

## Site Description

1. Diversity indices
2. Species abundance models
3. Species – area relationship

## Shannon diversity

$$H = - \sum_{j=1}^S p_j \log_b p_j$$

Originally information theory with base  $b = 2$ : Average length in bits of code with shortest possible unique coding

- The limit reached when code length is  $-\log_2 p_i$ : longer codes for rare species.

Biologists use natural logarithms (base  $b = e$ ), and call it  $H'$

Information theory makes no sense in ecology: Better to see only as a variance measure for class data.

## Simpson diversity

The probability that two randomly picked individuals belong to the same species in an infinite community is  $P = \sum_{i=1}^S p_i^2$ .

Can be changed to a diversity measure (= increases with complexity):

1. Probability that two individuals belong to *different* species:  
 $1 - P$ .
2. Number of species in a community with the same probability  $P$ ,  
but all species with equal abundances:  $1/P$ .

Claimed to be ecologically more meaningful than Shannon diversity, but usually very similar.

## Hill numbers

Common measures of diversity are special cases of Rényi entropy;

$$H_a = \frac{1}{1-a} \log \sum_{i=1}^S p_i^a$$

Mark Hill proposed using  $N_a = \exp(H_a)$  or the “Hill number”:

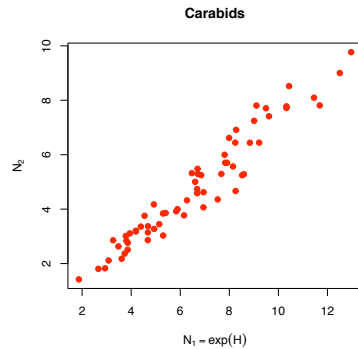
$$\begin{array}{lll} H_0 & = & \log(S) \quad N_0 = S \quad \text{Number of species} \\ H_1 & = & - \sum_{i=1}^S p_i \log p_i \quad N_1 = \exp(H_1) \quad \text{exp Shannon} \\ H_2 & = & - \log \sum_{i=1}^S p_i^2 \quad N_2 = 1 / \sum_{i=1}^S p_i^2 \quad \text{Inverse Simpson} \end{array}$$

Sensitivity to rare species decreases with increasing  $a$ :  $N_1$  and  $N_2$  are little influenced and nearly linearly related.

All Hill numbers in same units: “virtual species”.

## Choice of index

- Diversity indices are only variances of species abundances.
- It is not so important which index is used, since all sensible indices are very similar.



## Evenness

“If everything else remains constant”, diversity increases when

1. Number of species  $S$  increases, or
2. Species abundances  $p_i$  become more equal.

Evenness: Hidden agenda to separate these two components

For a given number of species  $S$ , diversity is maximal when all probabilities  $p_i = 1/S$ : in Shannon index  $H'_{\max} = \log(S)$

Pielou's evenness is the proportion of observed and maximal diversity

$$J' = \frac{H'}{H'_{\max}}$$

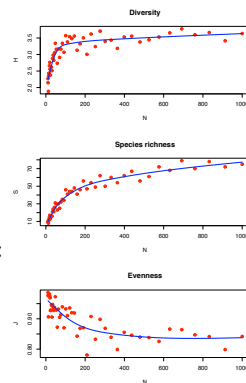
## Sample size and diversity

With increasing sample size

- Number of species  $S$  increases
- Diversity ( $N_1$  or  $N_2$ ) stabilizes
- Evenness decreases

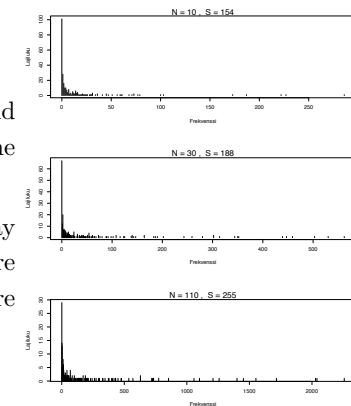
Diversity little influenced by rare species: a variance measure.

Evenness based on twisted idea.



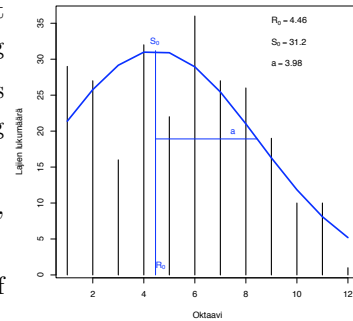
## Logarithmic series

- R.A. Fisher in 1940's
- Most species are rare, and species found only once are the largest group
- In larger samples, you may find more individuals of rare species, but you find new rare species



## Log-Normal model

- Preston did not accept Fisher's log-series, but assumed that rare species end with sampling
- Plotted number of species against 'octaves': doubling classes of abundance
- Modal class in higher octaves, and not so many rare species
- Canonical standard model of our times

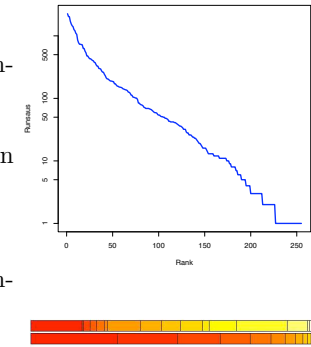


## Ranked abundance diagrams

- Horizontal axis: ranked species
- Vertical axis: Logarithmic abundance

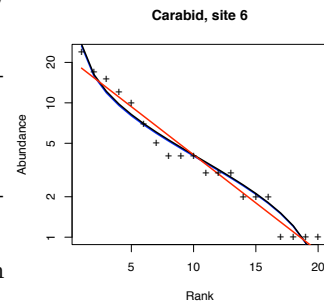
The shape of abundance distribution clearly visible:

- Linear: Pre-emption model
- Sigmoid: Log-normal or broken-stick



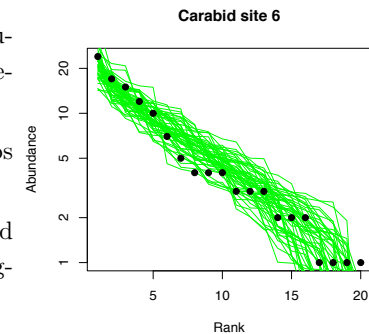
## Fitting RAD models

- Pre-emption model
  - Species abundances decay by constant proportion.
  - A line in the ranked abundance diagram.
- Log-normal model
  - Species abundances distributed Normally
  - Sigmoid: excess of both abundant and rare species to pre-emption model.



## Broken Stick

- Species 'break' a community ('stick') simultaneously in  $S$  pieces.
- No real hierarchy, but chips arranged in rank order:
- Result looks sigmoid, and can be fitted with log-Normal model.

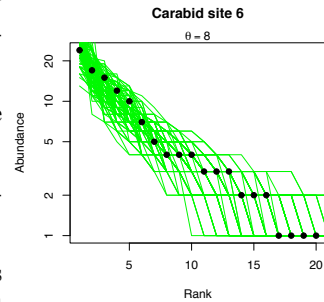


### Hubbell's abundance model

Ultimate diversity parameter  $\theta$

- $\theta = 2J_M\nu$ , where  $J_M$  is meta-community size and  $\nu$  evolution speed
- $\theta$  and  $J$  define the abundance distribution
- Simulations can be used for estimating  $\theta$ .

Species generator  $\theta/(\theta+j-1)$  gives the probability that  $j$ th individual is a new species for the community.

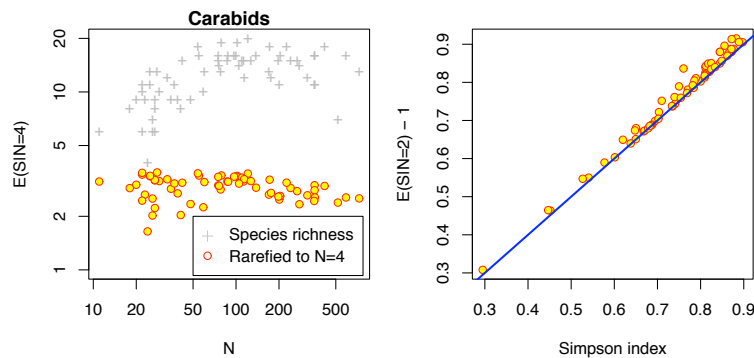


### Species richness: The trouble begins

- Species richness increases with sample size: can be compared only with the same size.
- Rare species have a huge impact in species richness.
- Rarefaction: Removing the effects of varying sample size.
- Sample size must be known in individuals: Equal area does not imply equal number of individuals.
- Plants often difficult to count.

### Rarefaction

Rarefy to a lower, equal number of individuals  
Only a variant of Simpson's index

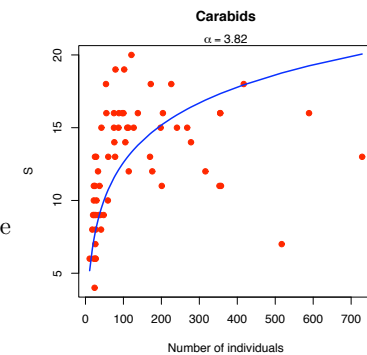


### Species richness and sample size

Fisher log-series predicts:

$$S = \alpha \ln \left( 1 + \frac{N}{\alpha} \right)$$

Species never end, but the rate of increase slows down.



## Species – Area models

- Island biogeography:  $S = cA^z$ .
- Parameter  $c$  is uninteresting, but  $z$  should describe island isolation.
- Regarded as universally good: Often the only model studied, so no alternatives inspected.
- Assuming that doubling area  $A$  brings along a constant number of new species fits often better.

