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EXploring PhenOtypic SpacE for mining genotypes and alleles in Maize - EXPOSE

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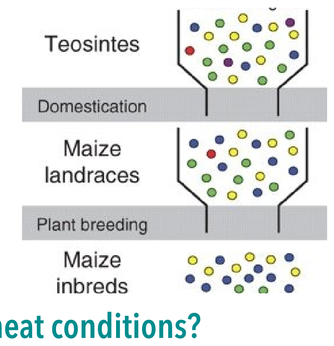
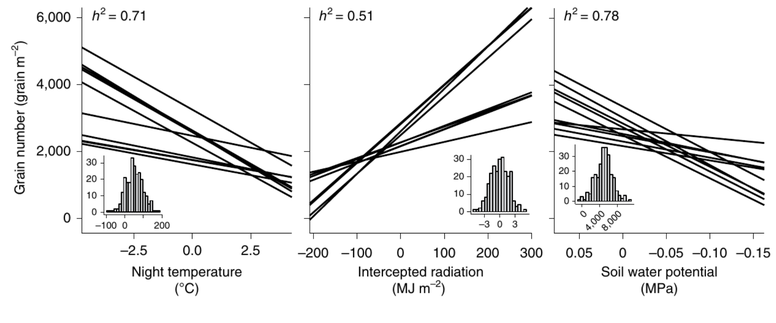
P10

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 × 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

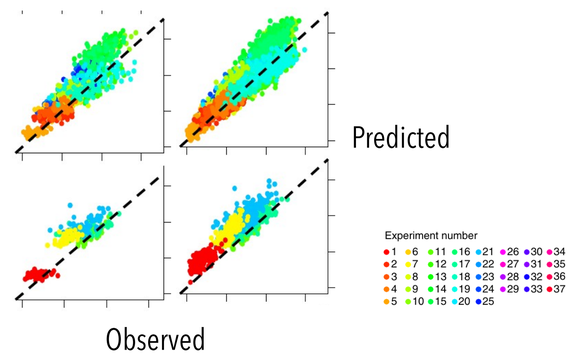
Model

Diversity of **modelling techniques**:

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

Crop models: APSIM, Sirius Quality, etc.

Prediction/Simulation **across environmental conditions:**

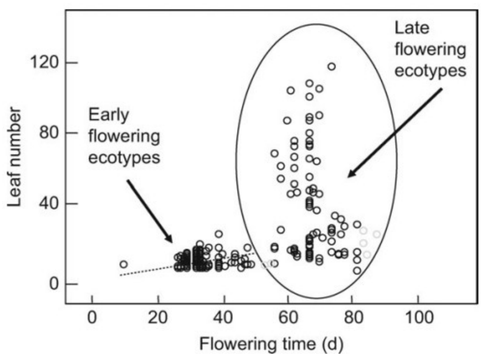


→ **However, a considerable effort still needs to be dedicated to understanding the distribution/structure/shape for combinations of correlated traits - phenotypic space.**

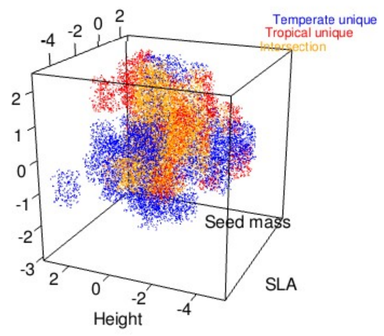
Objectives

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

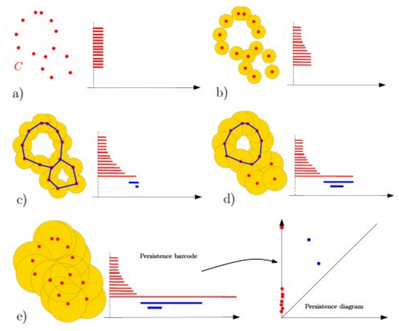


Hypervolume to investigate ecological niches : multidimensional trait space occupied by species in a community



→ 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

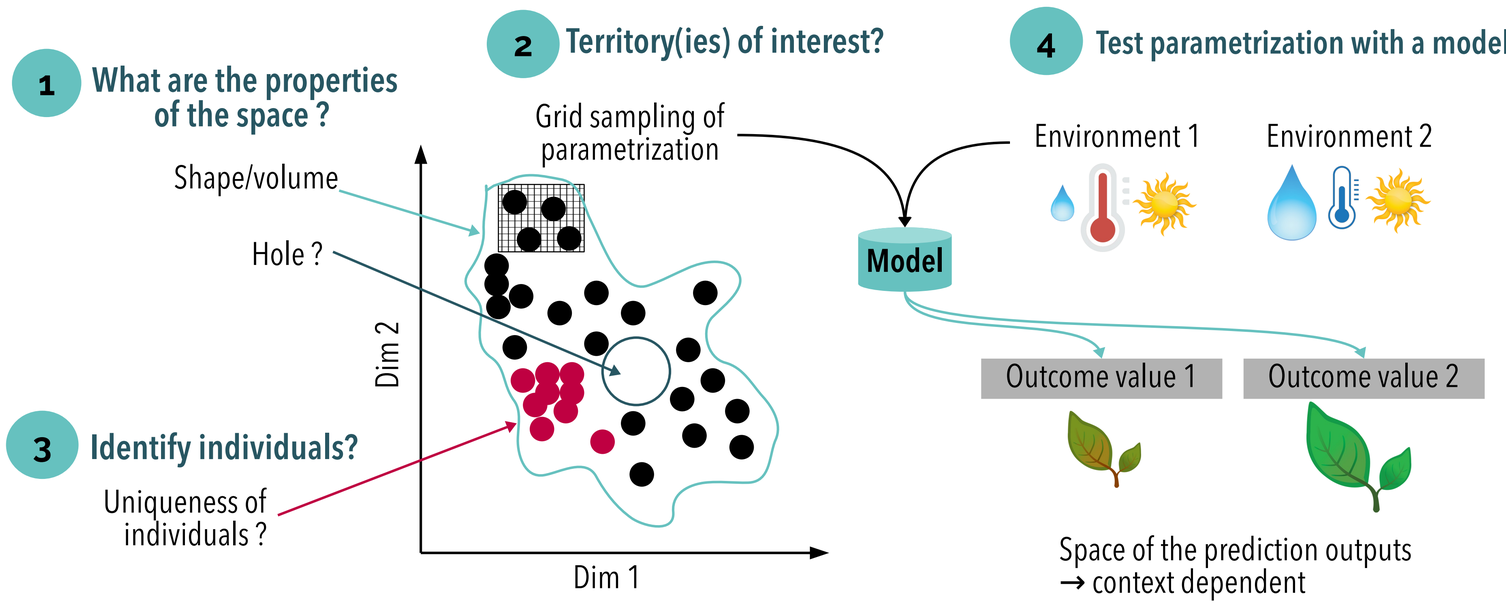


→ Application to plant phenotype: leaf and root shape + QTL

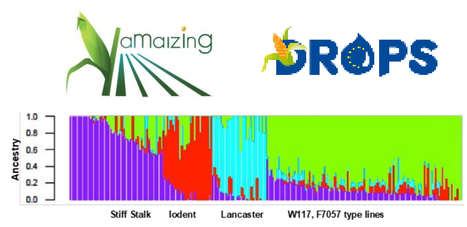
→ **Interfacing ecophysiological genetics, ecology/evolution and data science, we aim to EXPOSE new ways of framing and characterizing G×E for crops**

Strategy

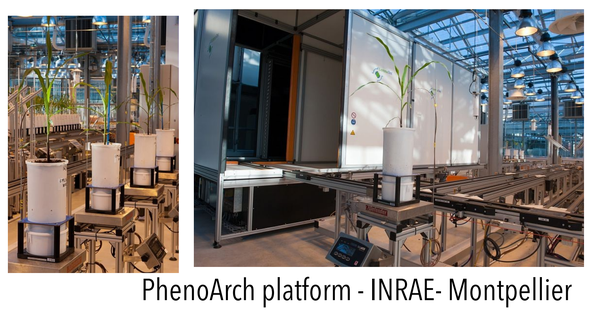
Toy example: 2-dimension space - 10 individuals - Dim 1 and Dim 2 are input of a **model** to simulate relevant outcome



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)

Lamanna et al. 2014 *PNAS* 111 (38) 13745-13750
Blonder et al. 2014 *Global Ecology and Biogeography* 23:595-609
Chazal et Michel 2017 *hal*-01614384
Li et al 2018 *Plant Physiol.* 177:1382–1395
Hutchinson 1957 *Cold Spring Harbor Symposia on Quanti. Biol.* 22:415–427
Pigliucci 2007 *Evolution*, 61: 2743-2749
Millet et al. 2019 *Nature Genetics* 51, 952–956
Alvarez Prado et al. 2018 *Plant, Cell & Env,* 41:314-326.
Cabrera-Bosquet et al. 2016 *New Phytologist* 212, 269-281
Lacube et al. 2020 *Journal of Exp. Bot.* 71 (18) 5577–5588
Yamasaki et al., 2005 *Ann Bot* 100: 967-973