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Tracking adaptation to environmental changes: selfing and detection of loci under selection

Miguel Navascués

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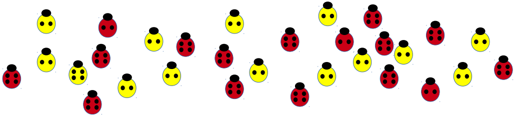
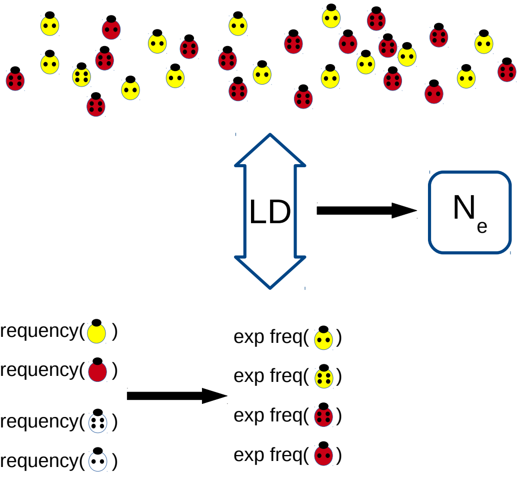
30/06/2015

Population genetics: sampling present generation



Population genetics: sampling present generation



LD

N_e

frequency(●)

frequency(●)

frequency(●)

frequency(●)

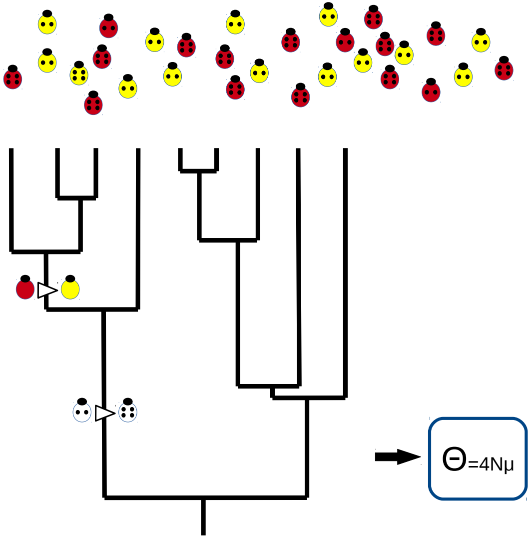
exp freq(●)

exp freq(●)

exp freq(●)

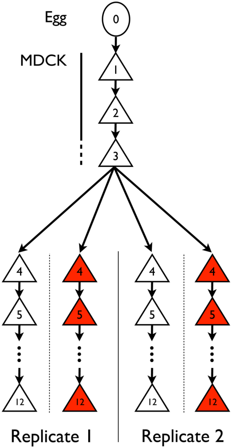
exp freq(●)

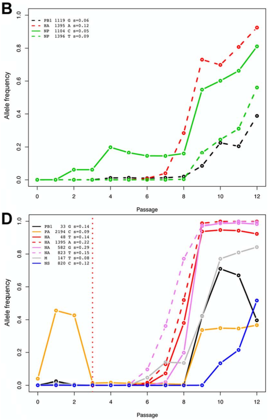
Population genetics: sampling present generation



Experimental evolution

Foll *et al.* (2014) Influenza Virus Drug Resistance
doi:10.1371/journal.pgen.1004185

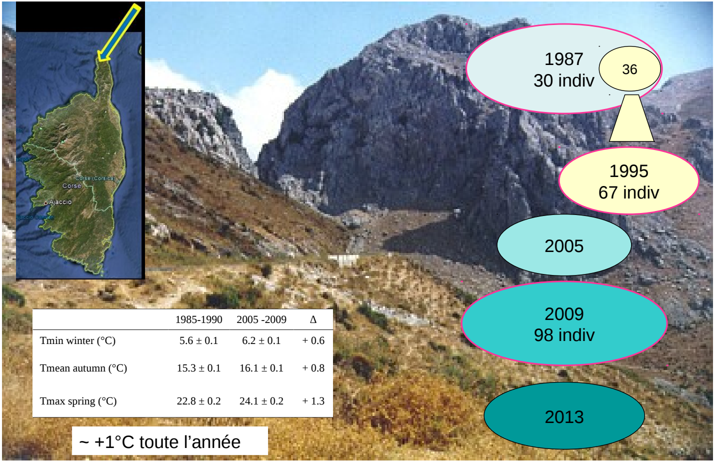




Temporal samples in natural populations

Medicago truncatula, Corsica

Pop Corse F20089



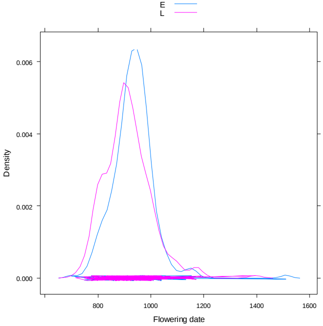
	1985-1990	2005 -2009	Δ
Tmin winter (°C)	5.6 ± 0.1	6.2 ± 0.1	+ 0.6
Tmean autumn (°C)	15.3 ± 0.1	16.1 ± 0.1	+ 0.8
Tmax spring (°C)	22.8 ± 0.2	24.1 ± 0.2	+ 1.3

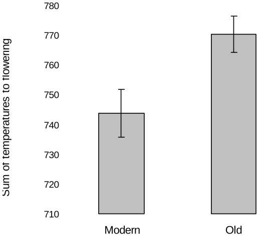
~ +1°C toute l'année

Medicago truncatula, Corsica

Changement phénotypique

- Mesure de la date de floraison en serre
  - 55 individus / année (/~100)
  - 5 blocs
  - 2 traitements vernalisation



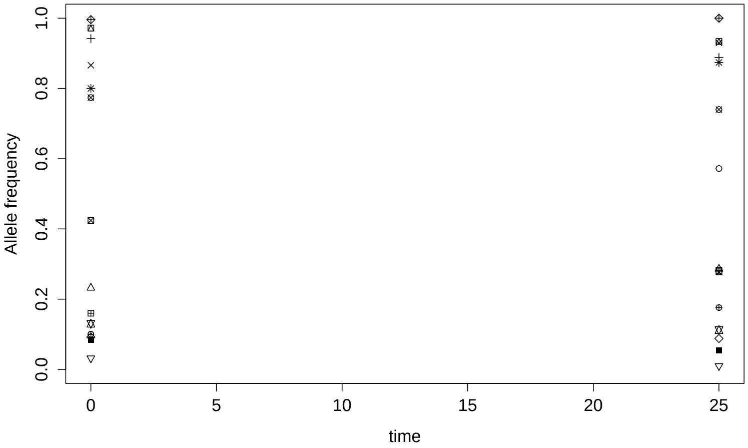


avancée de floraison +2 jour

Temporal F_{ST} outliers

A modified version of method proposed by Goldringer & Bataillon (2004) doi:10.1534/genetics.103.025908

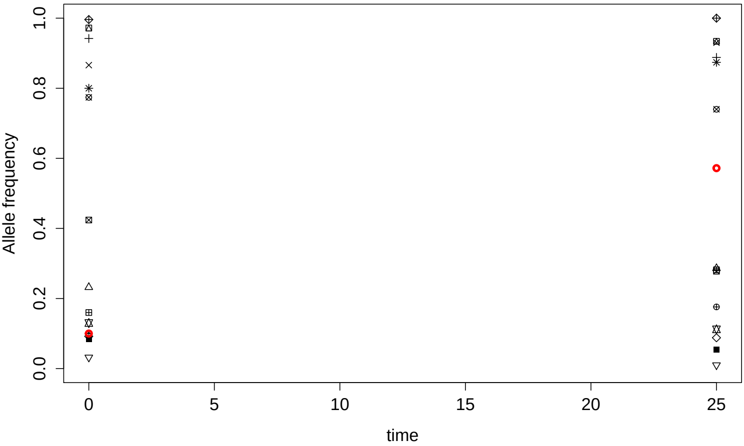
Variance in allele frequencies (F_C) from all loci: $\hat{N}_e$



Temporal F_{ST} outliers

A modified version of method proposed by Goldringer & Bataillon (2004) doi:10.1534/genetics.103.025908

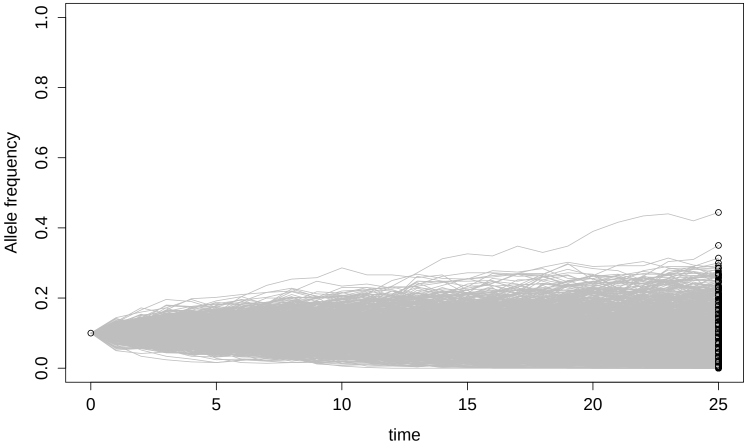
Is variance in allele frequencies (F_C) in a focal locus compatible with $\hat{N}_e$?



Temporal F_{ST} outliers

A modified version of method proposed by Goldringer & Bataillon (2004) doi:10.1534/genetics.103.025908

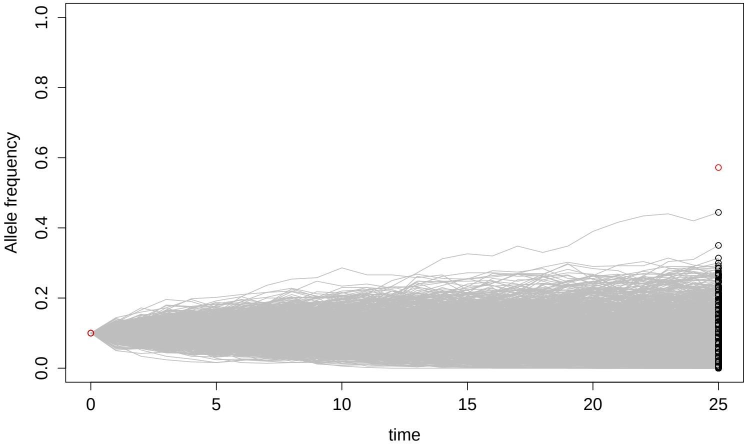
Simulation of drift from focal locus initial frequency and $\hat{N}_e$



Temporal F_{ST} outliers

A modified version of method proposed by Goldringer & Bataillon (2004) doi:10.1534/genetics.103.025908

Significance of observed F_C in focal locus is evaluated from distribution

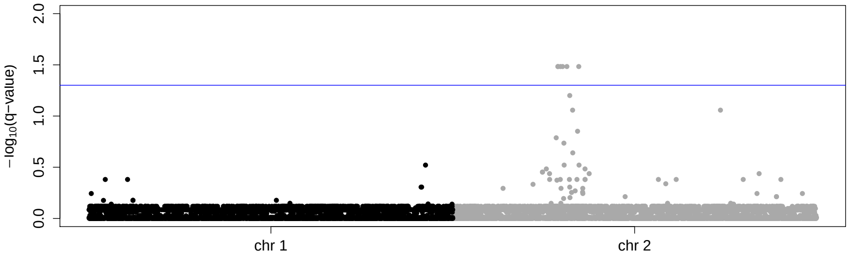


Simulations

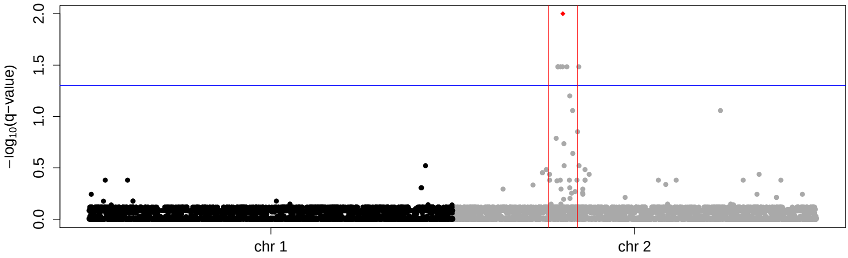
- Software: SLiM (Messer 2013, doi:10.1534/genetics.113.152181 messerlab.org)
- N=500 diploid individuals
- 2 chromosomes (500Mb), μ=1e-8, r=1e-8

- Neutral period (till mutation-drift equilibrium)
- New advantageous mutation/existing allele becomes advantageous (s=0.5)
- First sample: 50 diploid individuals
- Selection period (25 generations)
- Second sample: 50 diploid individuals
- 10000 polymorphic SNP loci are studied

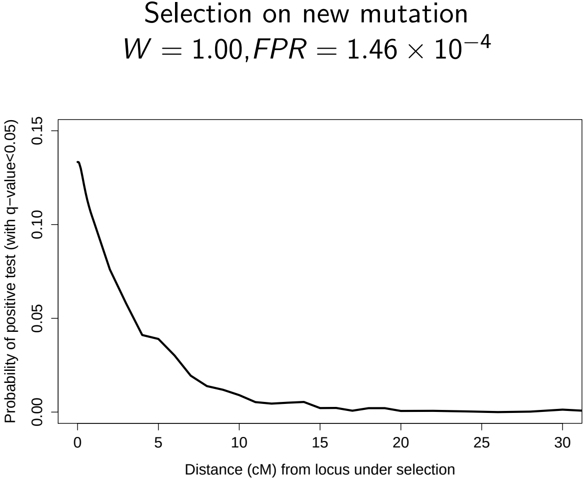
Manhattan plot: results from a single simulation replicate



Manhattan plot: results from a single simulation replicate



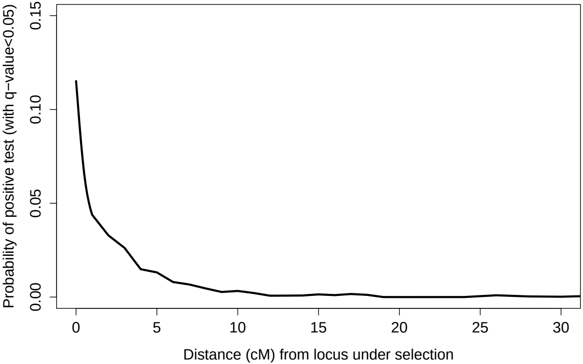
Power and False Positive Rate



Power and False Positive Rate

Selection on standing variation

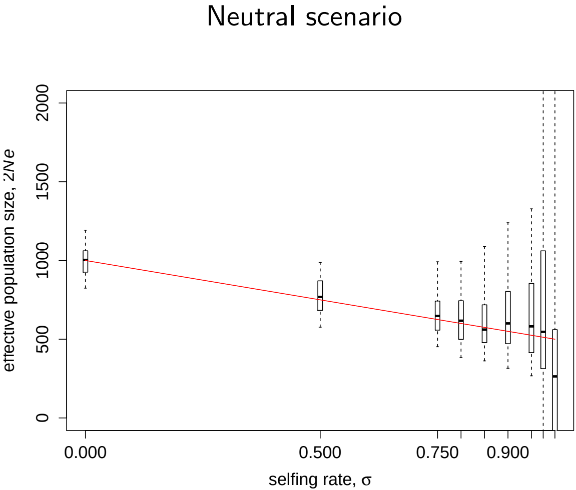
$W = 0.61, FPR = 2.92 \times 10^{-4}$



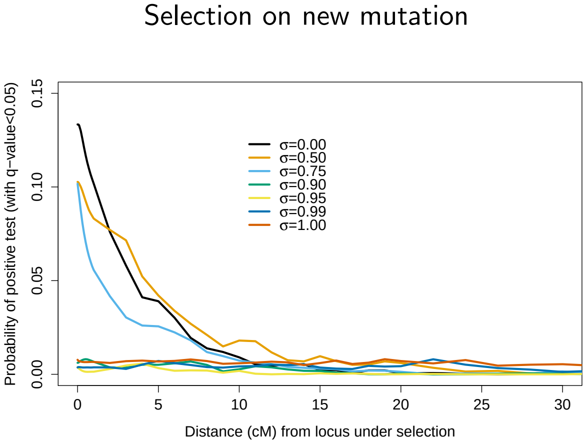
Consequences of selfing

- Reduction of effective population size
- Increase of homozygosity
    - reduction of effective recombination
    - increased LD
    - hitchhiking

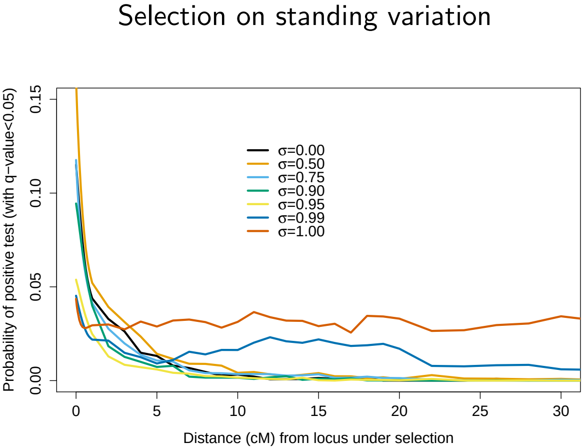
Effective population size



Power and False Positive Rate



Power and False Positive Rate



Conclusions

- Temporal F_{ST} outlier approach can detect regions under selection (parameter combination studied)
- Footprint of selection in a ∼20cM region (parameter combination studied)
- Selfing reduces power ($0.75 < \sigma < 0.90$)
- Increase of false positives with selfing is not very problematic ($FPR < 0.05$)

Acknowledgements

- Comité d'organisation ETEE 2015 - Empirisme et Théorie en Écologie et Évolution
- Collaborators:
  - Arnaud Becheler (currently at UMR EGCE, Gif-sur-Yvette) & Renaud Vitalis: Evaluation of temporal F_{ST} outlier method
  - Laurène Gay & Joëlle Ronfort (UMR AGAP): *Medicago truncatula*
- Project SelfAdapt funded by Métaprogramme ACCAF (INRA)

Images

- Figures 1 and 3 from Foll *et al.* (2014). CC BY doi:10.1371/journal.pgen.1004185
- Photos of Corsican sampling site and common garden experiments provided by Laurène Gay
- Signs. Public domain (Wikimedia Commons)

Abstract

In a single isolated populations, allele frequencies will change through time subject to the processes of selection (acting on specific loci) and genetic drift (acting on the whole genome). Genetic data collected at different times can be used to make inferences on the effective population size (i.e. strength of drift) and to detect outlier loci, whose changes in allele frequencies are unlikely to be only the product of the inferred demography. However, the presence of self-fertilization may pose a problem for the detection of loci under selection. Selfing reduces the effective size of populations and the effective recombination among loci (promoting hitch-hiking). We investigated the effect of the presence of partial selfing reproduction in the power and false discovery rate for the detection of selected loci. In addition, we characterized the footprint of selection along the chromosome containing the selected site.