

Multivariate statistics in R

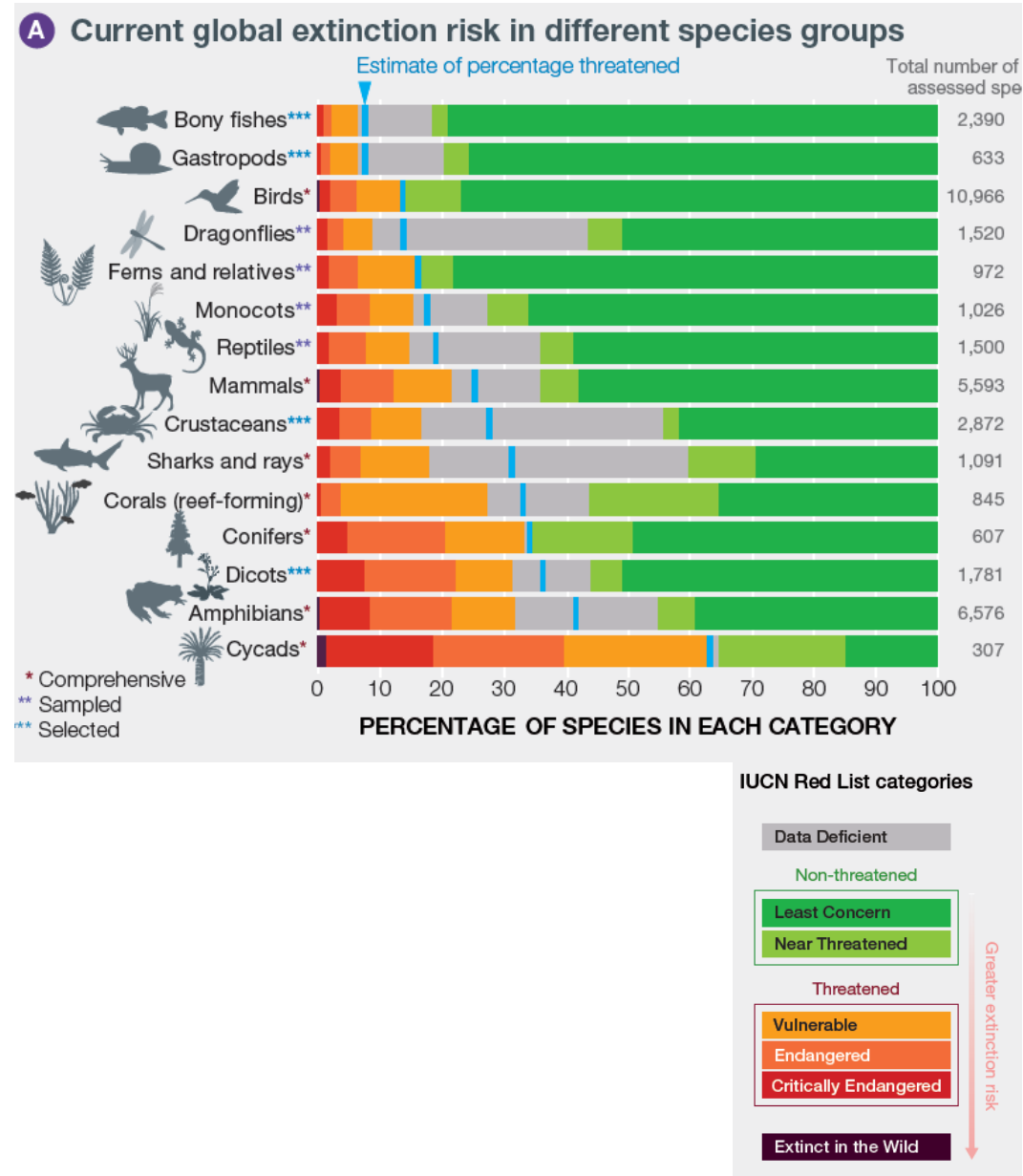
Hannes PETER
Martin BOUTROUX

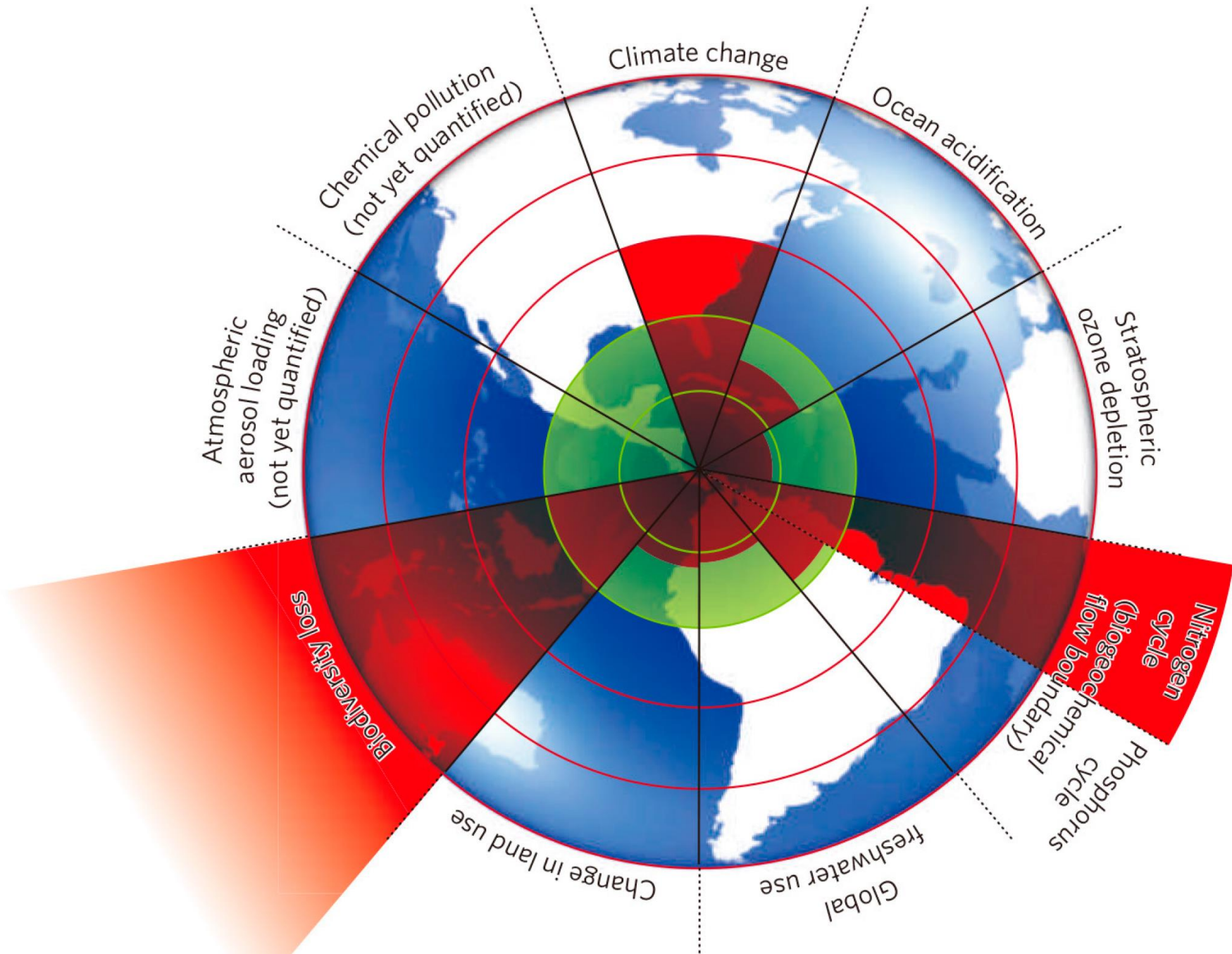
Estimating diversity using R

- Brief definition of diversity
- biodiversity under threat
- Estimating alpha diversity indices
- Assessing beta-diversity
- Rarefaction and extrapolation

Diversity

- Biodiversity is the variety of life, in all its manifestations (Gaston & Spicer 2004)
- Biodiversity is important for functioning, resistance and resilience of ecosystems
- Biodiversity is threatened
 - climate change, land-use, pesticide use, etc.
- A lot of unknown/uncharacterized diversity
 - Specific to groups of organisms/habitats





Multiple driver and aspects of diversity loss

DRIVERS

INDIRECT DRIVERS

Values and behaviours

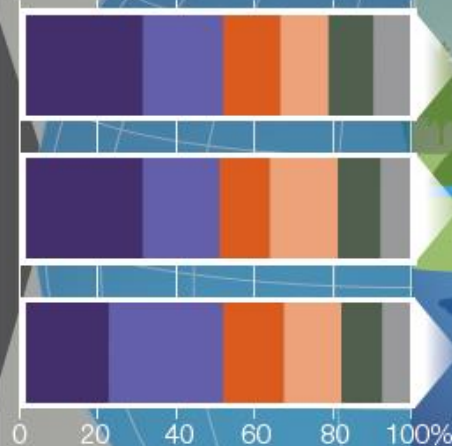
Demographic and sociocultural

Economic and technological

Institutions and governance

Conflicts and epidemics

DIRECT DRIVERS



Legend for Direct Drivers:

- Land/sea use change
- Direct exploitation
- Climate change
- Pollution
- Invasive alien species
- Others

EXAMPLES OF DECLINES IN NATURE

ECOSYSTEM EXTENT AND CONDITION

47%

Natural ecosystems have **declined by 47 per cent** on average, relative to their earliest estimated states.

SPECIES EXTINCTION RISK

25%

Approximately **25 per cent of species are already threatened with extinction** in most animal and plant groups studied.

ECOLOGICAL COMMUNITIES

23%

Biotic integrity—the abundance of naturally-present species—has **declined by 23 per cent** on average in terrestrial communities.*

BIOMASS AND SPECIES ABUNDANCE

82%

The global biomass of wild mammals has **fallen by 82 per cent**.* Indicators of vertebrate abundance have declined rapidly since 1970

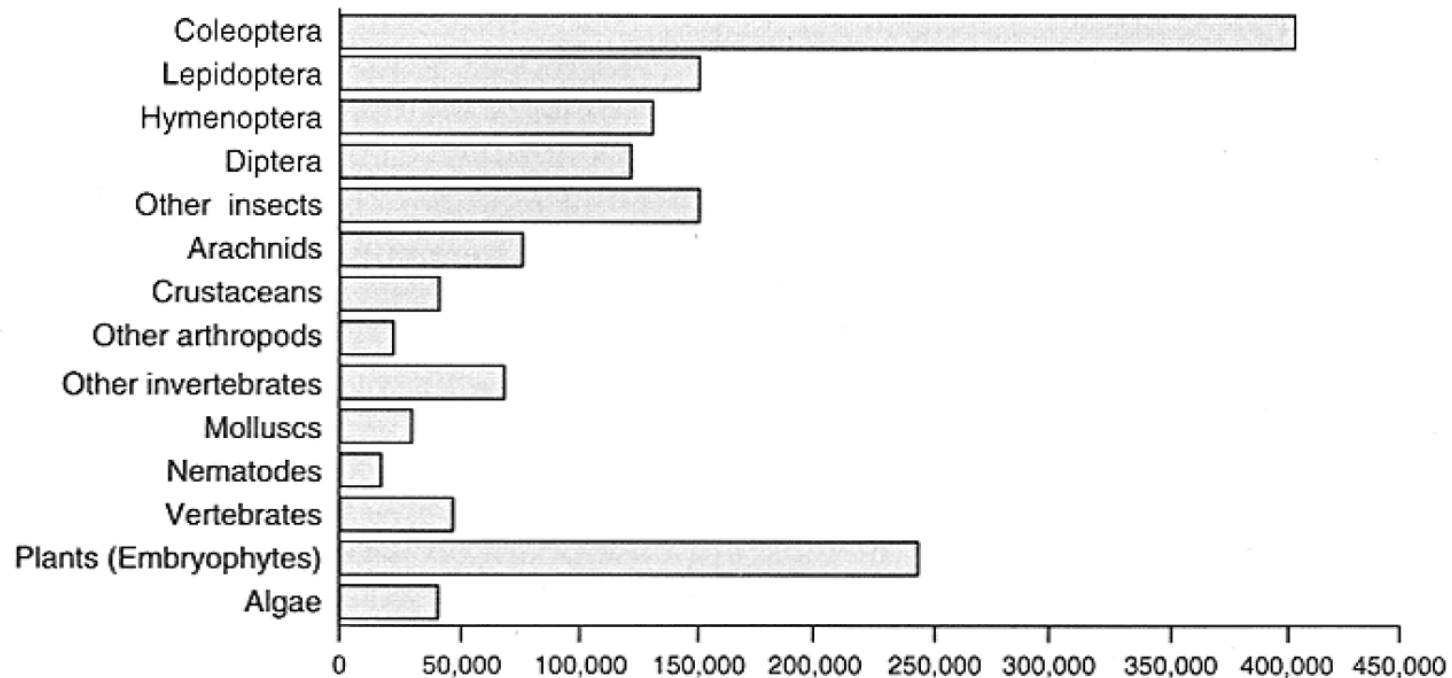
NATURE FOR INDIGENOUS PEOPLES AND LOCAL COMMUNITIES

72%

72 per cent of indicators developed by indigenous peoples and local communities show **ongoing deterioration** of elements of nature important to them

* Since prehistory

only few species are actually known...



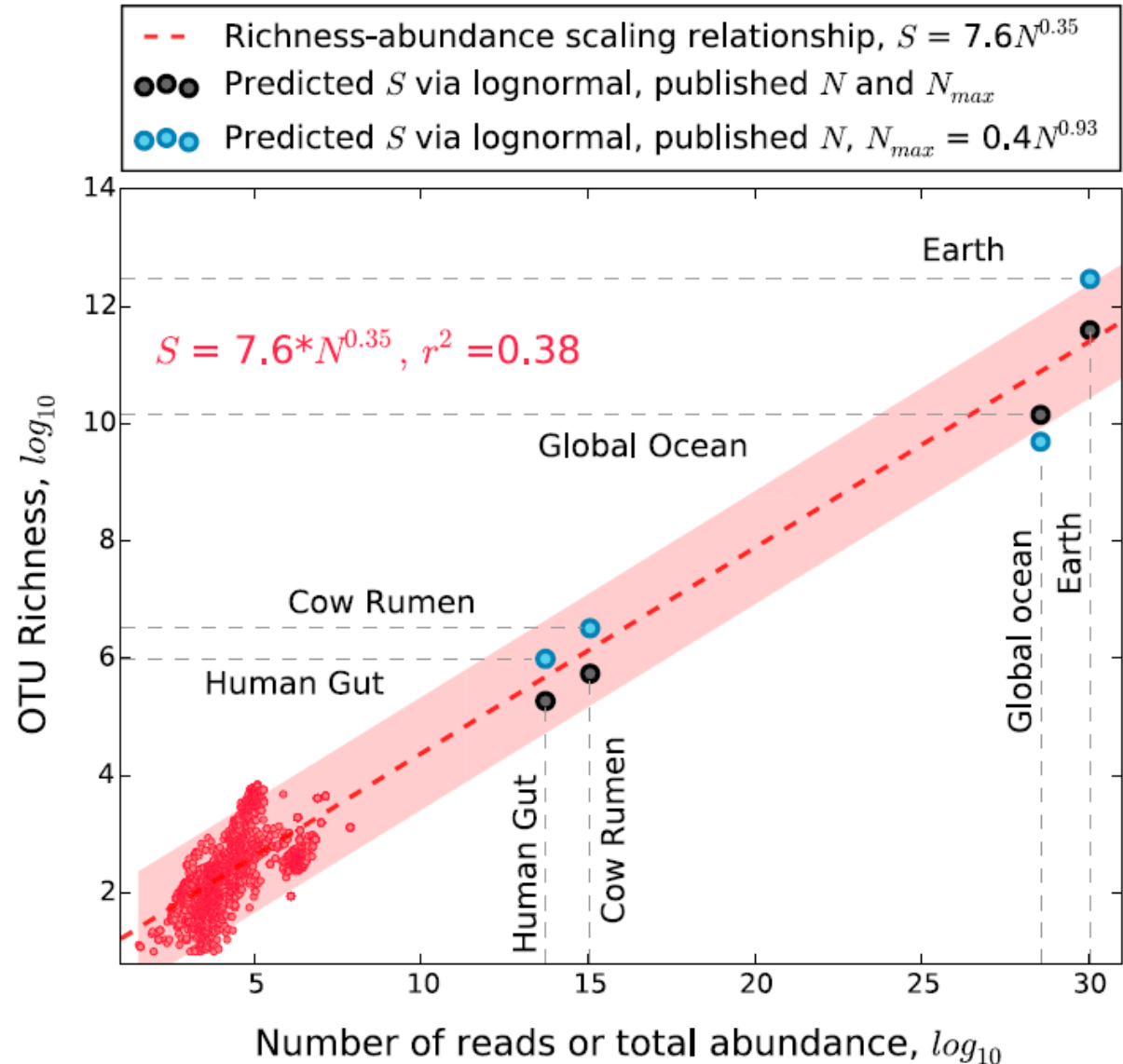
Hammond 1992, Stork 1993, Gaston & Spicer 2004

Scaling laws predict global microbial diversity

Kenneth J. Locey^{a,1} and Jay T. Lennon^{a,1}

^aDepartment of Biology, Indiana University, Bloomington, IN 47405

- 10^{30} bacterial cells
- 1 trillion (10^{12}) bacterial species on Earth

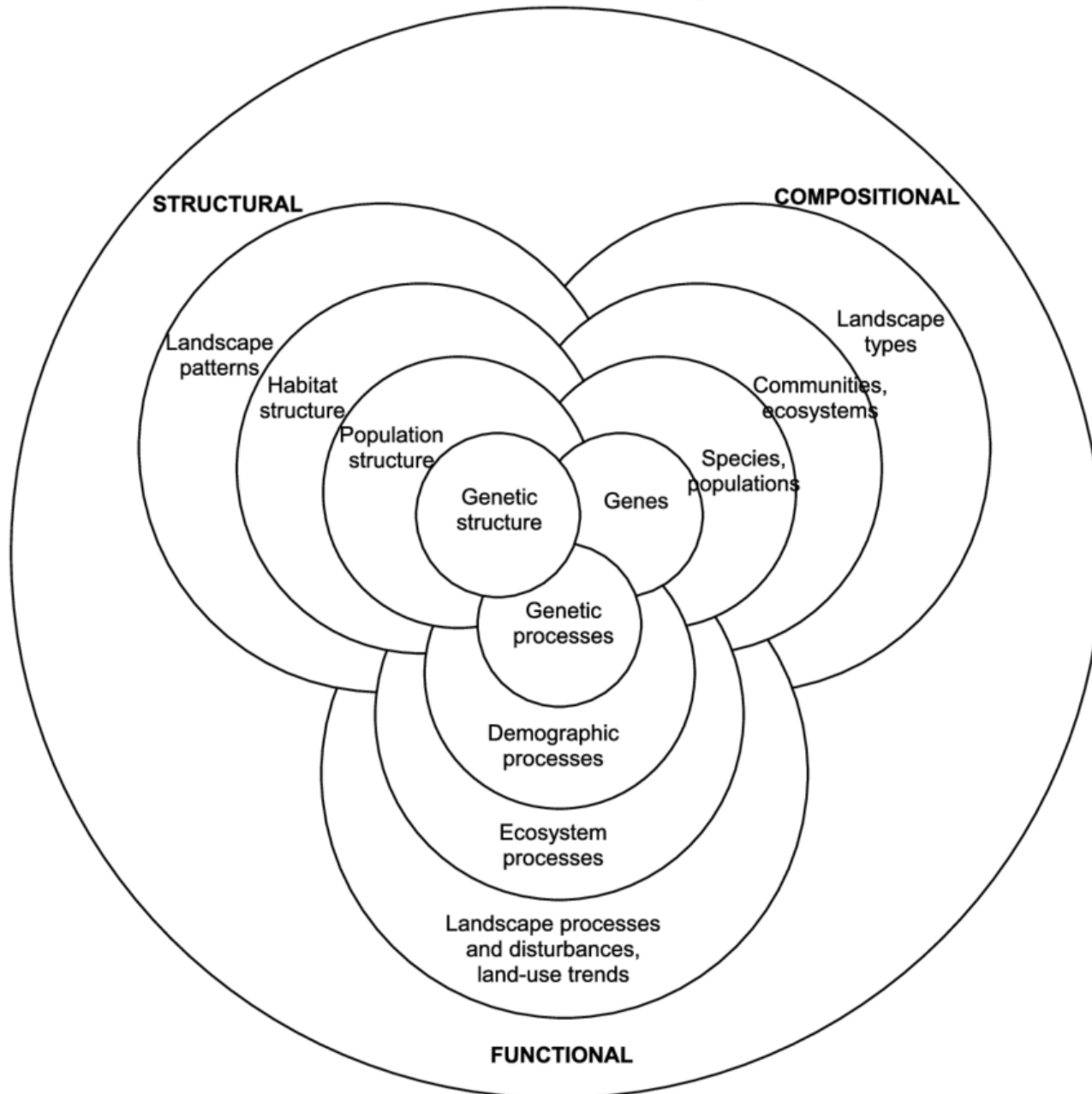


Elements of biodiversity

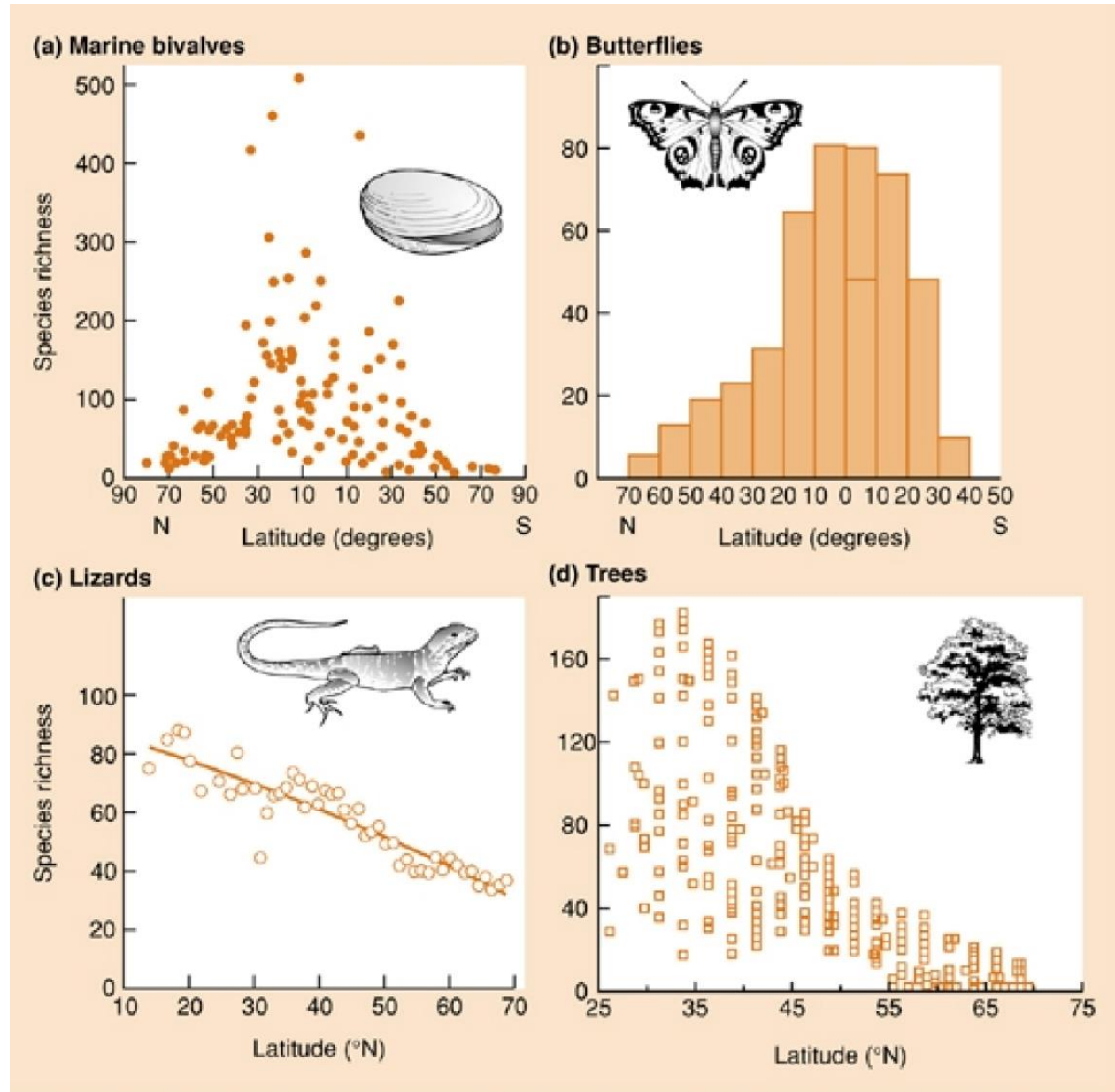
Table 1.1 Elements of biodiversity. (Adapted from Heywood & Baste 1995.)

Ecological diversity		Organismal diversity	
Biomes		Domains or Kingdoms	
Bioregions		Phyla	
Landscapes		Families	
Ecosystems		Genera	
Habitats		Species	
Niches		Subspecies	
Populations		Populations	
	Genetic diversity	Individuals	
	Populations		
	Individuals		
	Chromosomes		
	Genes		
	Nucleotides		

Elements of biodiversity

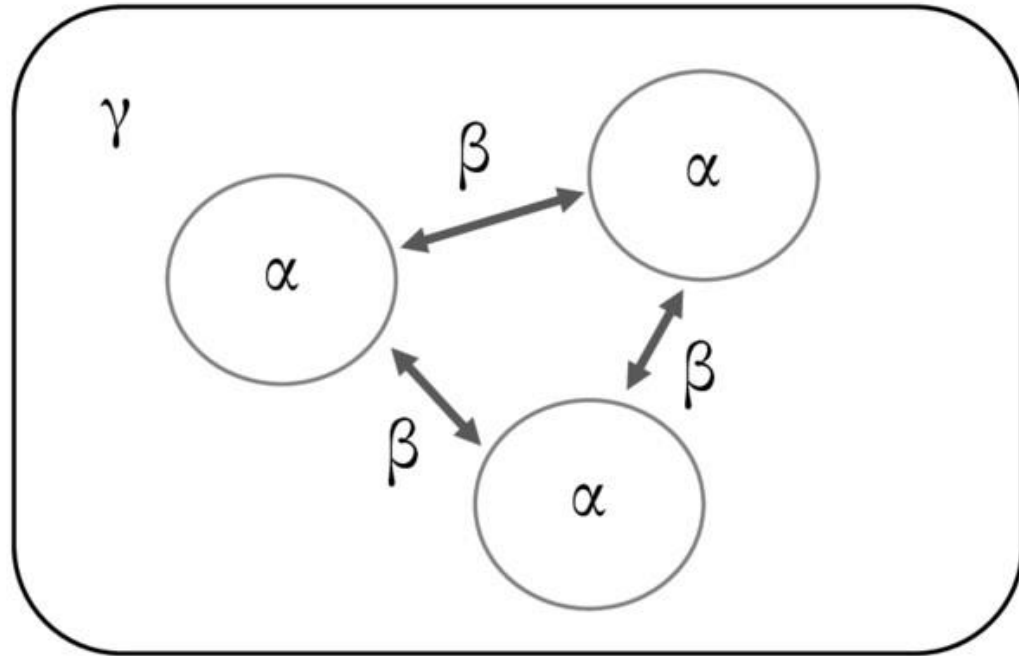


Latitudinal diversity gradients



Patterns of diversity

- α -diversity
 - local diversity
- β -diversity
 - diversity differences (turnover) across ecological gradients/locations
- γ - diversity
 - entire (regional) diversity

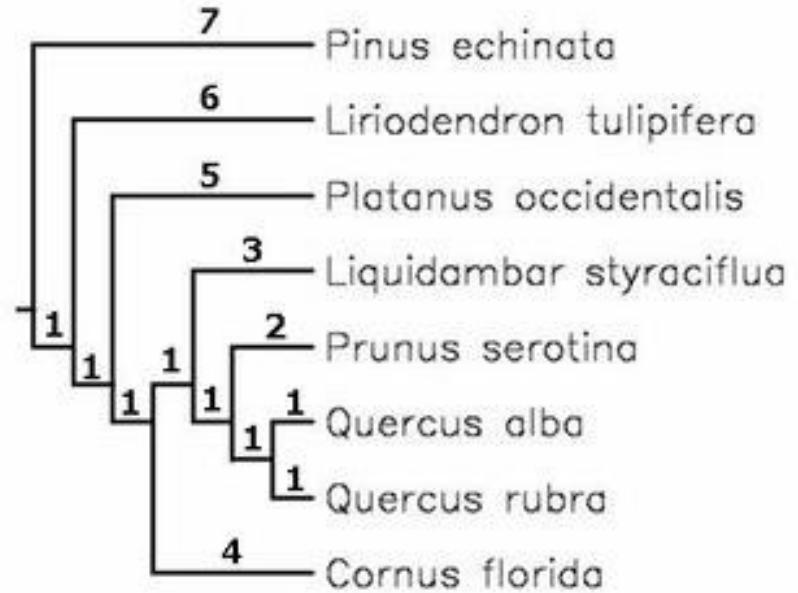
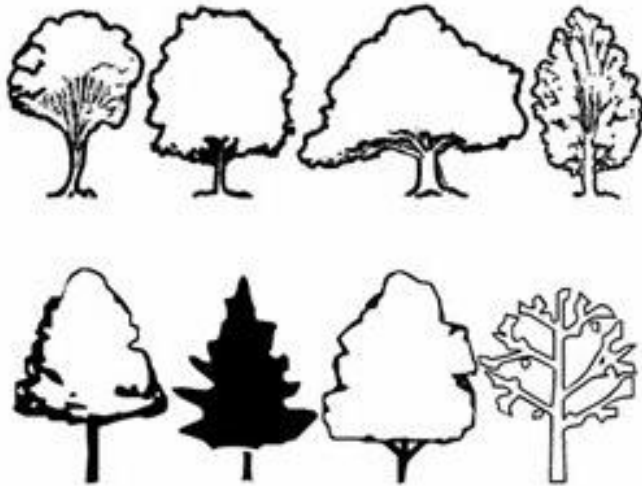


measures of biodiversity

- Species richness
 - Number of species in location/ecosystem
- Evenness
 - distribution of abundances (rarity/dominance)
- Genetic diversity
- Taxonomic diversity
- Functional diversity

...

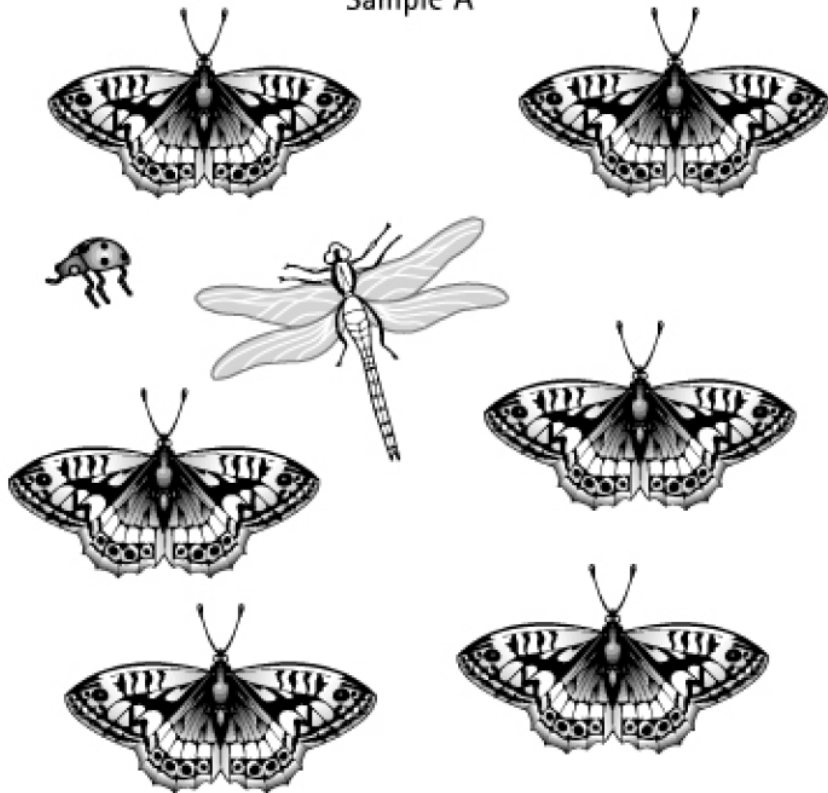
genetic (phylogenetic) diversity



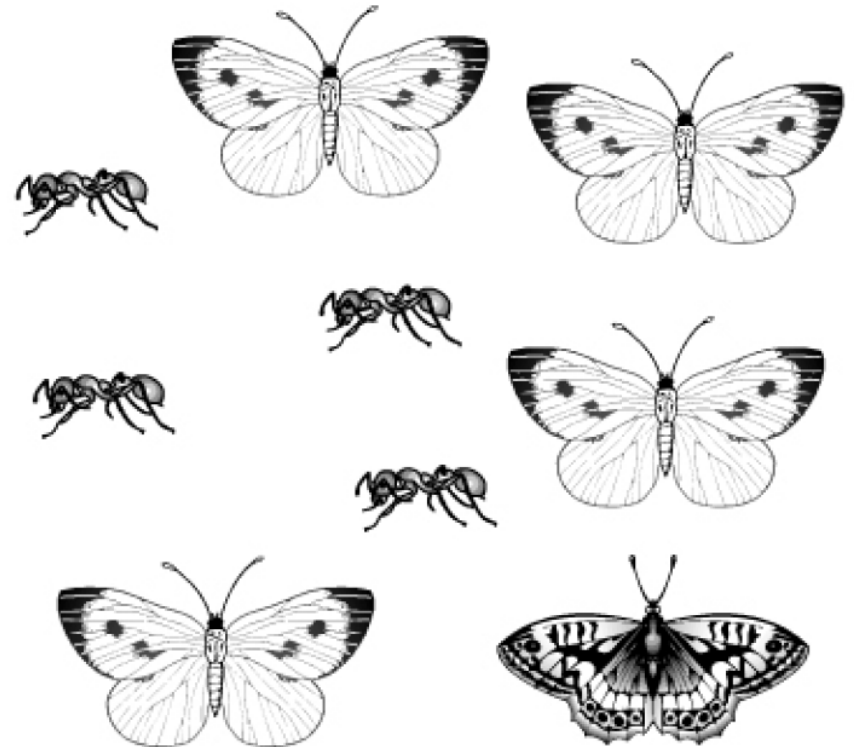
similar principals for taxonomic/functional diversity

Evenness

Sample A



Sample B



Alpha-diversity analysis using R

vignette: diversity-vegan

❑ `vegan:specnumber()`

- ❑ number of species

❑ `vegan:diversity()`

- ❑ returns common diversity indices for all sites

❑ `vegan:taxondive()`

- ❑ implements indices of taxonomic diversity (use `taxa2dist()` to convert taxonomic classification tables to distances)

❑ `vegan:treedive()`

- ❑ implements functional diversity based on branch length in a trait-based dendrogram

❑ `picante:pd()`

- ❑ Requires a species table and a phylogenetic tree and returns Faith's phylogenetic diversity index for each sample

$$H = - \sum_{i=1}^S p_i \log_b p_i \quad \text{Shannon-Weaver}$$

$$D_1 = 1 - \sum_{i=1}^S p_i^2 \quad \text{Simpson}$$

$$D_2 = \frac{1}{\sum_{i=1}^S p_i^2} \quad \text{inverse Simpson ,}$$

S number of species

p_i is the proportion of species i

b is the base of the logarithm

Hill numbers and diversity profiles

- most diversity indices are non-linear with respect to species addition (each added species leads to a smaller increment in the diversity measure than the species added before it)
- Hill proposed a statistical framework to transform classical diversity measures to ‘effective numbers of species’ (or ‘Hill numbers’)
- encompasses many diversity indices (e.g. richness, Shannon index, Simpson index), phylogenetic diversity (e.g. Faith’s PD, Allen’s H, Rao’s quadratic entropy) and dissimilarity (e.g. Sørensen index, Unifrac distances) metrics

library: *hilldiv*

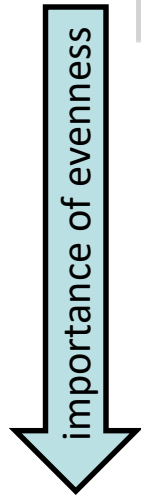
INVITED TECHNICAL REVIEW

MOLECULAR ECOLOGY
RESOURCES WILEY

A guide to the application of Hill numbers to DNA-based diversity analyses

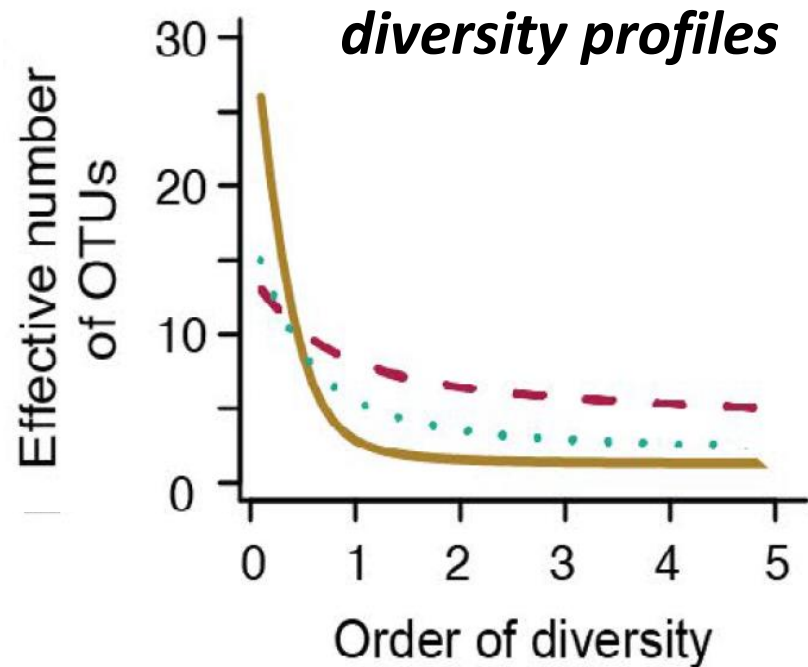
Antton Alberdi¹  | M. Thomas P. Gilbert^{1,2}

Hill numbers of order (q)



q	Diversity index qH	Hill number in terms of qH
0	Richness ${}^0H \equiv \sum_{i=1}^S p_i^0$	Richness ${}^0D = {}^0H$
1	Shannon entropy ${}^1H \equiv - \sum_{i=1}^S p_i^1 \ln p_i^1$	Shannon diversity ${}^1D = \exp({}^1H)$
2	Simpson index ${}^2H \equiv 1 - \sum_{i=1}^S p_i^2$	Simpson diversity ${}^2D = 1 / (1 - {}^2H)$

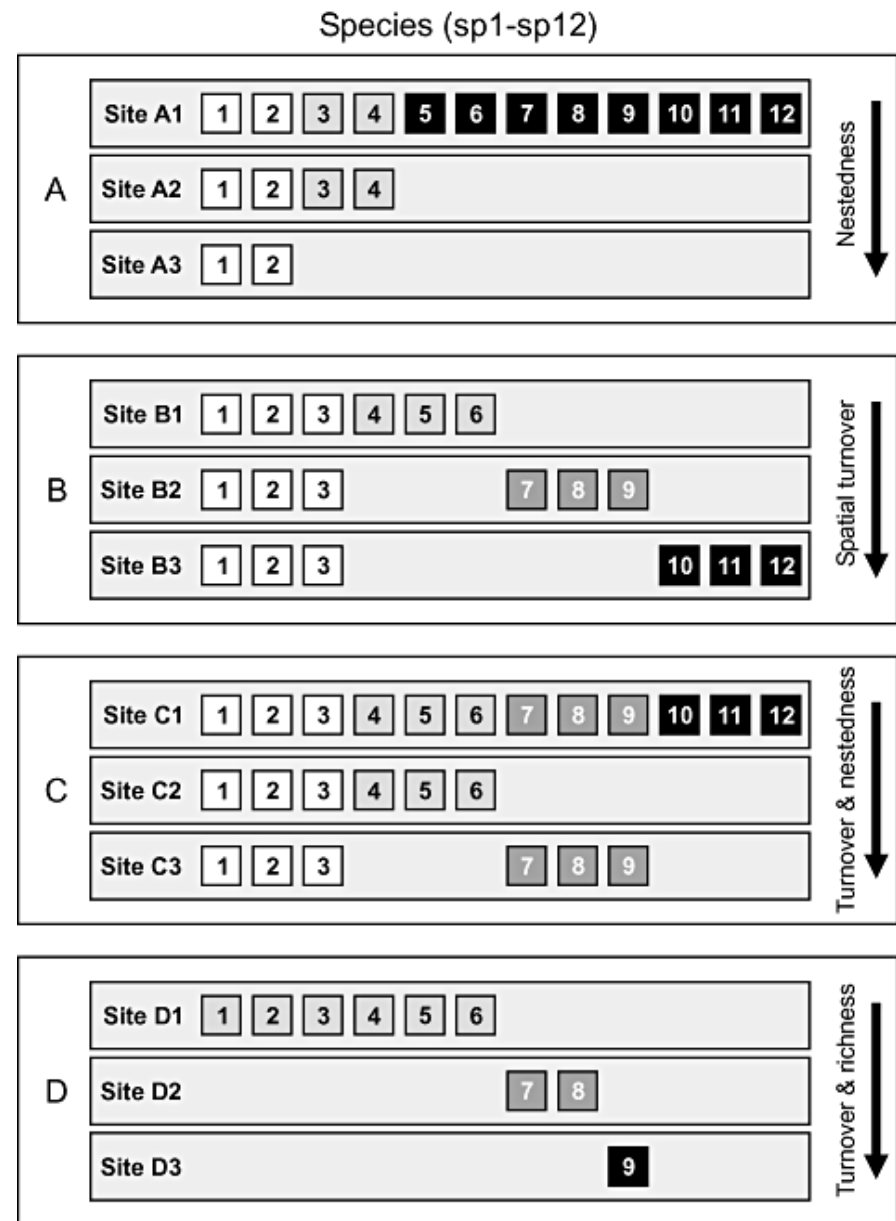
hilldiv:div_profile()



betadiversity

replacement of species is a measure of difference in composition between assemblages

- ❑ `vegan:betadiver()`
 - ❑ returns many beta-diversity indices
- ❑ `vegan:betadisper()`
 - ❑ measures group dispersion
- ❑ `betapart:betapart()`
 - ❑ partitiones betadiversity into nestedess and turnover
- ❑ `adespatial:beta.div()`
 - ❑ Species contributions to beta diversity (SCBD)
 - ❑ Local contributions to beta diversity (LCBD)



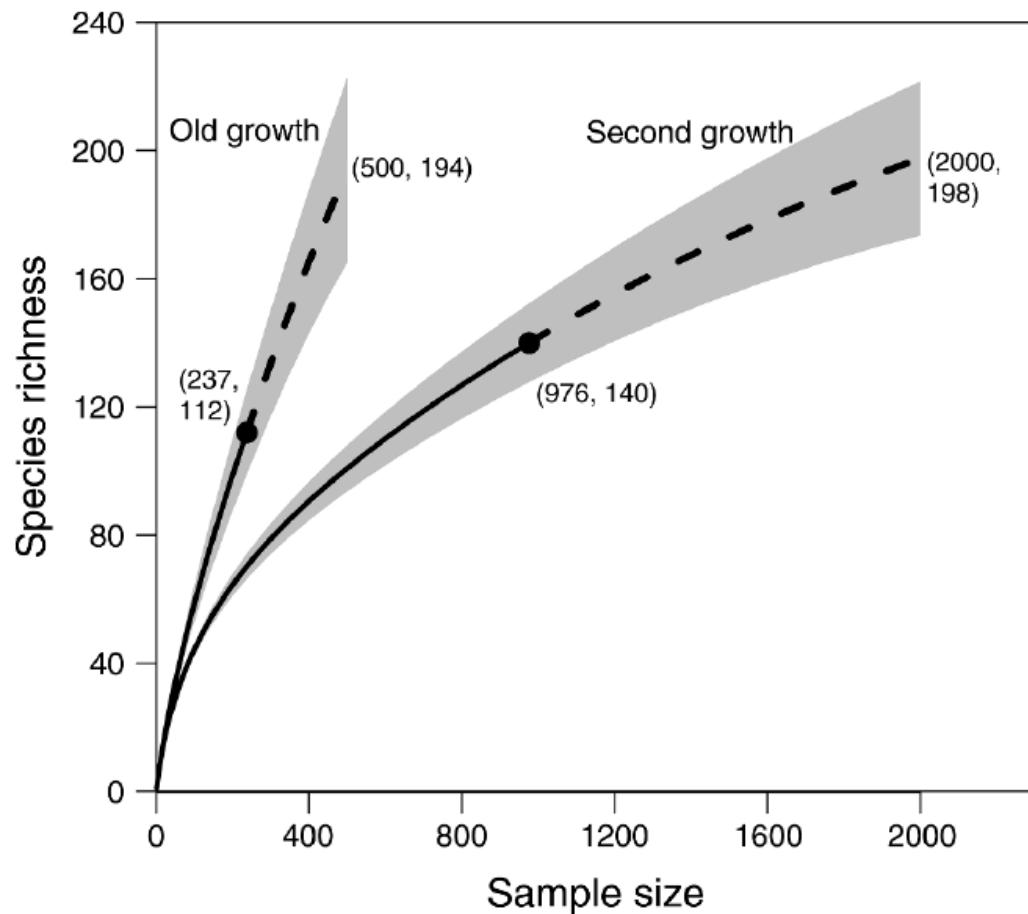
Rarefaction and extrapolation

rarefaction:

- ❑ `vegan: rarecurve(); rrarefy()`
 - ❑ rarefaction curve, subsampled community (i.e. rarified)
- ❑ `vegan: specaccum()`
 - ❑ species accumulation curve

extrapolation:

- ❑ Chao-1 estimate
 - ❑ `breakaway:chao1()`
- ❑ iNEXT
 - ❑ coverage-based rarefaction and extrapolation curves
 - ❑ `iNEXT:iNEXT()`



Take home messages