2. Species Richness and Diversity

Alpha Diversity

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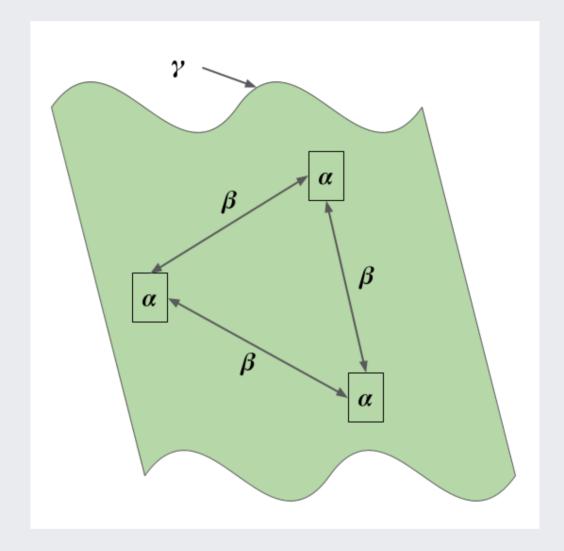
2022-02-01

The components of diversity

Alpha (α) = mean species diversity/richness within local-scale sites, habitats or communities (often termed "point diversity")

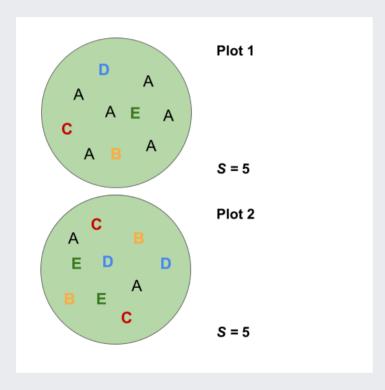
Beta (β) = diversity/richness differences between sites or habitats (attributable to species "turnover" or "nestedness")

Gamma (γ) = total landscape species diversity/richness

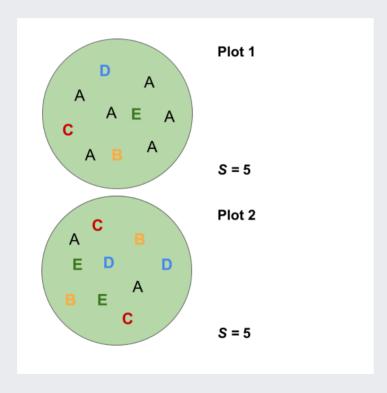


S = a simple count of species

Can be counts of the number of species in samples,

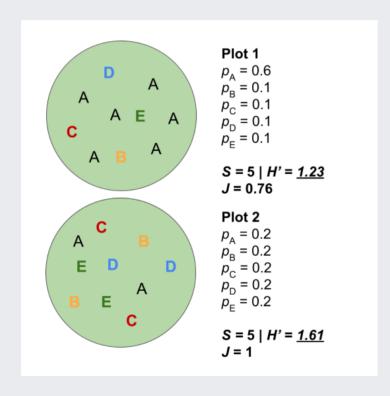


Can be counts of the number of species in samples,



S = a simple count of species, *but what of relative abundance?*

Can be counts of the number of species in samples,



or include information on their relative abundance

S = a simple count of species, *but what of relative abundance?*

A community is considered more diverse if the relative abundances are more evenly distributed

 because removing one individual is less likely to remove a species.

Shannon's index (*H'*) quantifies species diversity taking into account both species' richness and evenness in their relative abundance

$$H' = -\sum_{i=1}^n (p_i * ln(p_i))$$

where p_i is the proportion of individuals belonging to the ith species.

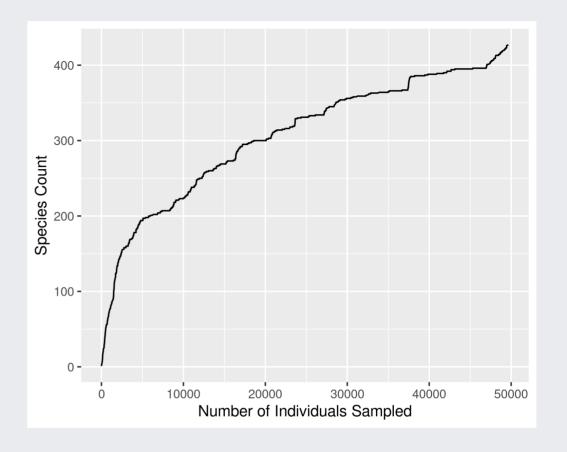
Pielou's measure of evenness ($\it J$) in the relative abundance (independent of $\it S$) can be calculated directly as $\it J=H'/log(\it S)$

Many studies will refer to species counts as "species richness", but this is often in error...

Species counts are sensitive to the number of individuals sampled.

More individuals means greater potential to encounter more species.

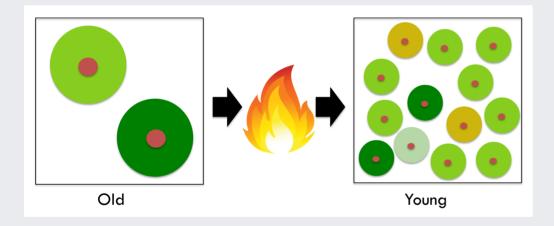




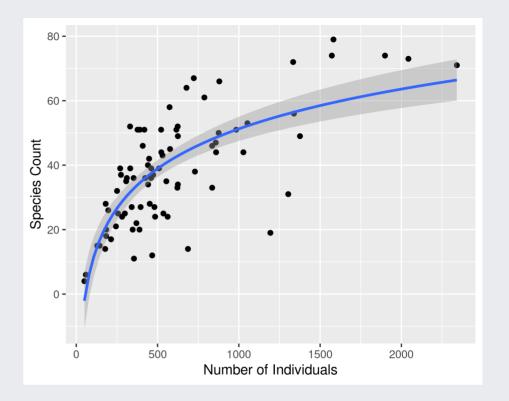
Species counts relative to number of individuals sampled across eighty-one 50m² vegetation plots in Table Mountain National Park (data from Slingsby et al. 2017).

The relationship is non-linear and asymptotic.

Dependence of species counts on number of individuals sampled is problematic when the number of individuals varies between samples (e.g. vegetation plots, netting events, etc).



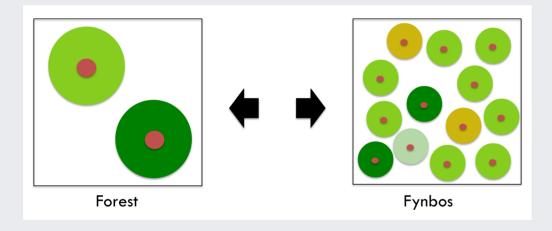
While raw species counts can still be useful for many purposes, it is also useful to have a metric that is independent of abundance and sampling effort.



Species counts relative to number of individuals sampled for each of eighty-one 50m² vegetation plots in Table Mountain National Park (data from Slingsby et al. 2017).

Since the samples are of a set unit area (50m²), the species counts in this figure can also be termed **species density**.

Dependence of species counts on number of individuals sampled is problematic when the number of individuals varies between samples (e.g. vegetation plots, netting events, etc).



While raw species counts can still be useful for many purposes, it is also useful to have a metric that is independent of abundance and sampling effort.

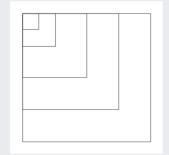




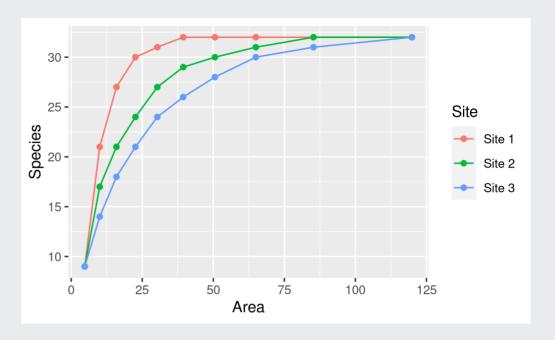
Species-Area relationship

The density (~size) of individuals can also affect the shape of the species-area relationship (SAR) at fine scales.

- Site 1 = many, small individuals
- Site 2 = intermediate
- Site 3 = fewer, large individuals



We estimate the SAR by sampling nested plots of increasing size, and can use it to estimate the diversity of a larger area by extrapolation.



When comparing sites, one solution is to sample enough area to reach the asymptote of the SAR, but this isn't often logistically (or logically) feasible...

Note that many other factors affect the SAR:

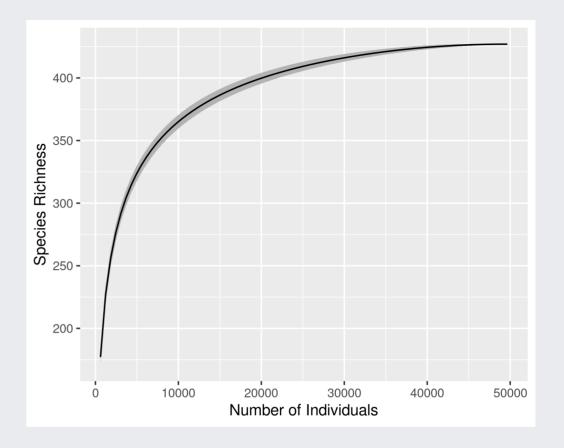
- patchiness/heterogeneity
- dispersal (limitation)
- immigration/extinction
- disturbance

Species richness

...is usually reserved to mean an estimate of the number of species while taking abundance and sampling effort into account (see Gotelli and Colwell 2001 for review).

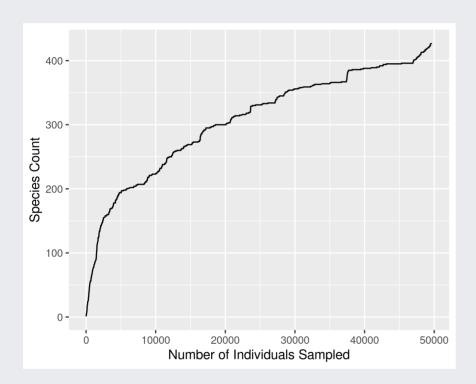
...is often estimated using individual or sample-based *rarefaction*.

i.e. resampling a set number (n) of individuals or samples from the data to determine the expected number of species for any given n. Resampling is repeated multiple times for each n and the results averaged.



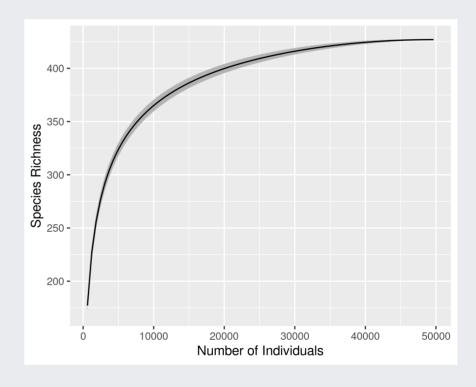
Individual-based rarefaction curve developed by sampling individuals from the pooled data from eighty-one 50m² vegetation plots in Table Mountain National Park (data from Slingsby et al. 2017).

Individual-based *accumulation* curve



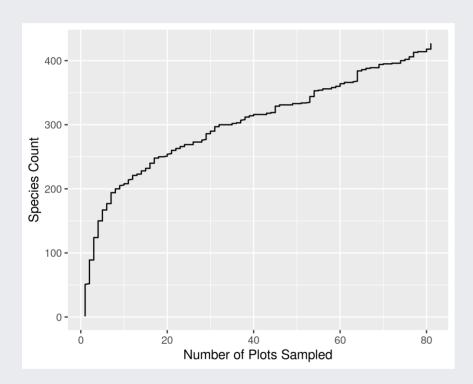
Curve is not smooth, because individuals (and thus species) are added in whatever order (in this case alphabetically by plot).

Individual-based *rarefaction* curve



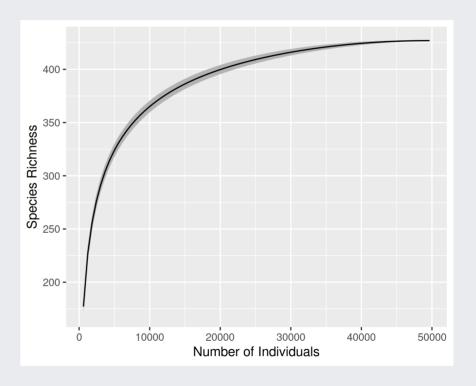
Curve is smooth, because individuals (and thus species) are repeatedly sampled and averaged for each sample size.

Sample-based accumulation curve



Curve is not smooth, because samples (and thus species) are added in whatever order (in this case by plot number).

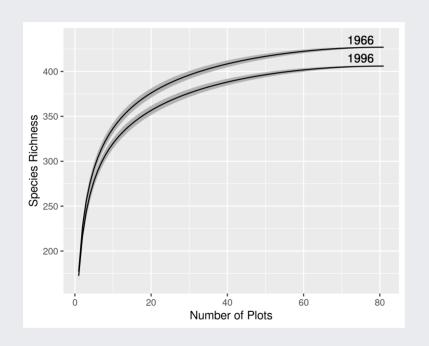
Sample-based rarefaction curve



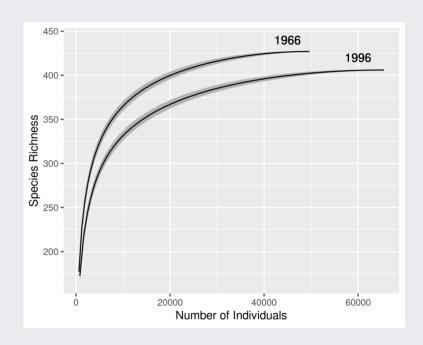
Curve is smooth, because samples (and thus species) are repeatedly sampled and averaged for each sample size.

Comparing diversity between sites or surveys

Sample-based rarefaction



Individual-based rarefaction

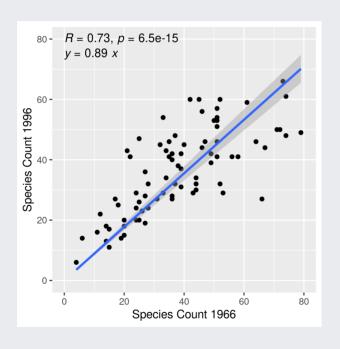


Note that you can compare between sites by rarefying for a set number of individuals or plots!

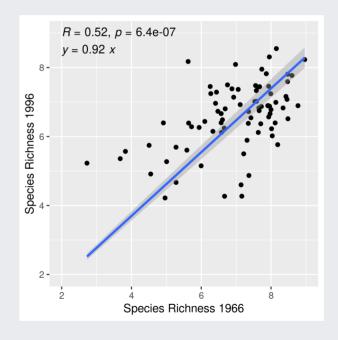
Rarefying by samples doesn't really get around the issue of different numbers of individuals...

Comparing diversity between samples

Raw species counts



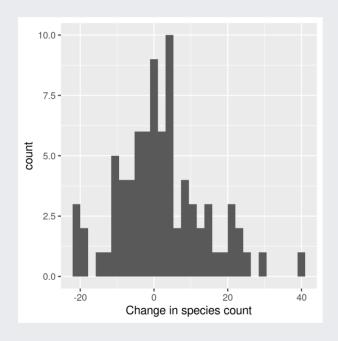
Individual-based rarefaction¹



¹for n = 10 individuals from each sample

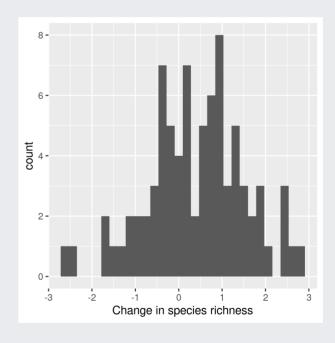
Comparing diversity between samples

Raw species counts



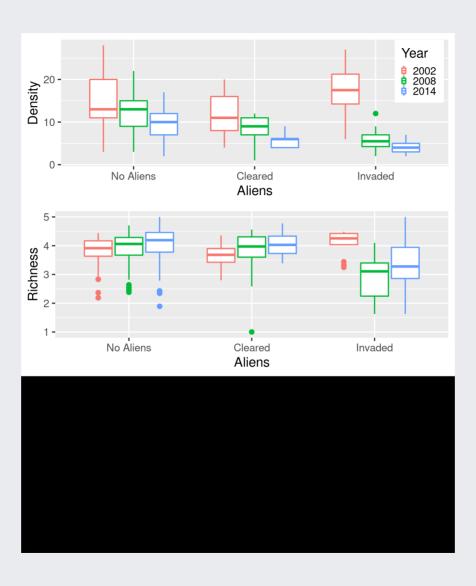
Paired T-test: t = 1.4957, df = 80, p-value = 0.1387

Individual-based rarefaction¹



Paired T-test: t = 3.2953, df = 80, p-value = **0.0015**

¹for n = 10 individuals from each sample



Take home

Measures of alpha diversity can be affected by factors like the area and number of individuals sampled.

Other factors can be important too, like the length of time sampled for (e.g. bird netting, fishing, etc).

You need to choose your measure of diversity carefully, and potentially correct for these sampling effects (e.g. by using rarefaction, sampling a larger area, etc), depending on your question and the group you're working on

References

Gotelli, N. J. and R. K. Colwell (2001). "Quantifying biodiversity: procedures and pitfalls in the measurement and comparison of species richness". In: *Ecology letters* 4.4, pp. 379-391. ISSN: 1461-023X, 1461-0248. DOI: 10.1046/j.1461-0248.2001.00230.x.

Slingsby, J. A., C. Merow, M. Aiello-Lammens, et al. (2017). "Intensifying postfire weather and biological invasion drive species loss in a Mediterranean-type biodiversity hotspot". En. In: *Proceedings of the National Academy of Sciences of the United States of America* 114.18, pp. 4697-4702. ISSN: 0027-8424, 1091-6490. DOI: 10.1073/pnas.1619014114.

Whittaker, R. H. (1972). "Evolution and measurement of species diversity". En. In: *Taxon* 21.2-3, pp. 213-251. ISSN: 0040-0262, 1996-8175. DOI: 10.2307/1218190.

Thanks!

Slides created via the R packages:

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gadenbuie/xaringanthemer