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Genomic prediction of the range of biological invasion

Louise Camus, Simon Boitard, Mathieu Gautier

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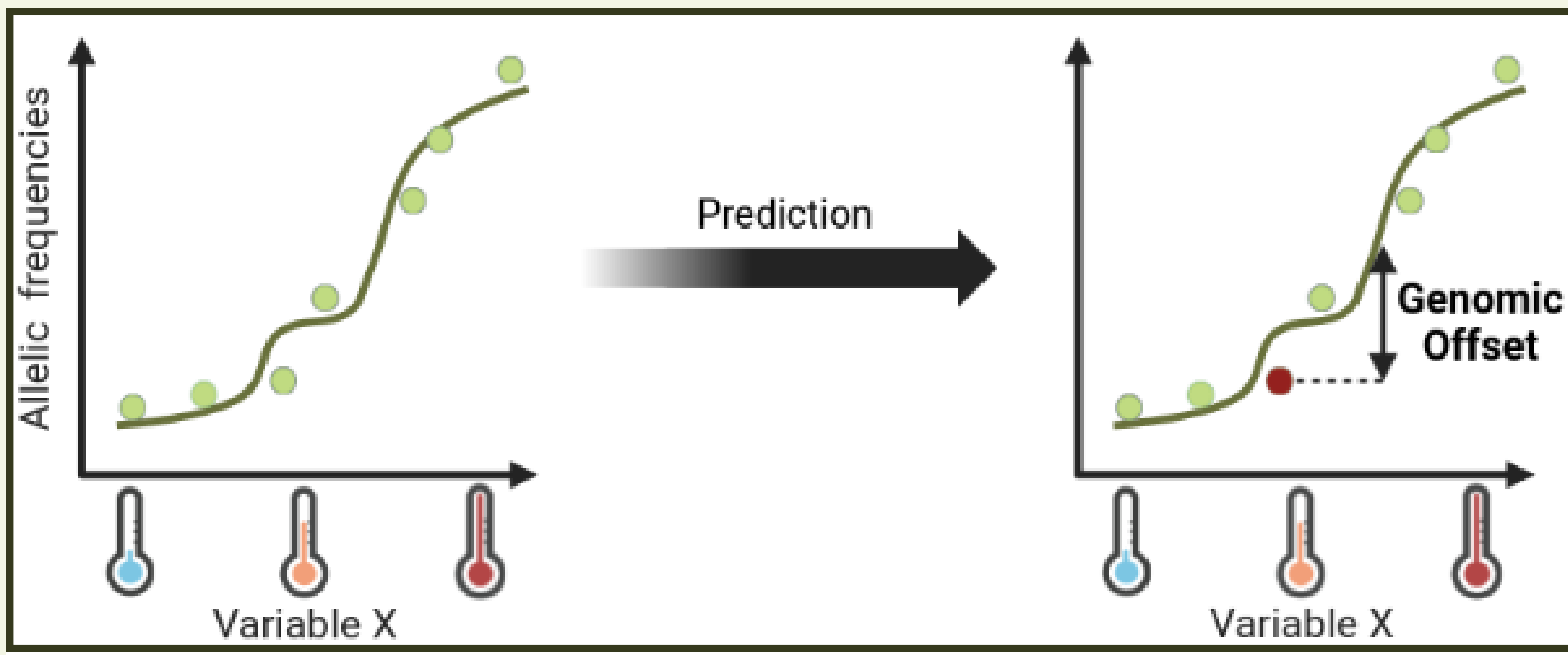
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1. Introduction

Question : Do population measures of "mal-adaptation" (a.k.a **Genomic Offset**) relate to their successful establishment ?

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



↳ **Prediction :** amount of allele frequency change required at environment associated variants for a population to be adapted in a new environment
= **Genomic Offset (GO)**¹

High GO \leftrightarrow High level of maladaptation \leftrightarrow ? Harder invasion

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 ?

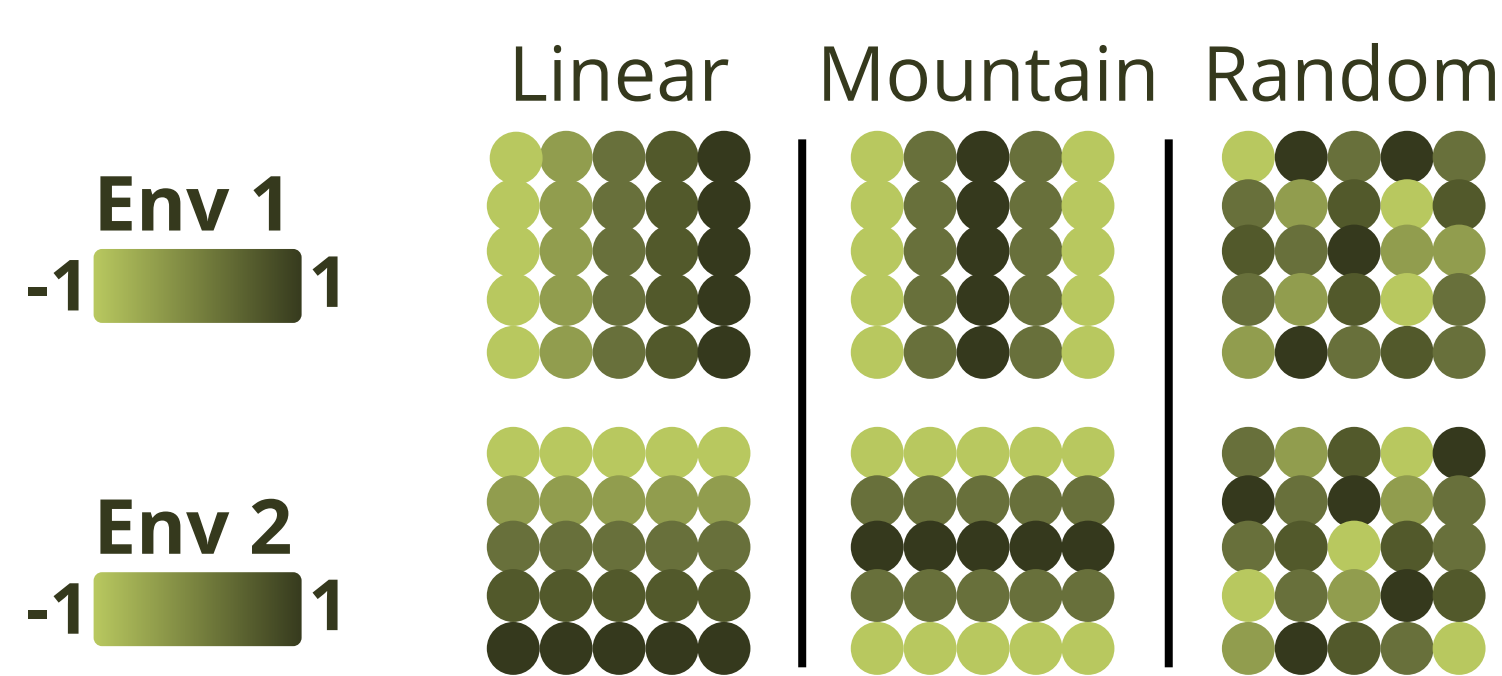
2. Which GO computation method performs best to predict EP ?

3. Would GO have informed us about the invasion of Europe and America by the **invasive pest** *D. sukuzii* native from Asia, in the early 2010s ?

2. Material and Methods

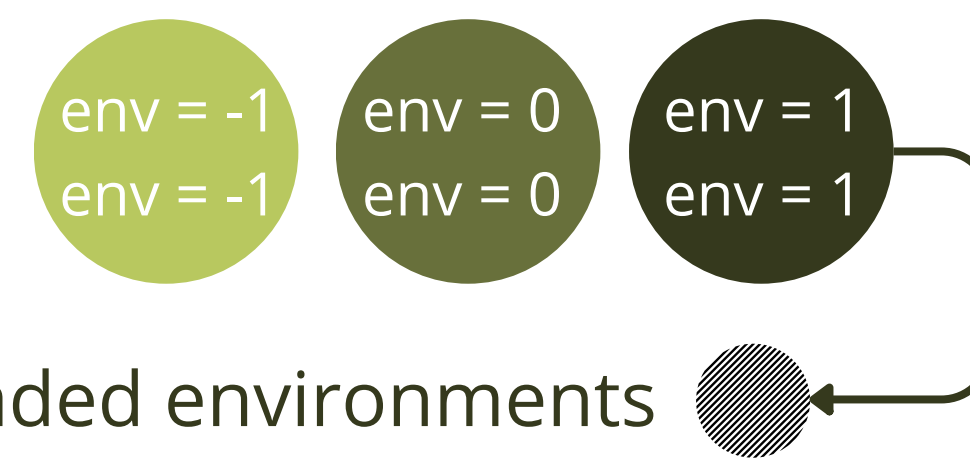
Simulated data (SLiM⁴):

3 "native" environment grid (5 x 5 pop.) with **two environmental variables**, polygenic local adaptation during 3000 generations.



10 individuals from a source population are randomly chosen to **invade a new environment**.

3 possible source populations :



Each invasion is replicated 50 times under a non-WF model

$$PE = \frac{n_{establishment}}{n_{replicates}}$$

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

- **Geometric GO** (GGO, linear, regression coefficients from **Baypass**⁵ or **LFMM**³)
- **Gradient Forest GO** (GF_GO, non-linear, based on Random Forest⁶)

Empirical data : Individual⁶ + pool⁷ sequencing for **30 populations** in the native (n=7) and invasive range (n_{europe}=9, n_{america}=14)
→ 4 millions SNPs + 21 bioclimatic variables → GO between invaded and source environments⁸



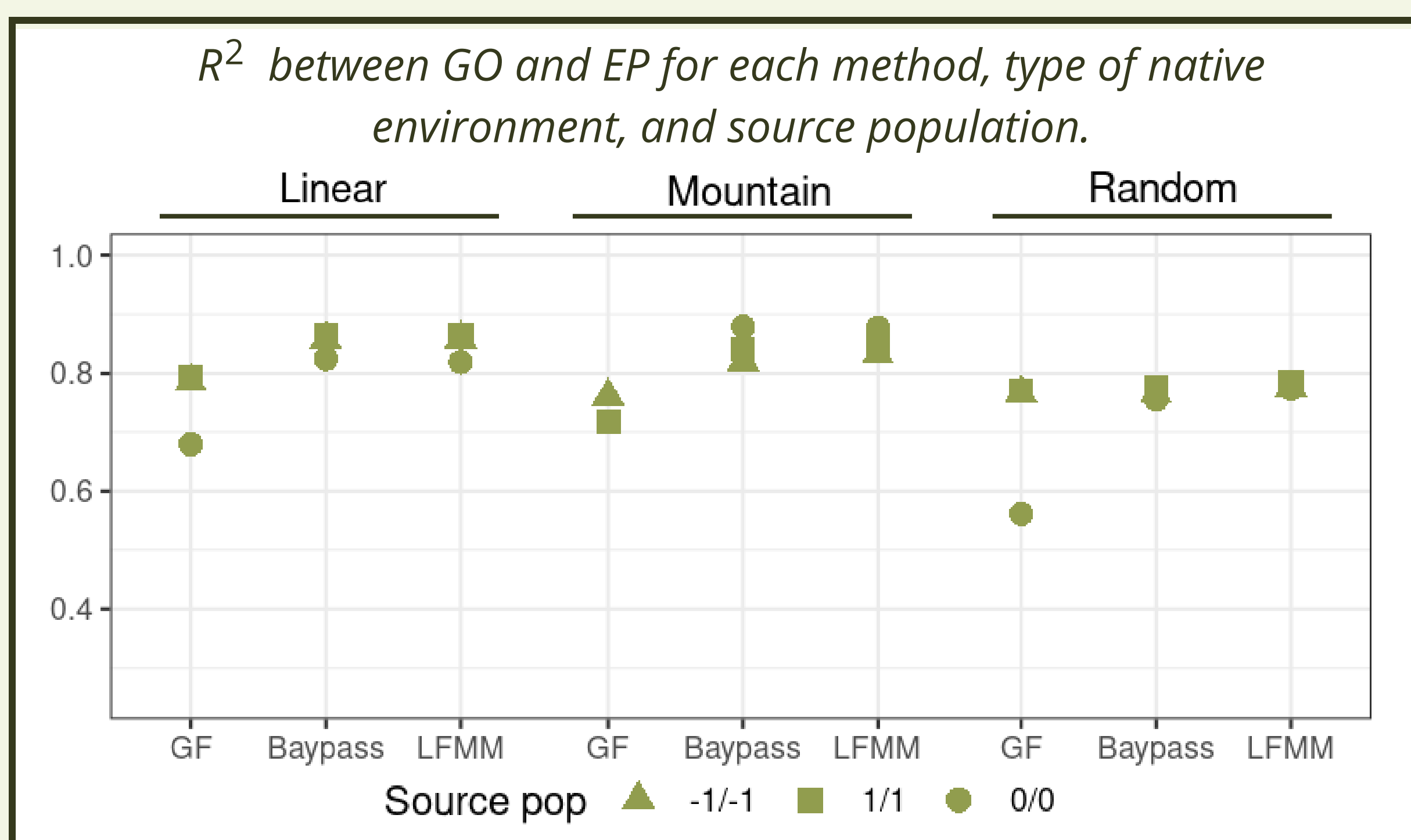
Europe \leftrightarrow Liaoyuan (China)

America \leftrightarrow Ningbo (China)

Are higher GO related to later invasion ?

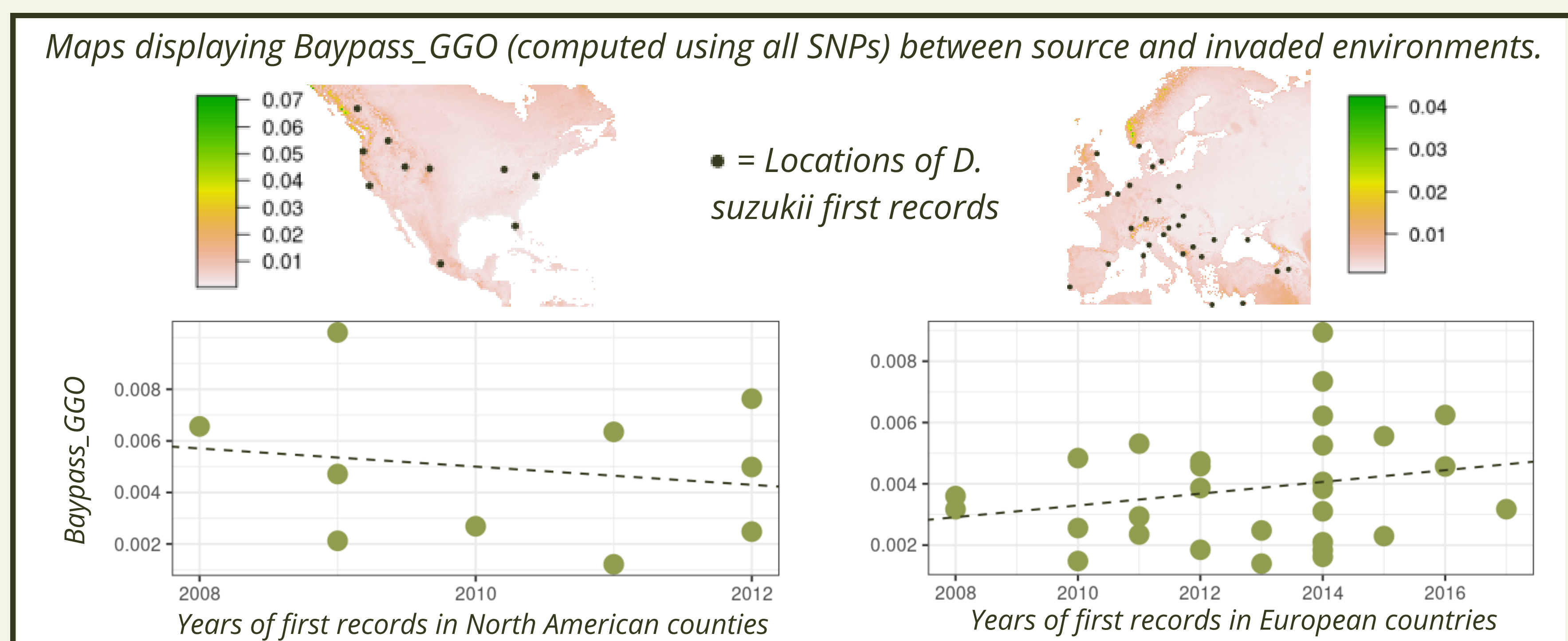
3. Results and perspectives

Simulated data :



- GO is related to EP / Baypass_GGO \approx LFMM_GGO
- GGO performs better than GF_GO

Empirical data :



- Overall, later invaded areas do not have higher GGO.
- GGO values are extremely similar → pre-adapted everywhere ?

GO could represent a good predictor of invasiveness, and may be valuable to inform invasion risk.

But with limitations : Successful invasion = more than only pre-adaptation : also a matter of historical chance (admixture, area accessibility, propagule pressure, source population origins) and other biological necessity (e.g purging of the genetic load).

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] Olazuaga et al. *Mol. Biol. Evol.* (2020) [7] Lewald et al., *G3* (2021). [8] Fraimout et al., *Mol. Biol. Evol.* (2017) [9] Di Castri, *Biological invasions in Europe and the Mediterranean Basin* (1990)