

Spatial Scaling of SAD: Update

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Re-working some results

For a few of the forest plots I have, I've re-evaluate the scaling of SADs using some new methods. The below analysis still uses the z^2 values that we discussed long ago. To jog your memory, z^2 is a description of goodness of fit derived from the likelihood of the data given the model of interest. In this case the model of interest is Fisher's log-series because we'd like to evaluate whether small scales conform to the log-series while large scales deviate from it. The standardization occurs as such:

$$z^2 = \left(\frac{\log\text{Lik}(x \mid \text{model}) - E[\log\text{Lik}(\log\text{Lik}(x_0 \mid \text{model}))]}{\sqrt{\text{Var}[\log\text{Lik}(\log\text{Lik}(x_0 \mid \text{model}))]}} \right)^2$$

where x is the observed data and x_0 is a hypothetical data set conforming perfectly to the model. Thus z^2 measures the likelihood of the observed data relative to the likelihood of a hypothetical data set generated by the model itself.

This measure is thus “standardized,” but unfortunately because of the Central Limit Theorem, it is sensitive to sample size (i.e. the number of species in the sample). Thus if we calculate z^2 from small sub plots to the entire plot, we expect it to increase across this range regardless of what the true underlying SAD is. We can get around this issue by comparing a spatial subset of the plot with a random subset of the plot of the same sample size. We take a representative random subset at any spatial scale by determining the number of individuals at that scale and randomly sampling that many individuals from the entire plot. In Figure 1 I implement such an analysis

What we see in Figure 1 is that for all plots at small scale both spatial and random subsets of the data match the log-series prediction (i.e. have small z^2 values). As we increase scale both spatial and random subsets deviate from the log-series. I expected the random subsets to look more like the large scale, while the spatial subset transitioned from conforming to log-series and then deviating from it at larger scale. I'm currently stumped as to why spatial and random subsets would follow the same pattern across scales.

A preliminary lit review

Borda-de-Água et al. (2012) focus on upscaling the SAD by estimating its moments at a smaller scale and then scaling those moments up. They re-iterate, as do many papers, that individuals are aggregated and so scaling the SAD does not preserve its shape—although it would under Poisson spatial process.

Chisholm and Lichstein (2009) relate the shape and size of a plot to the m immigration parameter of NTB. In the process they derive scaling for the SAD which they find goes from ZSM at small scale to logseries at large scale. They do not discuss the same nuance as Rosindell and Cornell (2013)

J. L. Green and Plotkin (2007) present a sampling theory for SADs based on random sampling (Poisson) or aggregated sampling (negative binomial). They confirm that random sampling preserves the shape of the SAD while aggregated sampling can interestingly often lead to something close to Fisher-looking.

Harte, Kinzig, and Green (1999) derive self-similar scaling of SAR and SAD (but see Pueyo 2006 who says they did it wrong for SAD).

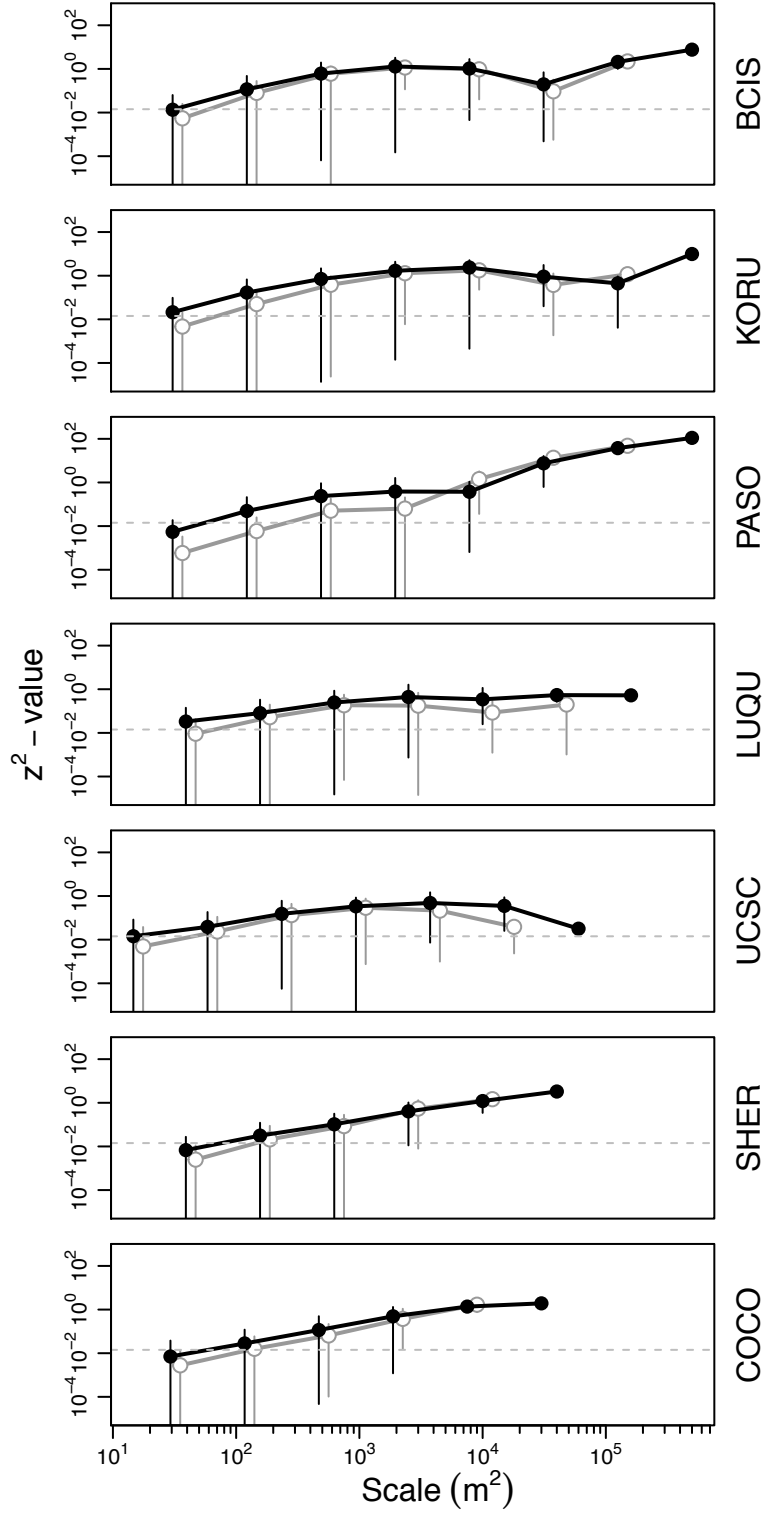


Figure 1: Relationship between z^2 value and scale. Black dots and lines represent spatial subsets while gray lines and open circles represent random subsets of comparable size (same number of individuals) as the nearest spatial subset point. Error bars are 95% confidence intervals. Gray dashed line corresponds to hypothesis test critical value, with points above rejecting the log-series at $\alpha = 0.05$

Hubbell et al. (2008) show power law scaling between nearest neighbor distance and rank of distance (this all in an effort to estimate number and abundance of tree species in Amazonia). Power exponent > 0.5 indicates non-Poisson aggregation. Some of these results might also show up in Harte’s MaxEnt book.

McGill (2003) argues that log right-skewed distributions, e.g. Fisher logseries, are sampling artifacts, that taking a small subsample of any large community will result in log right-skew. Does this mostly with simulation without considering spatial aggregation; but he also uses BCI, without much discussing it. Also misses the fact that Poisson sampling (as he does in “Model I”) will preserve the parametric form of the SAD, so skewness might not be the thing to look at, rather the parametric form could be more informative.

Myers et al. (2015) use burnt and unburnt plots to look at how disturbance influences turnover. Use spatial and non-spatial rarefaction to conclude that disturbance changes β -diversity patterns but not underlying processes.

O’Dwyer and Cornell (2017) provide an analytical solution to spatially explicit neutral theory and the spatial scaling of the SAD. They confirm work by Rosindell and Cornell (2013), including the scale collapse of the SAD when speciation rate is small. Could such scale collapse explain near universal success of Fisher at small scale? Also while they confirm the result of Rosindell and Cornell (2013) that at largest scale you get a log series, at intermediate, but still quite large, you get something hump-shaped on a log scale. This is also consistent with Rosindell and Cornell (2013) result that singletons first increase, then decrease, then increase again. Singletons increasing at largest scale is probably due to point mutation speciation—would be interesting to investigate with protracted speciation model. Most interestingly is that O’Dwyer and Cornell (2017) use spatially replicated plots to independently fit parameters of the model and then show that with these independent fits, the spatially explicit NTB does not fit BCI well at all.

Plotkin et al. (2000) show that power-law SAR is wrong from scales of 1 m^2 –50 ha (in the process of estimating species richness for tropical trees). Also show that upscaling SADs (various models) to get species estimates generally lead to over-estimate of S at 50 ha scale for Pasoh. Must be assuming Poisson spatial process, because no other process is mentioned.

Pueyo (2006) re-derives self-similar SAR and SAD, showing a power-law SAD leads to a power-law SAR. He does not consider how SAR will scale with area, we’re left to assume it’s the same shape everywhere.

Rosindell and Cornell (2013) explore scaling of the NTB. They find a tri-phasic accumulation of singleton species—first increasing with area, then decreasing, then increasing again. This pattern depends on the biogeographic range of the species considered—a quantity determined by speciation rate and dispersal kernel. This finding ties in with scale collapse of tri-phasic SAR (Harte and Storch).

Stegen et al. (2013) show that β -diversity is driven both by sampling and deterministic interactions with environment—namely heterogeneity and primary productivity. They do this with BBS.

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