

On estimating the shape and dynamics of phenotypic distributions in ecology and evolution

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Abstract

Estimating the distribution of phenotypes in populations and communities is central to many questions in ecology and evolutionary biology. These distributions can be characterized by their moments: the mean, variance, skewness, and kurtosis. Typically, these moments are calculated using a community-weighted approach (e.g. community-weighted mean) which ignores intraspecific variation. As an alternative, bootstrapping approaches can incorporate intraspecific variation to improve estimates, and also quantify uncertainty in the estimate. Here, we compare the performance of different approaches for estimating the moments of trait distributions across a variety of sampling scenarios, taxa, and datasets. We introduce the traitstrap R package to facilitate inferences of trait distributions via bootstrapping. Our results suggest that randomly sampling ~9 individuals per sampling unit and species, focusing on covering all species in the community, and analysing the data using nonparametric bootstrapping generally enables reliable inference on trait distributions, including the central moments, of communities.

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