Jeremy M. Beaulieu, Yale University, New Haven, CT, USA
Dwueng-Chwuan Jhwueng, Feng-Chia University, Taichung, TAIWAN
Carl Boettiger, University of California, Davis, CA, USA
Brian C. OMeara, University of Tennessee, Knoxville, TN, USA

Modeling stabilizing selection: expanding the OrnsteinUhlenbeck model of adaptive evolution

Comparative methods used to study patterns of evolutionary change in a continuous trait on a phylogeny range from Brownian motion processes to models where the trait is assumed to evolve according to an OrnsteinUhlenbeck (OU) process. Although these models have proved useful in a variety of contexts, they still do not cover all the scenarios biologists want to examine. For models based on the OU process, model complexity is restricted in current implementations by assuming that the rate of stochastic motion and the strength of selection do not vary among selective regimes. Here, we expand the OU model of adaptive evolution to include models that variously relax the assumption of a constant rate and strength of selection. In its most general form, the methods described here can assign each selective regime a separate trait optimum, a rate of stochastic motion parameter, and a parameter for the strength of selection. We use simulations to show that our models can detect meaningful differences in the evolutionary process, especially with larger sample sizes. We also illustrate our method using an empirical example of genome size evolution within a large flowering plant clade.