Inferring the Age of a Fixed Beneficial Allele in Natural Populations

Louise Ormond¹,², Matthieu Foli³, Gregory B. Ewing¹,², Susanne P. Pfeifer¹,² and Jeffrey D. Jensen¹,²

¹School of Life Sciences, École Polytechnique Fédérale de Lausanne, Switzerland
²Swiss Institute of Bioinformatics (SIB), Switzerland
³International Agency for Research on Cancer (IARC), Lyon, France

Do mutations pre-exist in populations to deal with new environmental challenges? Or is adaptation mutation-limited?

Estimating the age and strength of beneficial selected alleles is central to understanding how adaptation proceeds in response to changing environmental conditions. Several haplotype-based estimators exist for inferring the age of actively segregating beneficial mutations. Here we develop an Approximate Bayesian Computation approach that rather estimates these parameters for fixed beneficial mutations. Here we develop an Approximate Bayesian Computation approach that rather estimates these parameters for fixed beneficial mutations. We apply our method to estimating the age and selection strength of a previously identified mutation underpinning cryptic color adaptation in a wild deer mouse population.

To what extent can a Bayesian estimator of T and s take account of non-equilibrium demography, standing variation and dominance for application in natural populations?

Methods

1. Integrate summary statistics into an ABC approach by applying a Partial Least Squares method to a panel of 21 statistics (msstats-ABC).
2. Incorporate an LD-based statistic, into an alternative method (ωmax-ABC) which leverages differences in the upper tail of this statistic's distribution under selection in both equilibrium and non equilibrium scenarios.

References


Results

1: Inference of T alone

We can improve on results from Przeworski 2002 across different orders of magnitude.

2: Joint posterior density inference of s and T under equilibrium demography

We can estimate s and T well in equilibrium demographic scenarios, across different orders of magnitude, for both recent (T=0.01 x 4Ne generations) and old (T=0.1 x 4Ne generations) sweeps

3: Incorporate non eqm demography, stg variation and dominance

Eg under bottlenecks, we can estimate T and s well for strong selection, if the age of the sweep coincides with or post-dates the age of the bottleneck, but not for moderate or weak selection.

Conclusions and Next Steps

- Joint estimator for s and T is accurate for both old and young sweeps
- Flexible ABC approach allows non-equilibrium demography and dominance to be incorporated in simulations
- Next steps: Incorporate selection from standing variation

Contact

louise.ormond@epfl.ch
jensenlab.epfl.ch

www.isb-sib.org