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

Arnaud Becheler Renaud Vitalis Miguel Navascués

UMR CBGP (INRA Montpellier, France) Miguel.Navascues@supagro.inra.fr



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.

Motivation

A population of *Medicago truncatula* in Corsica has been studied by L. Gay and J. Ronfort (UMR AGAP, INRA Montpellier). Samples taken from 1987 and 2009 show a significant and heritable shift in flowering time (~ 2 days earlier), congruent with adaptation to climate change (increase of $\sim 1^\circ\text{C}$ in mean temperatures). Can we detect the loci involved? *Medicago truncatula* is a predominantly selfing plant, how does this affect the detection of loci under selection?

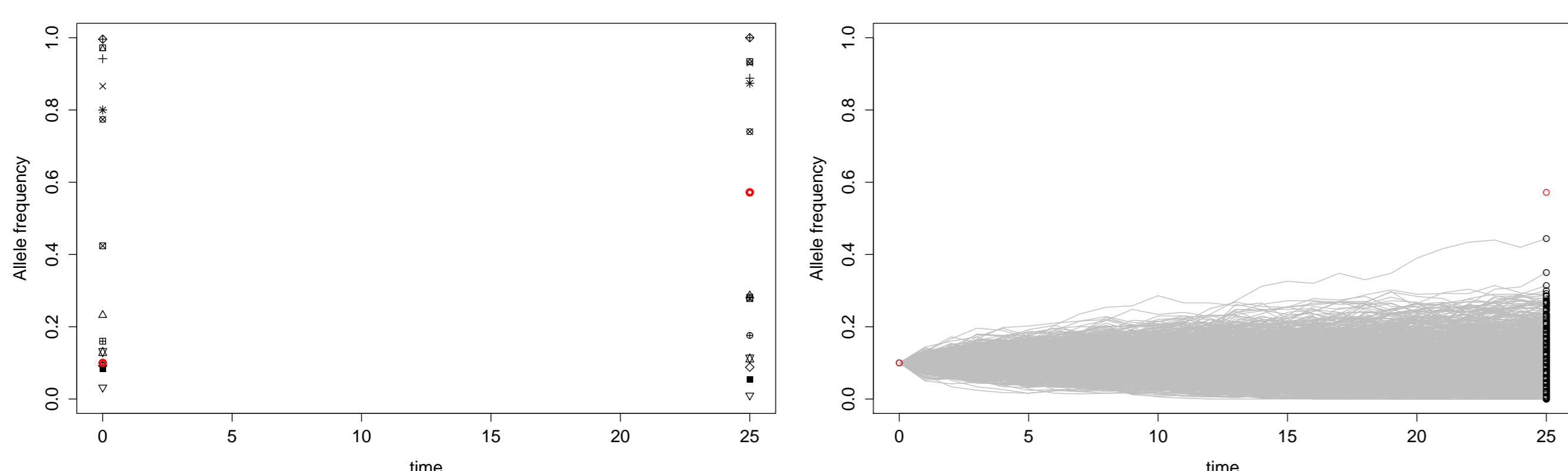


Consequences of selfing

- ▶ Reduction of effective population size
- ▶ Increase in homozygosity
 - ▷ reduction of effective recombination
 - ▷ increased linkage disequilibrium
 - ▷ hitch-hiking (genome wide)

F_C : a “temporal F_{ST} ” outlier method

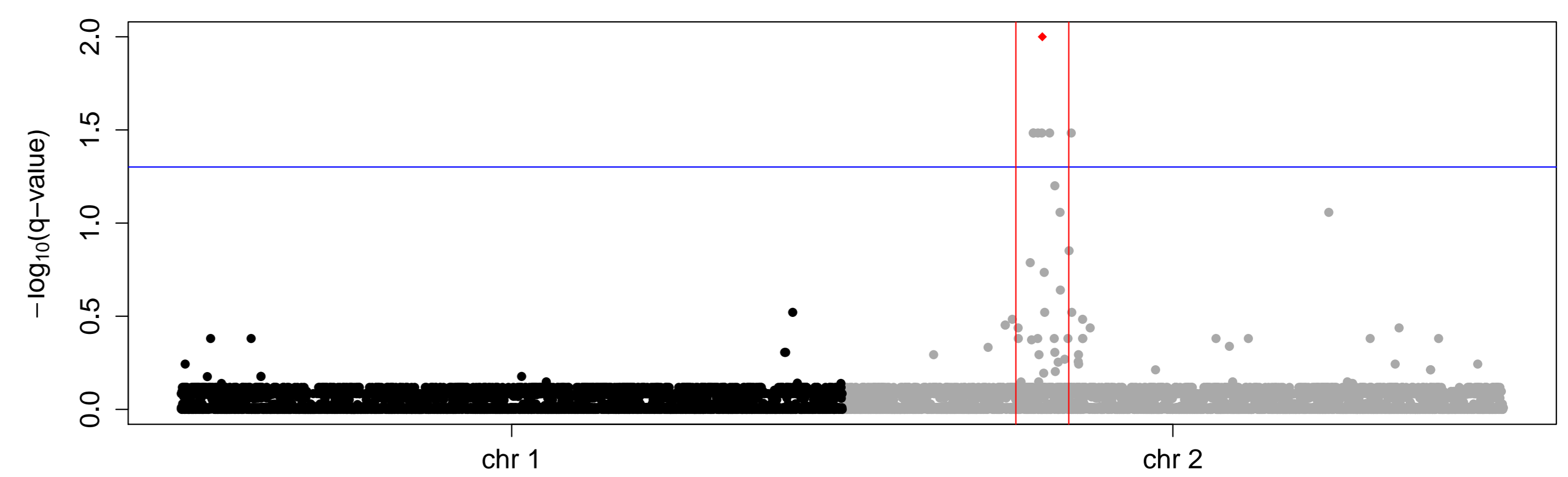
We evaluate a modified version of method proposed by Goldringer & Bataillon (2004, doi:10.1534/genetics.103.025908). Variance in allele frequencies (F_C statistic) from all loci is used to estimate effective population size (\hat{N}_e). Then we can ask if variance in allele frequencies (F_C) in a focal locus is compatible with \hat{N}_e . Simulations of drift from focal locus initial frequency and \hat{N}_e allows to test for it.



Simulations

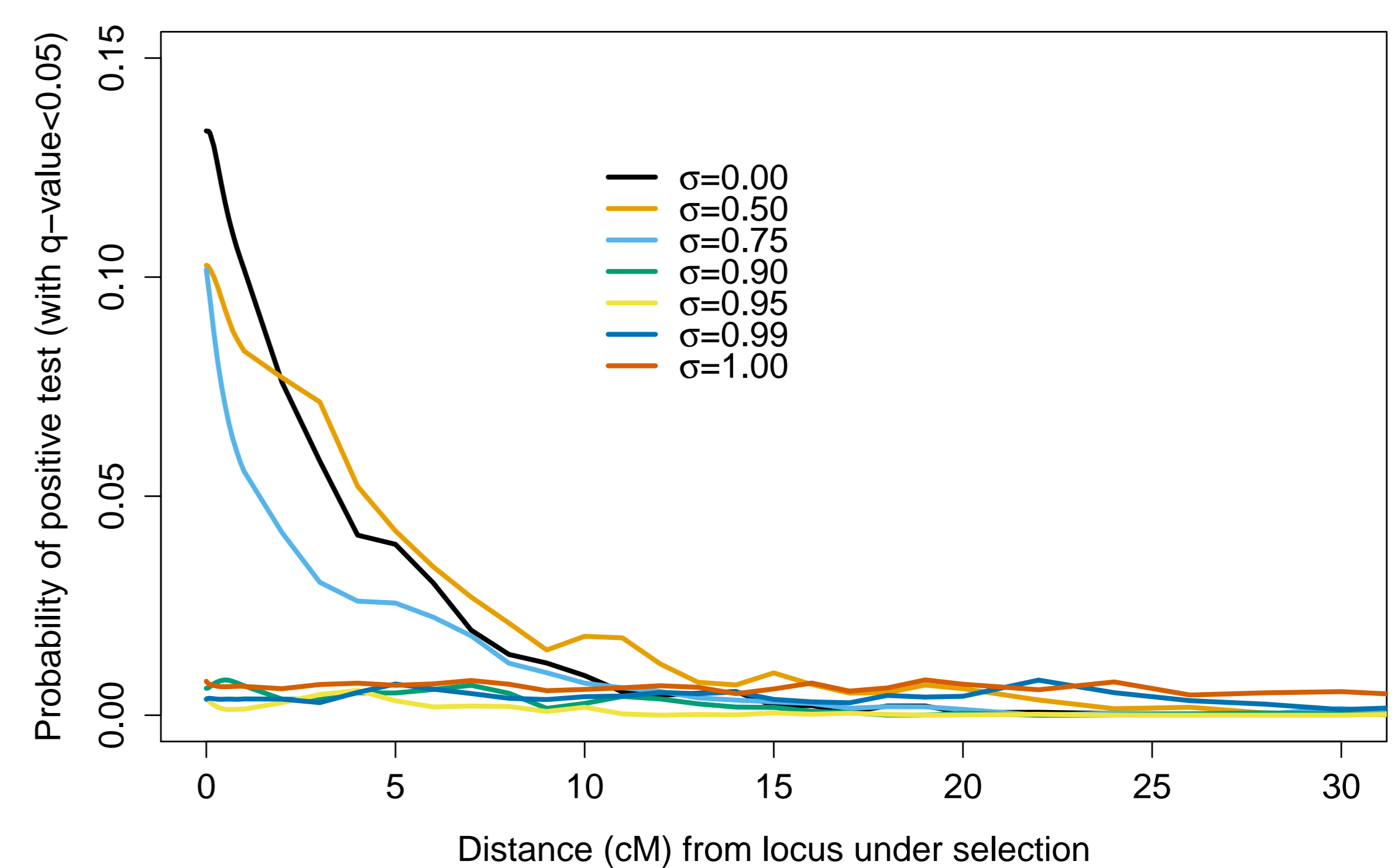
- ▶ Software: SLiM (Messer 2013, doi:10.1534/genetics.113.152181 messerlab.org)
 - ▷ N=500 diploid individuals
 - ▷ Selfing rate (σ): 0, 0.50, 0.77, 0.90, 0.95, 0.99, 1.00
 - ▷ 2 chromosomes (500Mb), $\mu=1e-8$, $r=1e-8$
 - ▷ 10000 polymorphic SNP loci are studied
- 1. Neutral period (till mutation-drift equilibrium)
- 2. New advantageous mutation/existing allele becomes advantageous ($s=0.5$)
- 3. First sample: 50 diploid individuals
- 4. Selection period (25 generations)
- 5. Second sample: 50 diploid individuals

Results from a single simulation

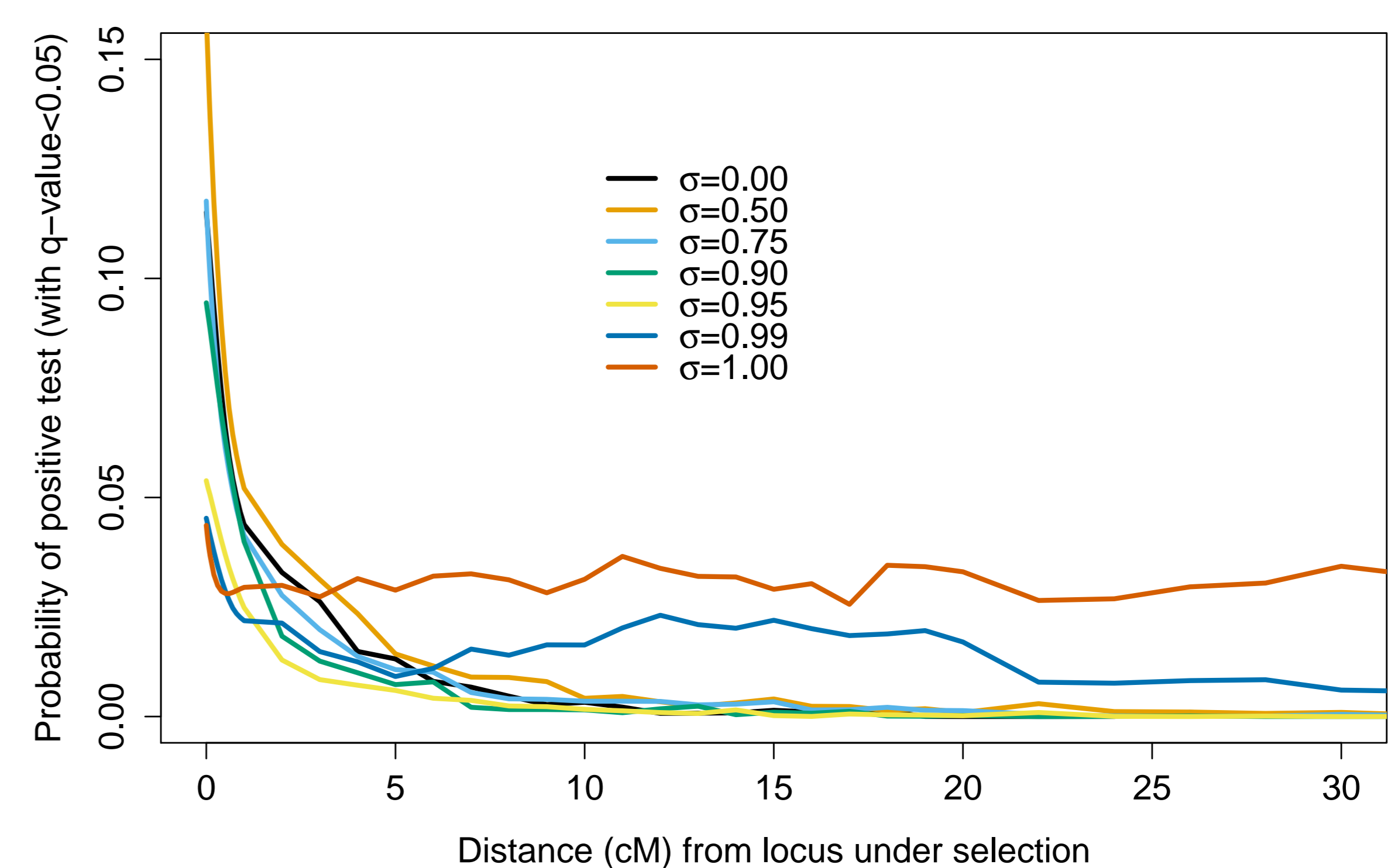


- ▶ Power: detection of selected site as under selection (red dot)
- ▶ False positive rate: detection of neutral sites as under selection (black dots)
- ▶ Footprint of selection: detection of neutral sites that have hitch-hiked with the selected site (grey dots)

Footprint of selection: new mutation



Footprint of selection: standing variation



Conclusions

- ▶ Temporal F_{ST} outlier approach can detect regions under selection (NB: for parameter values shown)
- ▶ Footprint of selection can be detected in a $\sim 20\text{cM}$ region (smaller region for selection on standing variation)
- ▶ Selfing reduces power (threshold for applicability between 0.75 and 0.90)
- ▶ Increase of false positives with selfing is not very problematic ($FPR < 0.05$)

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