Table 1. Definitions and interpretations of the summary statistics for simplified two-scale analysis

| Metric | Definition | Interpretation |
|---|---|---|
| $S$ | Observed richness, effective number of species of order 0 (Jost, 2007) | Number of species |
| $N$ | Total abundance across all species | Measure of density of individuals |
| $S_n$ | The expected richness for $n$ randomly sampled individuals (Hurlbert 1971). | Estimate of richness after controlling for differences due to aggregation or number of individuals (i.e., only reflects SAD) |
| PIE | Probability of intraspecific encounter ($S_{n=2} - S_{n=1}$, Hurlbert 1971, Olszweski 2004), | Measure of evenness, slope at base of the rarefaction curve, and sensitive to common species |
| $S_{\text{PIE}}$ | Number of equally abundant species needed in a hypothetical community to yield PIE using sampling with replacement (i.e. $^{k=2}\hat{E}$, Dauby and Hardy, 2012; $^{2}\widehat{D}(\infty)$, Chao et al, 2014) | Effective number of species of PIE that is easier to compare with $S$ (= 1 / (1 – PIE). asymptotic estimator of effective number of species of order 2, (Jost, 2007) |
| $S_{\text{asymptote}}$ | Extrapolated asymptotic richness via Chao1 estimator (Chao 1984). | Richness that includes unknown species but is highly correlated with $S$ (McGill 2011) |
| $f_0$ | Richness of undetected species ($S_{\text{asymptote}} - S$, Chao et al. 2009). | Measure of rarity at top of rarefaction curve, more sensitive to rare species than $S$ |
| $\beta_S$ | Ratio of total treatment $S$ and plot $S$ (Whittaker 1960) | More species turnover results in larger $\beta_S$ which may be due to increases in spatial aggregation, $N$, and/or unevenness of the SAD. |
| $\beta_{f_0}$ | Ratio of total treatment $f_0$ and plot $f_0$ | Like $\beta_S$ but emphasizes rare species |
| $\beta_{S_{\text{PIE}}}$ | Ratio of total treatment and plot $S_{\text{PIE}}$ (Olszewski 2004) | Like $\beta_S$ but emphasizes common species |

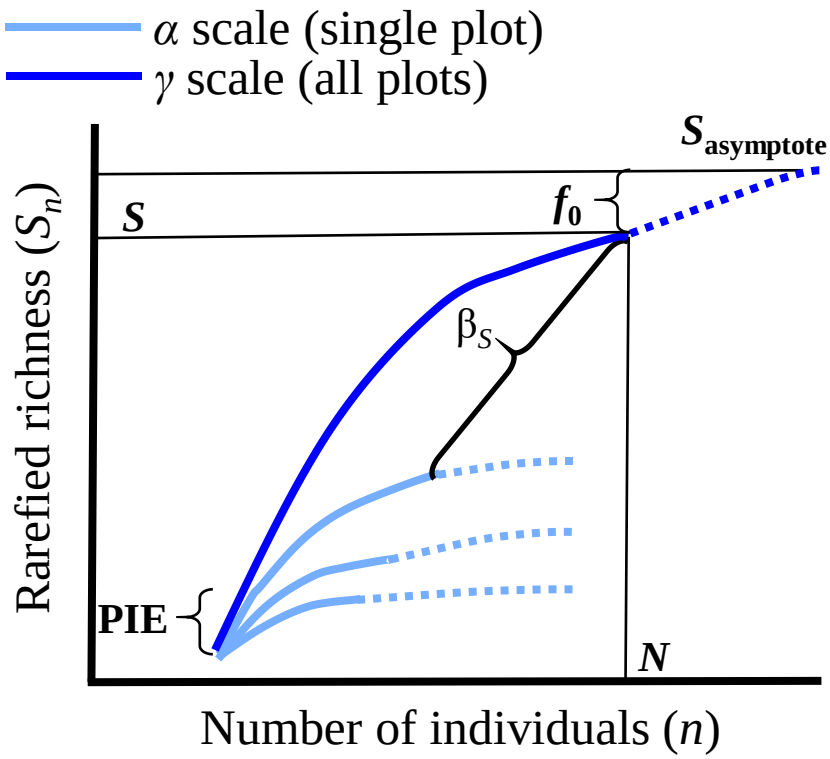


Figure 1. Illustration of how the key biodiversity metrics are derived from the individual-based rarefaction curves constructed at the $\alpha$ (i.e., single plot) and $\gamma$ (i.e., all plots) scales. The solid lines are rarefied richness derived from the randomly sampling individuals from each plot's SAD

Table 2. Rarefaction curve terminology (see McGlinn et al. https://www.biorxiv.org/content/early/2018/01/07/244103 for more details).

| Curve Name | Notation | Method for accumulation | Interpretation |
|---|---|---|---|
| Spatially constrained sample-based rarefaction | $\mathrm{E}\left[S_t \middle\vert k, \vec{n}_{t,+}, \vec{N}_t, \vec{d}_t\right]$ | Spatially explicit sampling in which the most proximate plots to a focal plot are accumulated first. All possible focal plots are considered and the resulting curves are averaged over. | This curve includes all information in the data including effect of SAD, effect of density of individuals, and effect of spatial aggregation. |
| Nonspatial, sample-based rarefaction curve | $\mathrm{E}\left[S_t \middle\vert k, \vec{n}_{t,+}, \vec{N}_t\right]$ | Random sampling of *k* plots after removing intraspecific spatial aggregation by randomly shuffling individuals across plots while maintaining average plot-level abundance ($\overline{N_{t,k}}$) and the treatment-level SAD ($n_{t,+,s} = \sum_k n_{t,k,s}$). In practice, we use an analytical extension of the hypergeometric distribution that demonstrates this curve is a rescaling of the individual-base rarefaction curve based on the ratio: (average density across treatments) / (average density of treatment of interest) | This curve reflects both the shape of the SAD and the difference in density between the treatments. If density between the two treatments is identical then this curve converges on the individual-based rarefaction curve. |
| Individual-based rarefaction curve | $\mathrm{E}\left[S_t \middle\vert N, \vec{n}_{t,+}\right]$ | Random sampling of *N* individuals from the observed SAD ($\vec{n}_{t,+}$) without replacement. | By randomly shuffling individuals with no reference to plot density, all spatial and density effects are removed. Only the effect of the SAD remains. |