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Integrating environmental gradients into forest tree breeding: genomic reaction norms in maritime pine

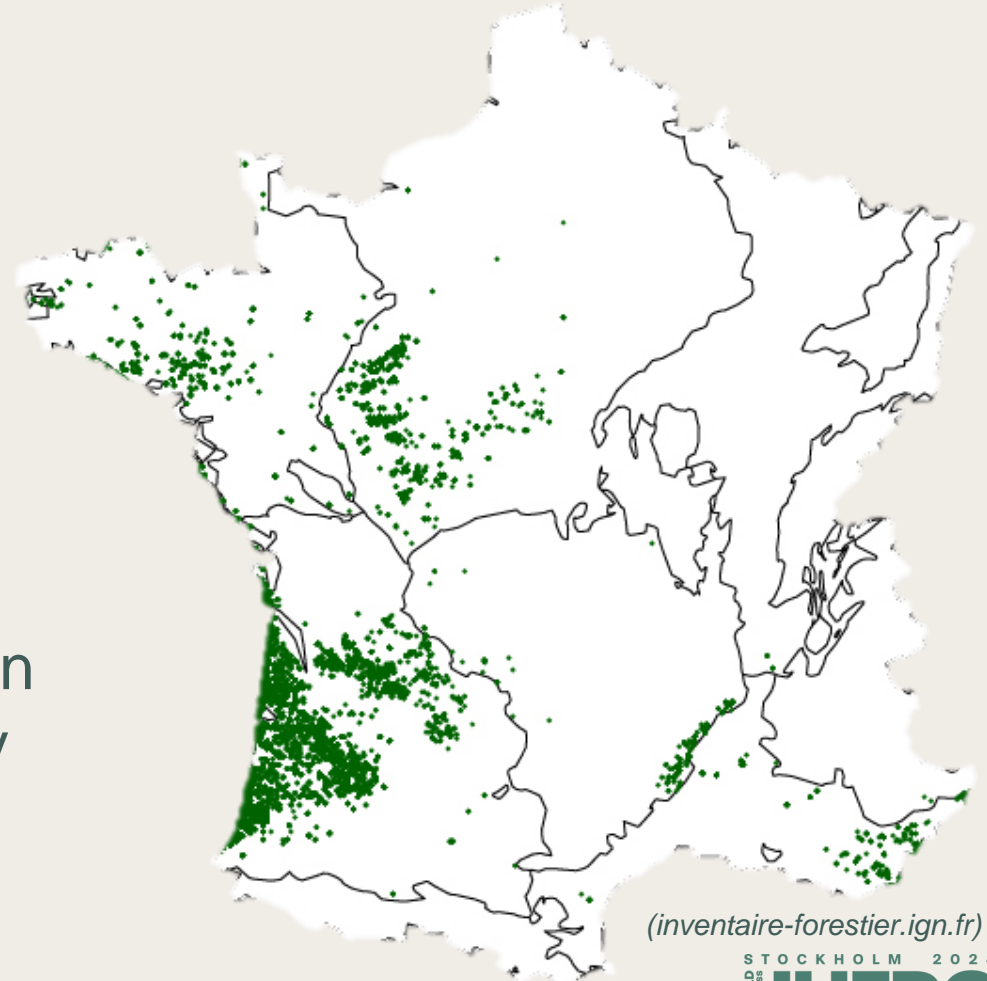
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Maritime pine breeding in France

Maritime pine distribution in France

- Most widely planted forest tree in France
- Recurrent breeding program since 1960s
 - Focus on **growth** and **straightness**
- The environment is becoming a major concern
 - Only assessed through complex and costly multi-environmental trials



(inventaire-forestier.ign.fr)

How can environmental information be effectively integrated into the genetic evaluation of forest trees?

→ Genomic reaction norms based on wood ring series

Presentation outline:

- Trial studied and data :
 - Phenotypes
 - Environmental data
 - Genetic data
- Random regression model
- Genomic prediction



Maritime pine trial used in this study



Site 1



Site 2



Polycross-progeny test: 174 half-sib families on two sites



Sample: 25 families with 13 individuals per site → 620 individuals

Phenotypes from wood ring series

1 Wood coring



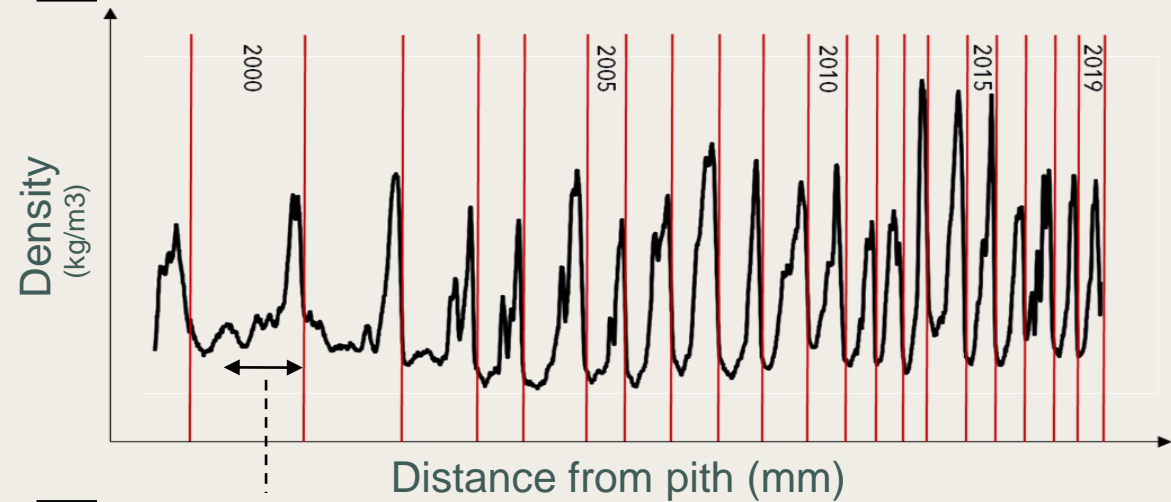
2 Cutting



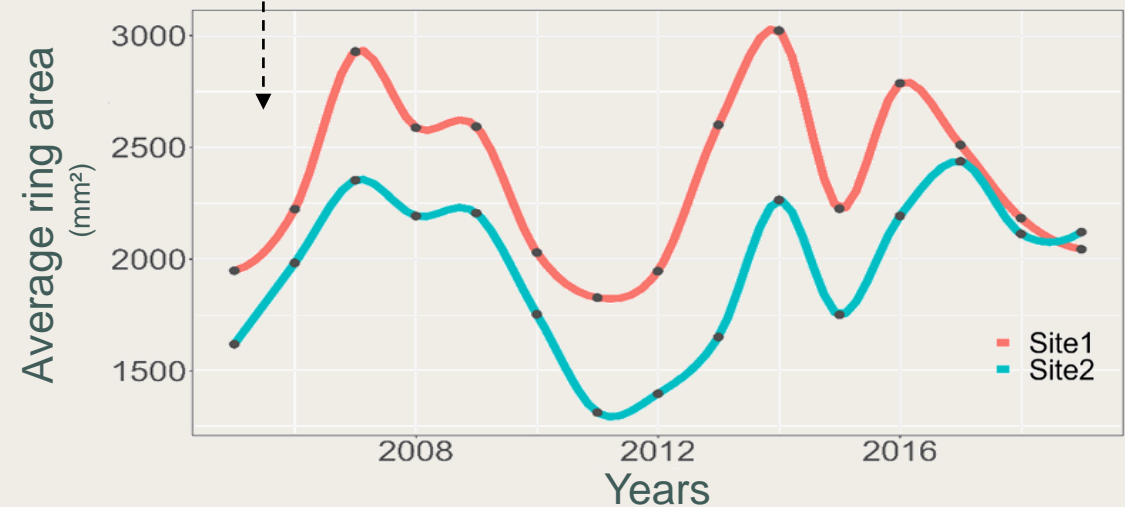
3 X-ray radiography



4 Densitometry profile



5 Annual growth



Environmental data



Climatic data

- Hourly rainfall
- Average hourly temperature
- Average hourly wind speed



Soil characterization

- Water table height
- Fertility



Silvicultural parameters

- Plantation density
- Thinnings



(Moreaux et al., 2020)



Microclimate temperature **per hour**
Trunk water potential **per hour**

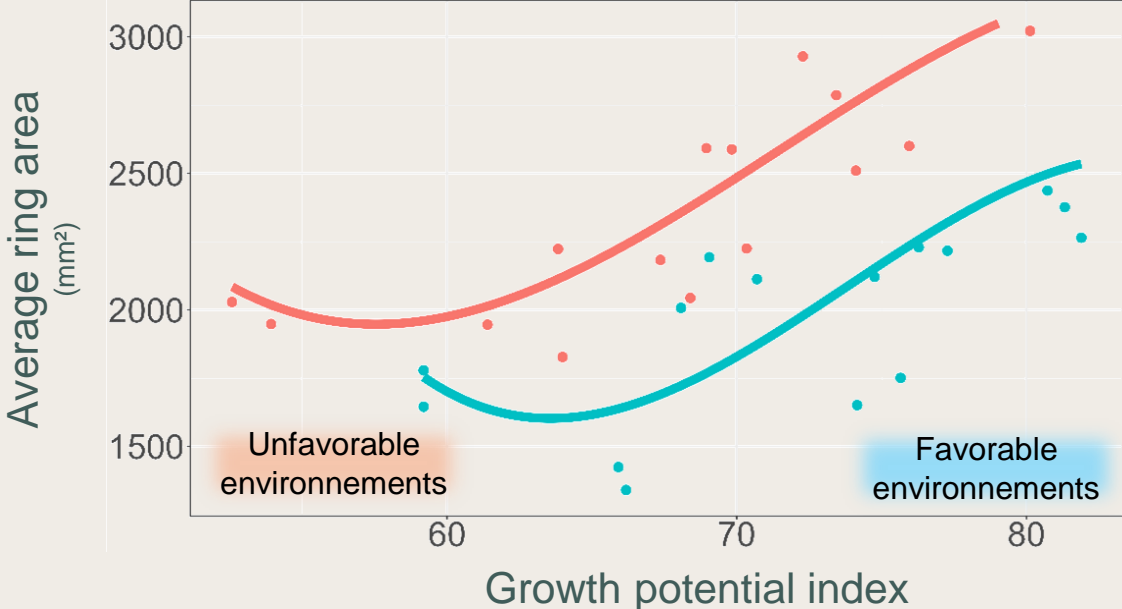
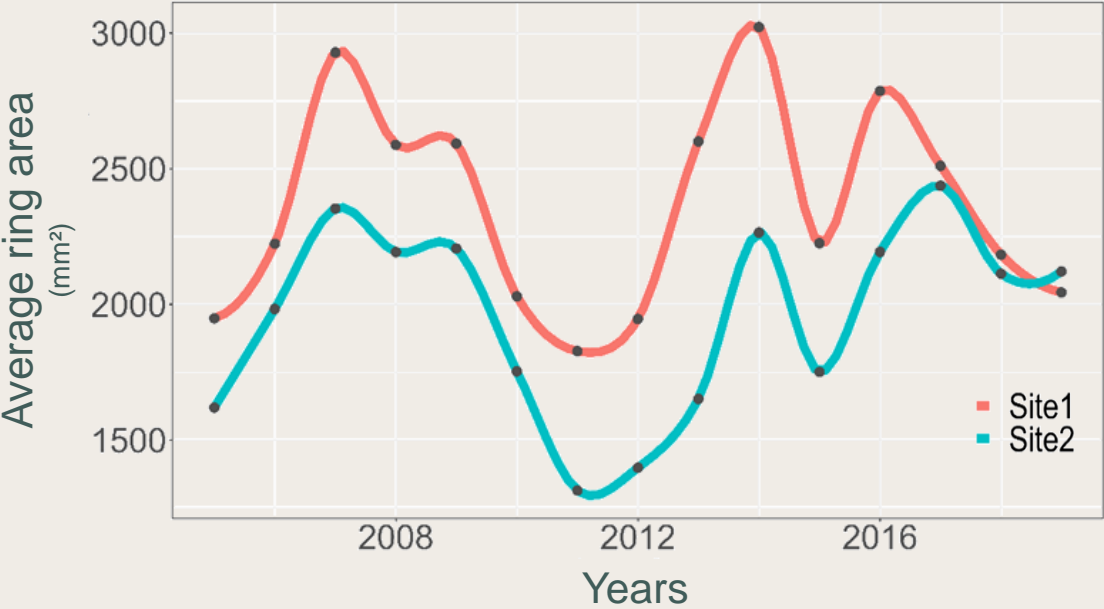


Growth potential **per day**



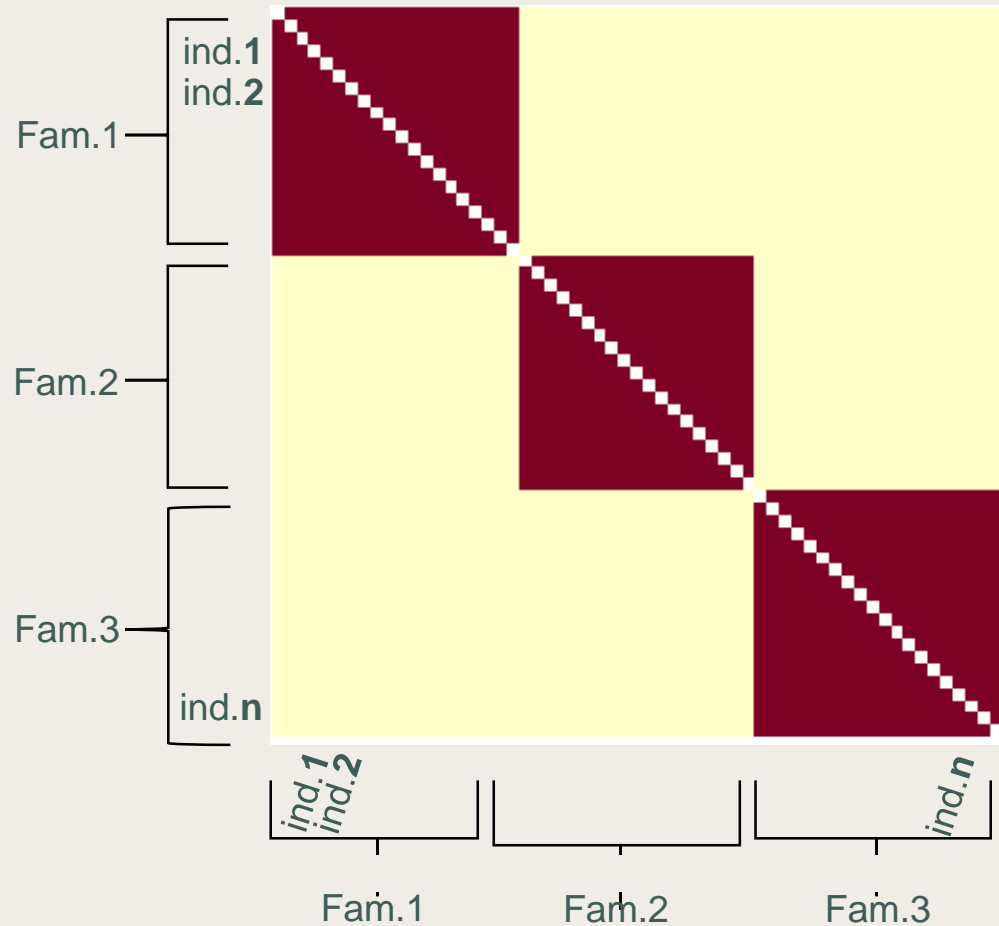
Growth potential **per year**

Phenotypes and environmental data

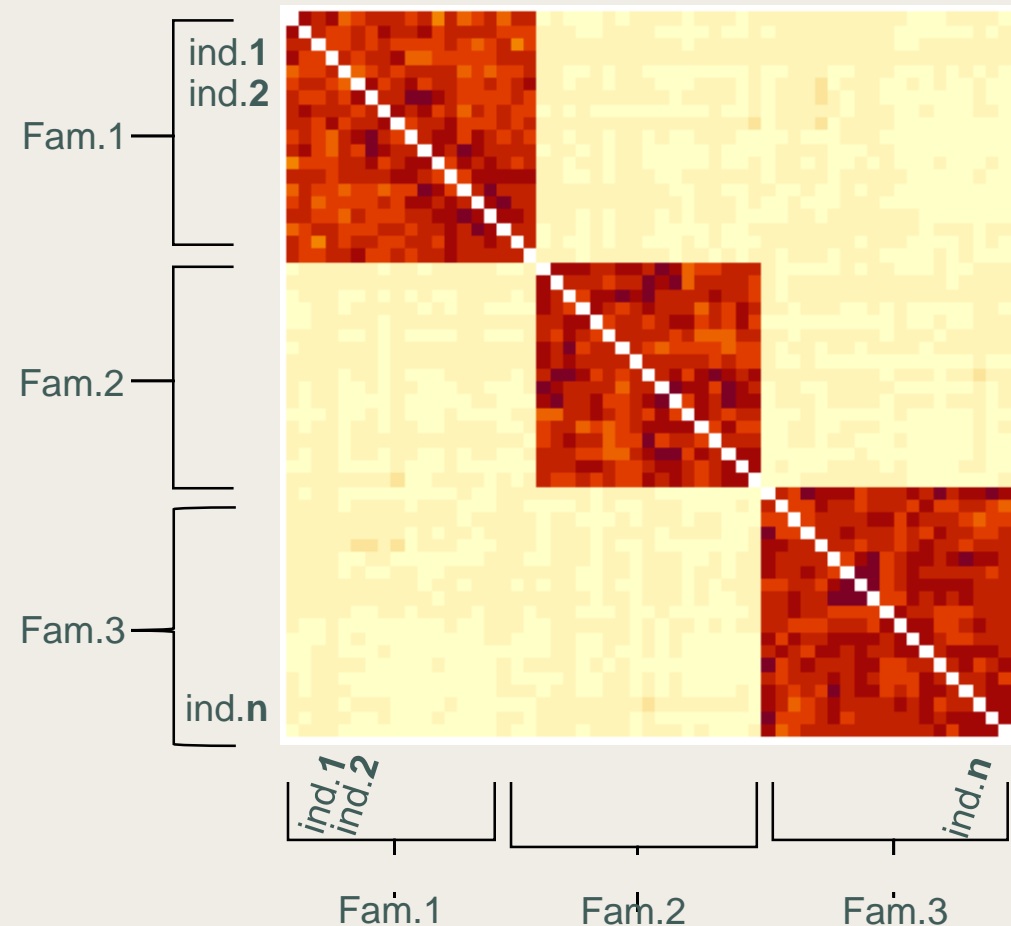


Genetic data

Pedigree-based relationship coefficients
(2 previous generations)



Genomic relationship coefficients
(3800 SNP)



Random regression model

$$y_{ijs} = \sum_{r=0}^{k_m} \varphi_{ijk} m_{sk} + \sum_{r=0}^{k_\alpha} \varphi_{ijk} \alpha_{ik} + \sum_{r=0}^{k_p} \varphi_{ijk} p_{ik} + \varepsilon_{ijs}$$



Individual (i) ring area for each environmental level j in site s

Mean trajectory per site (fixed effect)

Random additive genetic effect

With $\alpha \sim N(0, G \otimes \Omega)$

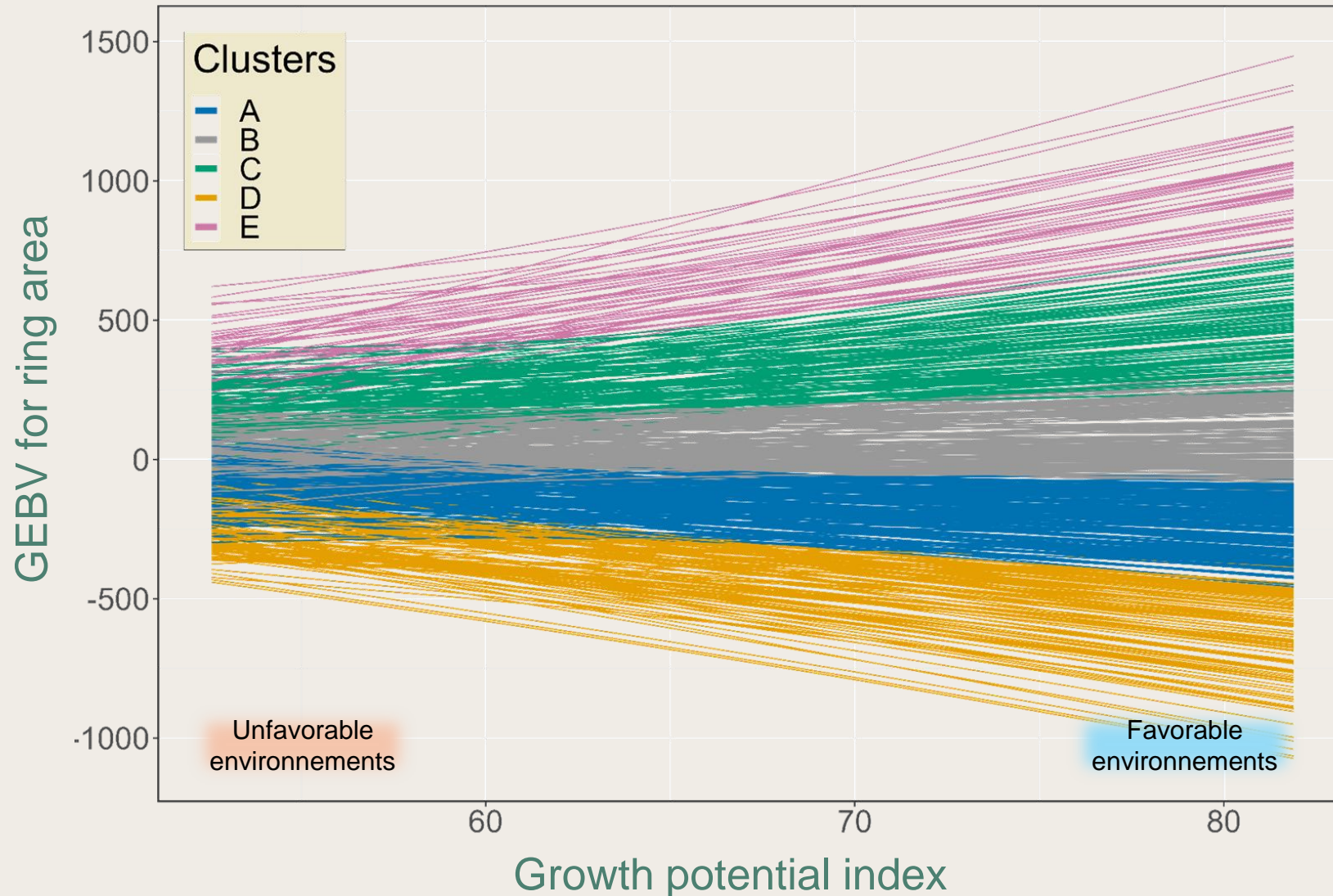
Random permanent environmental effect

With $\gamma \sim N(0, Id \otimes P)$

Residuals

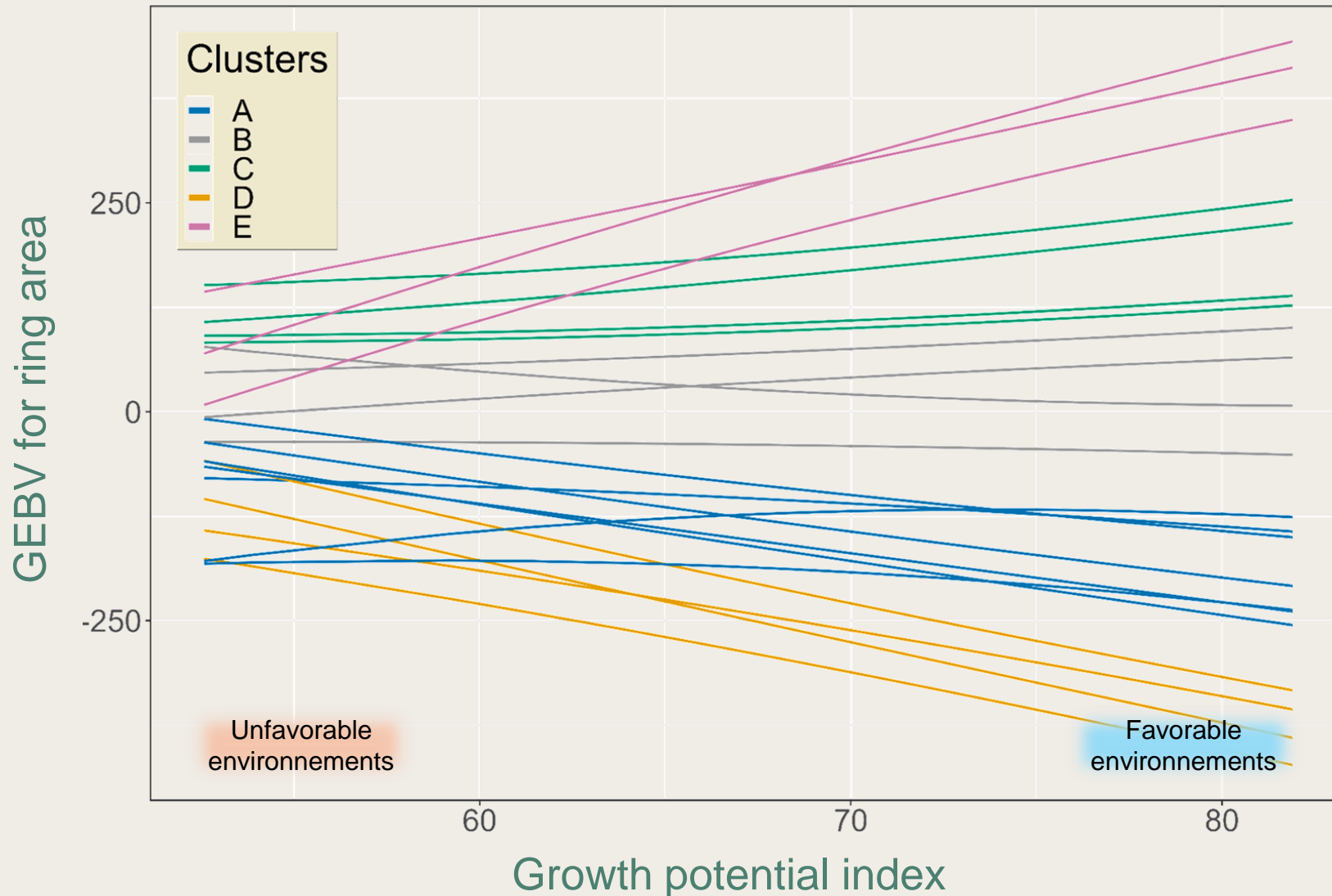
φ : Legendre polynomials coefficients

Trajectories of individual genetic values



- GxE interactions with reclassification of genotypes in the most unfavorable environments

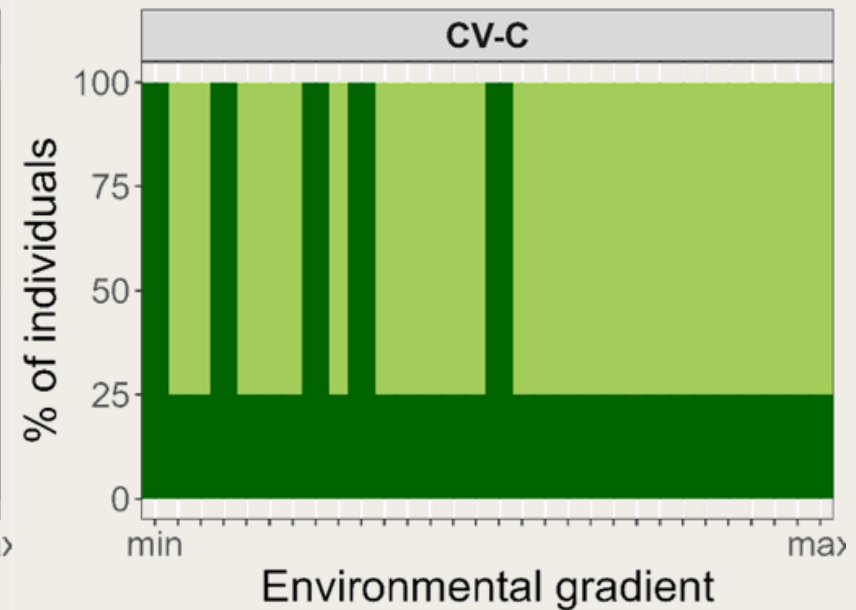
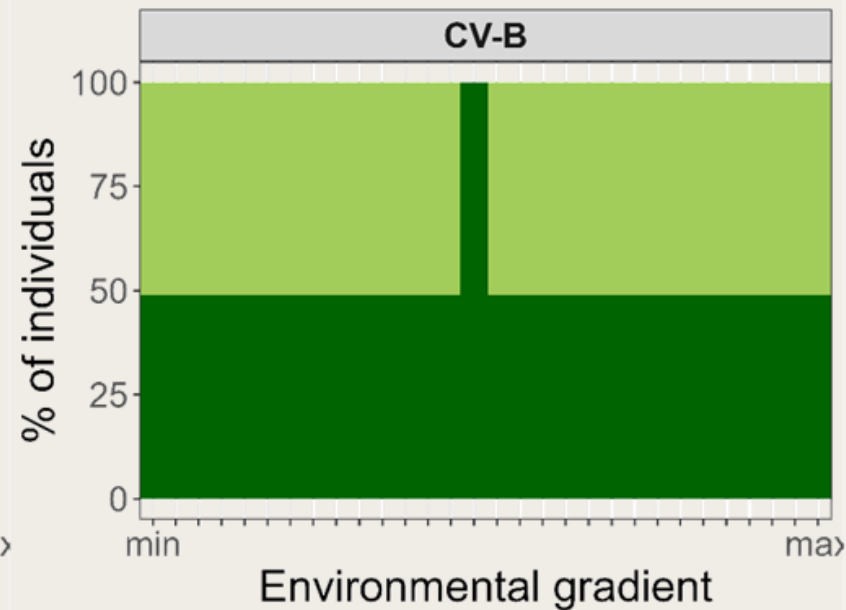
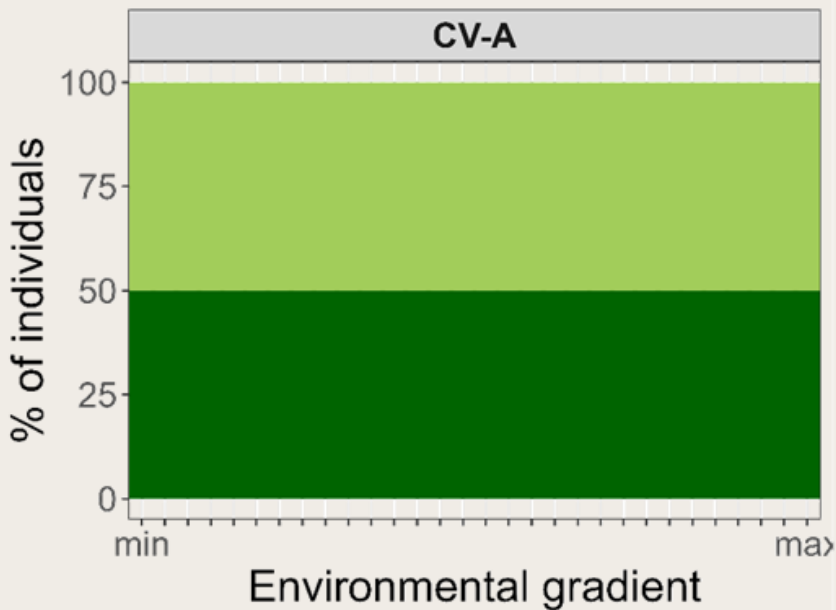
Trajectories of average family genetic values



- GxE interactions with reclassification of genotypes in the most unfavorable environments

Genomic prediction: cross-validation scenarios

Pop.validation
Pop.calibration



Genomic prediction: cross-validation scenarios



Conclusion

Modeling reaction norms through finer-grained phenotyping

- Key choice of environmental variable
- Re-ranking of individuals in the most likely future environments

Reaction norms and genomic selection

- Distribution of phenotypic information is key to prediction accuracy
- Genomic selection makes it easier to integrate new traits

Data availability

Papin, V., Bosc, A., Sanchez, L., & Bouffier, L. (2024). Integrating environmental gradients into breeding : Application of genomic reactions norms in a perennial species.
Accepted by Heredity in April 2024.

**Article
available on bioRxiv**



<https://doi.org/10.1101/2023.11.22.568058>

**Data and scripts
available on Data INRAE**



<https://entrepot.recherche.data.gouv.fr/datas/et.xhtml?persistentId=doi:10.57745/NUTK11>

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