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# Predicting the invasiveness of a species with genomic data: is Genomic Offset related to establishment probability ?

Louise Camus, PhD student

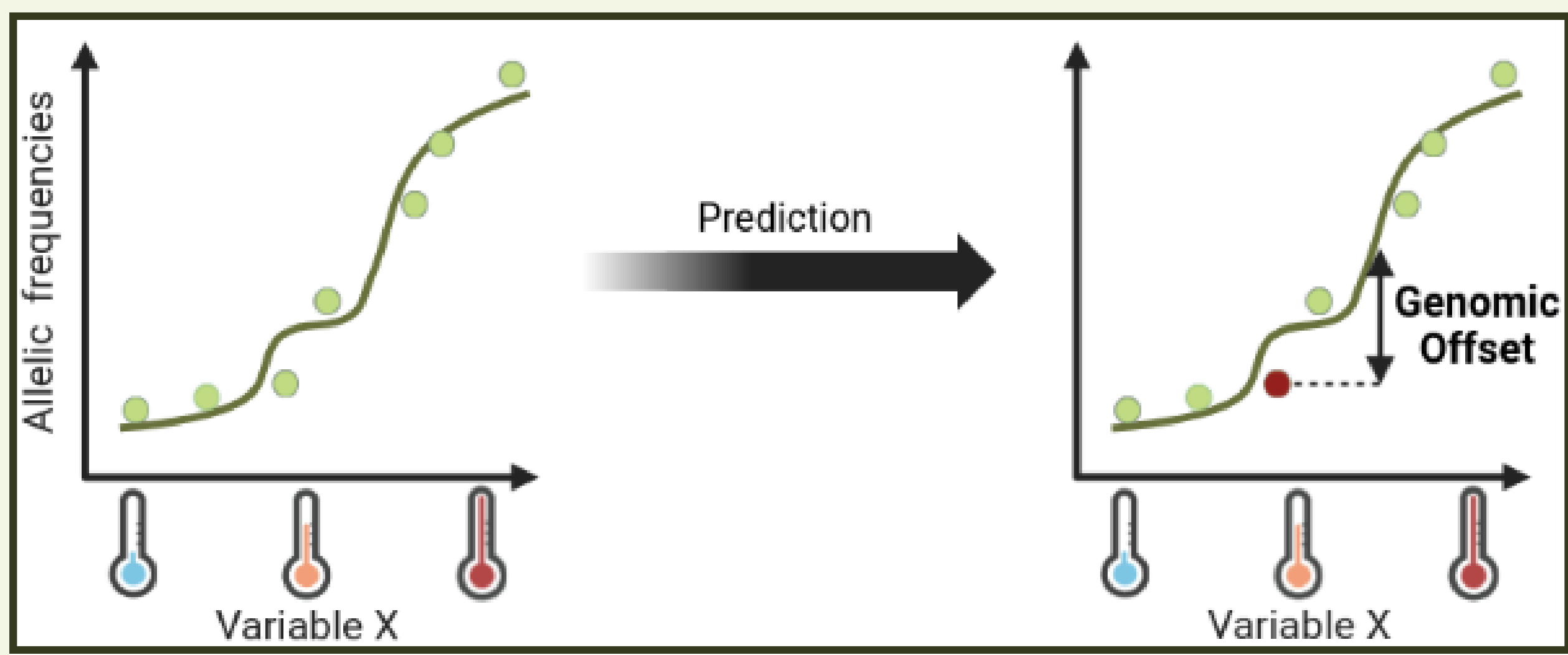
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Supervised by Simon Boitard & Mathieu Gautier

## 1. Introduction

**Question :** Can we predict biological invasion based on genomic data at the population level ?

Exploit observed **association** between allelic frequencies and the environment to take in account local adaptation



**Prediction :** if the environment of a given population changes, to extent the allelic frequencies must change for this population to be adapted ?

$$= \text{Genomic Offset (GO)}^{1,1}$$

High GO  $\longleftrightarrow$  High level of maladaptation  $\longleftrightarrow$  ? Harder invasion

The relationship between GO and fitness has already been demonstrated<sup>2,3</sup>, yet **the connexion between GO and invasiveness remains to be studied.**

**Objectives :** Use *in silico* and empirical approaches to evaluate the link between GO and establishment probability (EP)

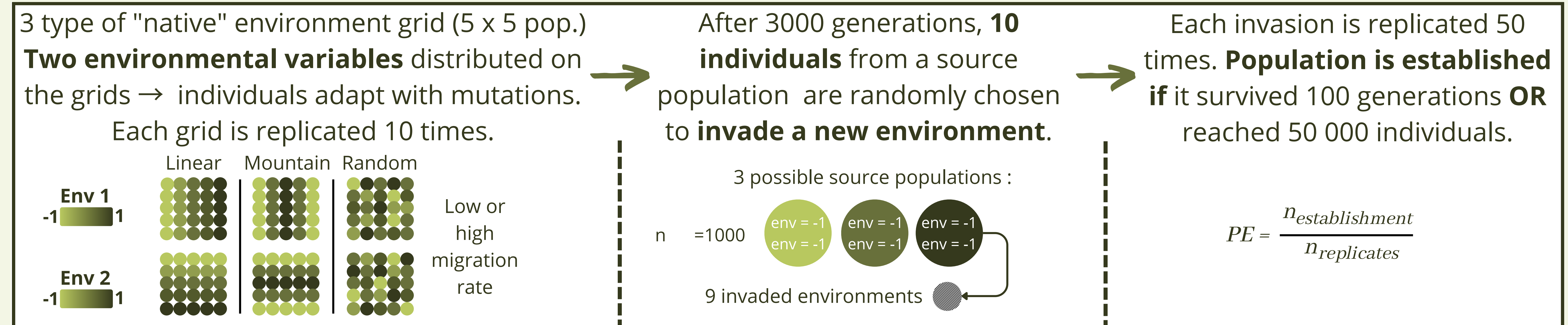
1. Is GO related to the EP of invasive population ?

2. Which GO computation method performs best to predict EP ?

3. For illustrative purpose, apply GO method to the **invasive pest *D. sukuzii***, native from Asia, which invaded American and European continent in the early 2010s.

## 2. Material and Methods

**Simulated data (SLiM<sup>4</sup>):**



Once EP is known, **GO between source population and the 9 invaded environments** are computed with several methods :

- **Geometric GO** (GGO, linear, using regression coefficients from **Baypass<sup>5</sup>** or **LFMM<sup>3</sup>**)
  - **Gradient Forest GO** (GF\_GO, non-linear, based on Random Forest<sup>6</sup>)
- Using all or pre-selected SNPs

**Empirical data :** Individual<sup>6</sup>+ pool<sup>7</sup> sequencing for **30 populations** in the native (n=7) and invasive range (n<sub>europe</sub>=9, n<sub>america</sub>=14) → 4 millions SNPs + 21 bioclimatic variables → GO between invaded and source environments<sup>8</sup>



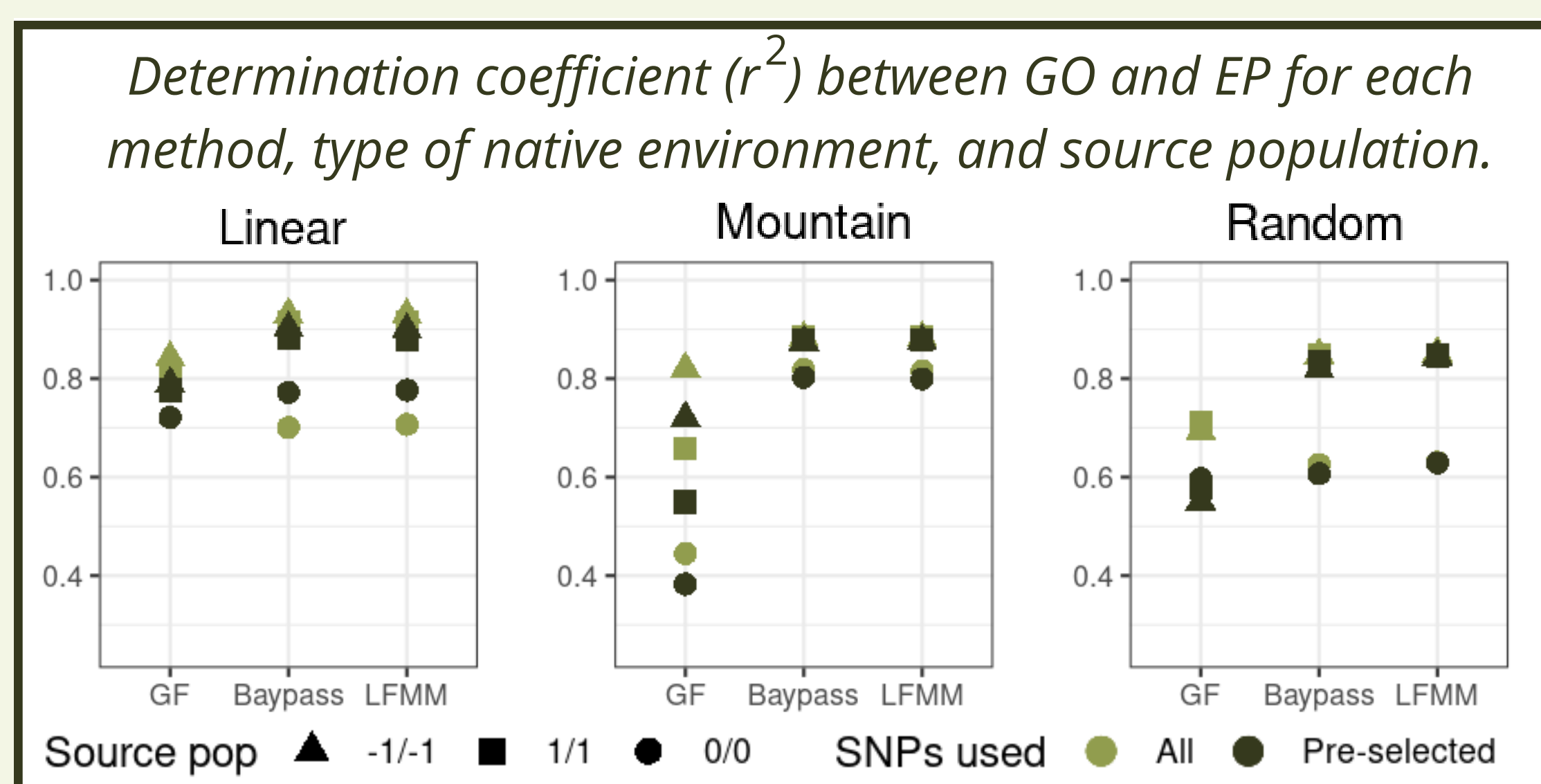
Europe  $\longleftrightarrow$  Liaoyuan (China)

America  $\longleftrightarrow$  Ningbo (China)

**Are higher GO related to later invasion ?**

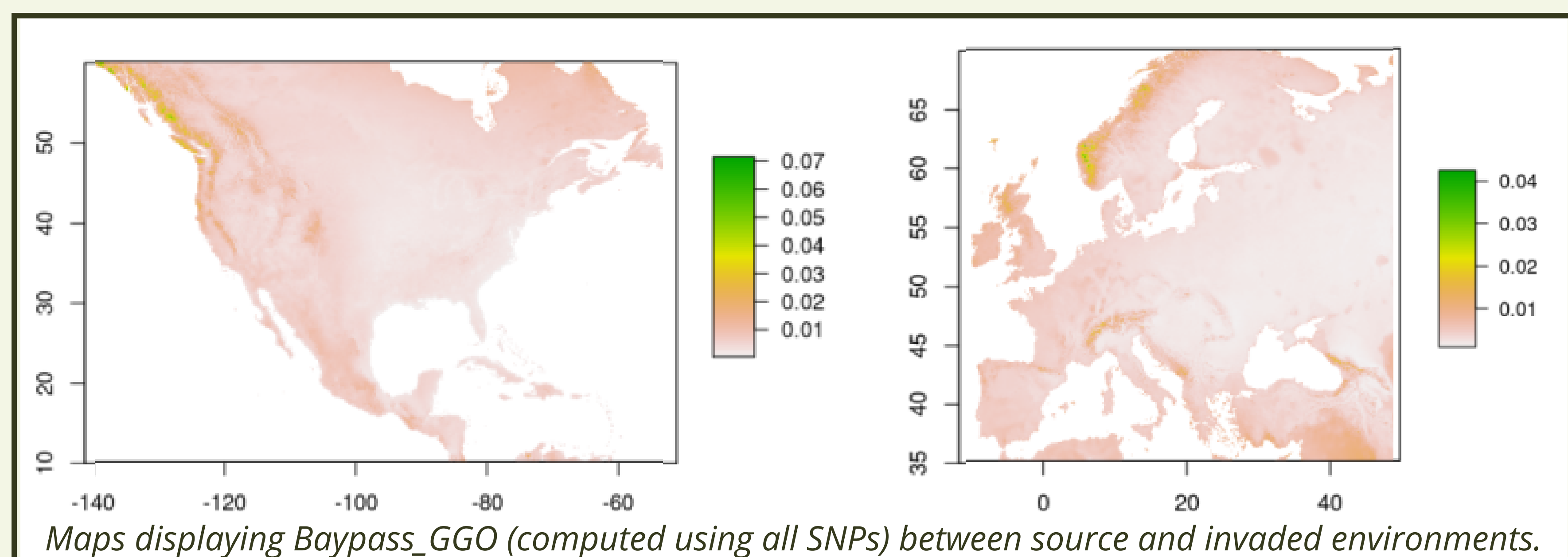
## 3. Results and perspectives

**Simulated data :**



- GO is related to EP.
- GGO performs better than GF\_GO
- Baypass\_GGO  $\approx$  LFMM\_GGO
- SNPs pre-selection lowers GF performances

**Empirical data :**



- Baypass\_GGO is overall coherent with invasion dates of *D. sukuzii*
- Very few areas have high GGO

**Overall GO seem to represent a good predictor of invasiveness, and may be a valuable tool to inform invasion risk.**

**Perspectives :** **Successful invasion = more than only adaptation.** Influence of : propagule pressure ? accessibility ? genetic load ?  
**Histories of invasion are complex.** Influence of : admixture ? "Source" population choice ?

**References :** [1] Fitzpatrick & Keller, *Ecol. Lett.* (2015) [2] Laruson et al., *Evol. Appl.* (2022) [3] Gain et al., *Mol. Biol. Evol.* (2023) [4] Haller & Messer, *Mol. Biol. Evol.* (2019) [5] Gautier, *Genetics* (2015) [6] Olazcuaga et al. *Mol. Biol. Evol.* (2020) [7] Lewald et al., *G3* (2021). [8] Fraimout et al., *Mol. Biol. Evol.* (2017)