**Overview of response (cover letter content?)**

[We are writing to resubmit the article … for consideration as a Review & Synthesis paper…]

In response to the reviewers’ questions, we have implemented a set of changes that we hope makes the manuscript more technically robust and more interesting and accessible to a general ecological audience. We have added two resampling analyses to explore how the tendency for rare species to escape detection during field sampling, and sampling error in the shape of the SAD more generally, affect our results. We have also added three metrics for describing deviations between observed and randomly-generated SADs, which provide a more nuanced picture of the magnitudeof observed deviations, how deviations vary over large ranges of species richness and total abundance, and how statistical deviations relate to ecological properties such as the number of rare species in a system. We situate these new results in a more extensive discussion of complexity science as it relates to the SAD and have expanded our discussion of how to interpret deviations from a statistical baseline in ecological terms.

**New results overview (for Morgan and Hao)**

**Rarefaction resampling**

Rationale: Sampling in the field often results in an underestimation of species richness, especially of the richness of rare species, because rare species are likely to escape detection. We explore how non-detection of rare species affects our results by calculating the estimated true number of species and adding any “missing” species as rare species with abundance equal to 1.

Specific methods: We estimate the true number of species by computing the bias-corrected Chao and ACE estimates for an observed SAD (as implemented in vegan::estimateR), adding one standard error to each estimate, and taking the mean. This yields a generous estimate of species richness. If the estimated species richness exceeds the sampled number of species, we add the missing species each with abundance 1. We then run the adjusted SADs through the computational pipeline as normal.

Results: Adjusting in this fashion consistently increases the deviation between the observed SAD and its feasible set. Compared to raw SADs, adjusted SADs are even more skewed, less even, have lower Shannon diversity, have greater absolute deviations from the rest of the feasible set and have a larger proportion of rare species than expected given their feasible sets. These results are not surprising, because increasing the number of rare species without changing the rest of the distribution naturally increases unevenness, etc. See Rarefaction.md.

**Jacknife resampling**

Rationale: There may also be sampling error in the abundances of all the observed species in a sample, not just the rare ones. To explore how variability across the entire distribution affects our results, we resample a subset of the observed individuals and analyze these resampled SADs.

Specific methods: For an observed SAD, we generate 10 resampled SADs by randomly sampling 60% of the individuals in the observed sample without replacement and without regard to species. We use 60% of the observed number of individuals to introduce substantial room for sampling variability without reducing the size of most communities (and, accordingly, the size of their feasible sets) beyond the realms where we believe our approach to be appropriate. We run each resampled SAD through the computational pipeline. For each observed SAD, we take the mean summary statistic – percentile score, effect size, etc – across the 10 resamples as the “resampled” statistic. Because resampling in this fashion increases computational effort up to tenfold, we used this resampling procedure on the entirety of the Mammal Communities, Misc. Abundance, and Gentry datasets, but only on a random sample of 300 (of ~2000) BBS sites and 2000 (of ~20,000) FIA sites.

Results: The proportion of extreme results is generally lower in resamples than in the raw values, but does not change the direction or the significance of the effect except for for the number of singletons for MCDB and BBS. BBS has a pretty weak singletons effect already, and MCDB has very low numbers of singletons across the board (<10). See jacknife.md.

**Number of rare (abundance = 1) species**

Rationale:

Specific methods:

Results:

**“Proportion off”**

Rationale:

Specific methods:

Results:

**Shannon diversity**

Rationale:

Specific methods:

Results:

**Response to reviewer comments**