Bayesian inference in evolutionary ecology: random drift vs. selection

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Abstract: One central aim in evolutionary ecology is to understand the causes and consequences of phenotypic variation, and to partition such variation into its genetic and environmental components (and their interaction) at different spatial scales, in particular within and among populations. Key parameters and concepts related to such research include e.g. individual- and population-level coancestry coefficients, the matrices of environmental and additive genetic variances and covariances, heritability, selection gradients, and the rates of mutation and migration. Typical data sets used to measure these parameters consist of phenotypic data from natural populations or breeding experiments (the latter possibly involving artificial selection), genotypic data on neutral or non-neutral marker genes, or data stemming from genome wide genotype or expression profiling. I discuss recent advances in mathematical theory and related Bayesian methods in this field of research, focusing on methods that aim to disentangle signals of diversifying or stabilizing selection from the null hypothesis of random genetic drift. In particular, I illustrate the use of the sparse Bayesian factor approach in identifying correlations (at the levels of phenotype, genotype or expression) from high-dimensional data.

References

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