# Integrative factorial methods to explore the relationships between genotypes, phenotypes and climate in Holstein cows

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# *Integrative factorial methods to explore the relationships between genotypes, phenotypes and climate in Holstein cows*

## *A first step: Synthesizing lactation curves*

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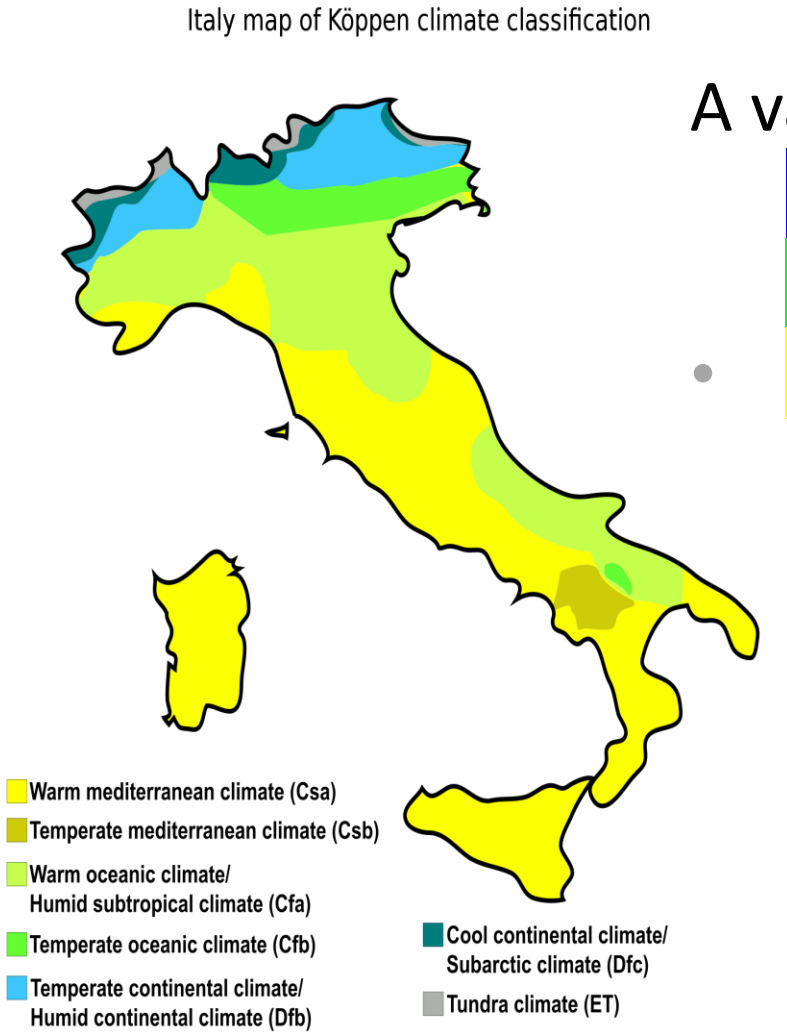
# Introduction
# The map of italian climates

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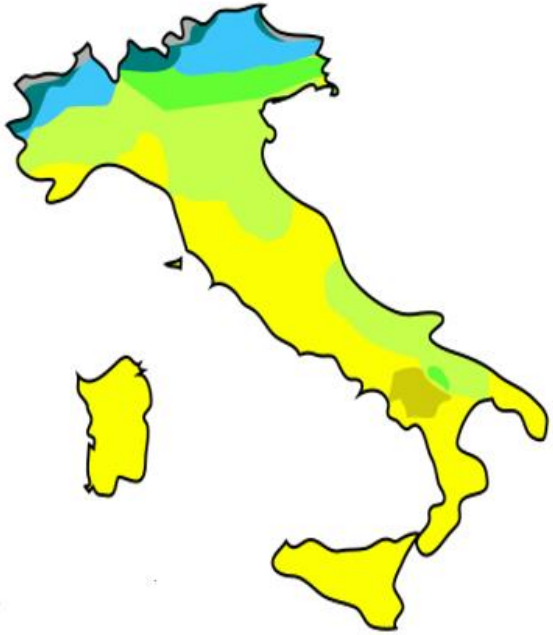
A variety of climates

- Continental
- Oceanic / Temperate
- Mediterranean

# Introduction
## The map of italian climates

### A variety of climates
(compared to other european countries)



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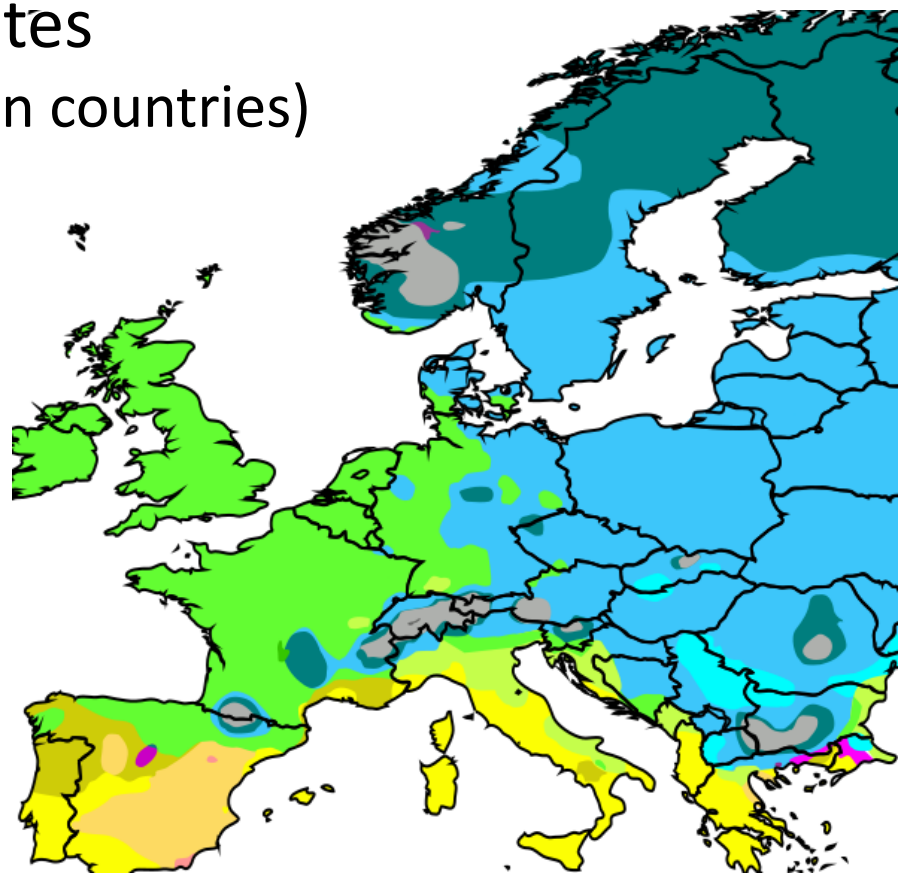


*en.wikimedia.org*

# Introduction
# Accounting for environment

The fine-scale (day) classical approach:
Reaction norms model on test-day records : test-day phenotypes linked to day-recorded meteo variables

*Bernabucci, U., Biffani, S., Buggiotti, L., Vitali, A., Lacetera, N., & Nardone, A. (2014). The effects of heat stress in Italian Holstein dairy cattle. Journal of dairy science, 97(1), 471-486.*

*Landi, V., Maggiolino, A., Cecchinato, A., Mota, L. F. M., Bernabucci, U., Rossoni, A., & De Palo, P. (2023). Genotype by environment interaction due to heat stress in Brown Swiss cattle. Journal of Dairy Science, 106(3), 1889-1909.*

*Vinet, A., Mattalia, S., Vallée, R., Bertrand, C., Cuyabano, B. C., & Boichard, D. (2023). Estimation of genotype by temperature-humidity index interactions on milk production and udder health traits in Montbeliarde cows. Genetics Selection Evolution, 55(1), 1-17.*

An other larger-scale approach:
Effect of general environment (through geography)

1. Functional PCA (fpca) on lactation curves (milk yield, fat, protein) -> a few synthetic variables
2. Links of fPCA results with geography / climate

# Methods: Functional Principal Components Analysis

**Data recorded at different discrete times-> Curve**

**Functional pca:**

- **Irregular measurement times, irregular number of measurements**
- **Extract the common temporal characteristics of a set of curves**
- **Essential modes of temporal variation: Principal Functions**
  - **% of variance**
  - **interpretation**

An extension of classical PCA (Macciotta et al (1015)

| | PCA | FPCA |
|---|---|---|
| Dimension | $P< \infty$ | $\infty$ |
| Mean | E(X) : scalar | E(X(t)) : function |
| Covariance | $Cov(x_p, x_q) = \Sigma$ | Cov (X(s),X(t) : surface |
| Eigenvectors / Eigenfunctions | $v_1$ , $v_2$ ,… | $f_1(t)$ , $f_2(t)$ ,… |


*Macciotta et al(2015). Genome-wide association analysis in Italian Simmental cows for lactation curve traits using a low-density (7K) SNP panel. *Journal of Dairy Science*, *98*(11), 8175-8185.

Yao F., Müller H.G., and Wang J.-L. (2005). Journal of the American Statistical Association 100 (470): 577–90. https://doi.org/10.1198/016214504000001745

Zhou Y et al (2022). _fdapace: Functional Data Analysis and Empirical Dynamics, R package

Arnal, M., Robert-Granié, C., & Larroque, H. (2018). Diversity of dairy goat lactation curves in France. *Journal of dairy science*, *101*(12), 11040-11051.

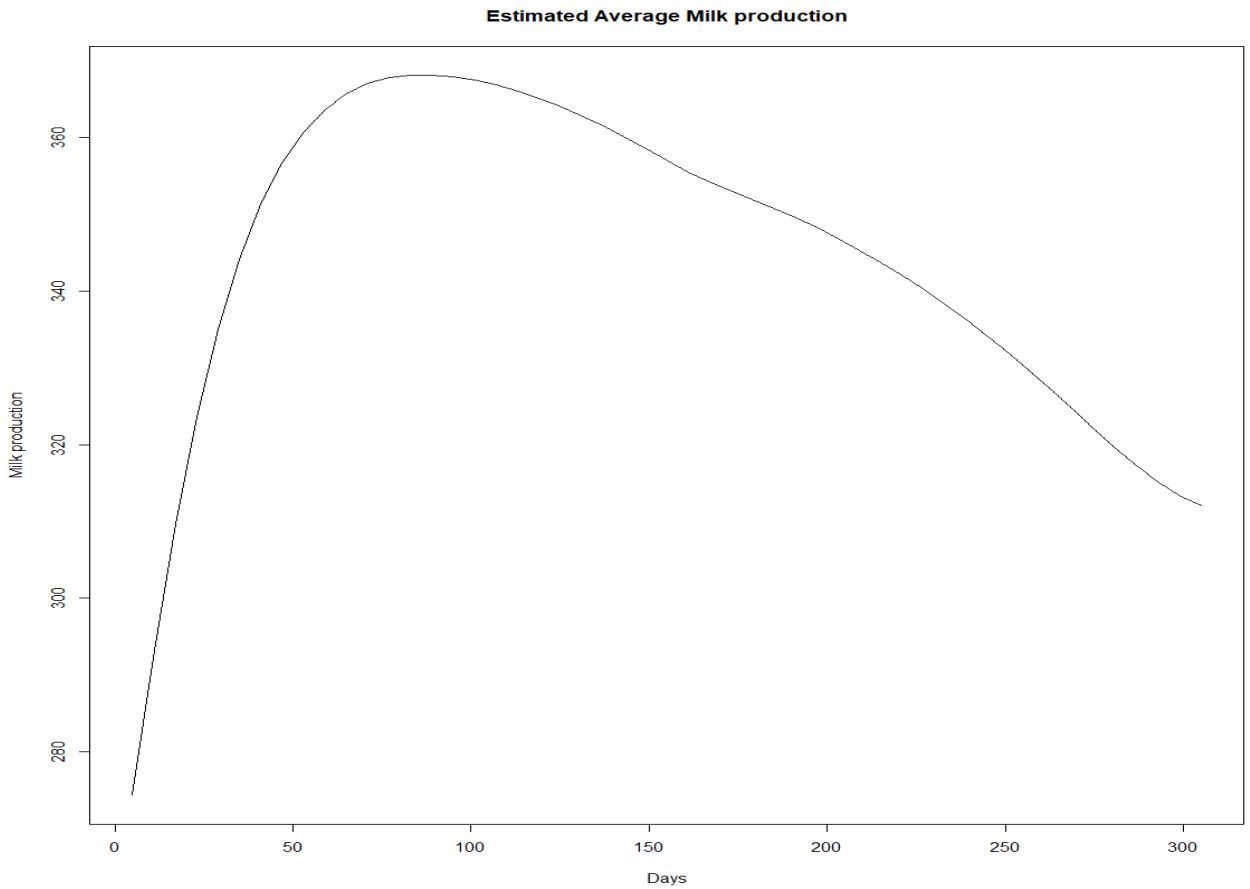
# Data (ANAFI): Milk records

- Editing : First lactations, in the same herd , with > 4 records.

| | Number |
|---|---|
| Records | 120245 |
| Lactations / Cows | 15545 |
| Herds | 881 |

| Number of records / lactation | Number |
|---|---|
| 5 | 898 |
| 6 | 1788 |
| 7 | 4162 |
| 8 | 4140 |
| 9 | 2845 |
| 10 | 1664 |
| 11 | 48 |

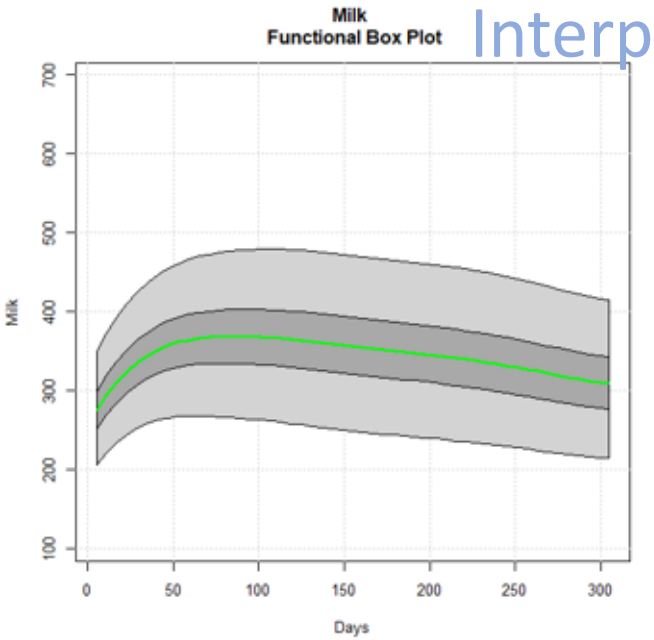
# Functional PCA Milk yield
# Average curve

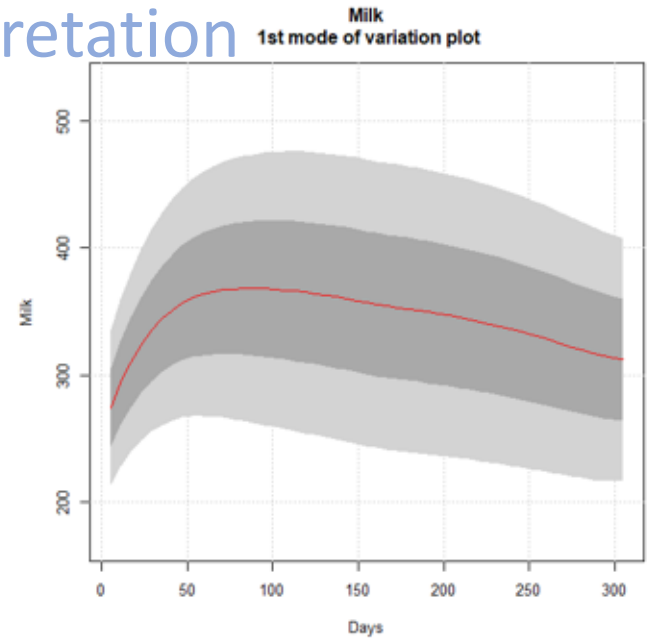


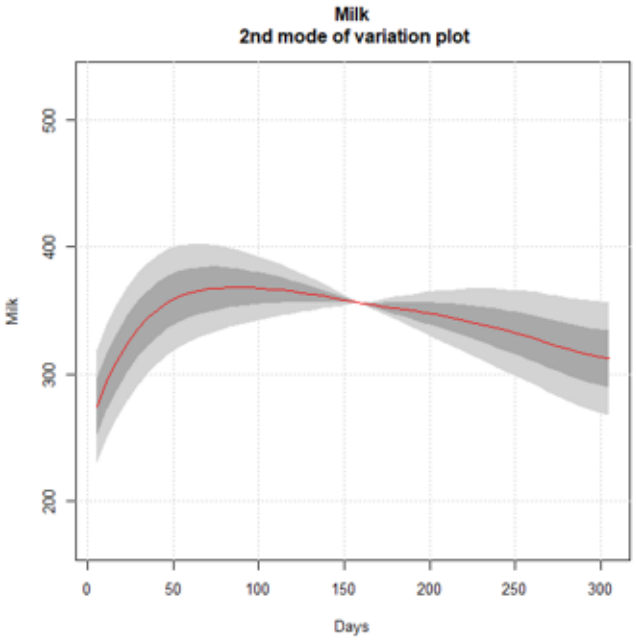
# Functional PCA Milk yield Interpretation

$$\bar{x}(t) \pm Q_\alpha \sqrt{d_i}\xi_i(t)$$

| | Milk Yield |
|---|---|
| 1 | 89,5 |
| 2 | 8,0 |
| Total(1+2) | 97.5 |




Variations around mean curves

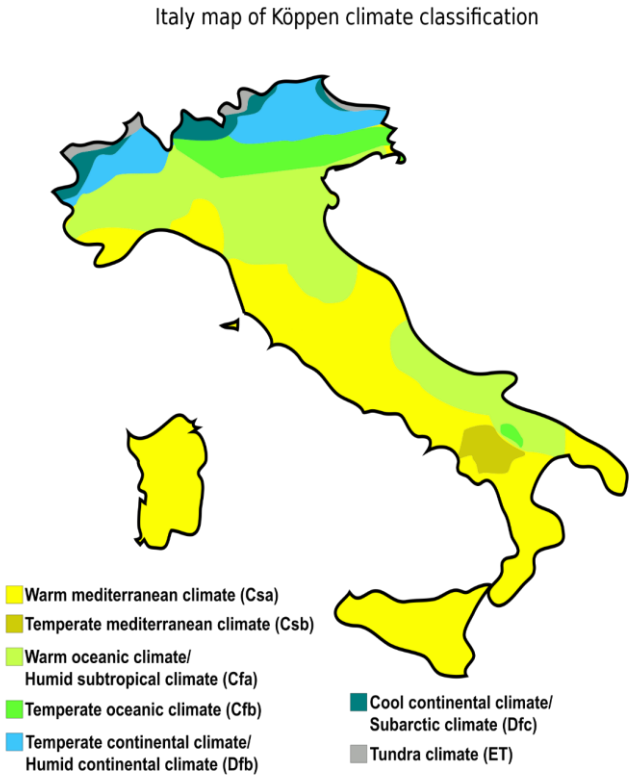
**K=1 : Level of production *(Size)***
**K=2: Persistency *(Shape)***

# Functional PCA applied to Milk yield, Protein (%), Fat(%)

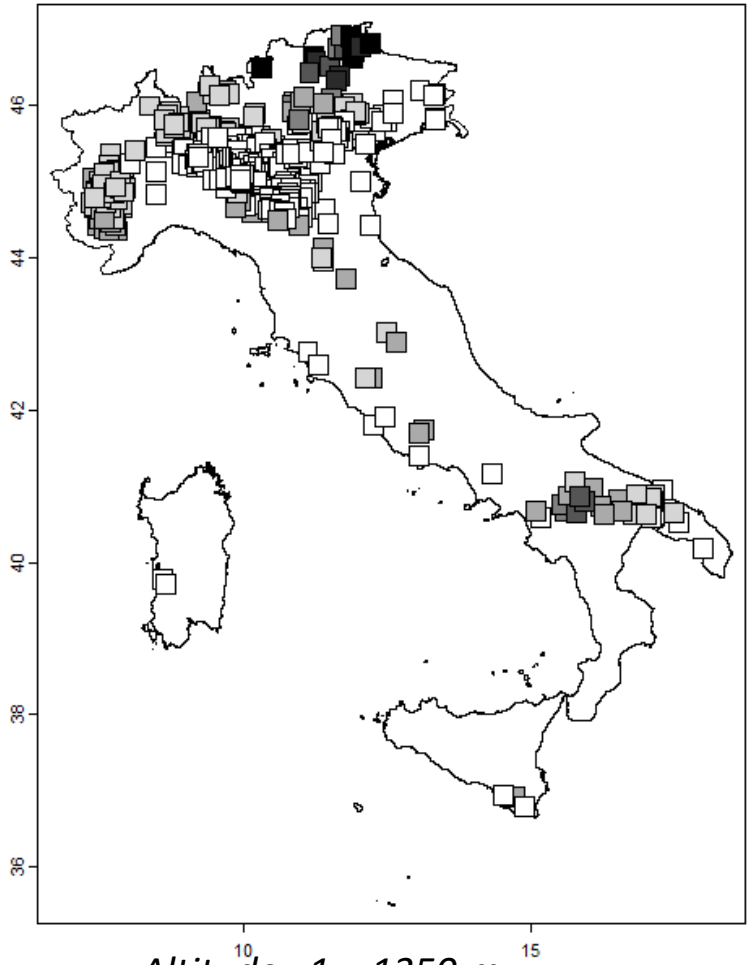
% of variance explained by the first 2 functional PCs

| | Yield | Protein % | Fat % |
|---|---|---|---|
| 1 | 89,5 | 85,2 | 88,8 |
| 2 | 8,0 | 11,7 | 7,3 |
| Total (1+2) | 97.5 | 96.9 | 96.1 |

# Data (ANAFI)
# Geography




Location of herds

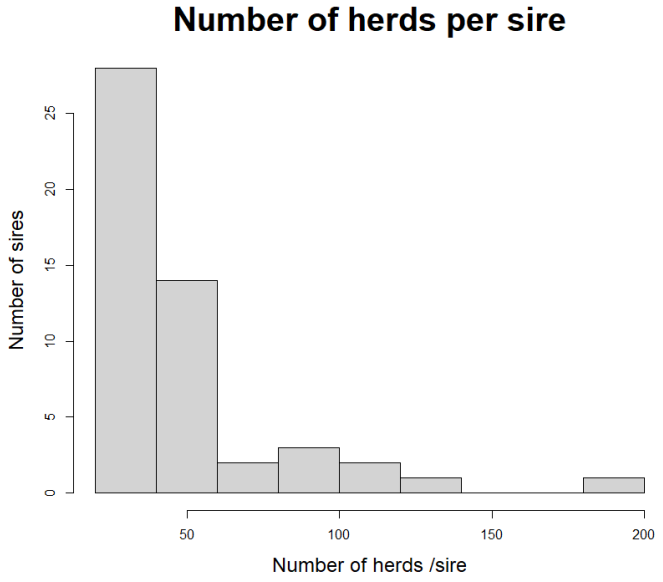


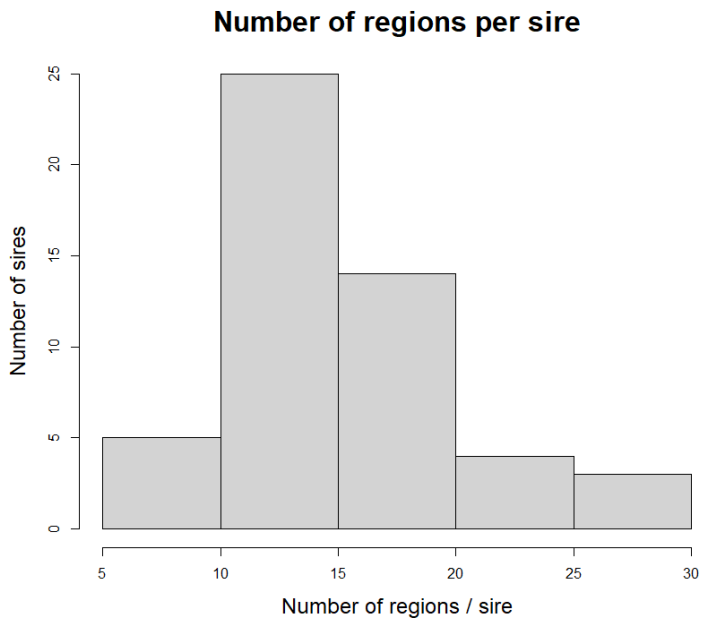

*Altitude : 1 – 1350 m*
*The darker, the higher*

# Adaptation to different environments
# Sire * geography interaction

2. Selection of « ubiquist » sires
   Sires that serve in > 25 herds

51 sires;
659 herds
42 provinces
6368 lactations



# A first attempt for the characterization of an interaction Geography * Genotype

A mixed linear sire model (R package « nlme »)
Fixed effets : Year calving, Month calving, latitude, longitude, altitude
Random effects: Sire, interactions Sire*latitude, Sire*longitude, Sire*altitude

* ML test Presence vs Absence interactions -> Significant (except when NS indicated)
* From 6 % to 25 % of the sire variance

| | Year | Month | Latit | Long | Altit | $\sigma^2_{sire}$ | $\sigma^2$ sire*lat | $\sigma^2$ sire*long | $\sigma^2$ sire*alt |
|---|---|---|---|---|---|---|---|---|---|
| Milk | NS | * | NS | * | NS | 0.056 | 0.014 | 0.006 | 0.014 |
| Prot% | * | * | * | * | NS | 0.108 | 0.011 | 0.007 | *0.003 (NS)* |
| Fat% | NS | * | * | NS | * | 0.068 | 0.006 | 0.006 | *0.004 (NS)* |

Pinheiro J, Bates D, R Core Team (2023). _nlme: Linear and Nonlinear Mixed Effects Models_. R package version 3.1-162, <https://CRAN.R-project.org/package=nlme>.

# Conclusion

For almost each trait*geographical coordinate, the interaction is significant, exhibiting a genotype*environment interaction

A (over?) simplified modelling
Environment (climate, breeding system, herd) synthetized by geography
Should be completed with more focused genetic studies (genetic / genomic studies )

Nevertheless,
Functional PCA allows us to synthesize a lactation curve into a few components;
- Can be seen as an extension of PCA
- Helps to relate milk yield to global climate parameters;
- could be used jointly with climate projections or scenarii (# genomic vulnerability)

A complementarity with reaction –norm approach


Thanks for Your Attention!!