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Model-based hypothesis testing for multivariate abundance data

Ecologists frequently wish to use multivariate abundance data to test hypotheses about ecological communities and their response to experimental treatments or environmental perturbations, currently achieved using resampling methods (e.g. via the mvabund or vegan package, or using PERMANOVA). However, this approach becomes problematic when random effects are desired in the model, e.g. for hierarchical or repeated measures sampling designs, because resampling techniques typically do not extend naturally to the mixed models setting. Here we instead explore a model-based inference approach, using generalised latent variable models fitted via the glmmTMB package in R. The glmmTMB package is an extension of lme4 for mixed modelling, capable of accommodating complex study designs, to which we have added factor analytical functionality (via the rr variance structure) to handle multivariate responses with high dimension.

We express the problem of testing for a (multivariate) treatment effect as a test of whether one (or more) variance components is zero, for random effects representing taxon-level treatment effects. Standard tests such as the likelihood ratio and Wald tests are not asymptotically Chi-squared distributed as standard regularity assumptions are not satisfied, because the null value of the variance component is on the boundary of the parameter space. We examine a few strategies for approximating the asymptotic null distribution of the likelihood ratio test and compare their performance to resampling.