

# Rarefaction techniques and temporal change in species richness

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## Introduction

- > Quantifying biodiversity change is an important task.
- > The number of species (richness) is a common indicator.
- > Comparing observed richness at different times is challenging.
- > Two common approaches taken are:
  - 1) **size-based rarefaction**; and
  - 2) **coverage-based rarefaction**.

Do these two methods reach the same conclusion indicating a richness increase or decrease?

## Results

- > **Size-** and **coverage-**based rarefaction methods can reach different conclusions (Figs 1 & 2).
- > They quantify different aspects of richness change:
  - 1) **size-based rarefaction** - the change in community composition;
  - 2) **coverage-based rarefaction** - the changes in both community size and composition.

Consider an ecological community potentially consisting of  $k$  species,  $i = 1, 2, \dots, k$ . When a rarefied sample of size  $n_t^*$  is taken from the observed  $n_t = \sum_{i=1}^k n_{it}$  individuals, the change (gradient) in each rarefied richness can be specified as:

### Size-based

$$\frac{d}{dt} \mathbb{E} [R_t(n^*)] \simeq \sum_{i=1}^k \gamma_1(n_t^* p_{it}) \frac{d}{dt} \log(p_{it})$$

### Coverage-based

$$\frac{d}{dt} \mathbb{E} [\tilde{R}(n_t^*)] \simeq \frac{\mathbb{E} [S_1(n_t^*)]}{\mathbb{E} [S_1(n_t)]} \frac{d}{dt} \mathbb{E} [S_1(n_t)] + \frac{d}{dt} \mathbb{E} [R(n_t^*)]$$

Here,  $\gamma_1(n_t^* p_{it})$  is the probability of species  $i$  to be singleton,  $p_{it}$  is the relative abundance and  $S_1$  is the number of singleton species.

## Rarefaction techniques

**Size-based rarefaction** counts the number of species found amongst a fixed number of individuals,  $n_t^*$ , the minimum number of individuals of a community at different occasions,  $n_t^* = \min_t \{n_t\}$ . The rarefaction draws a single subsample of  $n_t^*$  individuals from the pooled sample of size  $n_t$ , and then counts the number of species found.

$$R_t(n^*) = S \left( \min_t \{n_t\} \right)$$

**Coverage-based rarefaction** counts the number of species conditioning on a certain coverage,  $q$ , that yields the size of the rarefied sample as  $n_t^* = s_{1t}/(1-q)$  where  $q = \min_t \{q_t\}$  and  $q_t = 1 - s_{1t}/n_t$ .

The rarefaction draws a single subsample of  $n_t^*$  individuals from the pooled sample of size  $n_t$ , and then counts the number of species found.

$$\tilde{R}(n_t^*) = S(\lfloor s_{1t}/(1-q) \rfloor)$$

## Reference

Hideyasu Shimadzu (2018). On species richness and rarefaction: size- and coverage-based techniques quantify different characteristics of richness change in biodiversity. Journal of Mathematical Biology. DOI: 10.1007/s00285-018-1255-5

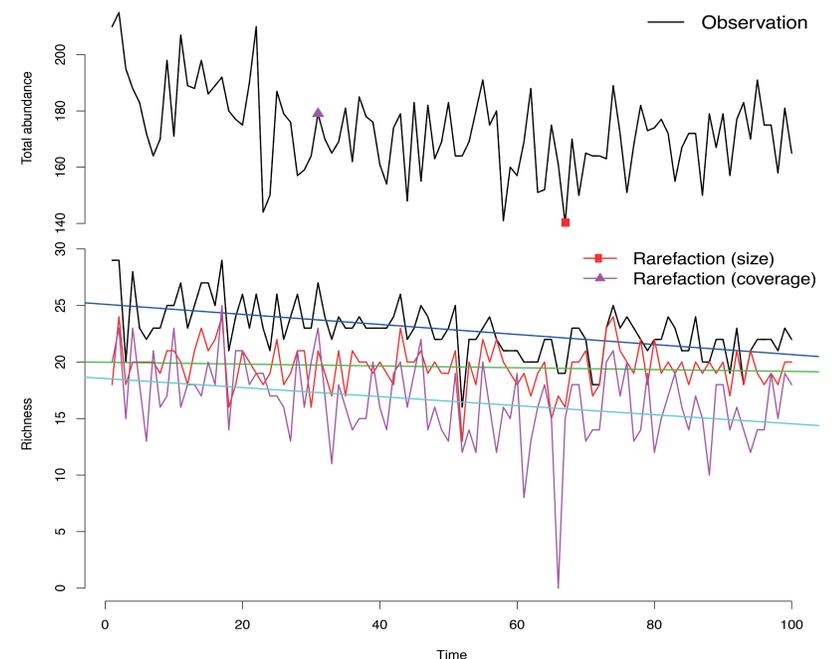


Fig 1: (Top) An observed series of total abundance. (Bottom) The solid black line is observed richness. The red line represents size-based rarefied richness and the purple line represents coverage-based rarefied richness. The three superposed straight lines are the linear trend of each richness series over time.

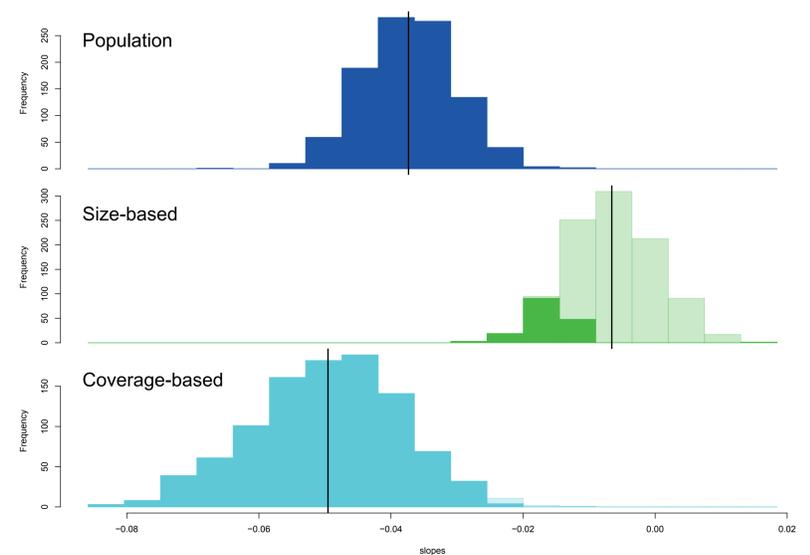


Fig 2: The histograms of the slope coefficients from the 1000 simulation study. The blue one (top) represents the distribution of the slope coefficients of the observed richness series. The green (middle) and the cyan (bottom) histograms show the distribution of the slope coefficients of size-based rarefied richness and of coverage-based rarefied richness, respectively. The transparent colour highlights statistically non-significant coefficients.

## Simulation study

Consider an ecological community potentially consisting of 100 species. Each species abundance is assumed to be  $N_{it} \sim \text{Pois}(\Lambda_{it})$  where  $\Lambda_{it} = \mathbb{E} [N_{it}] = \max\{0, \Lambda_{i0} + r_i t\}$  with a linear trend. A total of 1000 simulations were run. At each simulation, size- and coverage-based richness measures were calculated.

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