



HAL
open science

Predicting the invasiveness of a species with genomic data: A case study on the fruit pest *Drosophila suzukii*

Louise Camus, Mathieu Gautier, Simon Boitard

► To cite this version:

Louise Camus, Mathieu Gautier, Simon Boitard. Predicting the invasiveness of a species with genomic data: A case study on the fruit pest *Drosophila suzukii*. SMBE Regional Meeting on The Role of the Genome in Biological Invasion, Society for Molecular Biology and Evolution (SMBE), Nov 2022, Online, New Zealand. hal-04659207

HAL Id: hal-04659207

<https://hal.inrae.fr/hal-04659207v1>

Submitted on 22 Jul 2024

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution - NonCommercial - NoDerivatives 4.0 International License



Source : Katja Schultz

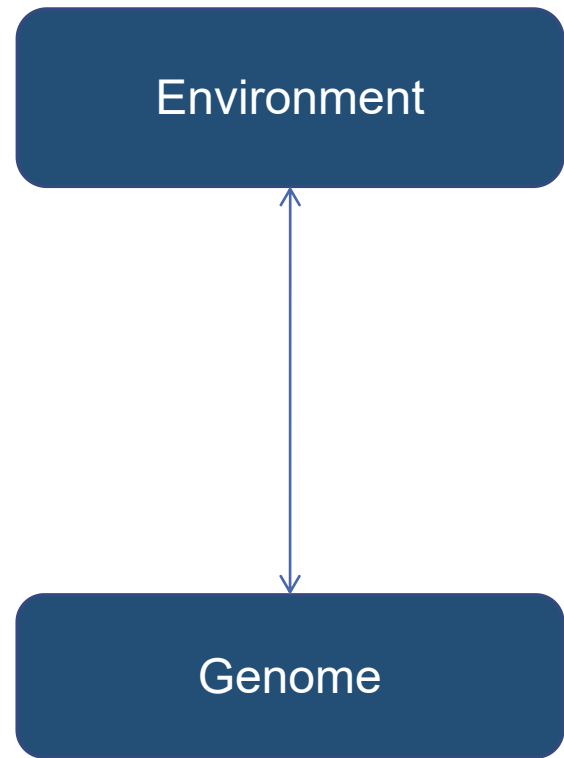
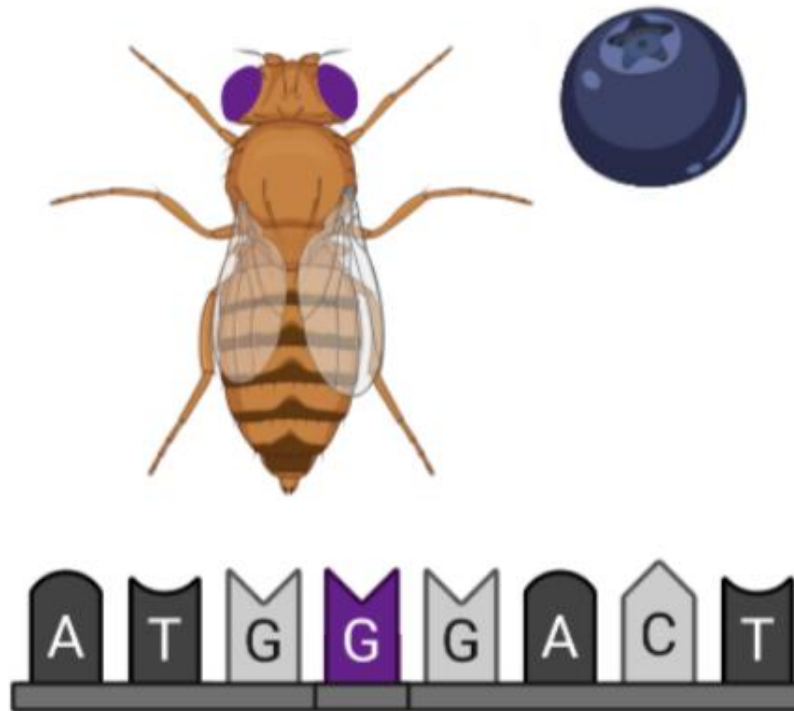
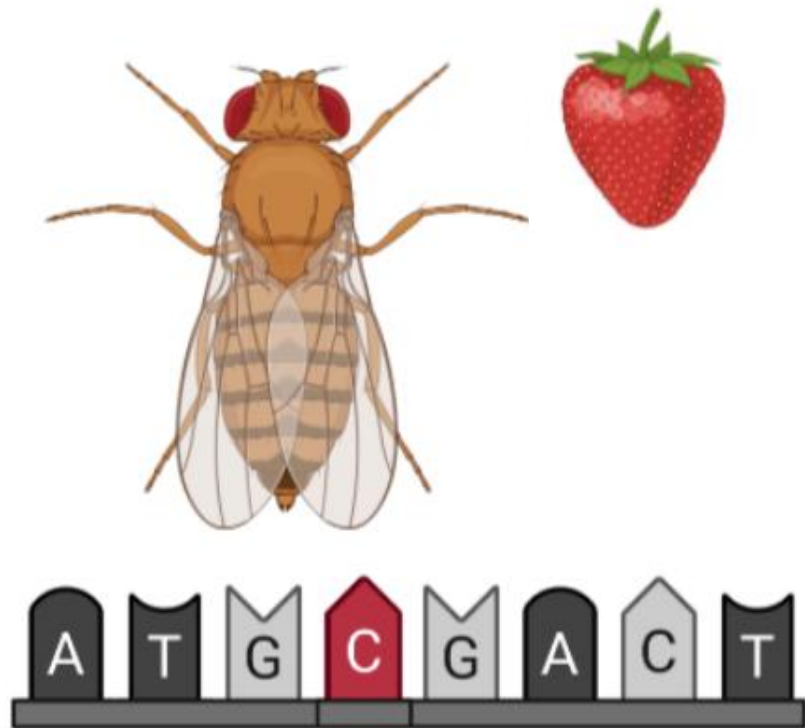
Predicting the invasiveness of a species with genomic data : a case study on the fruit pest *Drosophila suzukii*

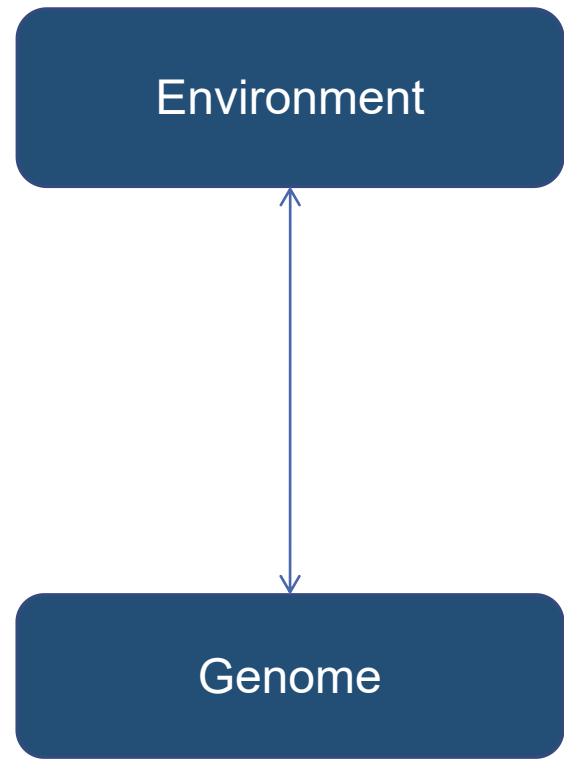
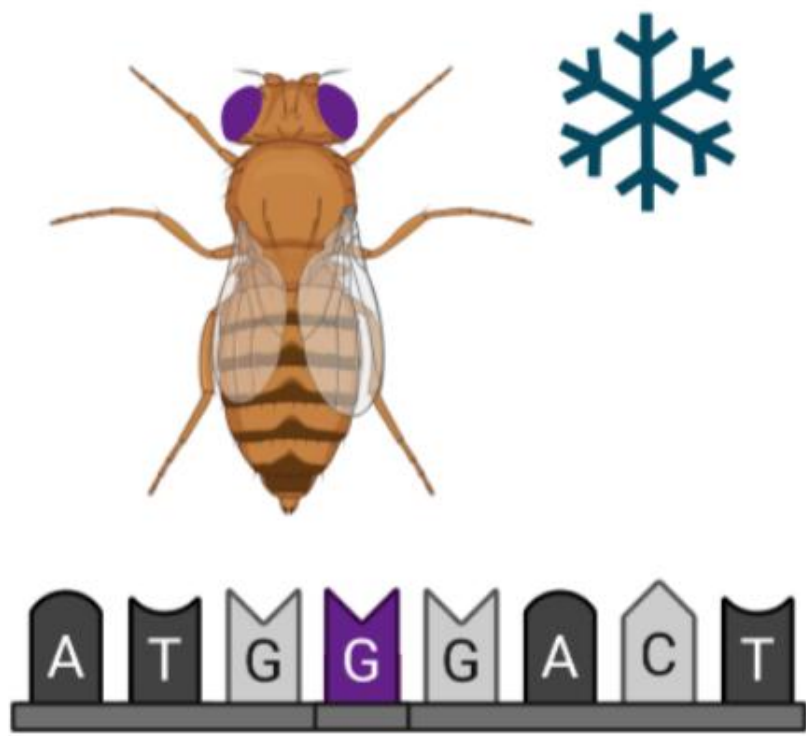
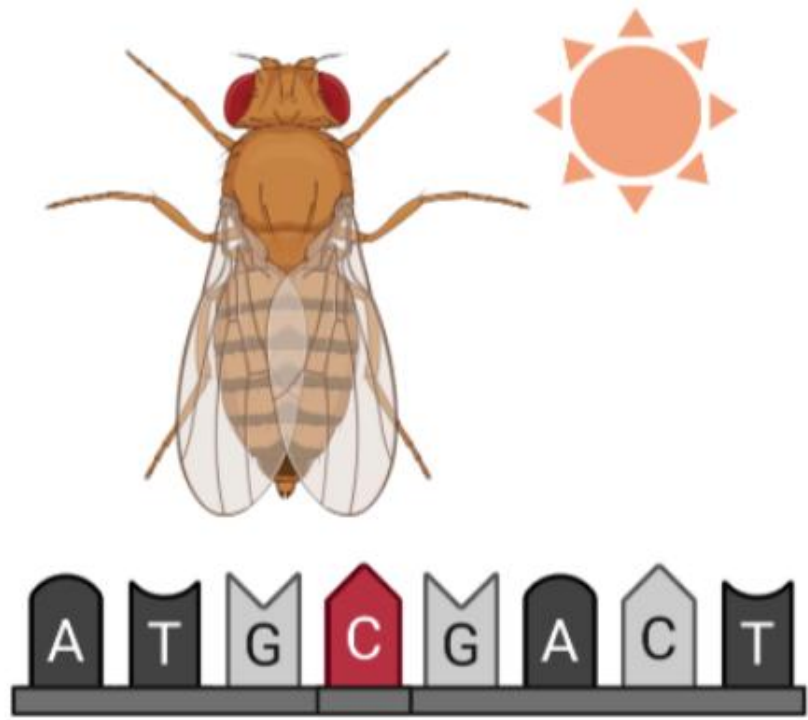
LOUISE CAMUS

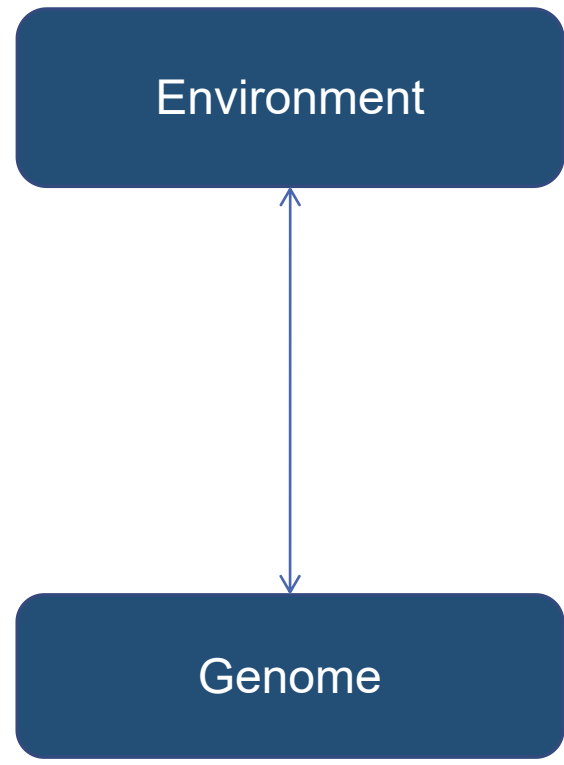
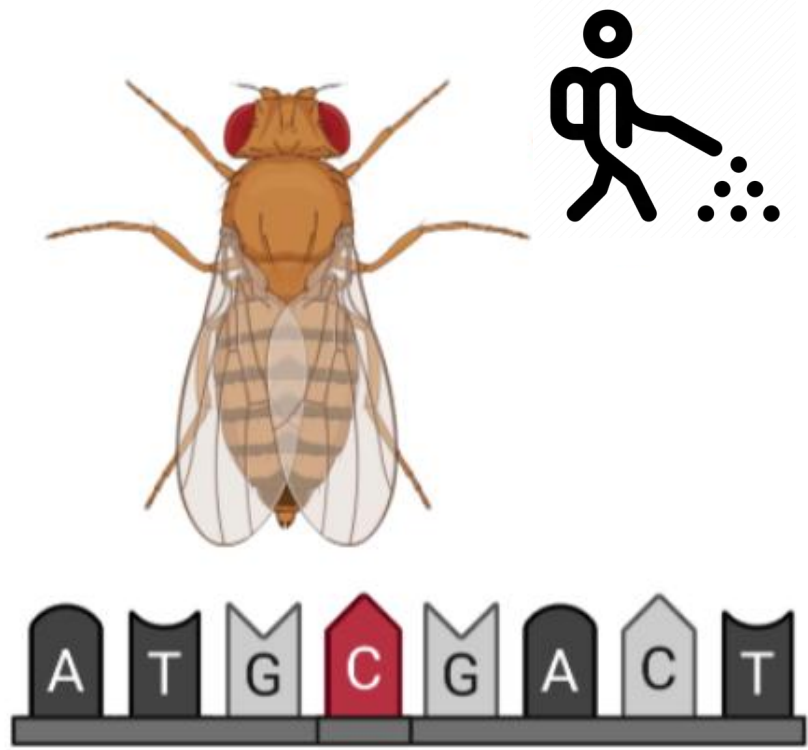
Supervised by Mathieu Gautier et Simon Boitard

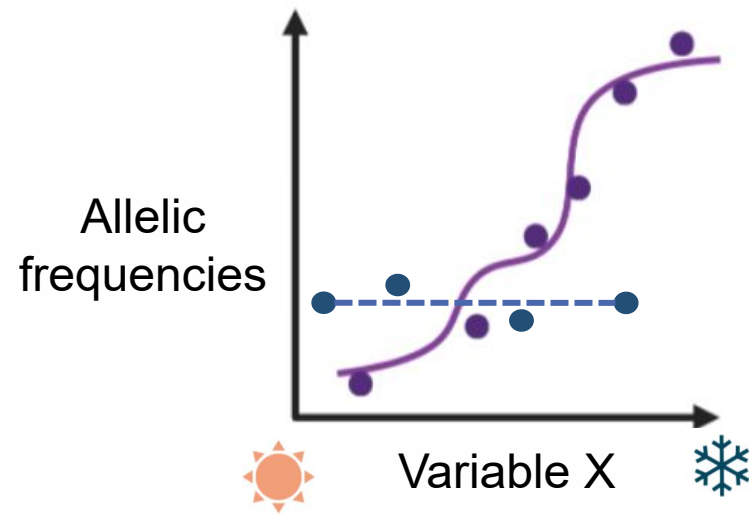
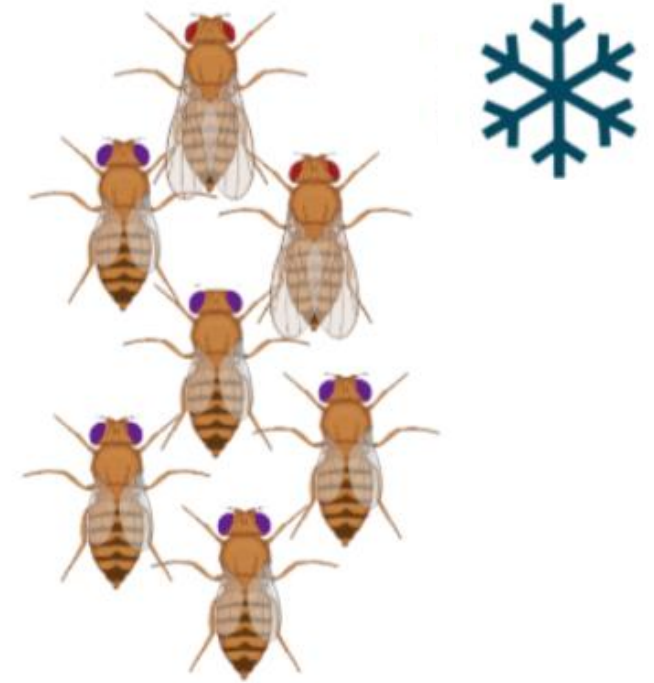
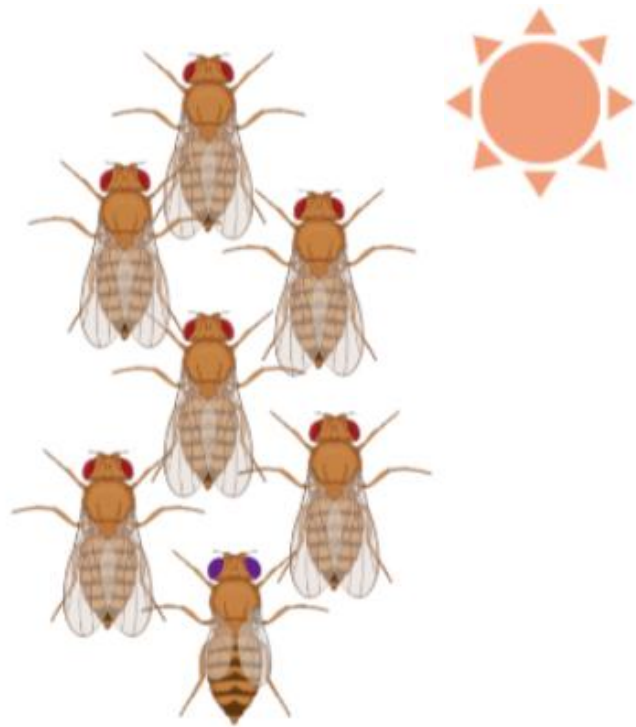
Centre de Biologie pour la Gestion des Populations (CBGP)

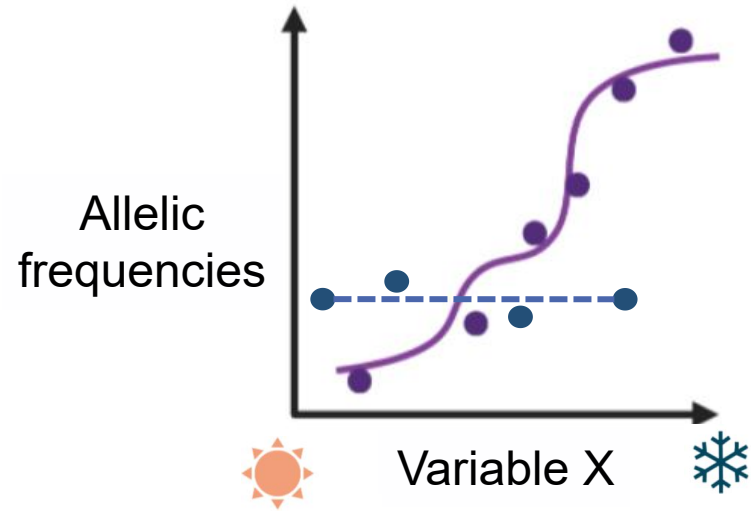
Invasomics conference, November 8th 2022





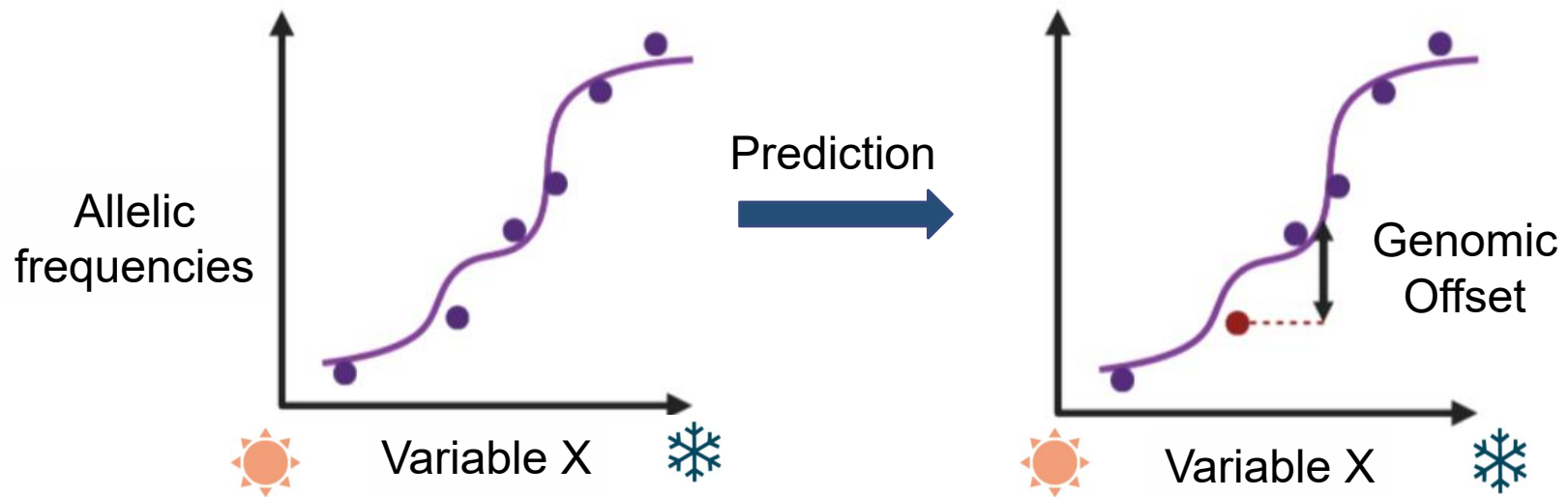


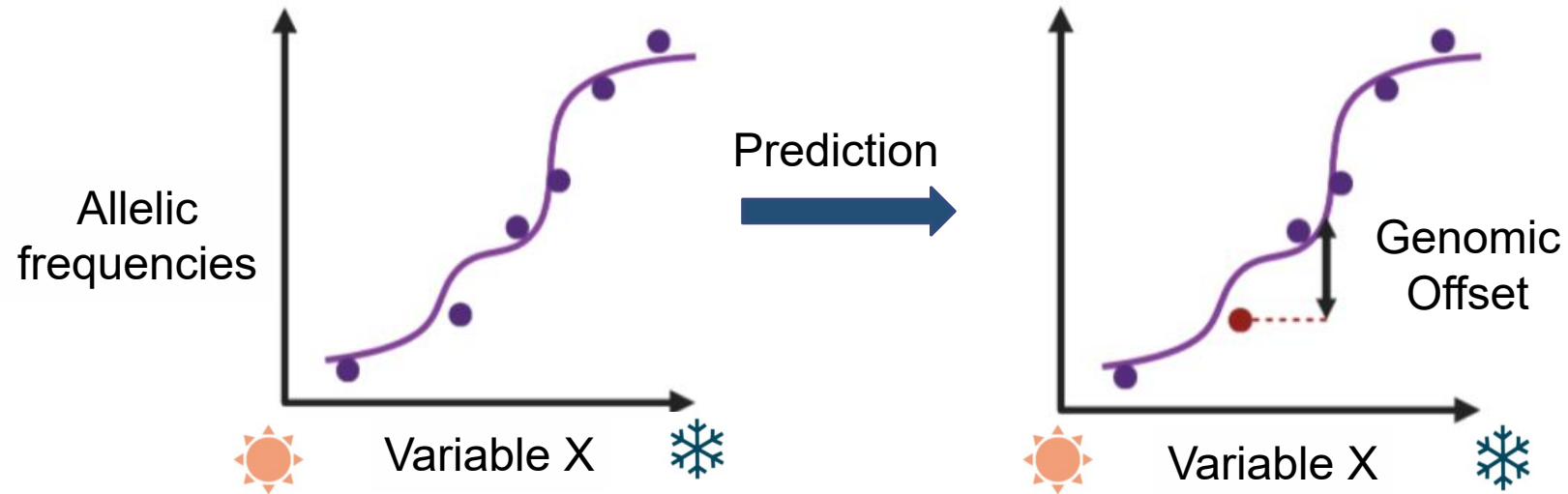




Identification of markers with specific roles in adaptation

Which environmental variables play a role in local adaptation ?





Genomic Offset = a measure of the level of maladaptation

Temporal (future climatic conditions) or spatial (conditions in other geographic areas)

→ Interesting for invasive species

Objectives

Tools

Many methods (Gradient Forest, Baypass, General Dissimilarity Modelling,...), few validations



Evaluation of some methods
How to improve them ?

Simulated data (SLiM)

Real data for two species :
Drosophila suzukii and
Harmonia axyridis



Objectives

Tools

Many methods (Gradient Forest, Baypass, General Dissimilarity Modelling,...), few validations

Evaluation of some methods
How to improve them ?

Simulated data (SLiM)
Real data for two species :
Drosophila suzukii and
Harmonia axyridis

Methods not yet applied to
invasive species

Methods application

Real data for two species :
Drosophila suzukii and
Harmonia axyridis

Two objectives :

- Which variables are more related to invasion ?

Two objectives :

- Which variables are more related to invasion ?
- To what extent is Genomic Offset a good indicator of invasive potential ?
 - Genomic Offset of native populations for an environment different from the one they originated from

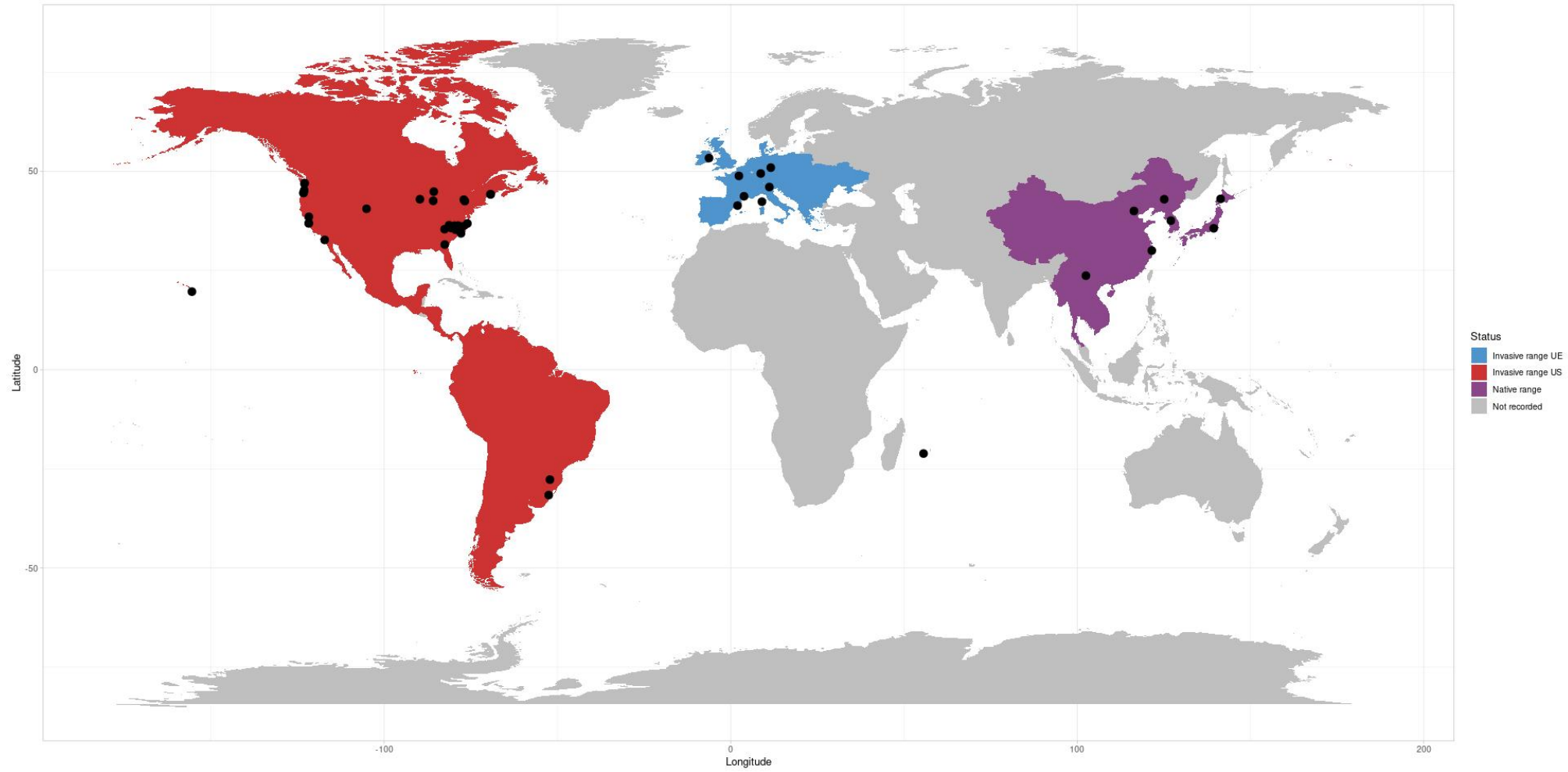
Two objectives :

- Which variables are more related to invasion ?
- To what extent is Genomic Offset a good indicator of invasive potential ?
 - Genomic Offset of native populations for an environment different from the one they originated from
 - Is Genomic Offset related to what we know about *D. sukuzii* invasion ?

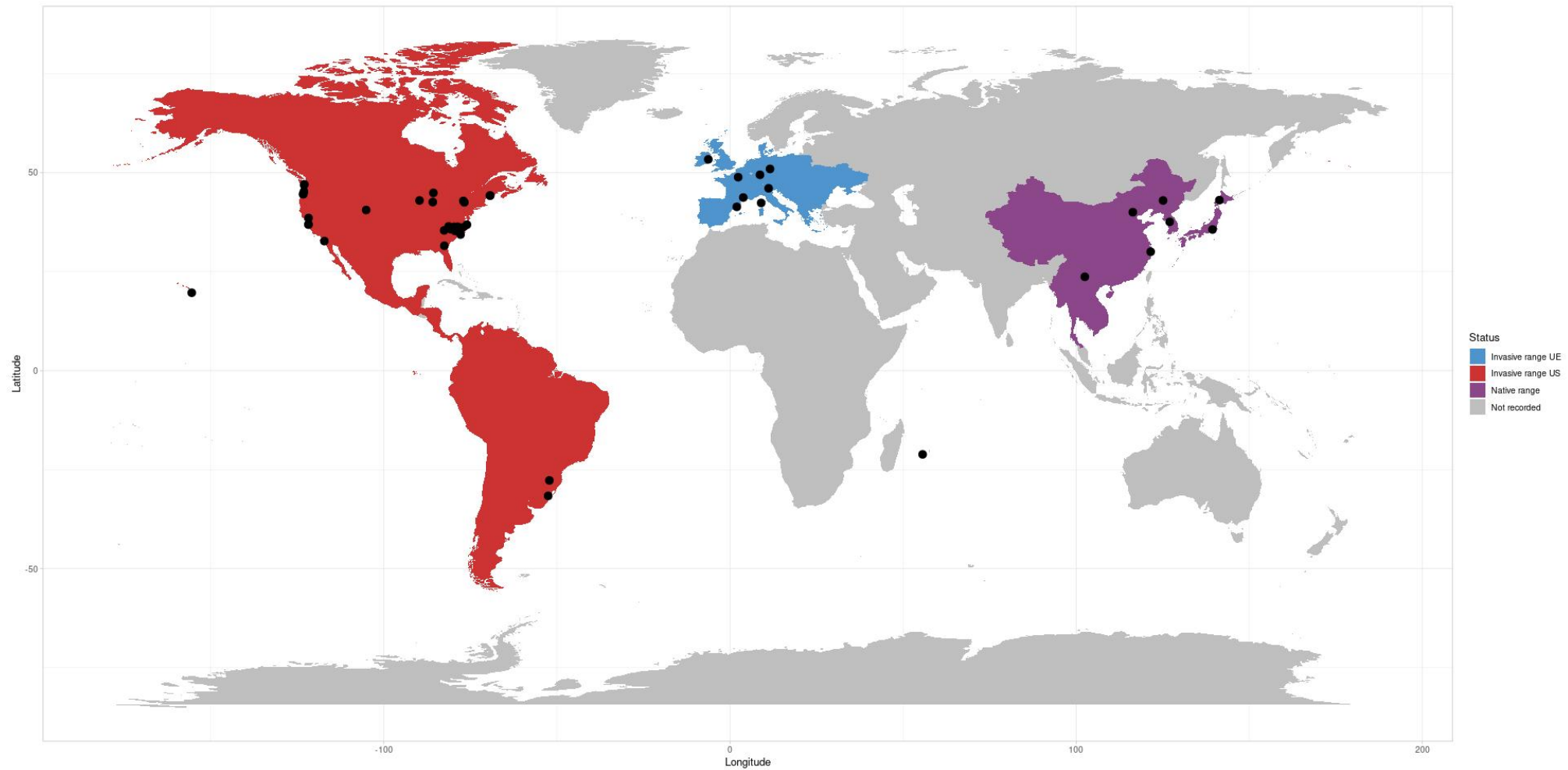
Two objectives :

- Which variables are more related to invasion ?
- To what extent is Genomic Offset a good indicator of invasive potential ?
 - Genomic Offset of native populations for an environment different from the one they originated from
 - Is Genomic Offset related to what we know about *D. sukikii* invasion ?





Individual and pooled resequencing : 43 populations (Public data¹)

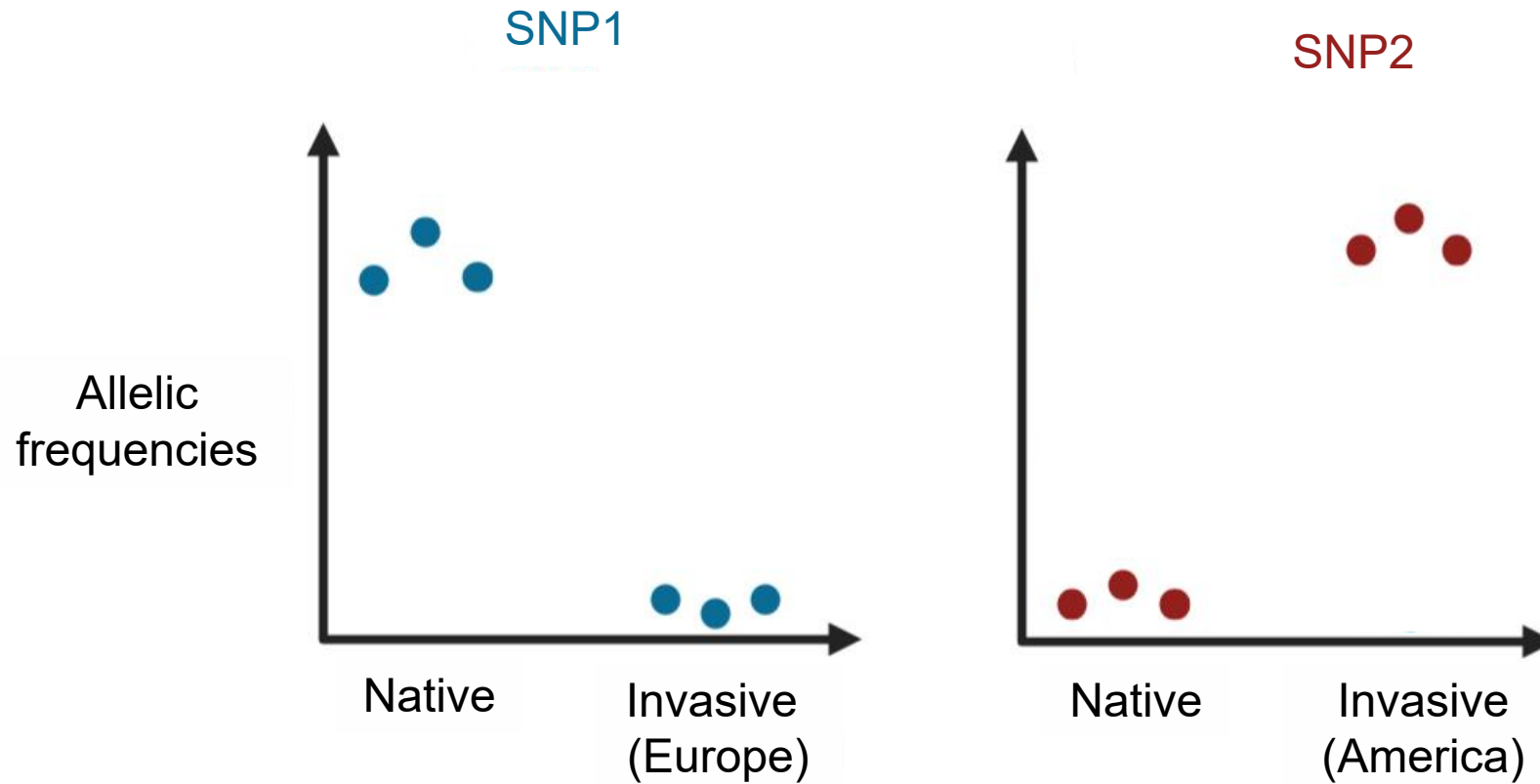


→ Identification of 3 117 246 Single Nucleotide Polymorphism (SNPs)

¹Lewald *et al.* (2021) , Olazcuaga *et al.* (2020)

- Which variables are most related to invasion ?

Contrast index (C2) :



Genome

Allelic frequencies
(2 dataset)

19 bioclimatic variables (WorldClim) for 2012

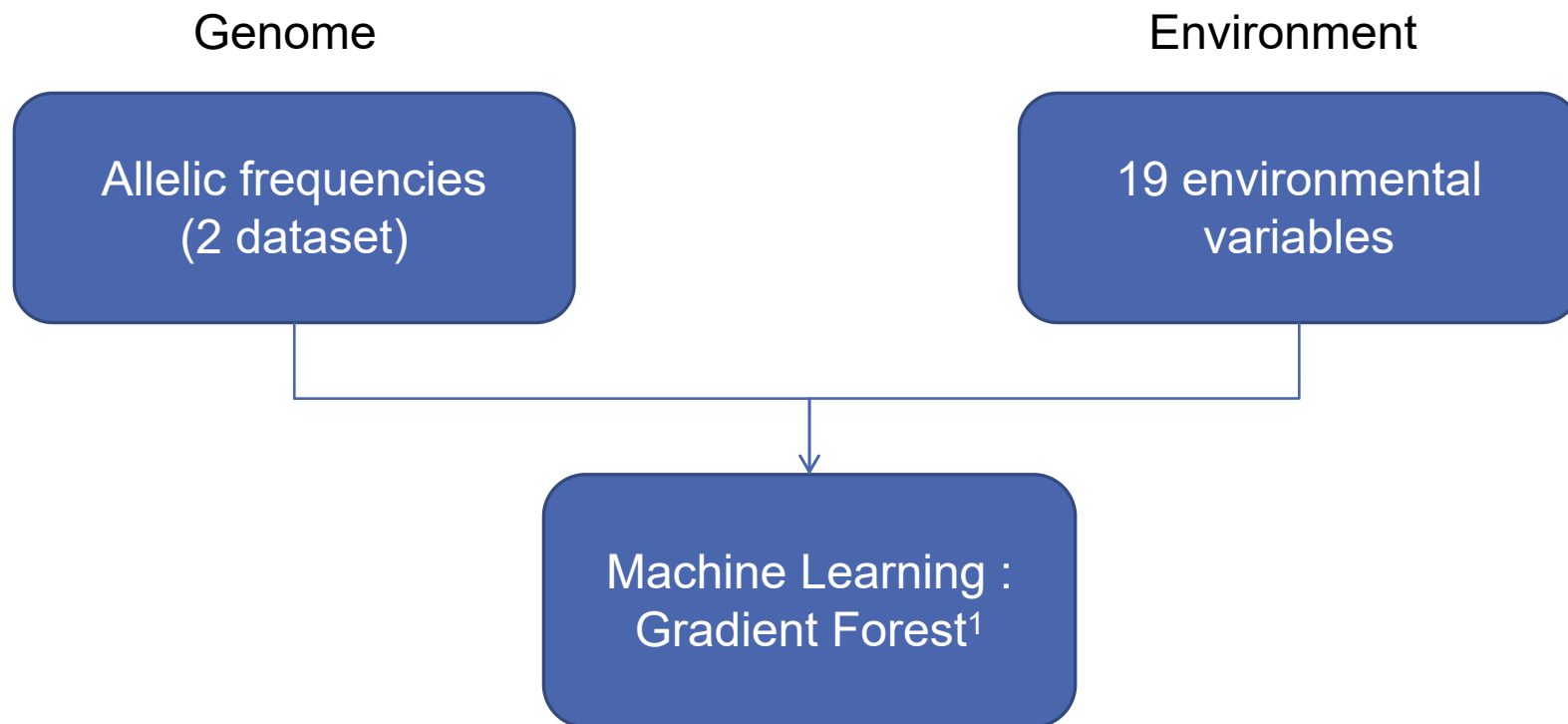
Genome

Allelic frequencies
(2 dataset)

Environment

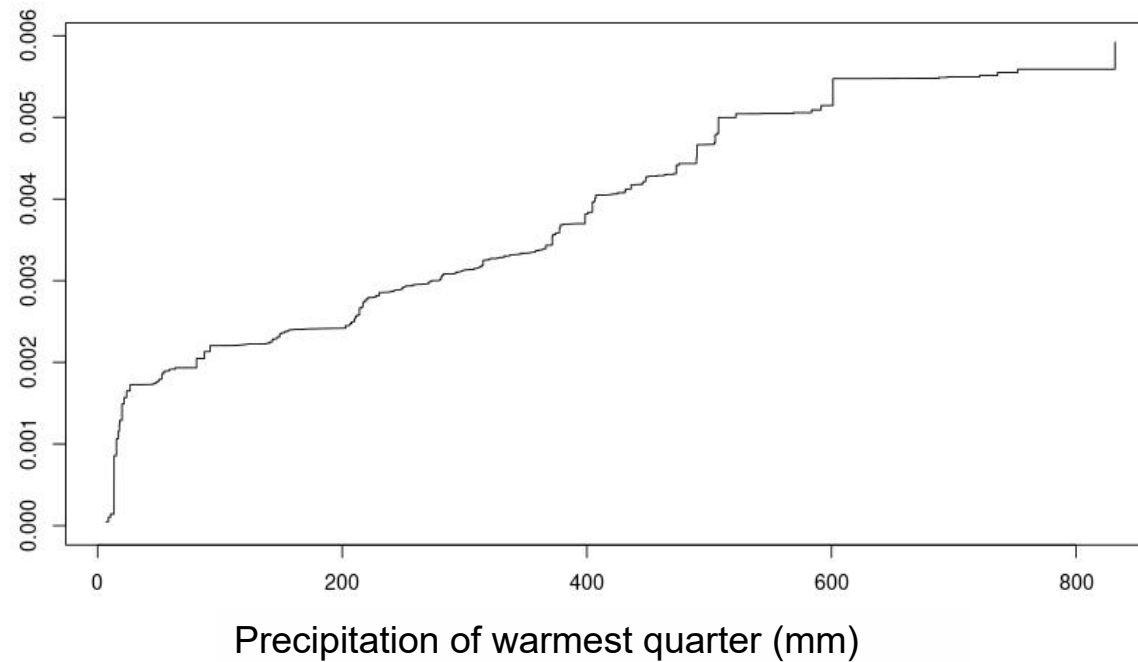
19 environmental
variables

19 bioclimatic variables (WorldClim) for 2012



¹ Ellis *et al.* (2012)

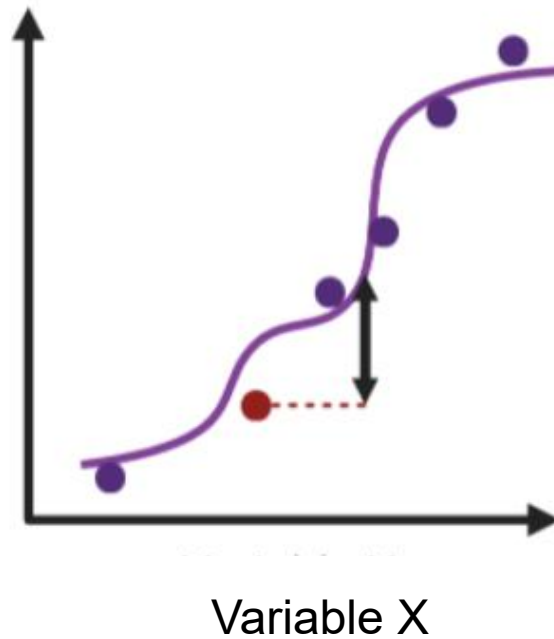
Cumulative importance of allelic frequencies turnover for each variable



Modelisation for each SNP (Sorts non informative SNPs)
Non linear relationship

Prediction :

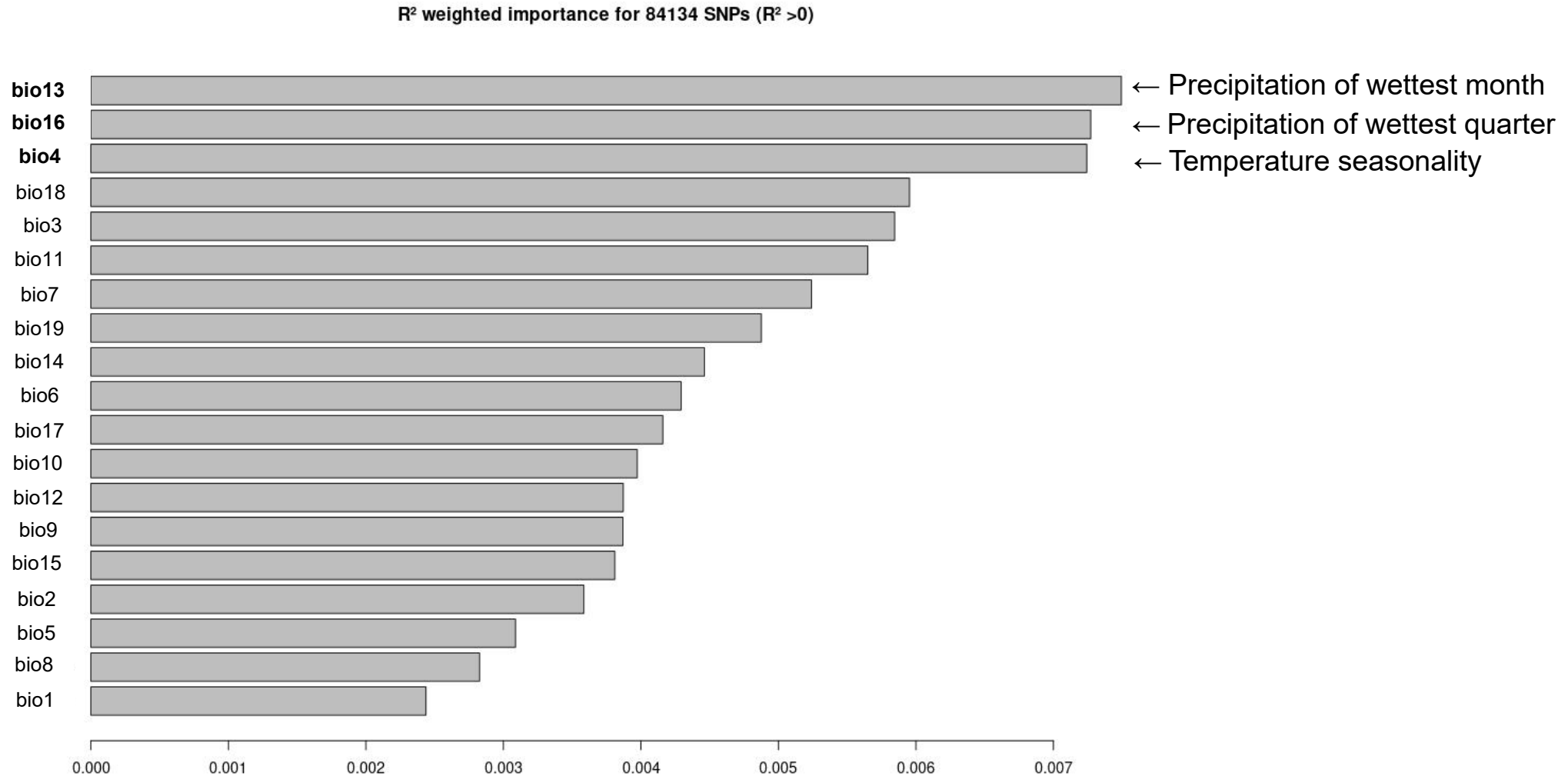
SNPs
cumulative
turnover
=
cumulative
importance



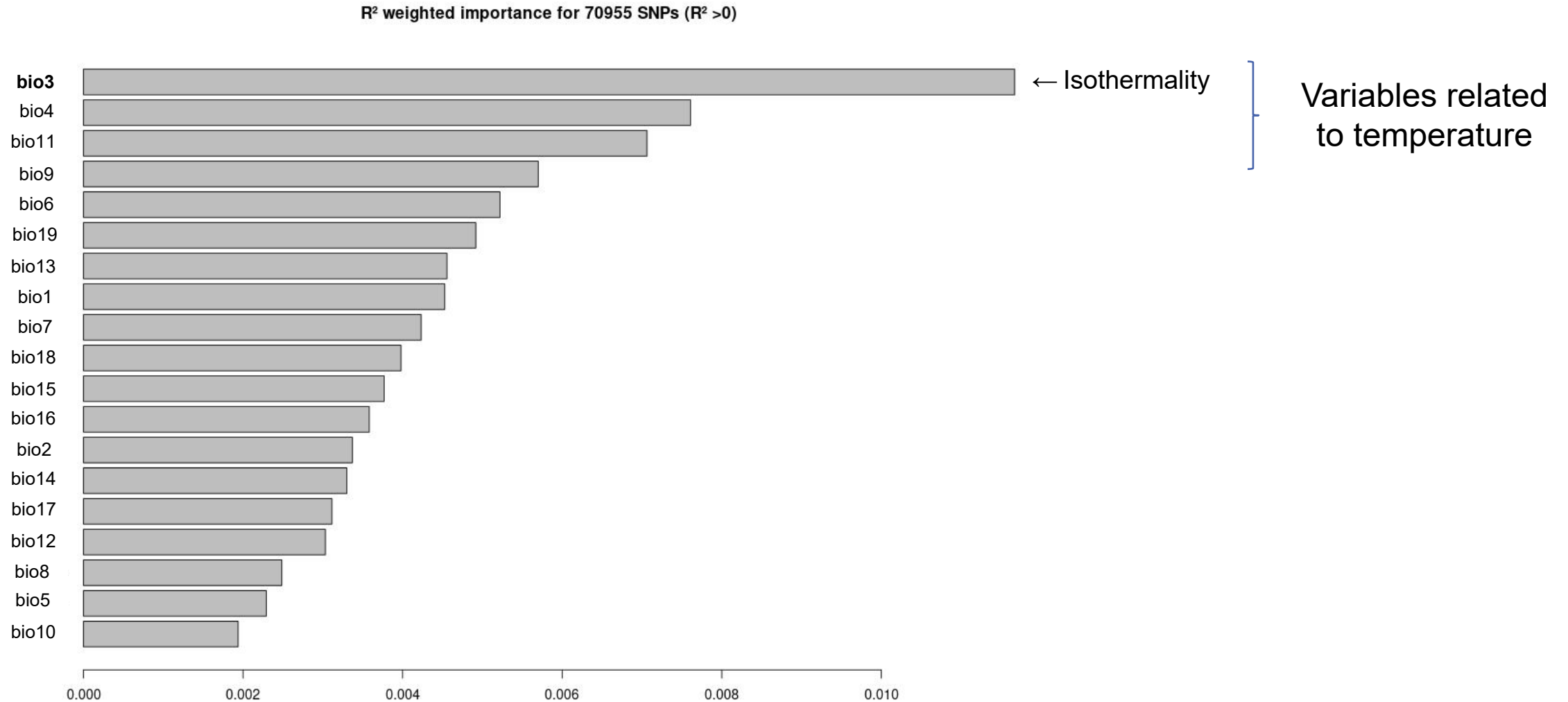
Distance for the importance
of every variables,
between the two
compared environment

Variables weighting !

- Which variables are more related to invasion for **European** invasive populations ?

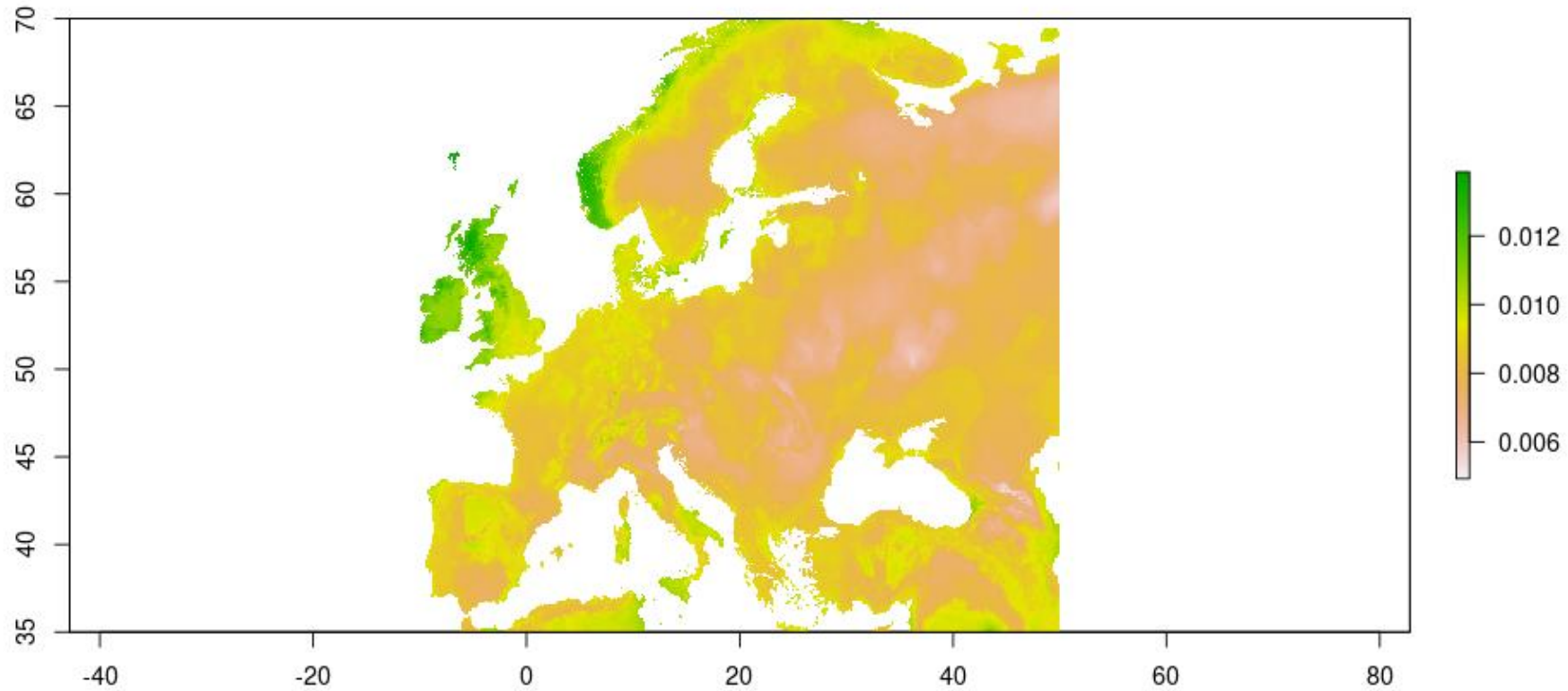


- Which variables are more related to invasion for **american** invasive populations ?



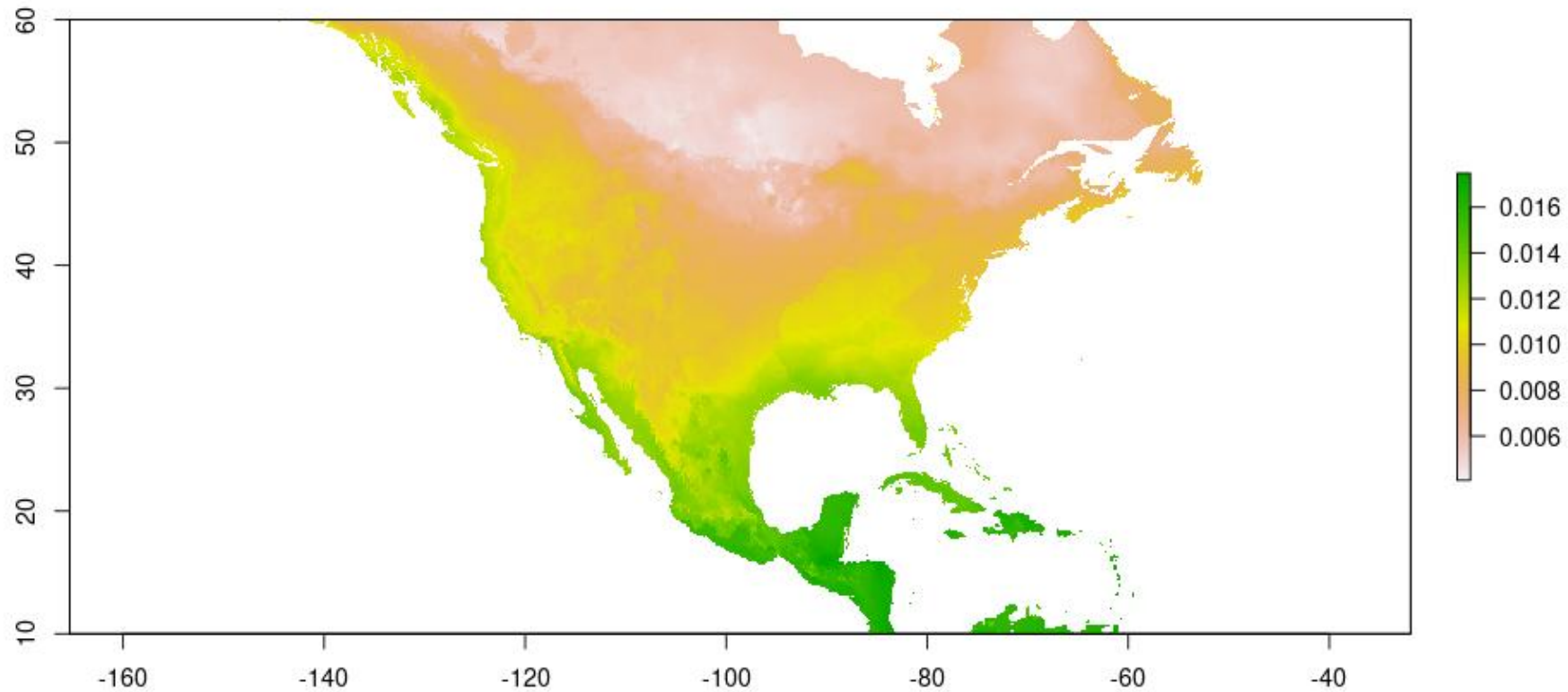
Genomic Offset of native populations for an environment different from the one they originated from

Genomic Offset (“european” model)



Genomic Offset of native populations for an environment different from the one they originated from

Genomic Offset (“american” model)



- Which variables are more related to invasion ?
 - Different depending on the continent : Precipitations and seasonality in Europe
Temperature in America

- Which variables are more related to invasion ?
 - Different depending on the continent : Precipitations and seasonality in Europe
Temperature in America
 - Probably different adaptation basis for invasion : interest of genomic

- Which variables are more related to invasion ?
- To what extent is Genomic Offset a good indicator of invasive potential ?

Genomic Offset of native populations for an environment different from the one they originated from

Is Genomic Offset related to what we know about *D. sukikii* invasion ?

- Which variables are more related to invasion ?
- To what extent is Genomic Offset a good indicator of invasive potential ?

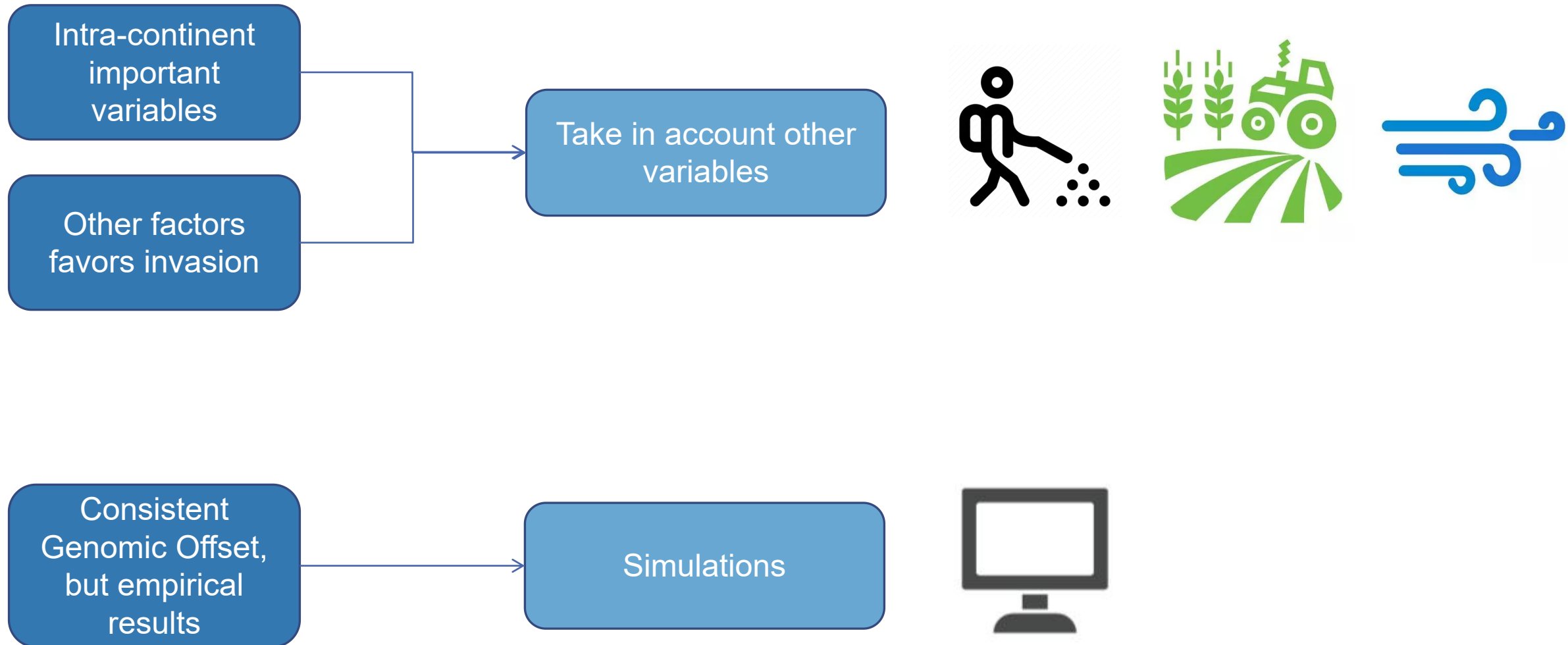
Genomic Offset of native populations for an environment different from the one they originated from

Is Genomic Offset related to what we know about *D. sukikii* invasion ?

Genomic offset is consistent :

- None of the first invaded areas have a high Genomic Offset
- Every high Genomic Offsets areas are late invaded
- However : areas with low Genomic Offsets are not always the first invaded

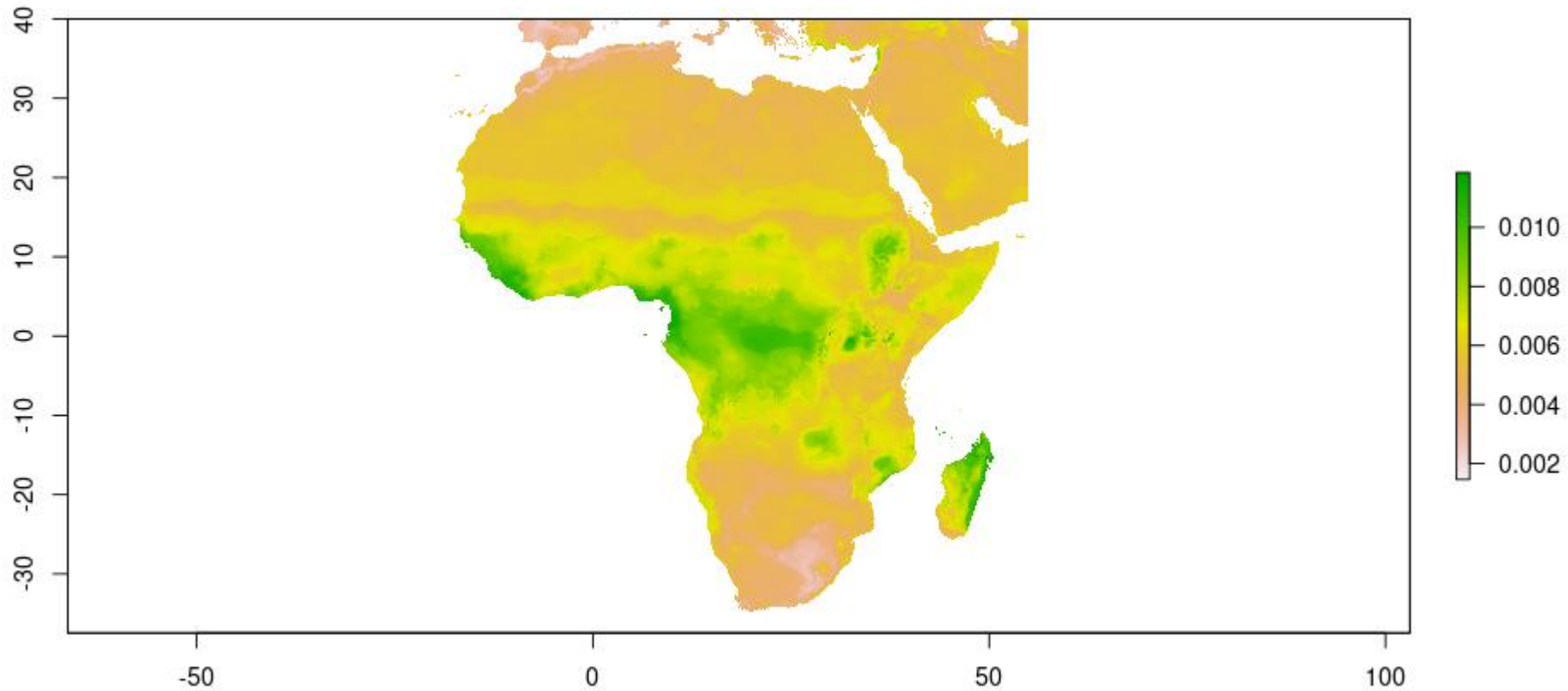




Thank you for your attention !

- Le Genomic Offset est-il lié à ce que l'on connaît de l'invasion de *D. sukii* ?

Genomic Offset (modèle "européen") entre l'Espagne (Barcelone) et l'Afrique



Avec le même nombre de SNPs sélectionnés au hasard

