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Norms of reaction for maritime pine

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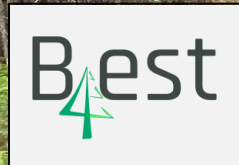
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B4EST international conference – Managing Forest Genetic Resources for an uncertain future

Norms of reaction for maritime pine

***Session A** : Accelerating breeding to cope with new challenges and uncertain future – 20th June 2022*

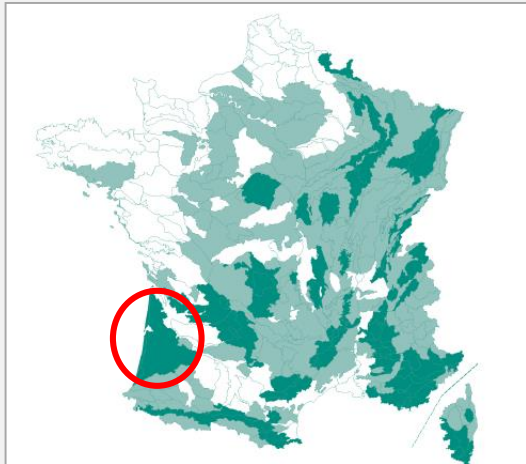
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Laurent Bouffier, INRAE (UMR BIOGECO Pierroton)
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Maritime pine (*Pinus Pinaster*) breeding in France

« Landes de Gascogne » forest

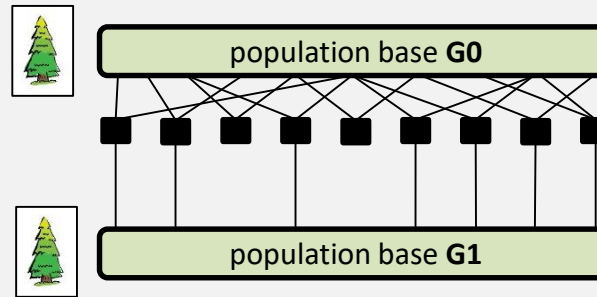
- 0,8 million hectares (24% of French wood harvest)
- Main uses in carpentry, joinery, stationery



- Plantations with **improved seedlings**
- Mainly based on the **Landes provenance**

Recurrent selection scheme

- Started in the ~1960 → 3rd generation today

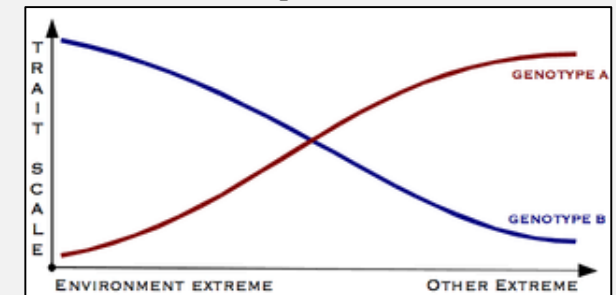


- Targeted traits :
 - **Growth** (height, circumference, straightness)
 - **Adaptation** to the environment
 - **Wood quality**
- **Genetic values** estimated with **pedigree**

Dynamic phenotypes : NoR

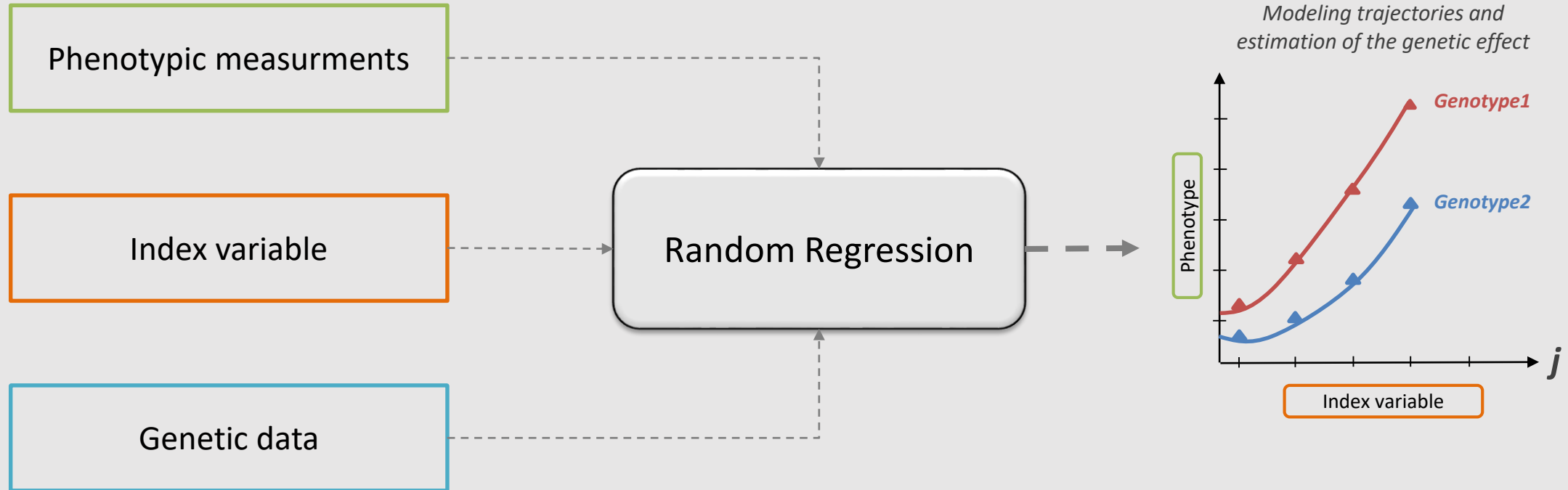
- Classical selection focuses on **final growth traits**
- Integrative phenotypes with **no consideration of the environment**

NoR : pattern of phenotypic expression of a single genotype across a range of environments

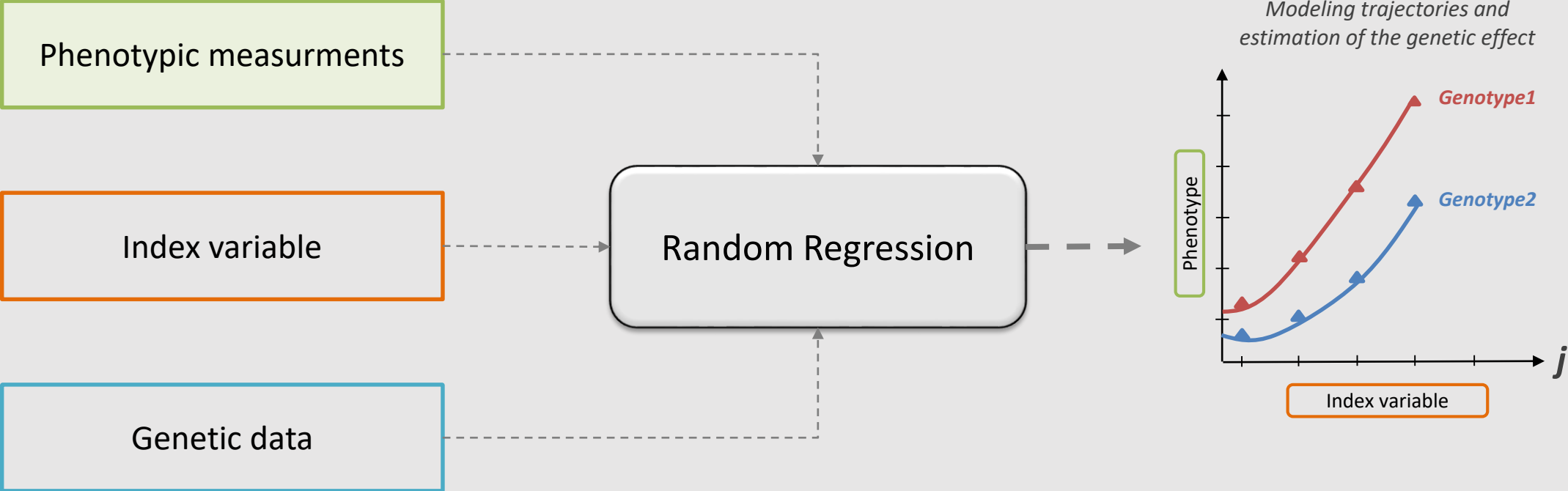


- Consideration of **dynamic** and **explicative** traits
- Evaluation and prediction of **genetic values** taking account of the **environnement** (even in unobserved environments)

Construction of norms of reaction

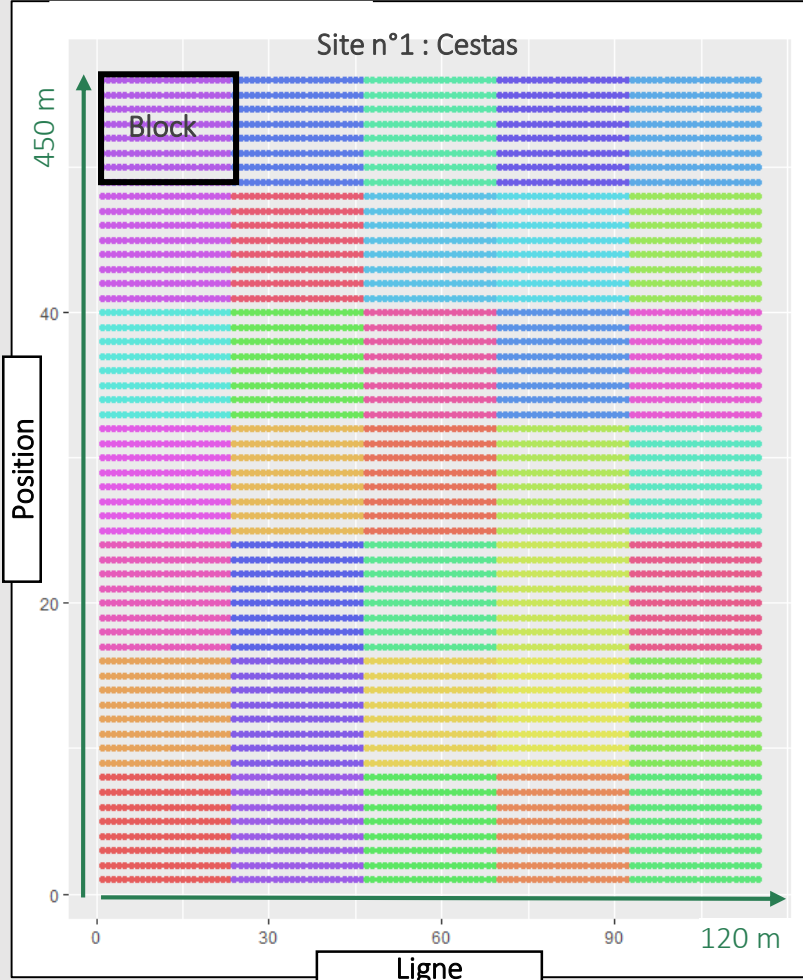


Construction of norms of reaction



Experimental design and measurements

Experimental design for maritime pine (6300 trees)

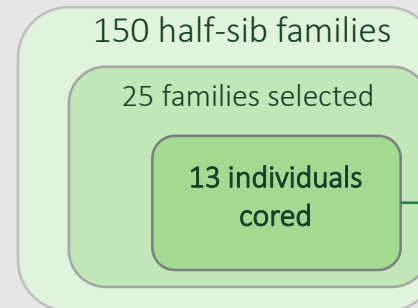


Experimental design

- 2 locations : Cestas (humid) & Escource (dry)
- Installation in **1996** : **26** years old trees
- **150** half-sib families with **35** individuals/family → **6300** trees per site
- **Complete** block design (1 individual of each family per block)

Phenotypic measurements :

- Classical growth measures at different ages (height, circumference, straightness)
- Core sampling of **325** trees per site :



Environmental measurements :

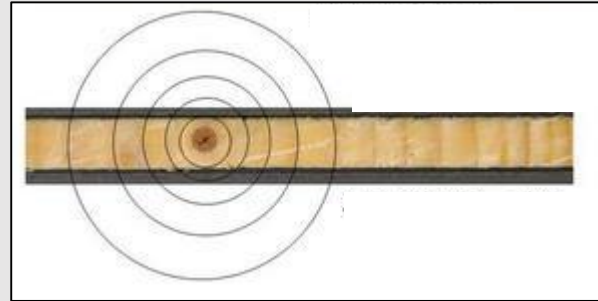
- Conventional annual climate measurements (temperature, rainfall...)

Experimental design and measurements

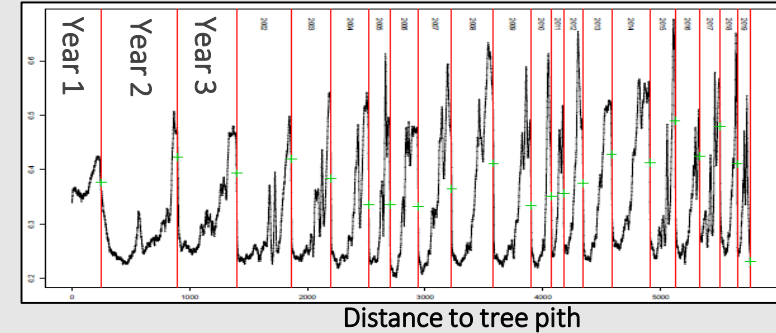
Core sampling



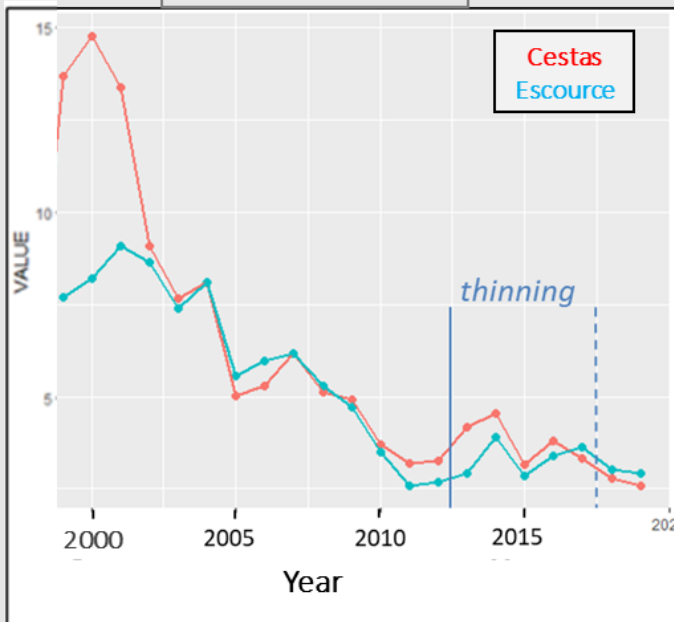
Cutting in boards



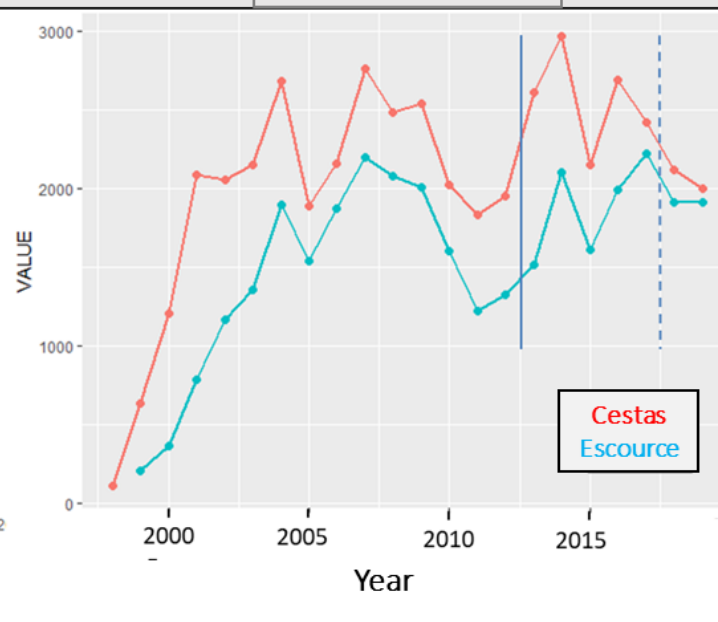
Density profile after X-ray radiography



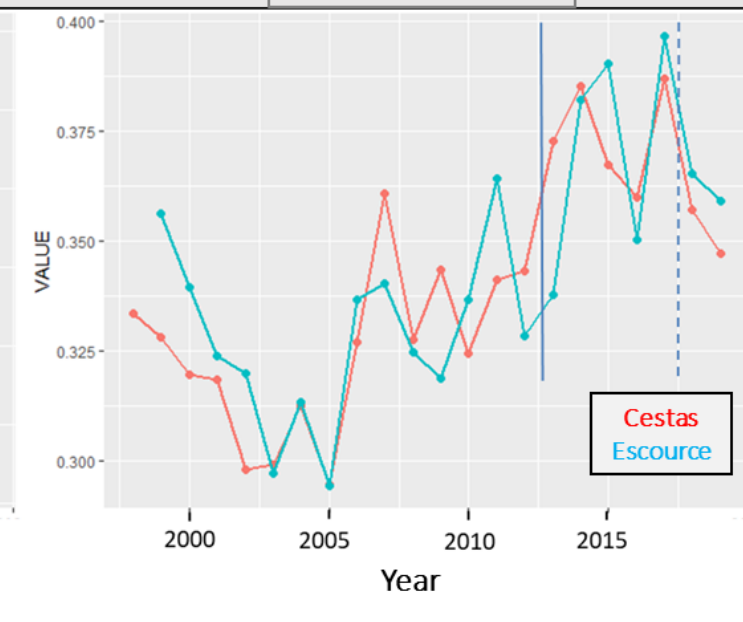
Ring width



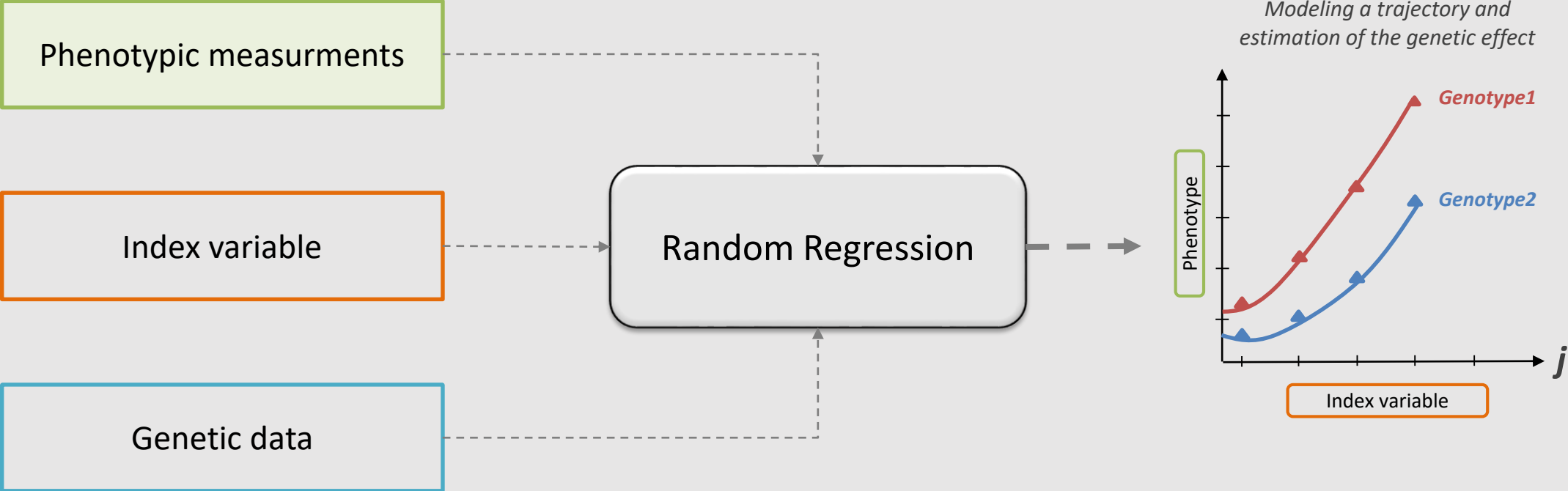
Ring surface



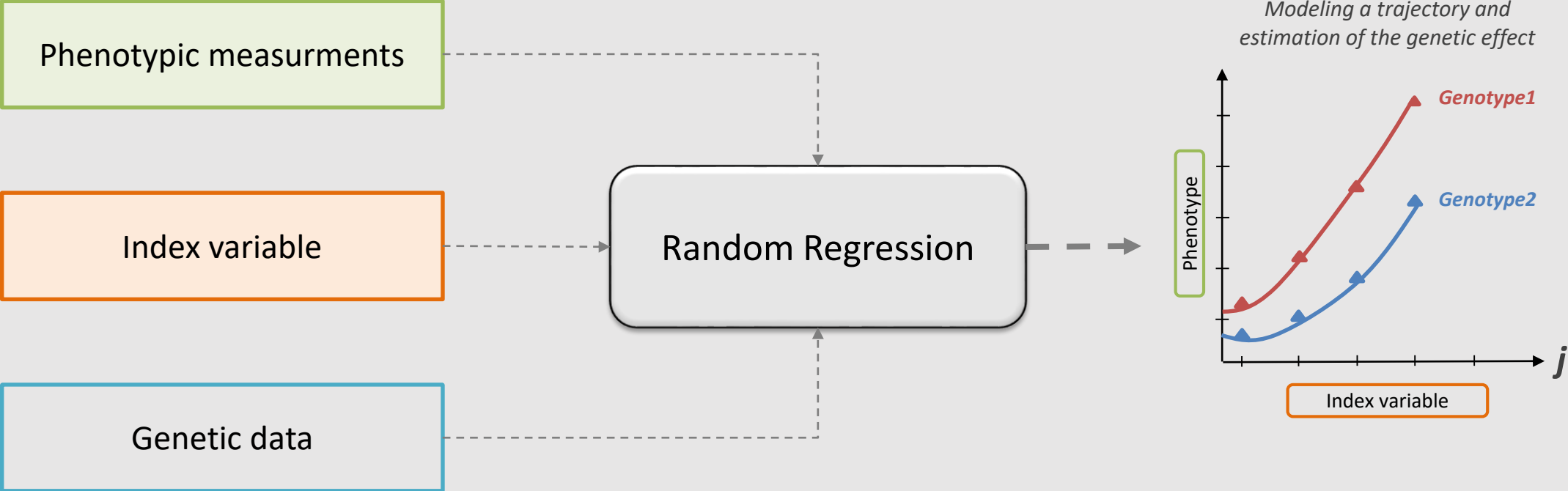
Ring mean density



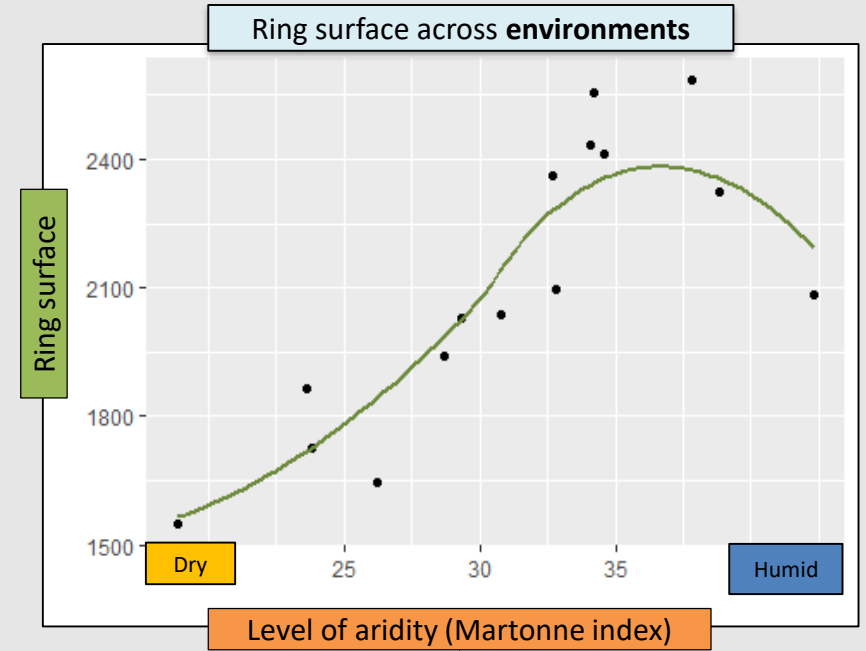
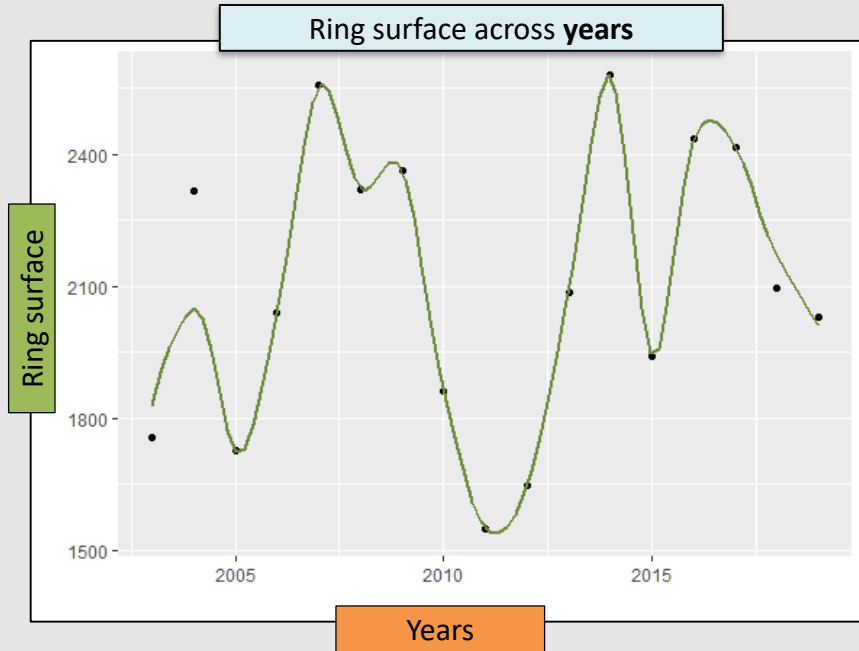
Construction of norms of reaction



Construction of norms of reaction



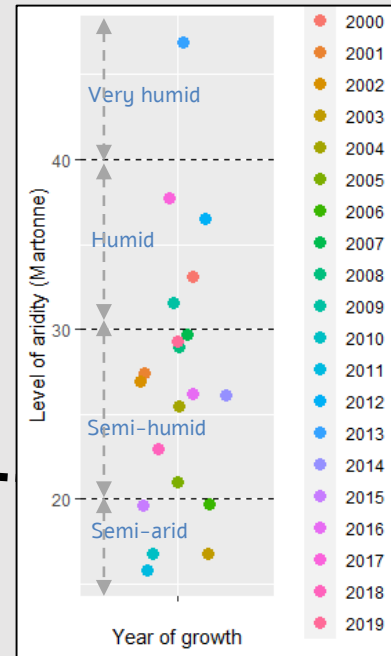
Construction of norms of reaction



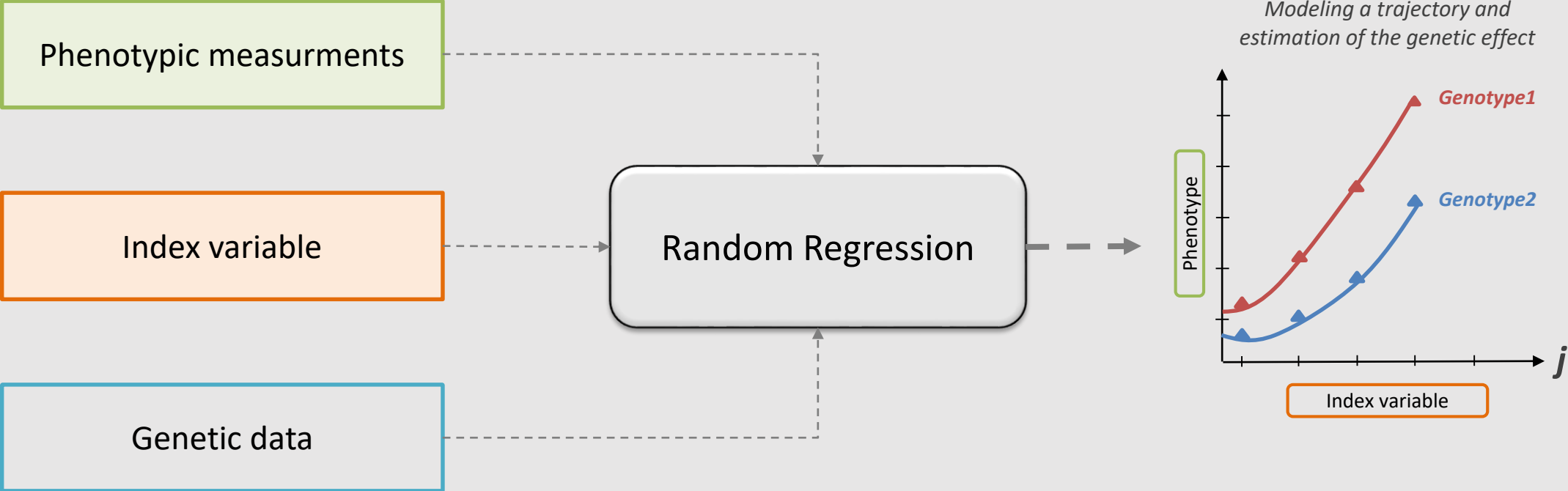
For each year, characterization of global aridity with Martonne index

$$I = \frac{12p}{t + 10}$$

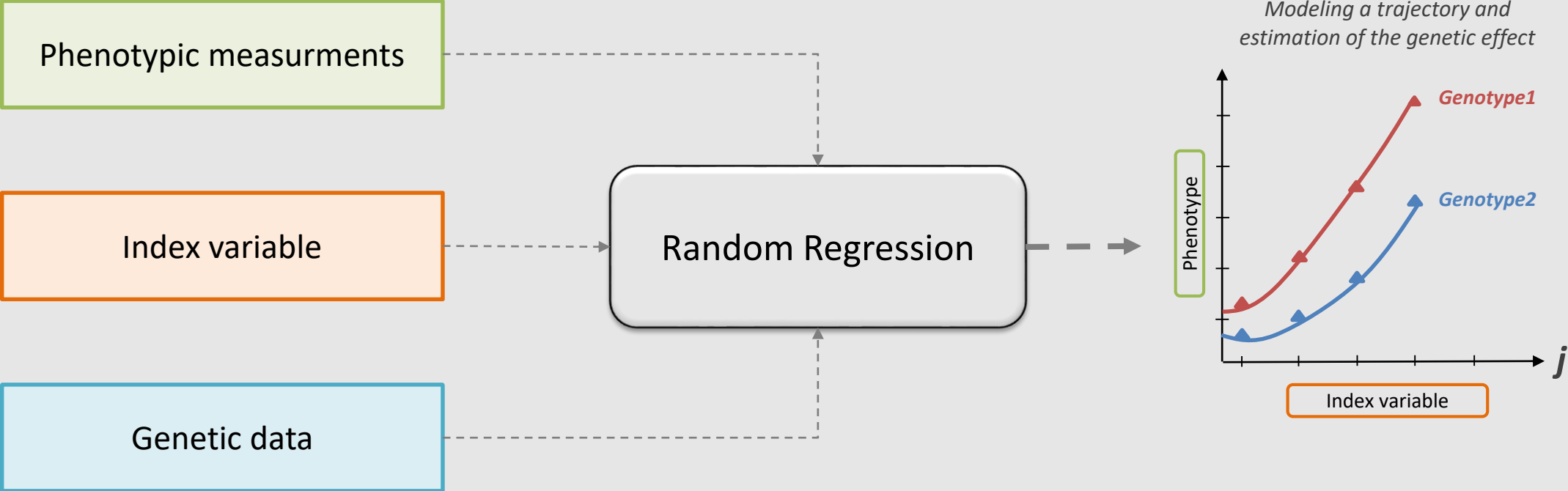
p : cumulative rainfall (mm)
t : mean temperature (°C)



Construction of norms of reaction

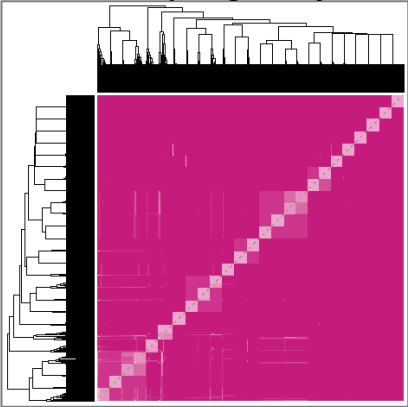


Construction of norms of reaction

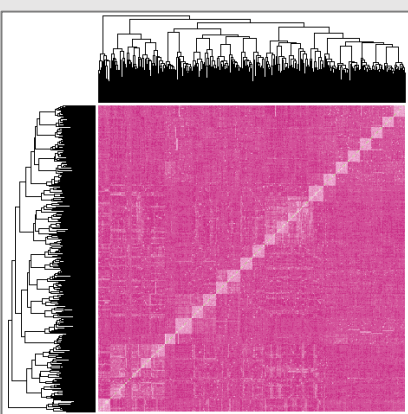


Construction of norms of reaction

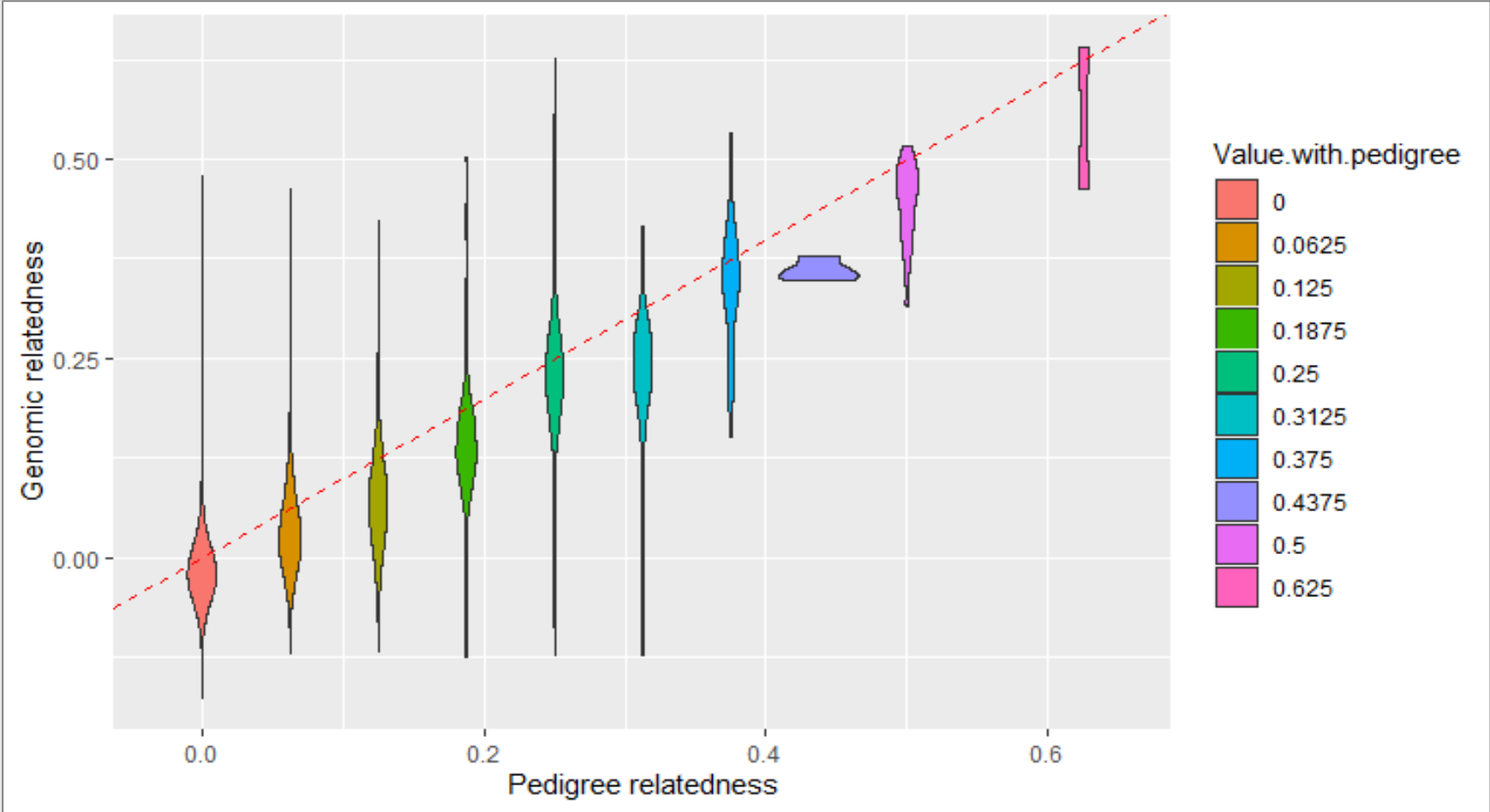
A matrix
calculated with pedigree information



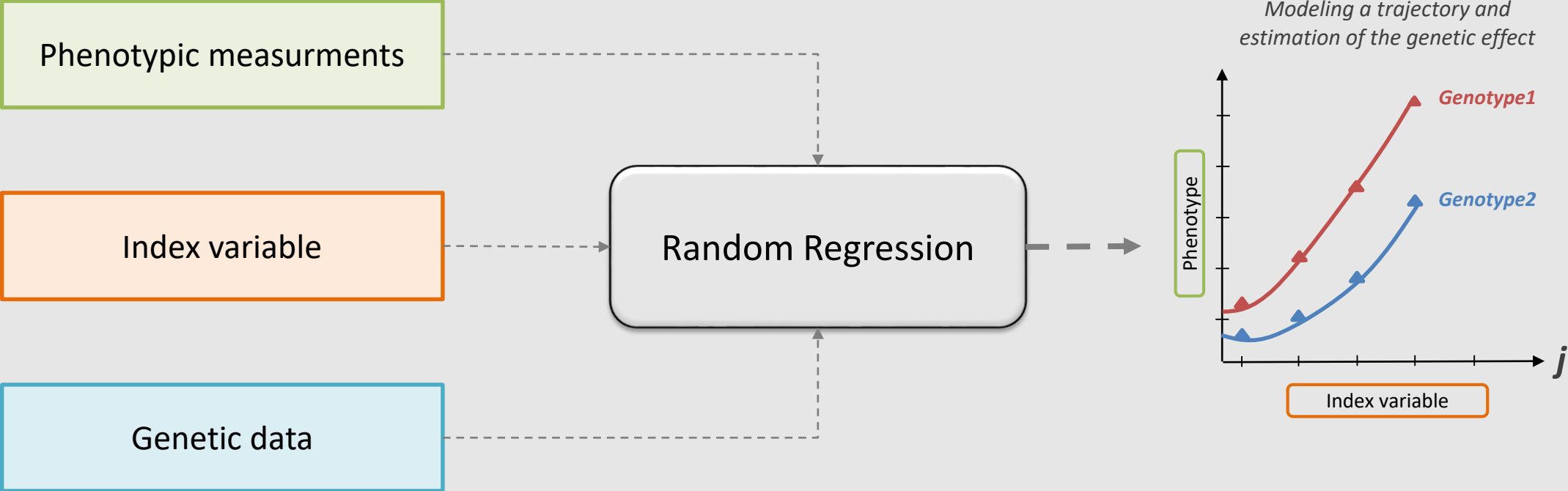
G matrix (VR1)
Calculated with 3000 SNPs information



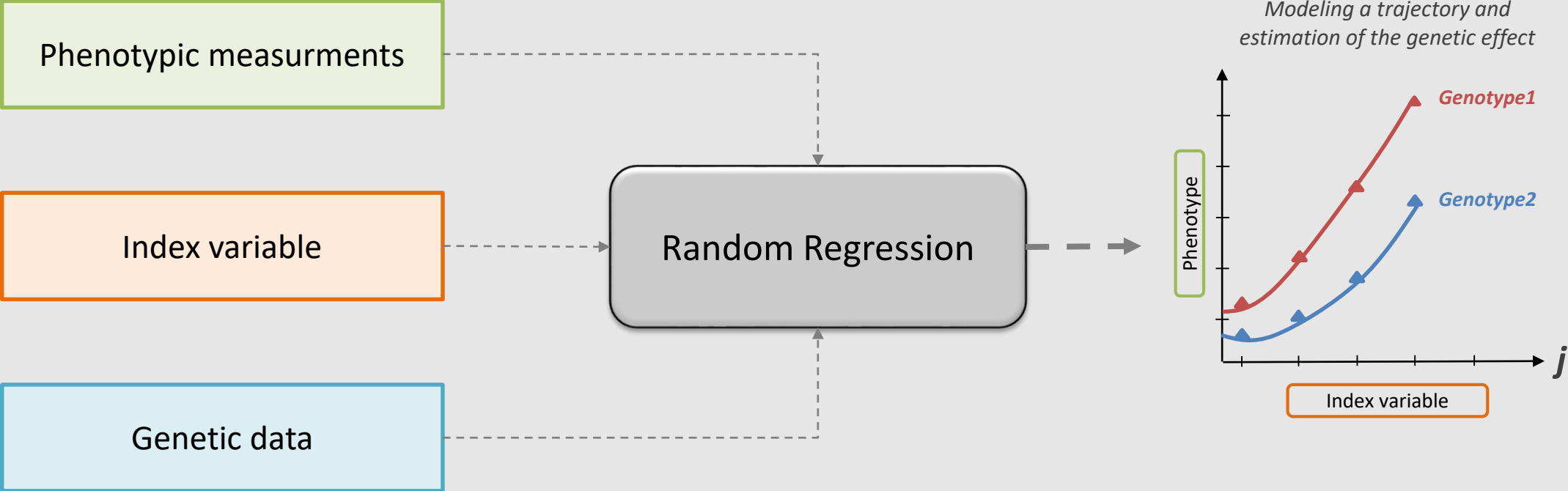
Comparison of relatedness calculated with genomic data and relatedness calculated with pedigree data



Construction of norms of reaction

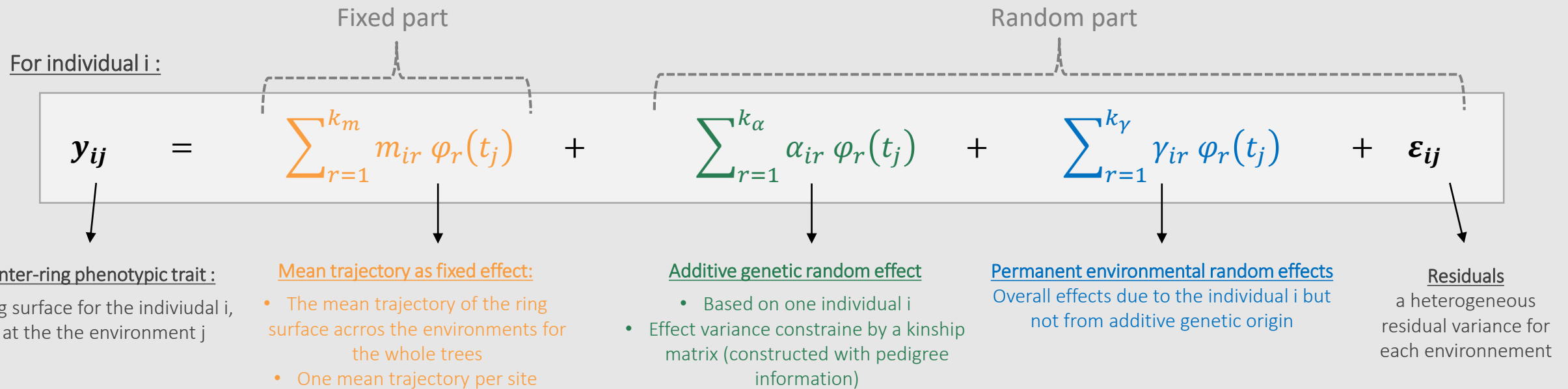
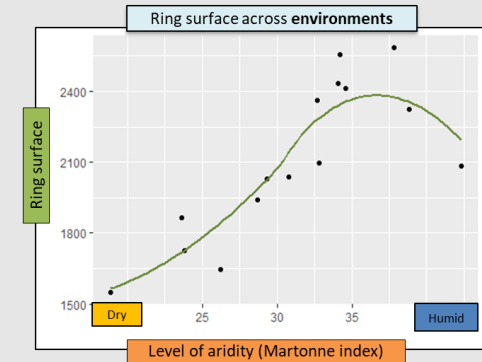


Construction of norms of reaction



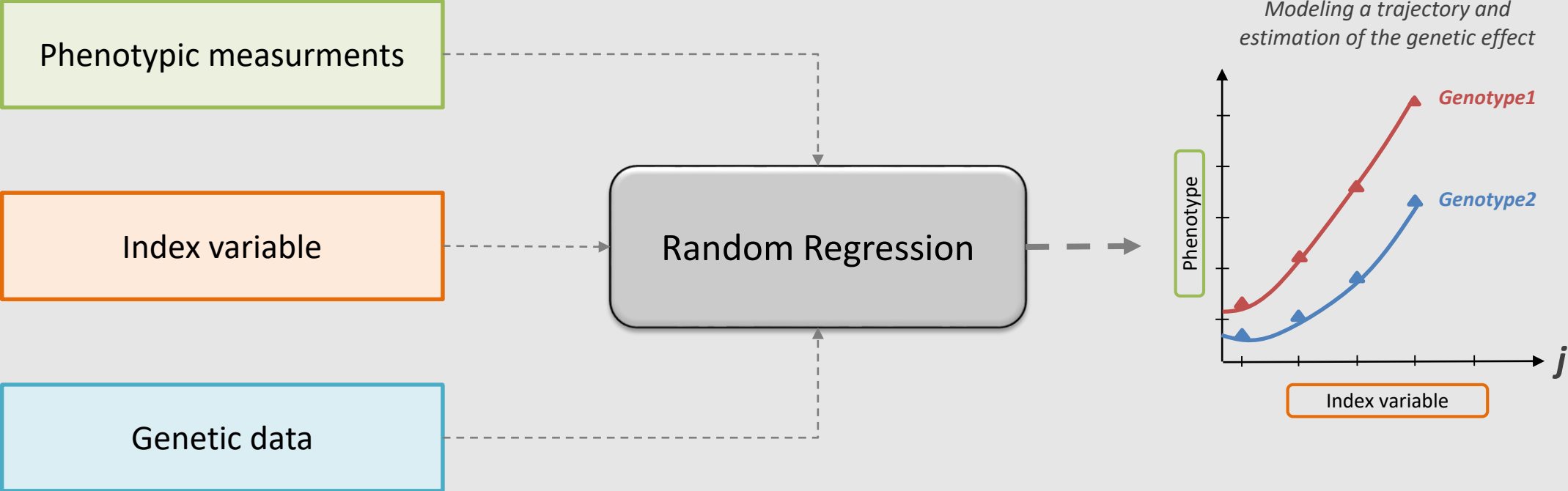
Random regression model (RRM)

- We model individual trajectories according to the level of aridity of the environment (Martonne index)

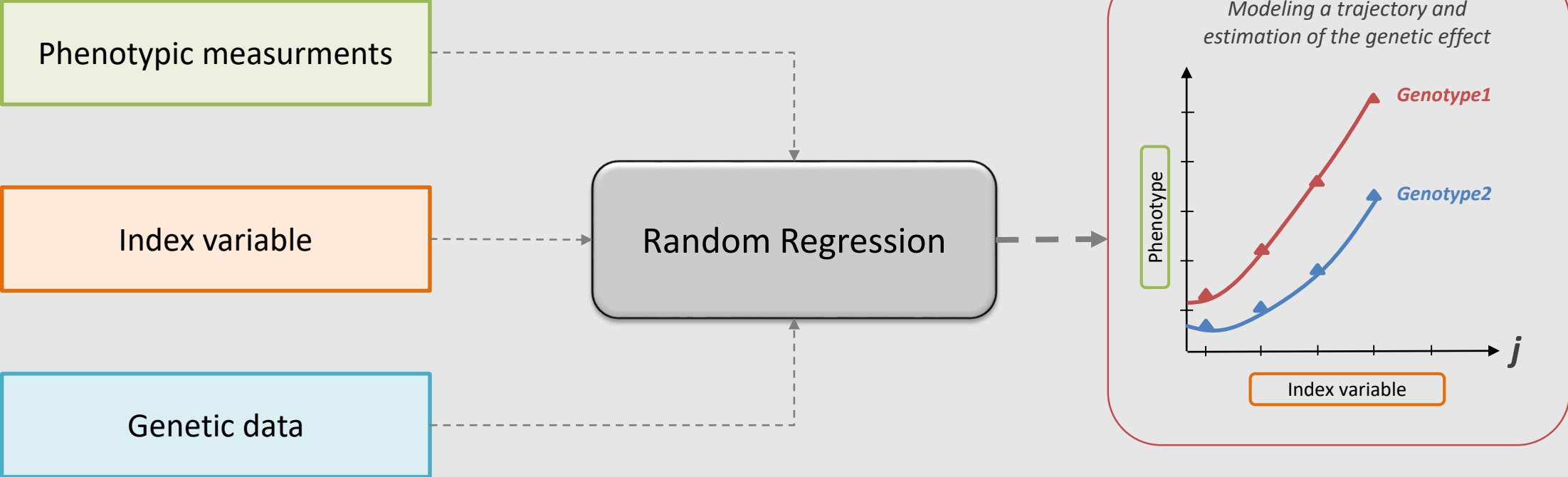


- Mean trajectories, additive genetic effect and permanent environmental effects are modeled by 2-order Legendre polynomials

Construction of norms of reaction



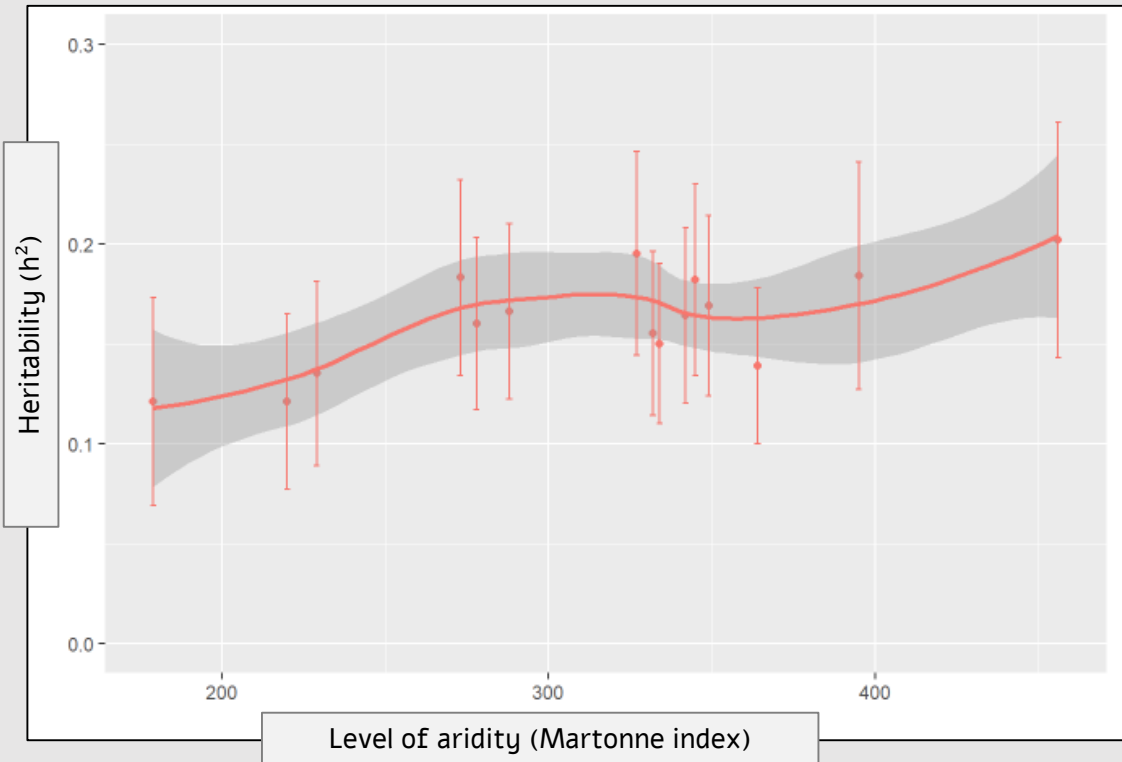
Construction of norms of reaction



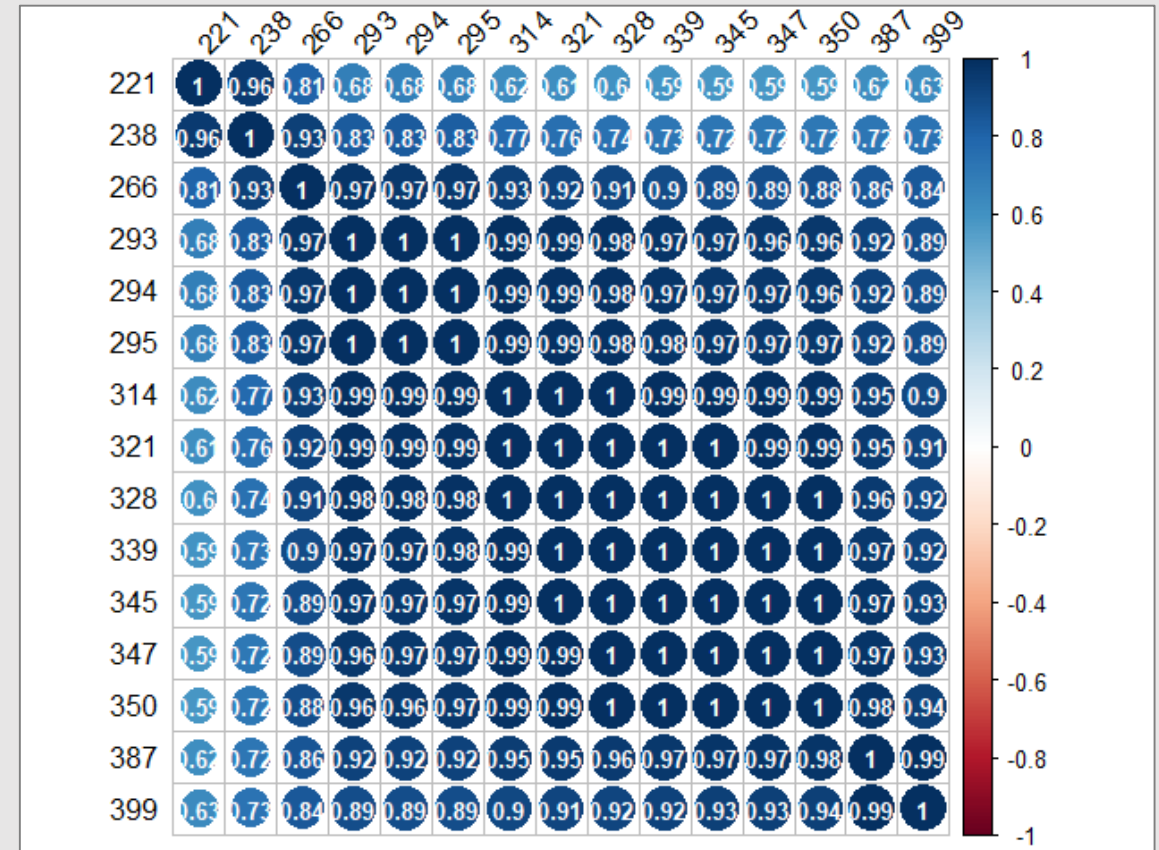
Norms of reaction : heritability and genetic correlations

$$y_{ij} = \text{Mean trajectory } (t_j) + \text{Additive genetic effect}_i(t_j) + \text{Permanent environmental effect}_i(t_j) + \varepsilon_{ij}$$

Heritability of ring surface estimated with a random regression model of order 2 (RRM2)



Genetic correlations between environments (levels of aridity) estimated with RRM2



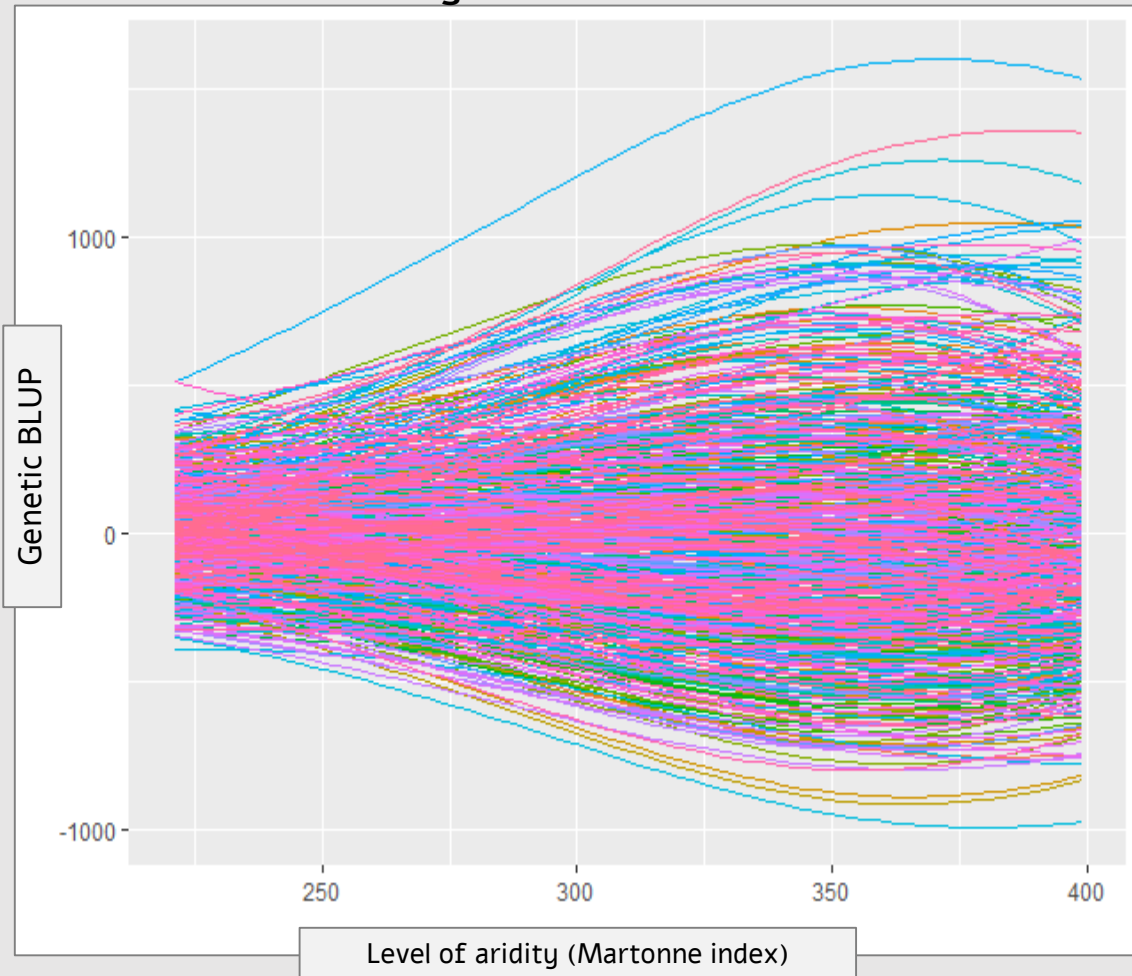
Norms of reaction : additive genetic trajectories

$$y_{ij} = \text{Mean trajectory } (t_j) + \text{Additive genetic effect}_i(t_j) + \text{Permanent environmental effect}_i(t_j) + \varepsilon_{ij}$$

Norms of reaction : additive genetic trajectories

$$y_{ij} = \text{Mean trajectory } (t_j) + \text{Additive genetic effect}_i(t_j) + \text{Permanent environmental effect}_i(t_j) + \varepsilon_{ij}$$

Evolution of individual genetic values across environments

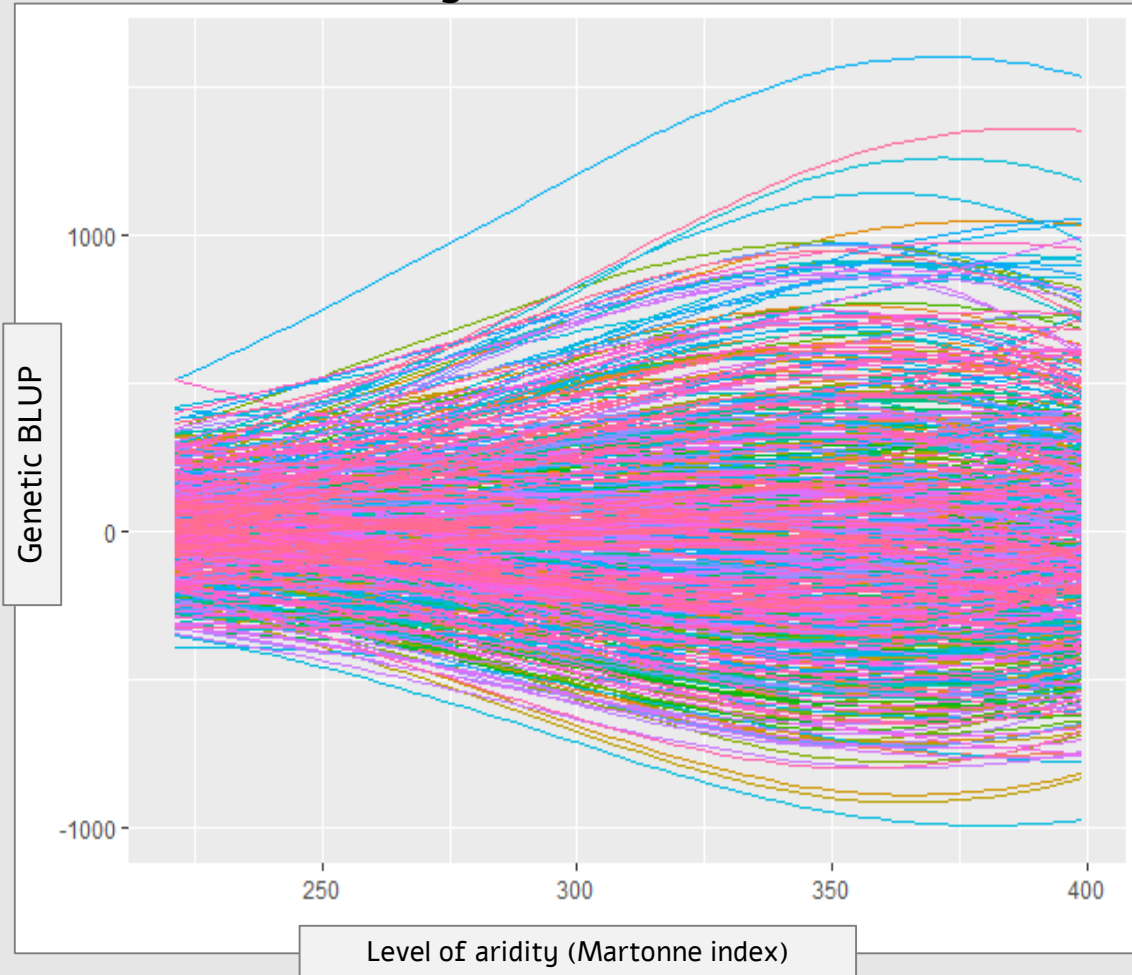


Norms of reaction : additive genetic trajectories

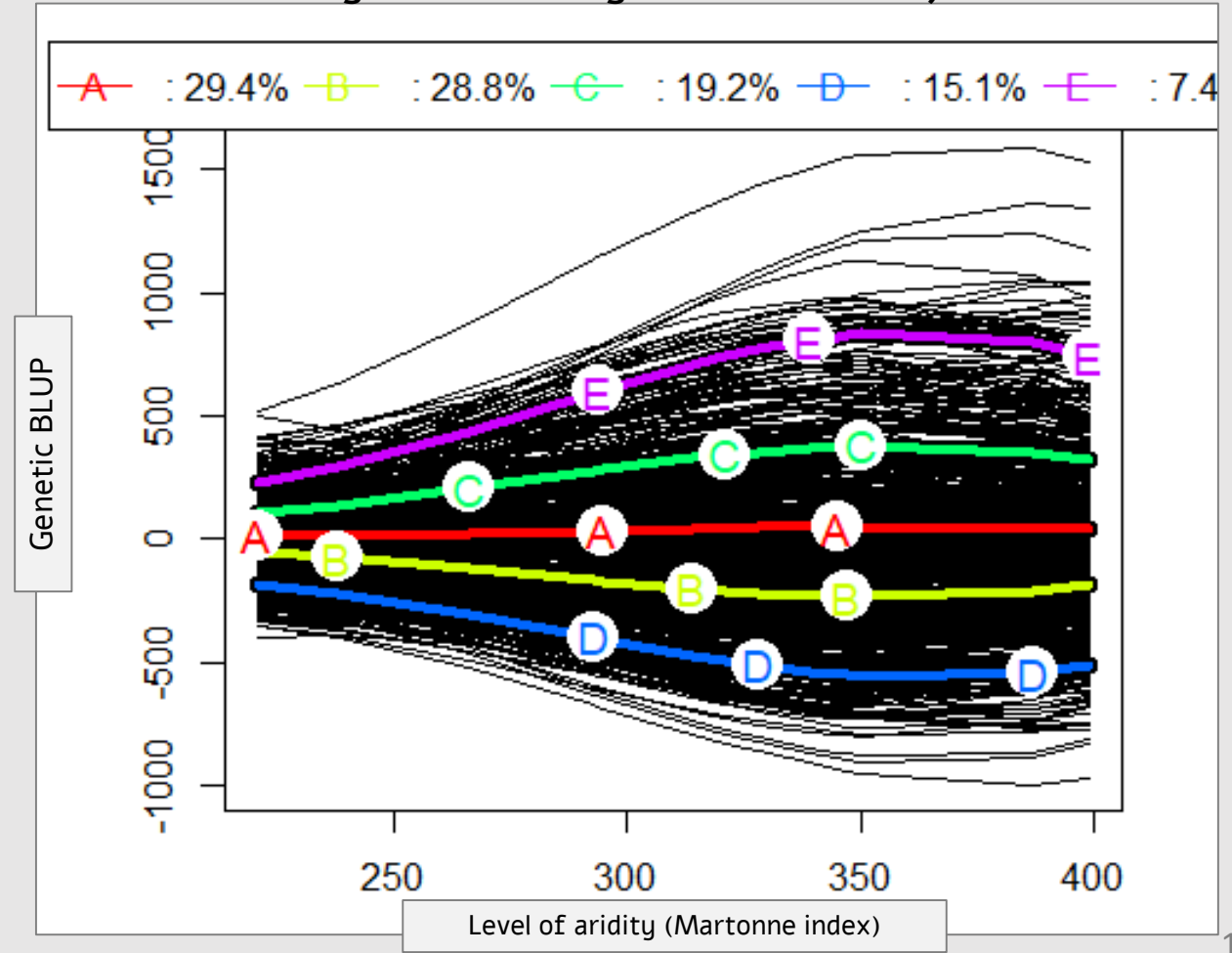
$$y_{ij} = \text{Mean trajectory } (t_j) + \text{Additive genetic effect}_i(t_j) + \text{Permanent environmental effect}_i(t_j) + \varepsilon_{ij}$$

Clustering of trajectories (Genolini et al. 2015)

Evolution of individual genetic values across environments



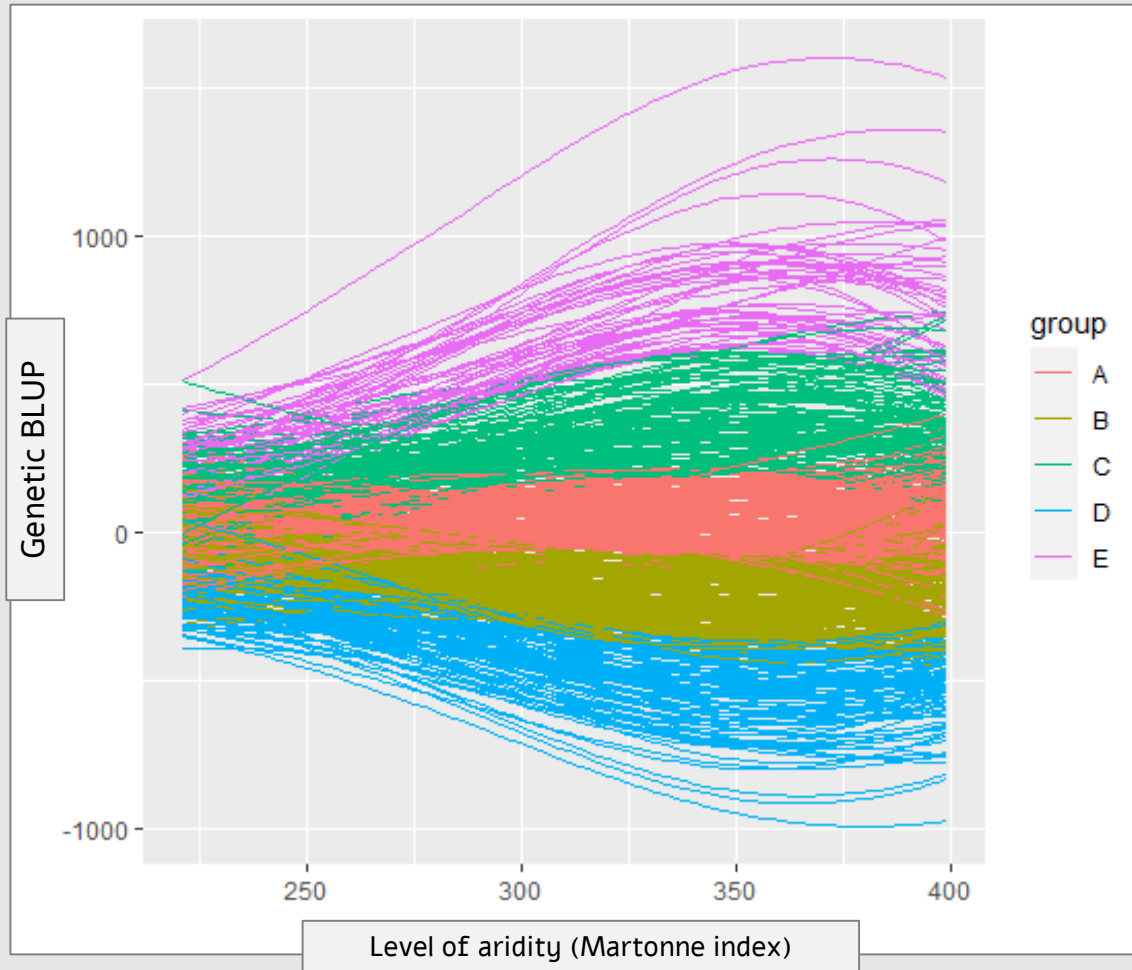
Clustering of individual genetic values trajectories



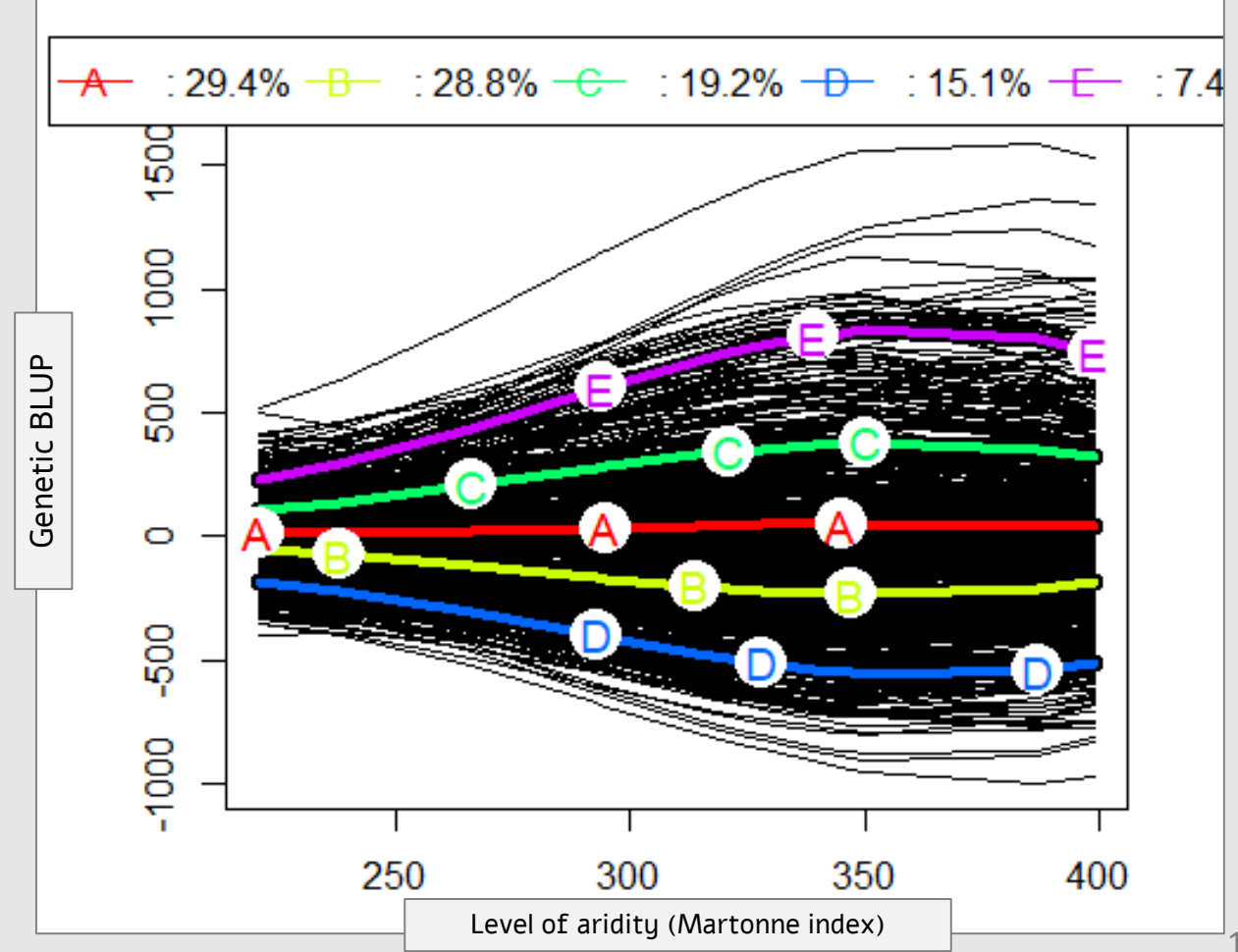
Norms of reaction : additive genetic trajectories

$$y_{ij} = \text{Mean trajectory } (t_j) + \text{Additive genetic effect}_i(t_j) + \text{Permanent environmental effect}_i(t_j) + \varepsilon_{ij}$$

Evolution of individual genetic values across environments



Clustering of individual genetic values trajectories



Conclusion and prospects

- With :

- Phenotypic measurements : densitometric profiles
- Simple climatic characterization : Martonne's aridity index
- Genetic data : pedigree or molecular markers information

→ Norms of reaction : individual genetic values across a range of environments

- Main prospects :

- Improve environmental characterization :
 - Consideration of previous years, better differentiation of experimental sites...
 - Use of a growth simulation model (GO+ : based on environmental characteristics of each site (stand density, groundwater height)) to incorporate more explanatory parameters into the annual index (soil water reserve, evapotranspiration demand)
- Extend to other inter-ring phenotypic traits (ex: average ring density)
- Construct NoR for intra-ring growth



B4EST international conference – Managing Forest Genetic Resources for an uncertain future

Thank you for your attention

