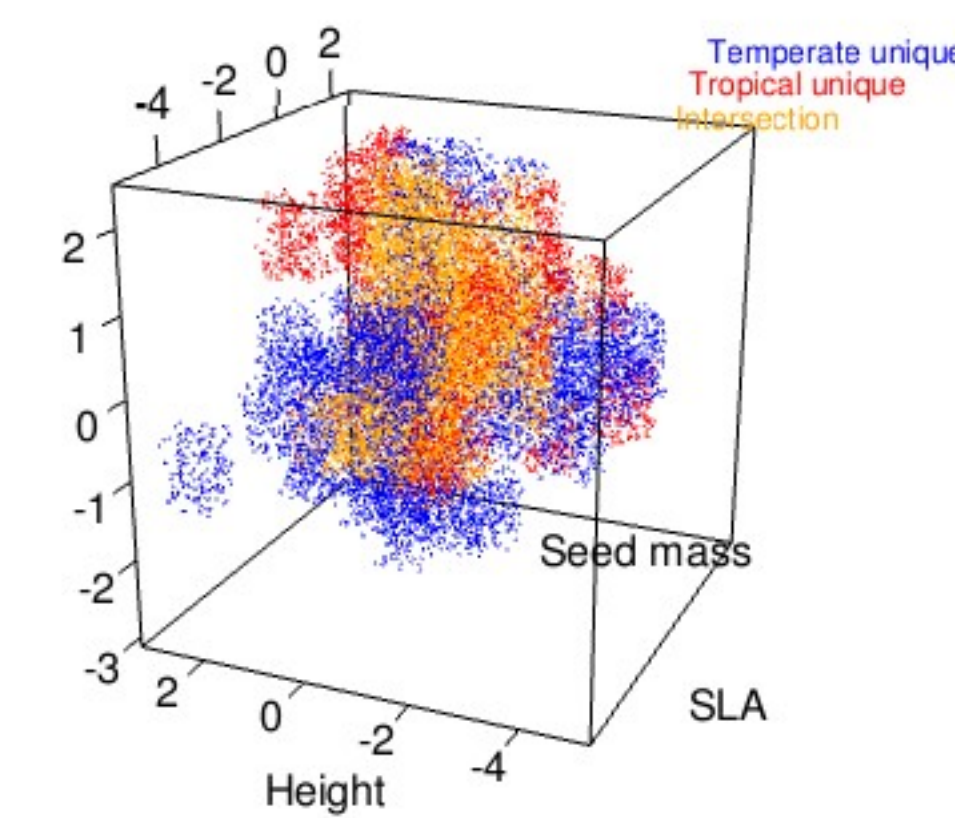
Objectives

The **phenotypic space** is not a new concept:

- Hutchinson (1957) : niche = n-dimensional hypervolume describing the set of environments that permit a species to exist
- Pigliucci (2007): a phenotypic space shaped by the interaction of various kinds of constraints and selective pressures

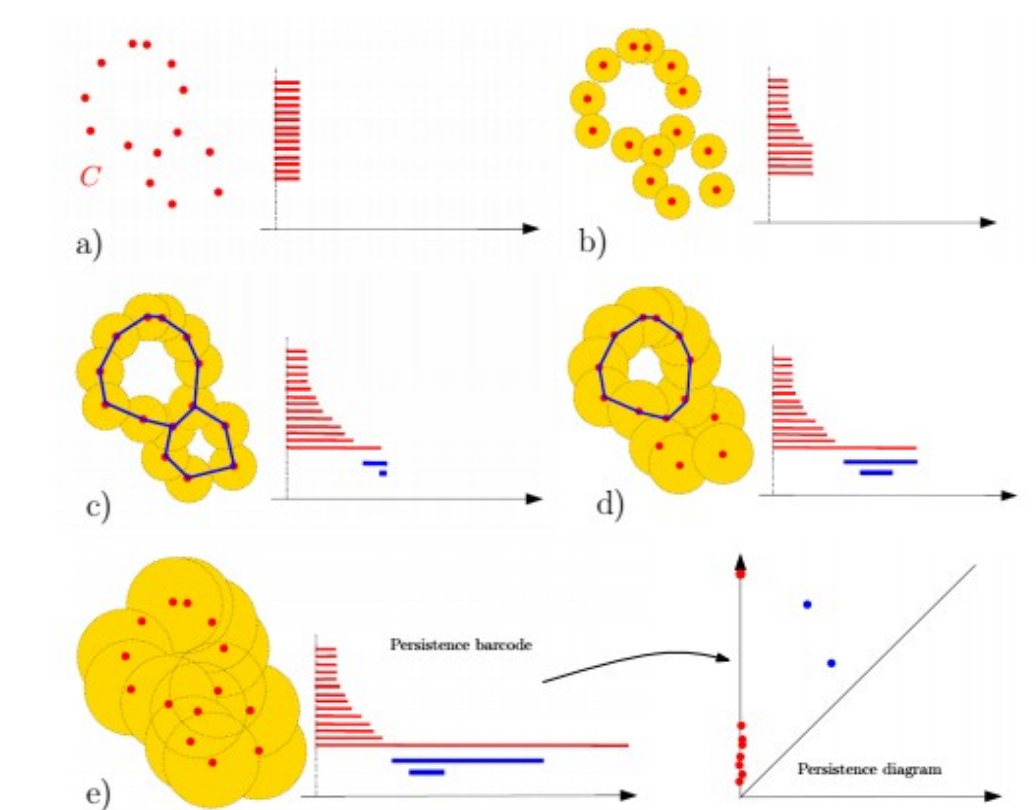


Hypervolume to investigate ecological niches: multidimensional trait space occupied by species in a community



→ geometrical shape can then be delineated within this space and used to describe the **size, position and geometry of the system**

Topological Data Analysis aims at analysing the structures underlying data represented as point clouds in metric spaces

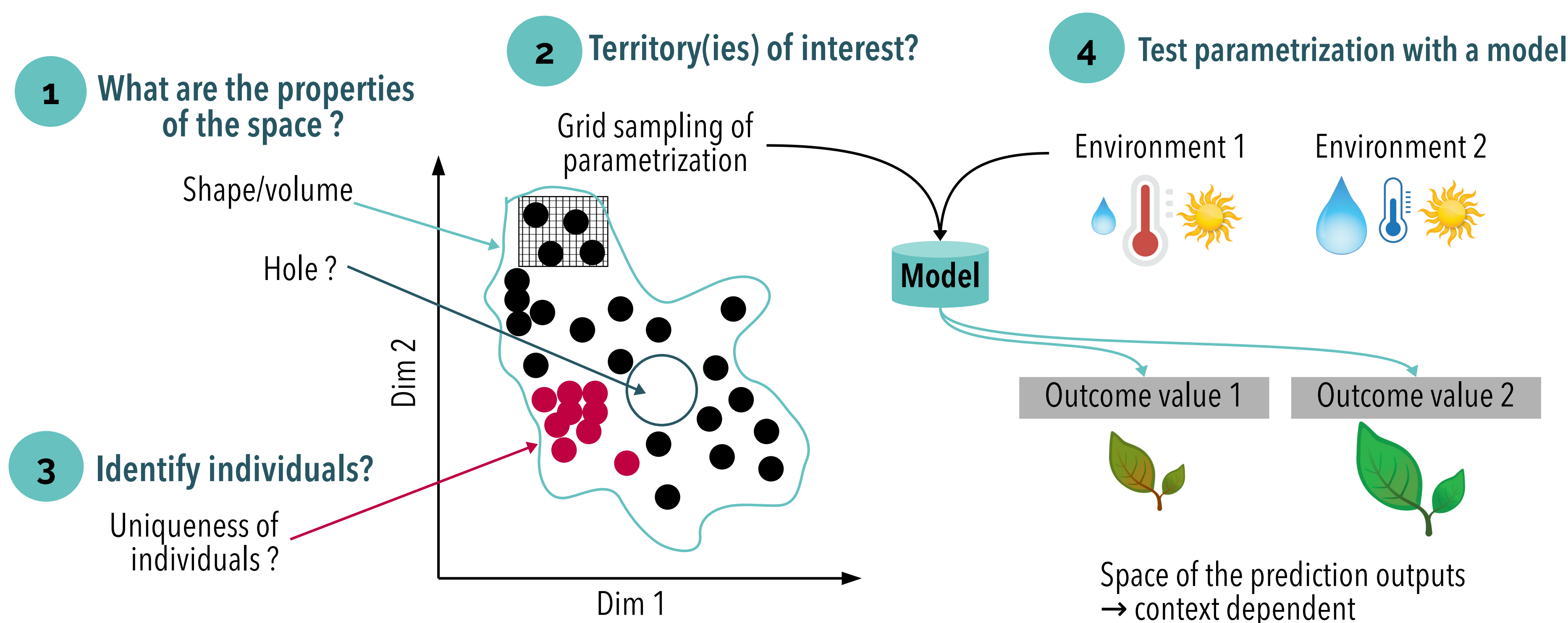


→ Application to plant phenotype: leaf and root shape + QTL

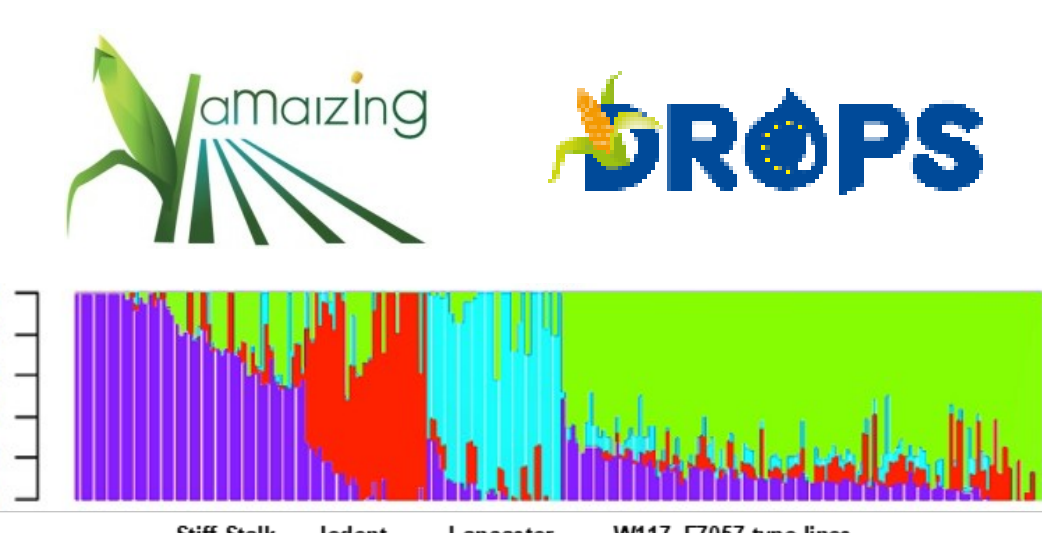
→ Interfacing ecophysiological genetics, ecology/evolution and data science, we aim to EXPOSE new ways of framing and characterizing G×E for crops

Strategy

Toy example: 2-dimension space - 10 individuals - Dim 1 and Dim 2 are input of a model to simulate relevant outcome



Step 1 : framework development Existing datasets



Step 2 : framework test Datasets generation



PhenoArch platform - INRAE- Montpellier

Expected outcomes

- Development of novel approaches for the analysis of phenomics data using cross-disciplinary ideas and methods
- Generation of new datasets on immortalized genetic stocks (public resources).
- Perspective in genomic prediction
- Breeding for changing climate (identification of unique adaptation)