Ghat: An R package for Quantifying selection and adaptation on polygenic traits

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Ghat

We introducing a method to identify selection on complex traits by evaluating the relationship between genome-wide changes in allele frequency and estimates of effect-size. The method involves calculating a composite-statistic across all markers that captures this relationship, followed by implementing a linkage disequilibrium-aware permutation test to evaluate if the observed pattern differs from that expected due to drift during evolution and population stratification. In this manuscript, we describe "Ghat", an R package developed to implement the method to test for selection on polygenic traits.

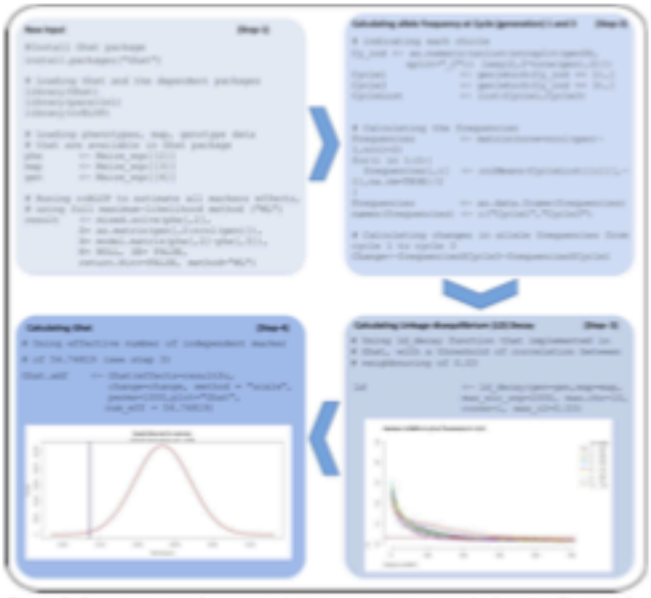

Figure 1. Four steps to go from raw individual marker data to results from the Ghat test for selection. An illustrated example using the "Maize_wgs" data available in the Ghat package.

Testing for selection during 50 years of wheat breeding

To demonstrate the power and flexibility of the Ghat package, we used it to test for selection during the past 50 years of wheat breeding in Europe.

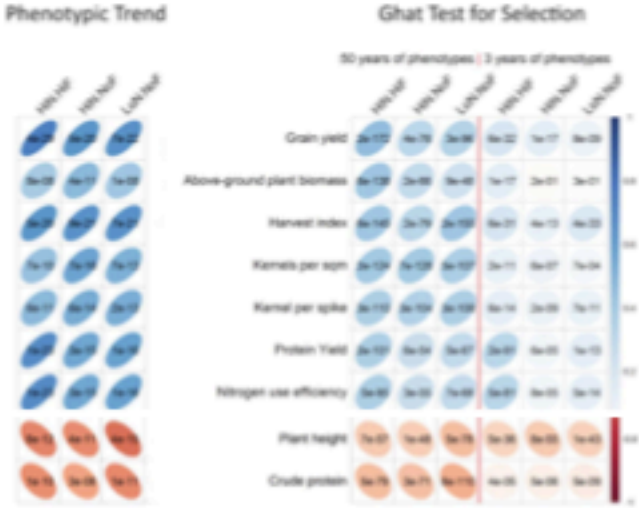

Figure 2. The power of Ghat test of selection in European winter wheat under three agrochemical treatments.

Adaptation history in the European winter wheat.

To more precisely dissect the history of selection in wheat, we divided the 50 years of breeding into 10 adaptation periods and applied Ghat successively between each period.

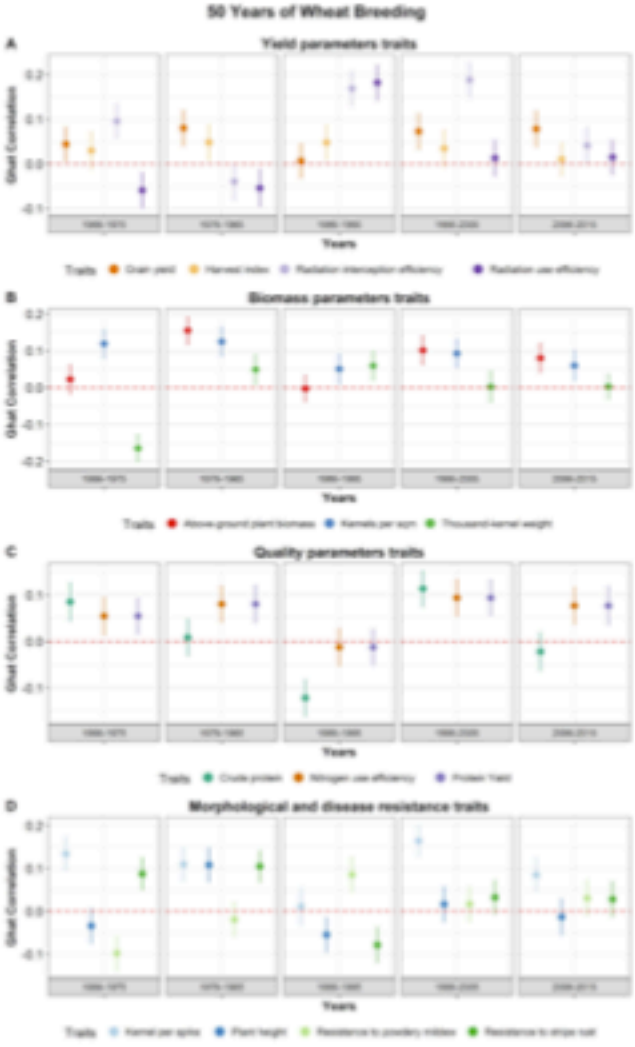

Figure 3. Cumulative selection in European winter wheat. Results are for the 14 traits of wheat during the past 50 years ago.

Conclusion:

For breeders and breeding organizations, Ghat represents a practical solution for tracing selection and adaptation history based on their recorded traits. Furthermore, Ghat test and its implementation via the package described herein does not require immense sample size, individual genotypes and/or genome-wide significant SNPs, as demonstrated by our implementation with a relatively modest sample size of 191 wheat individuals genotyped for 8,710 SNPs. Notably, this approach is more powerful when traits are controlled by large number of QTLs. These advantages allow the Ghat package to be used for identifying selection for various complex traits in other species of plants, animals and in humans.

Availability:
On CRAN: https://cran.r-project.org/package=Ghat
And on GitHub: https://github.com/timbeissinger/ComplexSelection