Scaling the species abundance distribution: annotated bibliography

A. J. Rominger

May 29, 2017

Borda-de Água et al. [1] focus on upscaling the SAD by estimating its momenst 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 [2] 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 [10]

Green and Plotkin [3] 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 et al. [4] derive self-similar scaling of SAR and SAD [but see 9, who says they did it wrong for SAD].

Hubbell et al. [5] 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 exponant > 0.5 indicates non-Poisson aggregation. Some of these results might also show up in Harte's MaxEnt book.

McGill [6] argues that log right-skewed distributins, e.g. Fisher logseries, are sampling artifacts, that taking a small subsample of any large community will result in log right-skew. Does 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. [7] 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.

Plotkin et al. [8] 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 [9] 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 [10] 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 on the biogeoraphic range of the species considered—a qunatity determined by specieation rate and dispersal kernal. This finding ties in with scale collapes of tri-phasic SAR (Harte and Storch).

Stegen et al. [11] show that β-diversity is driven both by sampling and deterministic

interactions with environment—namely heterogeneity and primary productivity. The do this with BBS.

References

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