Performance evaluation of adaptive introgression classification methods

Jules Romieu, Ghislain Camarata, Pierre-André Crochet, Miguel de Navascués, Raphaël Leblois, François Rousset

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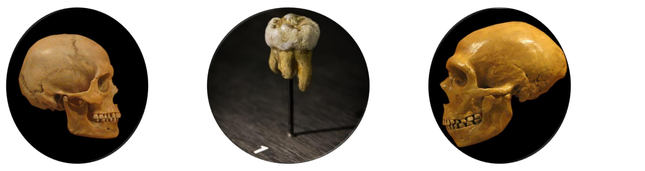
1 Background and objective

Current adaptive introgression classification methods

Developped and tested → **Human lineages**



Homo sapiens — *Denisovan* — *Homo neanderthalensis*

Recent divergence time

Performance ? → ***Other lineage***

Podarcis genus

Ancient divergence time

Objective: Performance tests of AI methods on simulated datasets under *Podarcis* scenarios

2 Summary statistic and methods tested

Q95 (1%,100%) (Racimo *et al.* 2017)

- **Summary statistic**
- 50kb windows
- **High frequency** of alleles uniquely shared between the donor and the recipient populations
- Uses samples from 3 populations

VolcanoFinder (Setter *et al.* 2020)

- **Composite likelihood-based** genomic scan
- One test site every kb
- **Excess intermediate frequency polymorphism** in the flanking region of the genome
- Uses only the **recipient population** sample

Simulation-based classification methods

Genomatnn (Gower *et al.* 2021)

- **Deep learning** (Convolutional Neural Network)
- 100kb windows
- **Black box** (train on genotype matrix)
- Uses samples from 3 populations

MaLAdapt (Zhang *et al.* 2023)

- **Machine learning** (Extra Trees Classifier)
- 50kb windows
- Train on **summary statistics** (alleles shared between donor and recipient, linkage desequilibrium, genetic diversity, etc)
- Uses samples from 3 populations

3 Simulation test approach

Simulation	Simulated test sets	Classification methods	Classification metrics
Backward + Forward ms prime + SLiM	Simulated genome: Known states: Non-AI window — AI window	• Q95[1] (Summary statistics) • VolcanoFinder[2] (Composite likelihood) • Genomatnn[3] (Deep learning) • MaLAdapt[4] (Machine learning)	Known states Versus Predicted states ROC, TPR, AUC, FPR

4 Demographic model

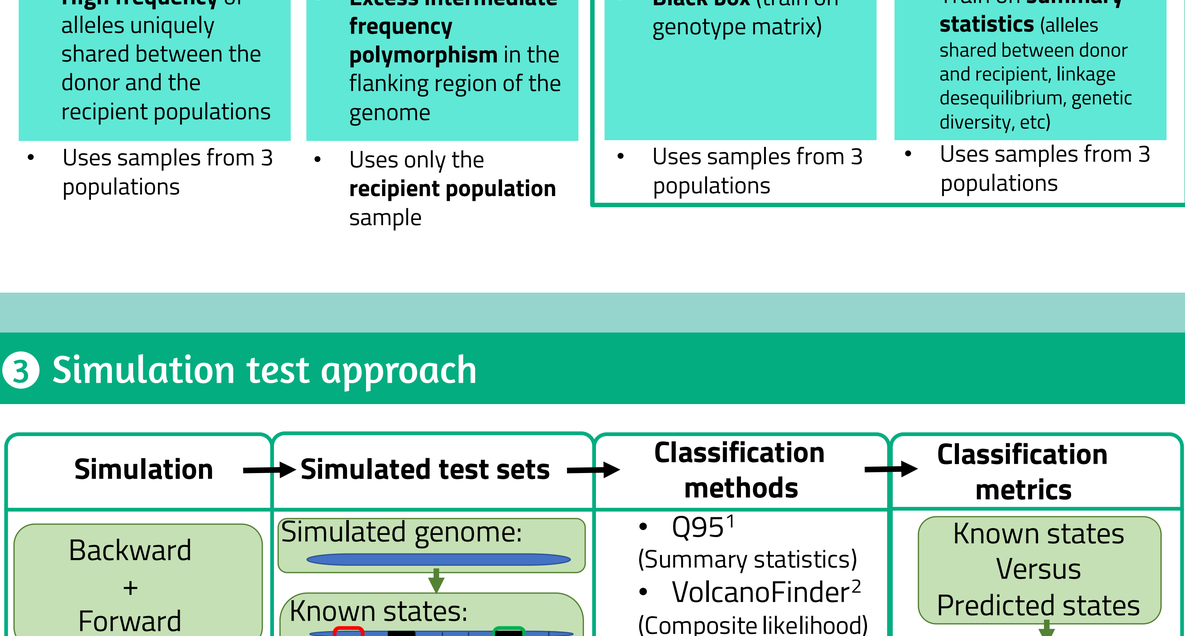
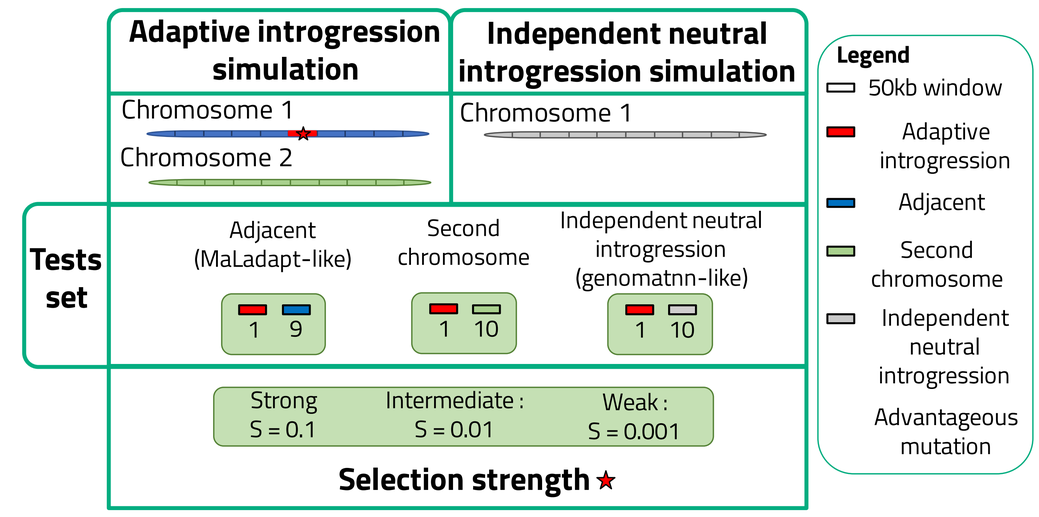


Figure 1 – Demographic model used to generate simulated dataset. Anc_O_I = Outgroup and Ingroup ancestral population, O = Outgroup population, I = Ingroup population, Anc_D_DS = Donor and non-introgressing ancestral population, Anc_R_RS = Recipient and non-introgressed ancestral population. DS = sister to the donor population (non-introgressing population), D = Donor population (introgressing population), R = Recipient population (introgressed population), RS = Recipient sister population (non-recipient population), Population size (N) = 10,000.

5 Importance of genetic architecture

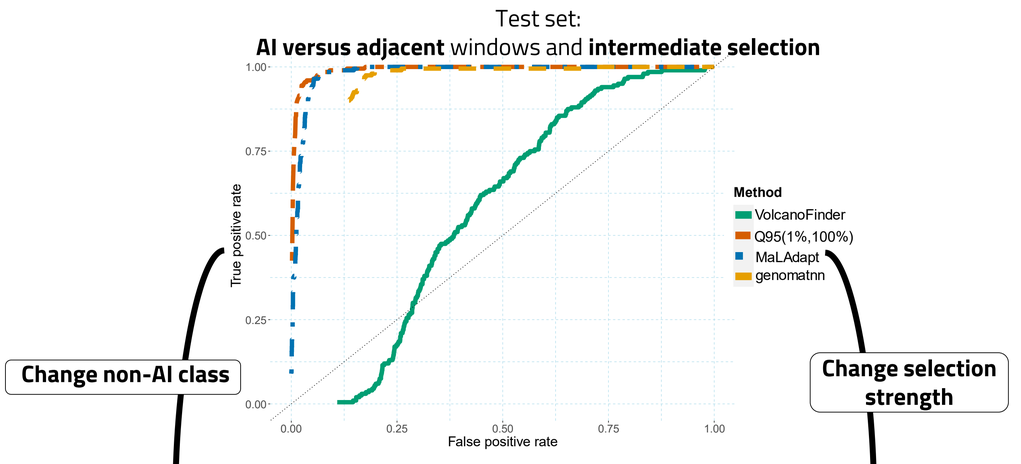
Hitchhiking effect on method's performance?

→ **non-AI window types : adjacent, second chromosome and independent neutral introgression**



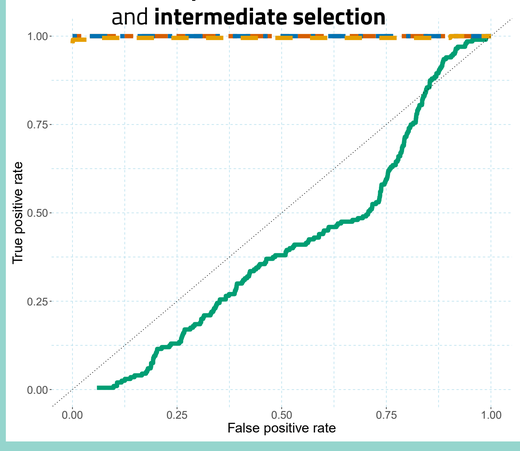
6 Results: ROC curves

Test set:
AI versus adjacent windows and **intermediate selection**



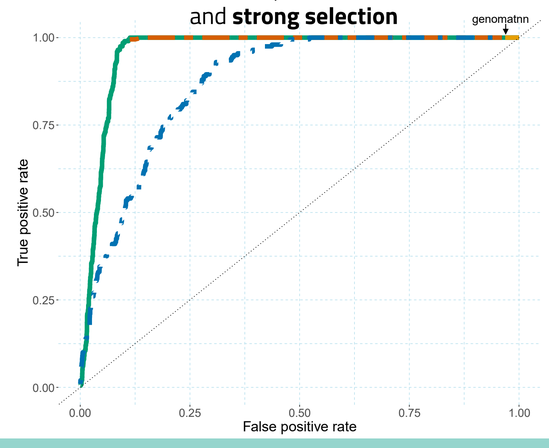
Change non-AI class

Test set:
AI versus independent neutral windows and **intermediate selection**



Change selection strength

Test set:
AI versus adjacent windows and **strong selection**



7 Discussion and conclusion

- Best method in our tests: Q95 summary statistic
- Better performance with strong selection but leads to an increase in hitchhiking effect

  → Take adjacent windows into account

- Simulation-based inference methods: Factors that have negative impacts on performance:
  - Test sets with non-AI windows types non-used in train sets (ex :genomatnn)
  - Misspecification of demographic model used in train sets

  → Importance to take into account different types of neutral windows in trained sets

- Classification methods problems:
  - Define a threshold to discriminate AI/non-AI windows
  - Necessity to use FDR control methods

  → Solution: Develop methods to estimate genomic-level introgression

Bibliography

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