

Measuring, exploring and estimating biodiversity

Jonathan Dushoff, McMaster University

McMaster CSE Seminar, March 2022

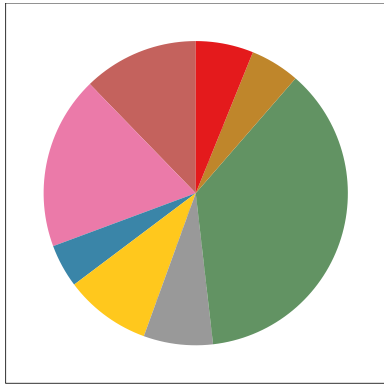
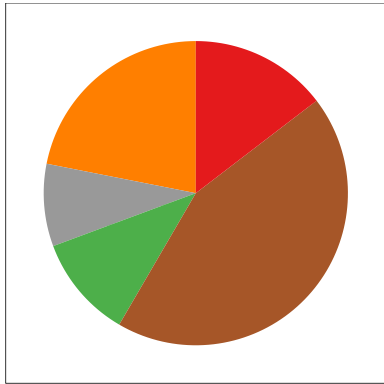
Why do we measure biodiversity?

- ▶ It seems practically important:
 - ▶ How does it correlate with ecosystem function?
 - ▶ What can we do to protect it?
- ▶ It seems scientifically important
 - ▶ Maybe we can understand the world better even if we can't protect it
- ▶ But there's no consensus on how best to measure it, or how to compare the metrics themselves

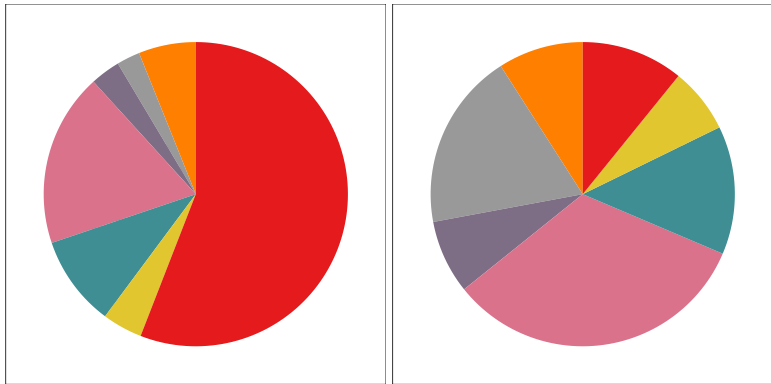
Community diversity

- ▶ I am going to be talking about community diversity, often called α -diversity
 - ▶ How different are individuals in a given sampling unit?
- ▶ I am not going to be talking about diversity of units themselves, often called β -diversity
 - ▶ How different are two sampling units from each other?
- ▶ When I compare two different sampling units, I will be asking which one is more diverse, not how different they are

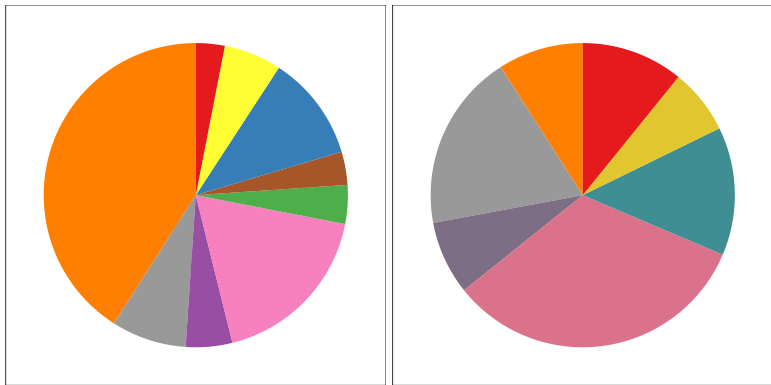
Comparing diversity



Comparing diversity



Comparing diversity



Richness

- ▶ How many species are there?
 - ▶ This is apparently what aliens want to know
- ▶ Can we ever know?
 - ▶ Other “diversity” measures combine diversity with relative abundance
 - ▶ ... but so does this one!
 - ▶ In practice

Simpson diversity

- ▶ What is the probability that two different individuals are from different species?



$$1 - \sum p_i^2$$

Shannon diversity

- ▶ How much Shannon information is there in a particular observation?
- ▶ How many distinct ways of combining individuals?
- ▶

$$\sum -p \log(p)$$

Richness is unstable

- ▶ If we assume an effectively infinite population, it's impossible to get good estimates of population richness
 - ▶ We don't know what we don't know

Simpson diversity *seems* stable

- ▶ We can get an unbiased estimate of Simpson diversity from two individuals!
- ▶ Recall: unbiased means that the expected value of the estimate is equal to the true value of the estimand
- ▶ This is equivalent to saying we get an “unbiased” estimate of an unfair coin from a single flip
- ▶ Of course, we’ll always have more than 2 individuals, but we can always get an unbiased estimate

Effective number of species

- ▶ The value of Simpson or Shannon diversity is hard to interpret.
 - ▶ Or at least, easy to misinterpret.
- ▶ We can ask how do they map to an effective number of species?
 - ▶ On a given scale, the observed diversity is equivalent to E *evenly distributed* species

Hill diversity

$$H_q = \left(\sum p_i^q \right)^{1/1-q}$$

- ▶ Take limits as necessary
- ▶ Spans from richness ($q = 0$) to Hill-Shannon ($q = 1$) to Hill-Simpson
- ▶ Gives an effective species number
- ▶ Decreases with q

Rarity perspective

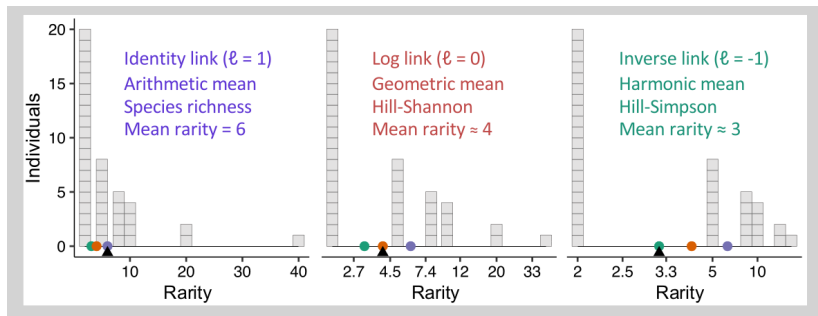
$$D_\ell = \left(\sum p_i (r_i)^\ell \right)^{1/\ell},$$

- ▶ where $r_i = 1/p_i$ is the rarity
- ▶ $\ell = 1 - q$ has a natural interpretation in terms of power means:
 - ▶ $\ell = 1$ is the arithmetic mean, corresponds to richness
 - ▶ $\ell = 0$ is the geometric mean, corresponds to Hill-Shannon
 - ▶ $\ell = -1$ is the harmonic mean, corresponds to Hill-Simpson

Leverage of rare species

- ▶ The higher values of ℓ are often described as giving more *weight* to rare species
- ▶ But this doesn't correspond to an actual weighting
- ▶ We use “leverage” to describe the increasing importance of rare species
- ▶ And illustrate with “seesaw” plots

DiversitySeesaw

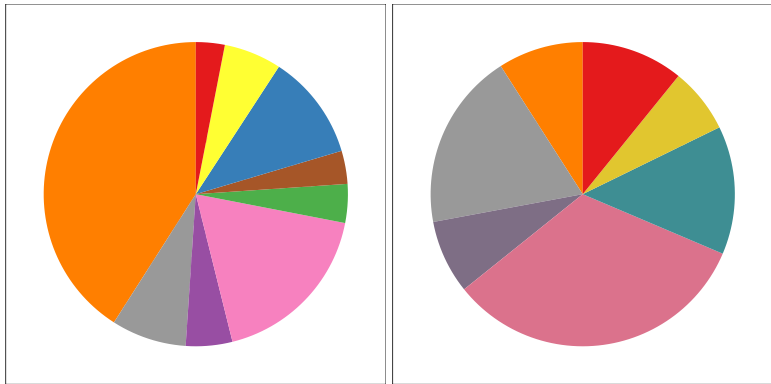


<https://github.com/mikeroswell/MeanRarity>

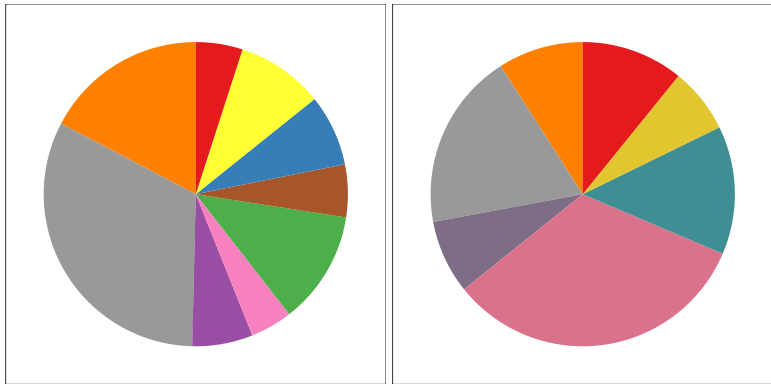
Is Hill-Shannon just better?

- ▶ Geometric mean corresponds to ratio-based distance: 1:5 as 5:25
- ▶ E.g., The difference between 20% abundance (rarity of 5) and 10% abundance
 - ▶ Hill-Simpson: the same as the difference between 10% and 0% (∞ rarity)!
 - ▶ Richness: the same as the difference between 10% and 6.7%
 - ▶ or 2% and 1.8%
 - ▶ Hill-Shannon: the same as the difference between 10% and 5%

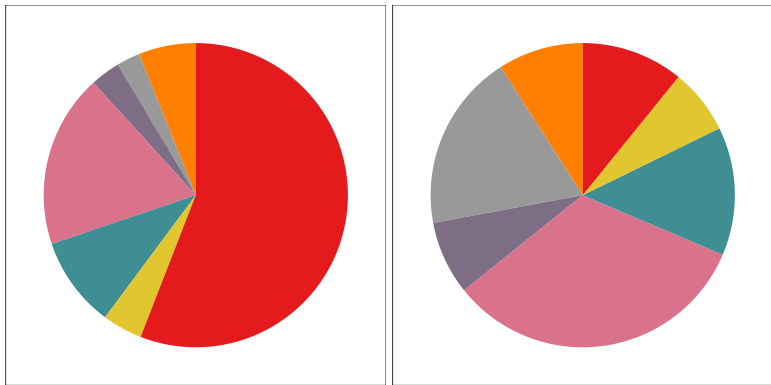
Shannon equivalence



Simpson equivalence



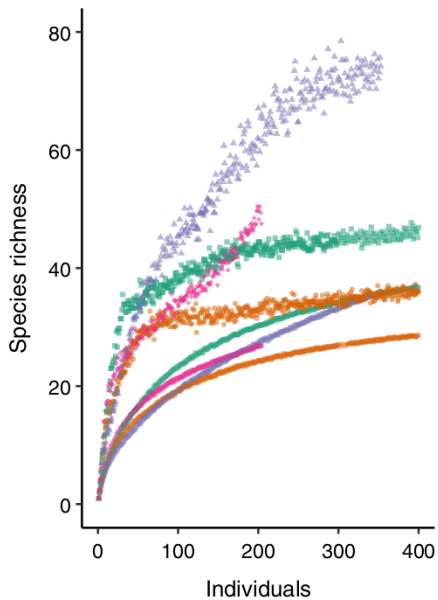
Richness equivalence



How to compare *sampled* communities?

- ▶ We don't know the true diversity
- ▶ Rarefaction
 - ▶ Compare at equal number of individuals sampled
 - ▶ Or at equal “coverage”
- ▶ Asymptotic estimation
- ▶ Much of this goes back to the work of Turing, who was interested (effectively) in diversity metrics on coded messages and ciphertext

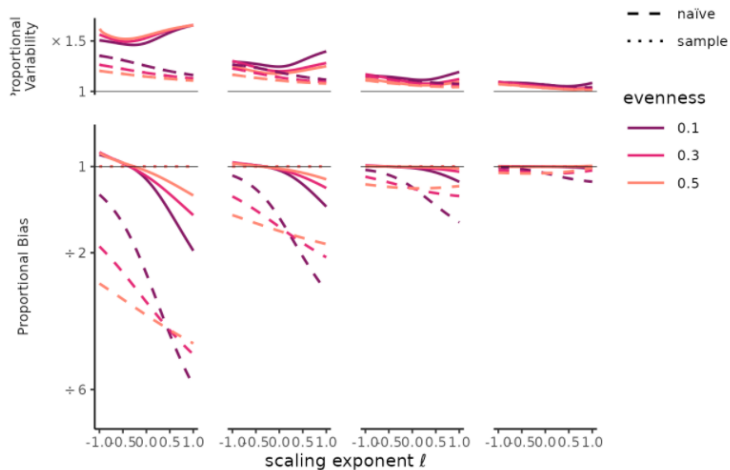
Comparing observed diversity



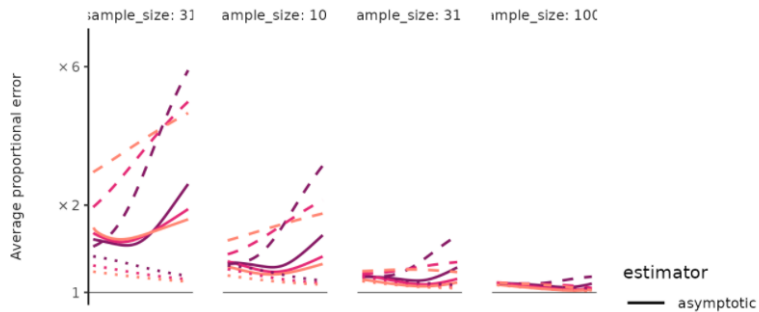
Ongoing work

- ▶ How *biased* are different asymptotic or sample-based measures?
- ▶ How *variable* are different asymptotic or sample-based measures?
- ▶ <https://github.com/mikeroswell/MeanRarity>

Bias-variance tradeoff



Bias-variance tradeoff



Future work

$$\hat{D}_\ell = \left(\sum p_i (\hat{r}_i)^\ell \right)^{1/\ell},$$

- ▶ Does the rarity perspective provide insight into estimation methods?
- ▶ p and r are typically treated the same, but actually play different roles:
 - ▶ if we had good estimates of \hat{r} , then \hat{D} becomes an unbiased estimator
 - ▶ not *necessarily* a low-variance estimator
- ▶ Does the rarity perspective allow us to expand our concept of coverage?

Thanks

- ▶ Collaborators: Mike Roswell, Rae Winfree and others
- ▶ Organizers
- ▶ Audience