Multivariate statistics in R

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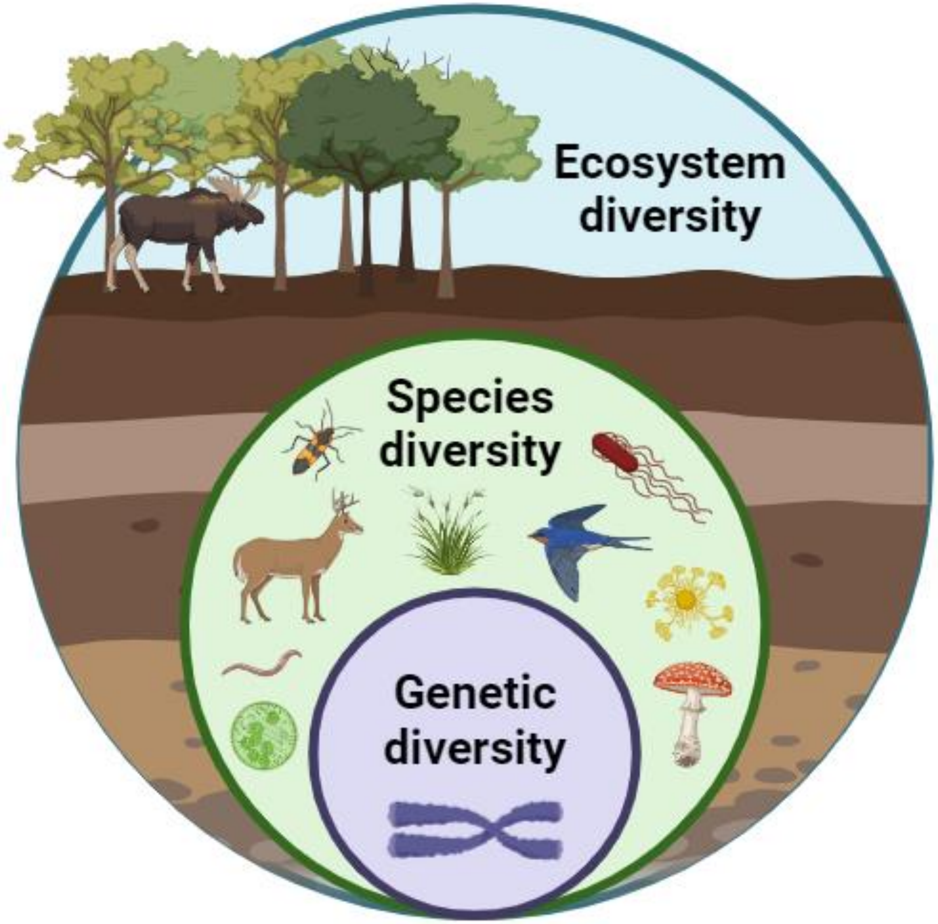
Exploring biodiversity using R

- brief definition of diversity
- estimating alpha diversity indices
- assessing beta-diversity/turnover
- rarefaction and extrapolation

Biodiversity

- Comprises the multitude and complexity of living systems, from genes to species and ecosystems
- Evolutionary processes (e.g. speciation, extinction) and ecological factors (e.g. competition, dispersal) shape biodiversity
- Biodiversity is important for humanity!

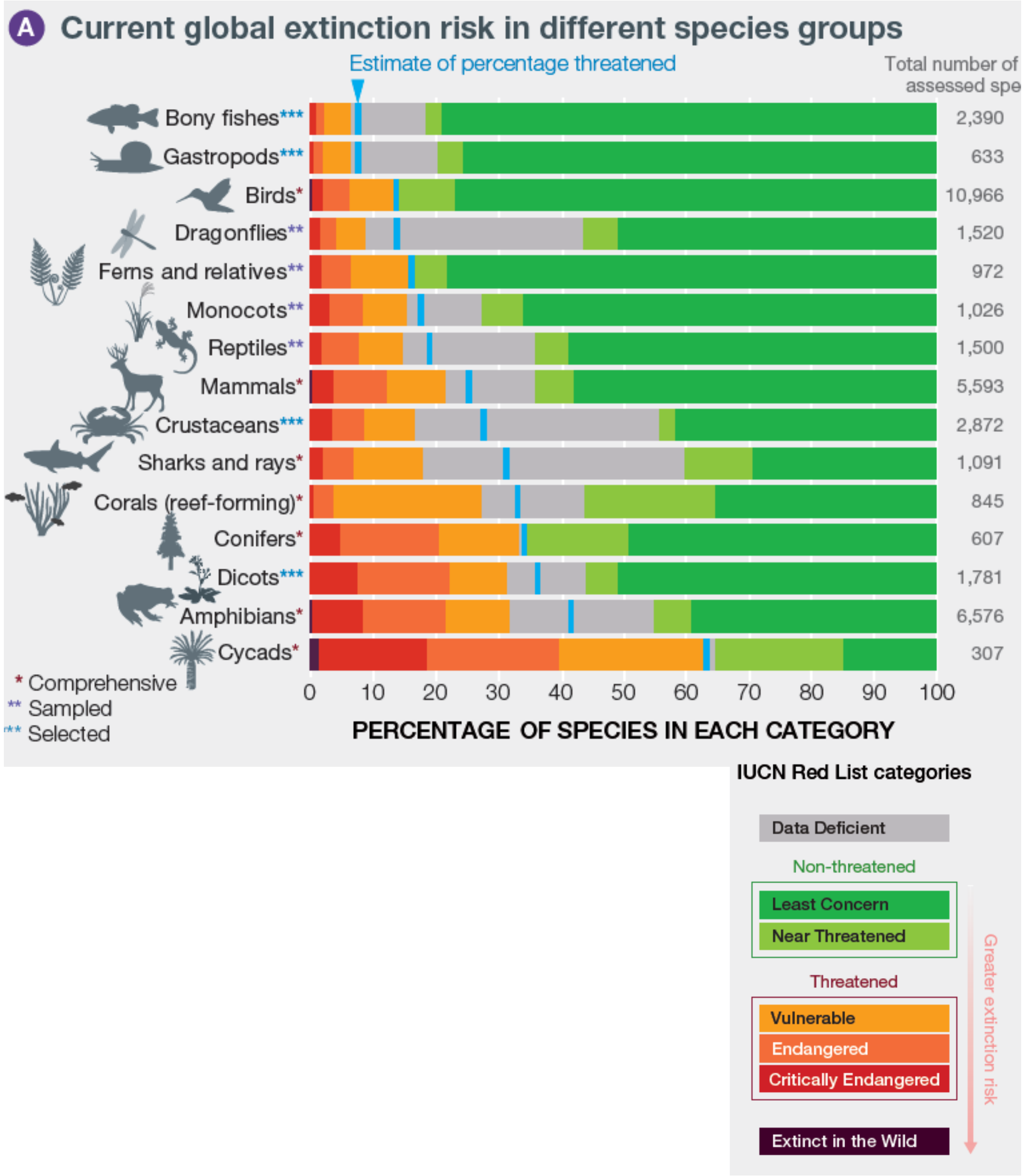


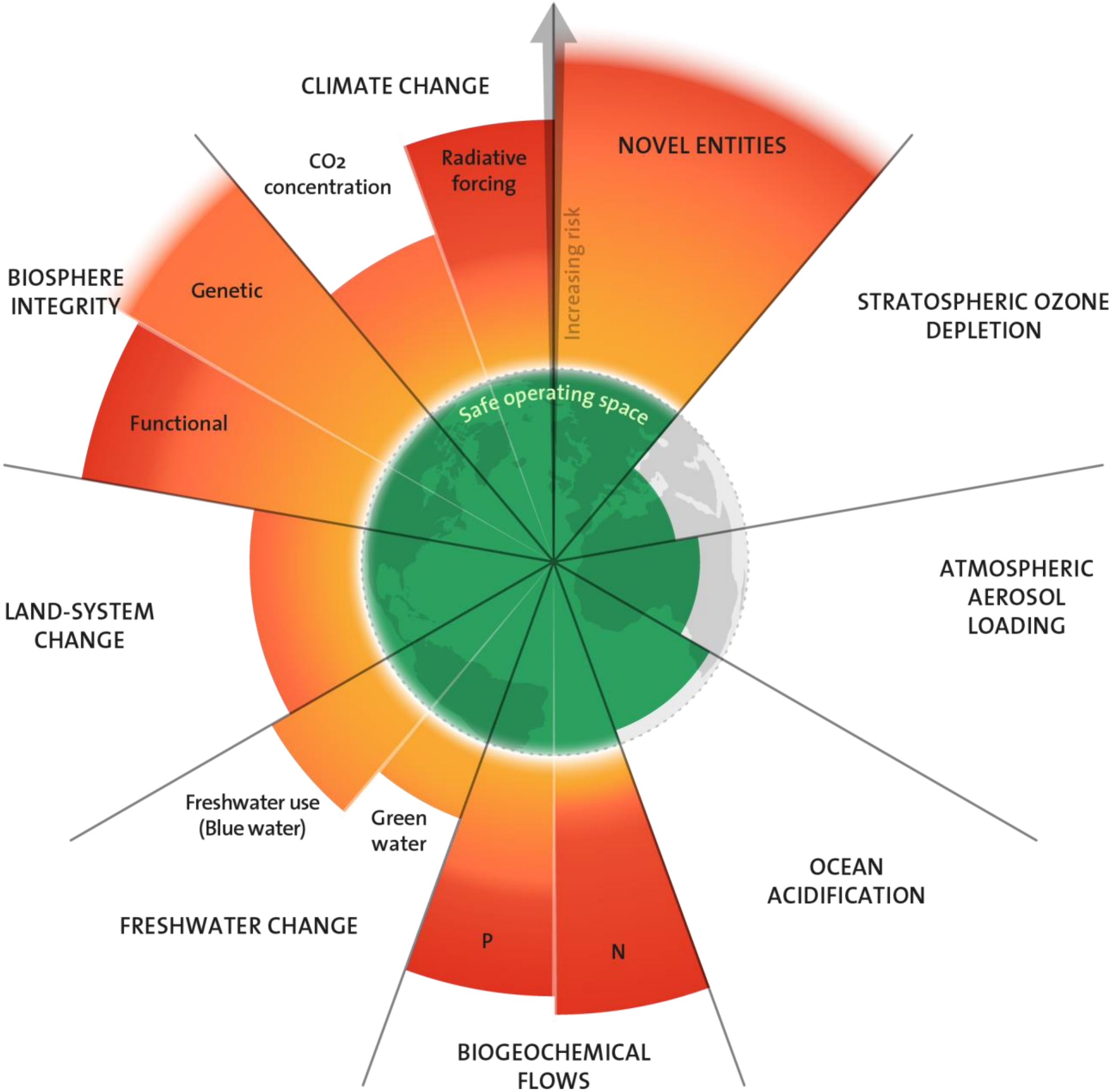
Biodiversity crisis

- Biodiversity is important for functioning, resistance and resilience of ecosystems

- Biodiversity is threatend
  - climate change, land-use, pesticide use, etc.

- A lot of unknow / uncharacterized diversity
  - Specific to groups of organisms/habitats





Stockholm Resilience Centre

much is unknown…

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

Scaling laws predict global microbial diversity

Kenneth J. Locey[a,1] and Jay T. Lennon[a,1]

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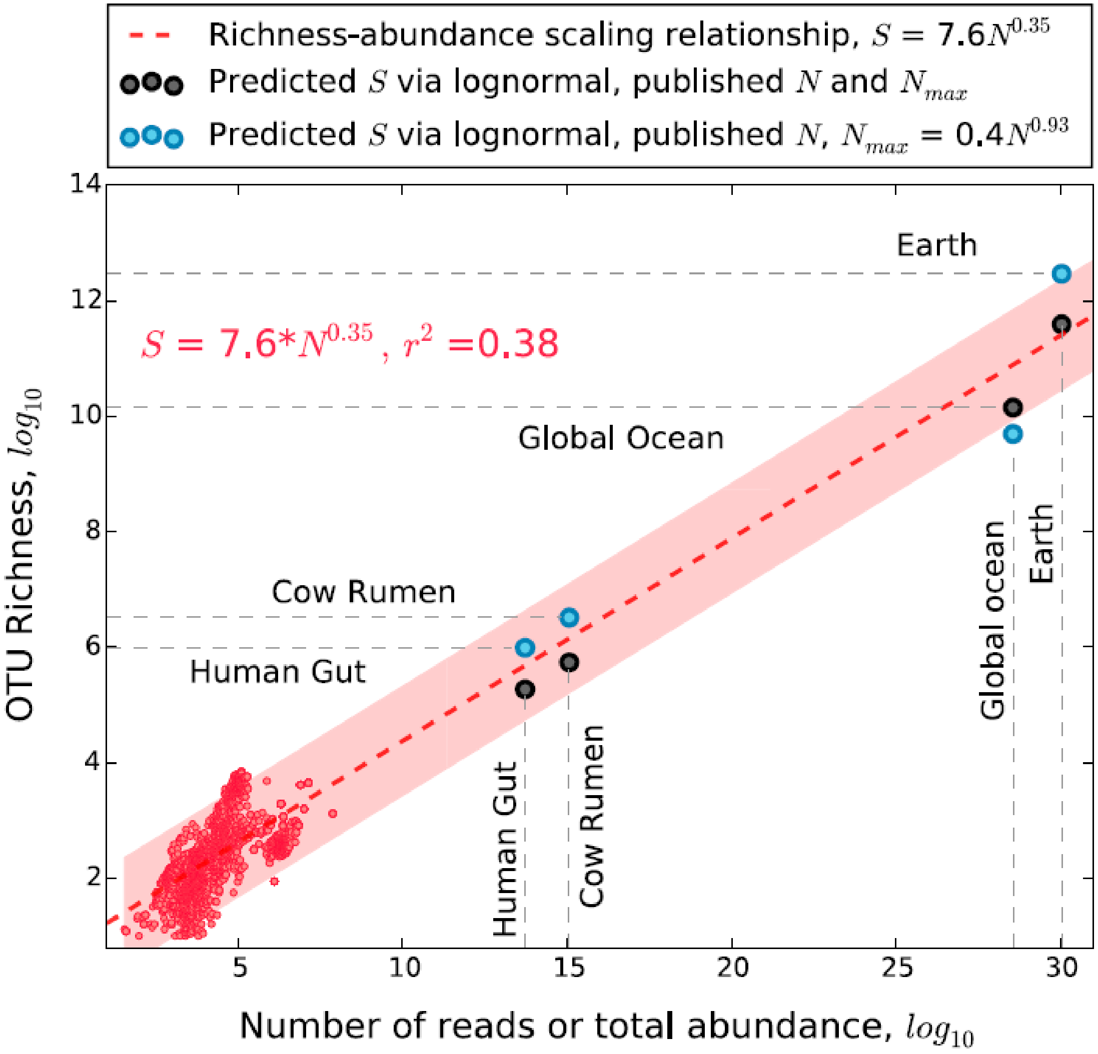
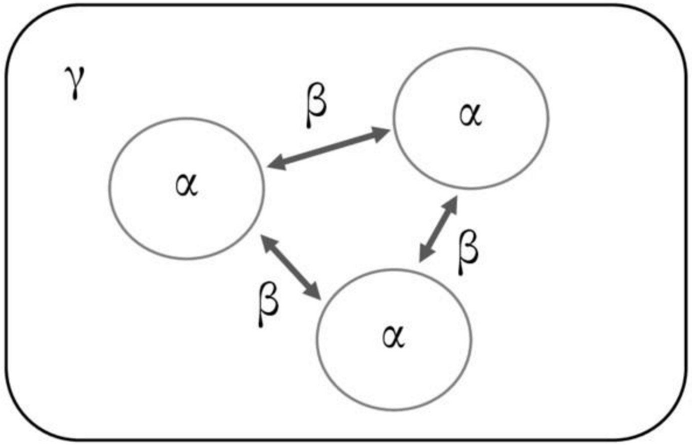


spatial scales of diversity

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

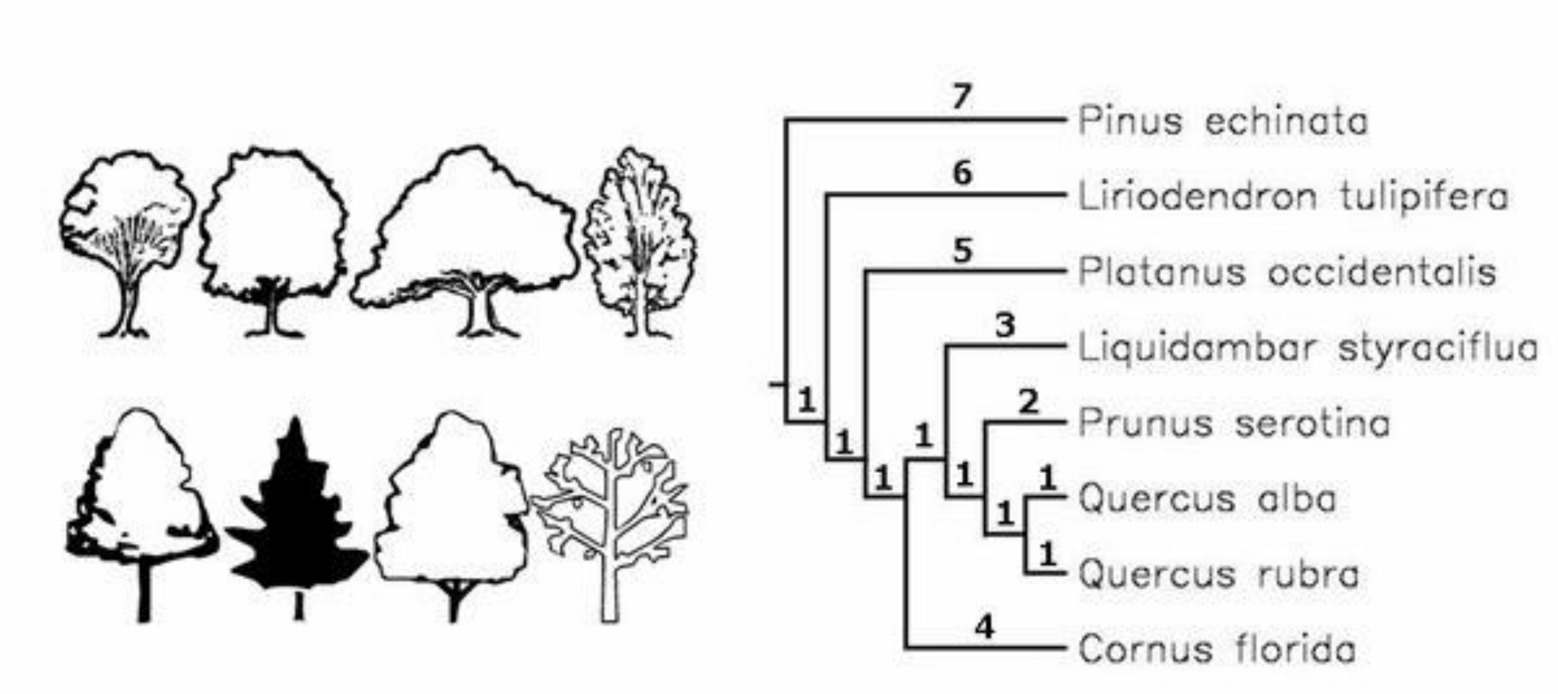


measures of biodiversity

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

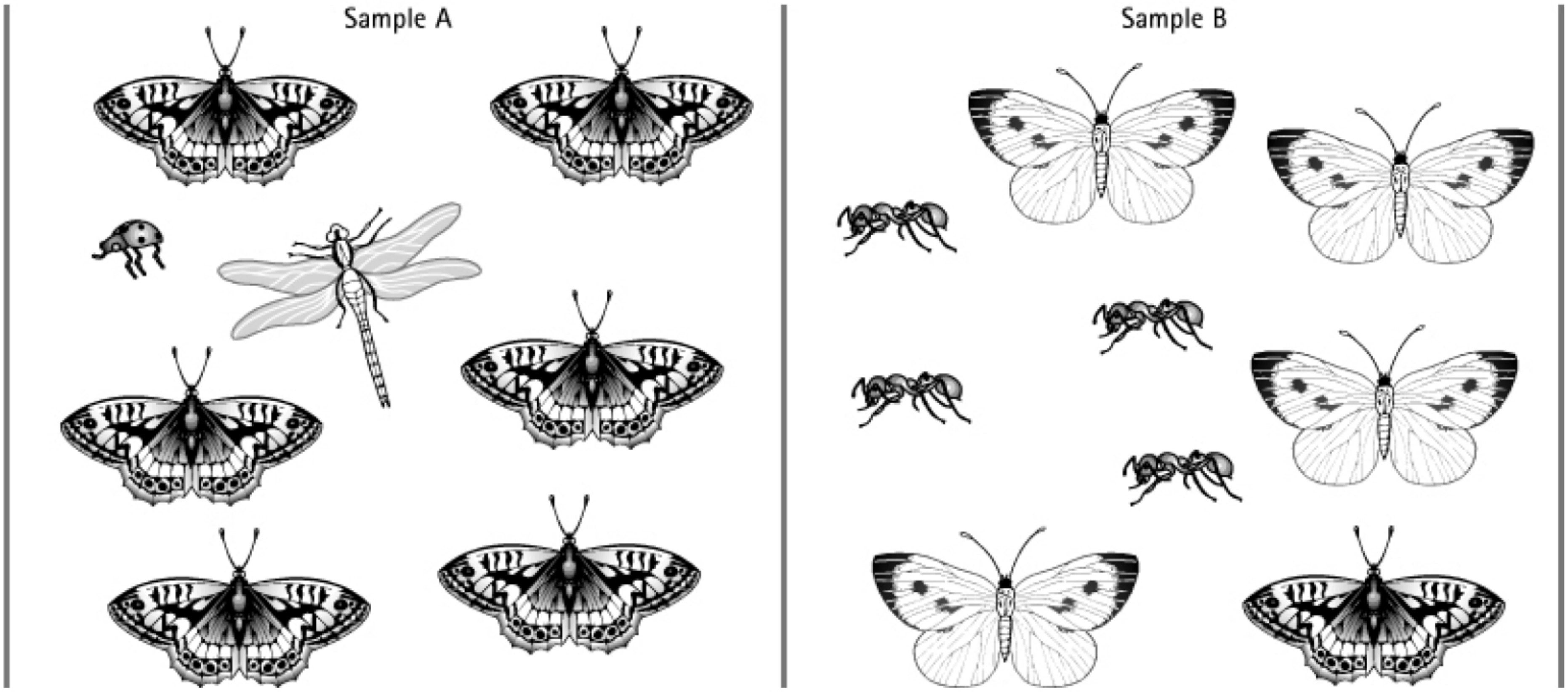
…

genetic (phylogenetic) diversity



similar principals for taxonomic/functional diversity

Evenness



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 (see Gower's Distance)
- picante:pd()
  - requires a species table and a phylogenetic tree and returns Faith's phylogenetic diversity index for each sample

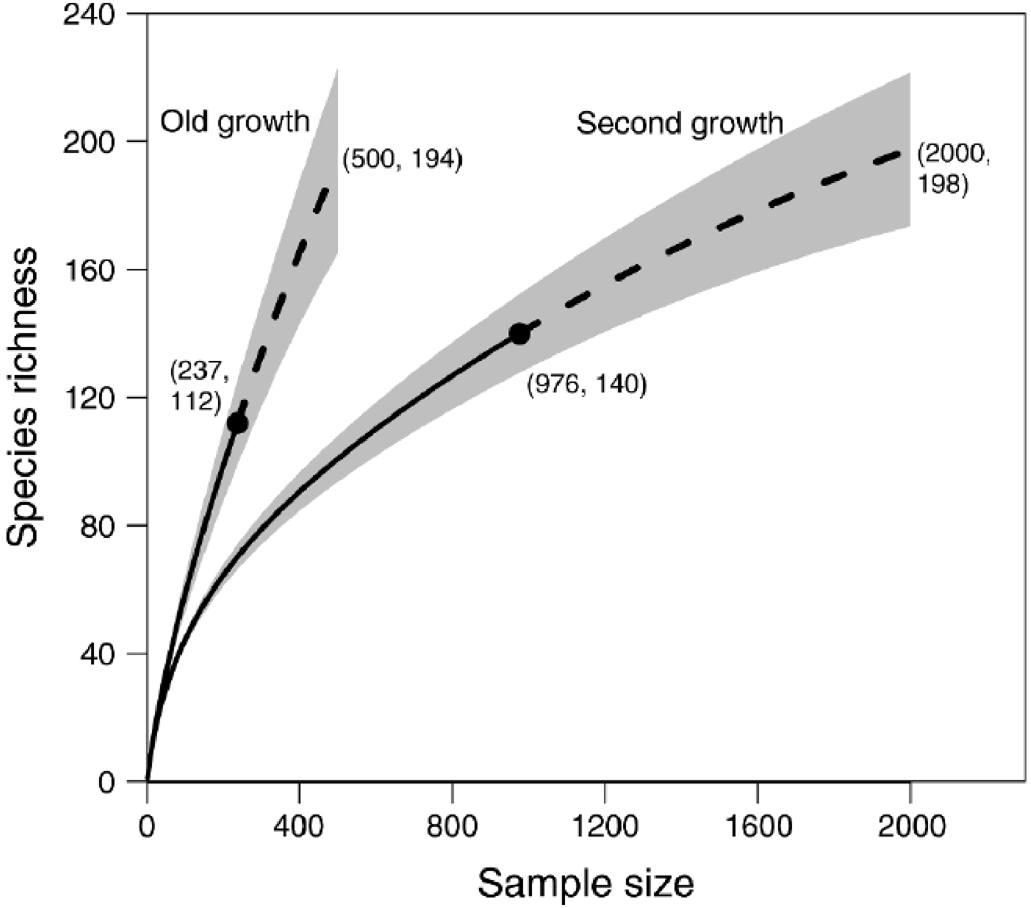
Rarefaction and extrapolation

rarefaction:

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

extrapolation:

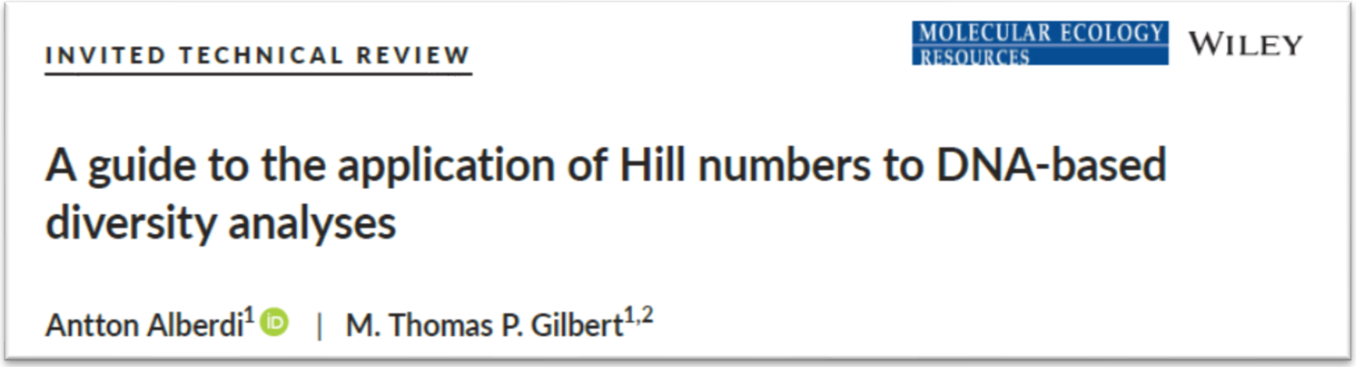
- Chao-1 estimate
  - breakaway:chao1()
- Abundance-based coverage
  - fossil: ACE() / ICE()
- coverage-based rarefaction and extrapolation curves (iNEXT)
  - iNEXT:iNEXT()



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

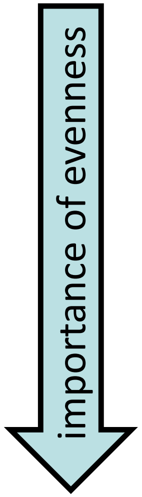
MOLECULAR ECOLOGY RESOURCES

WILEY

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

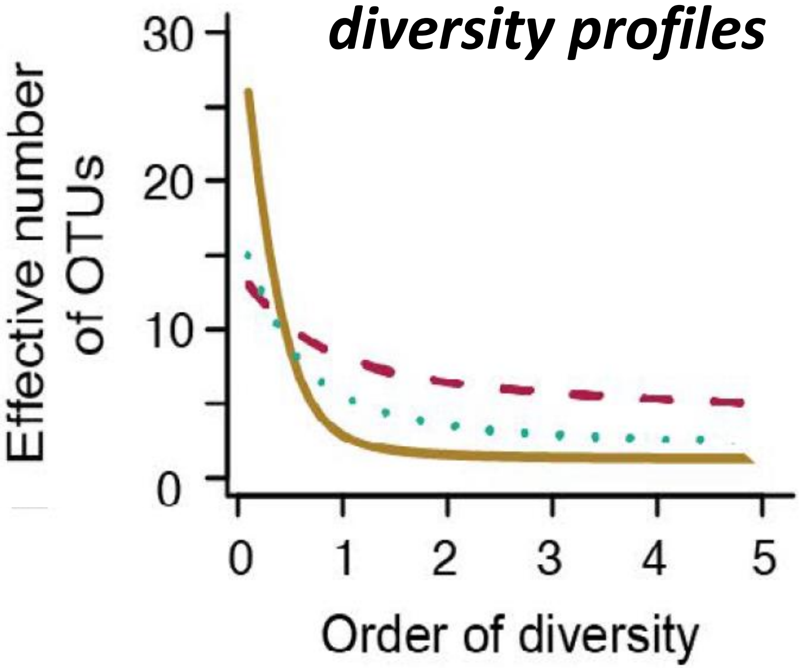
Antton Alberdi[1] | M. Thomas P. Gilbert[1,2]

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 $^1D = exp\left({}^1H\right)$
2	Simpson index $^2H \equiv 1 - \sum_{i=1}^{S} p_i^2$	Simpson diversity $^2D = 1/\left(1 - {}^2H\right)$

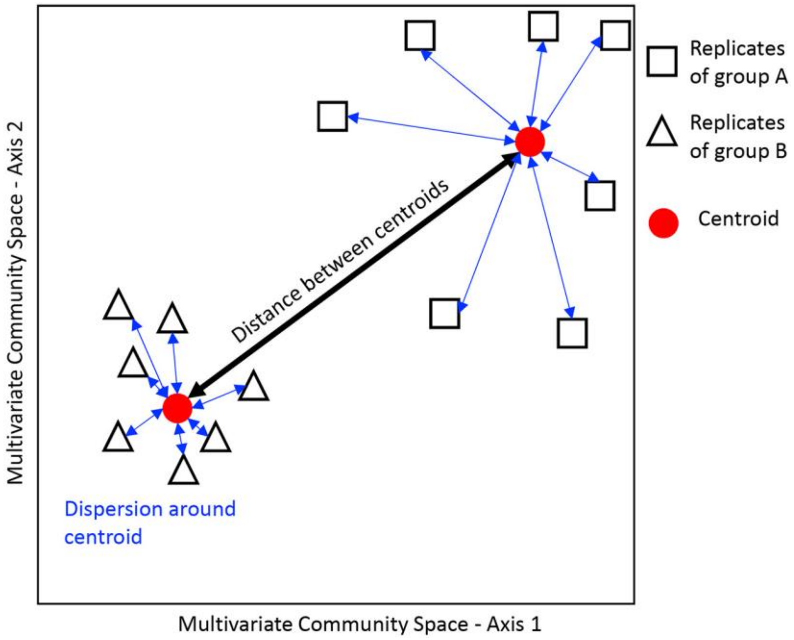
hilldiv:div_profile()

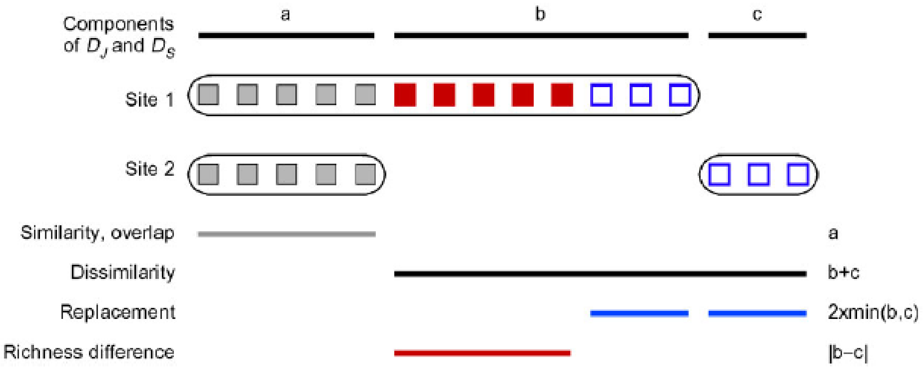


betadiversity

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

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





Baselga 2009 *Global Ecology and Biogeography*
Legendre 2014 *Global Ecology and Biogeography*

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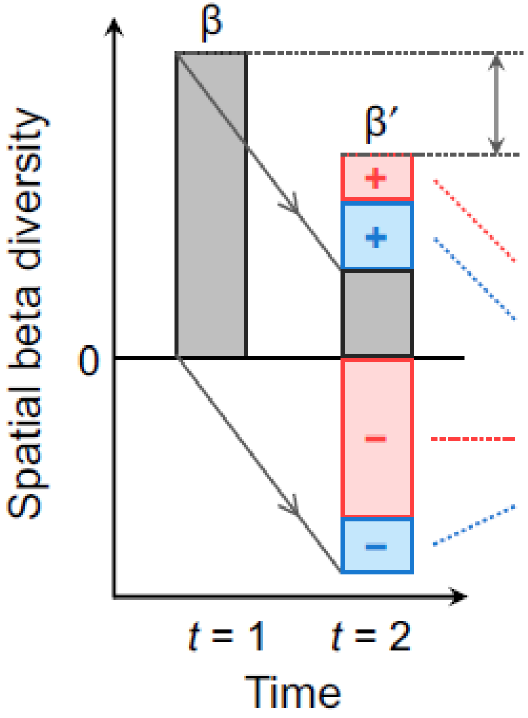
RESEARCH ARTICLE

Methods in Ecology and Evolution
BRITISH ECOLOGICAL SOCIETY

Partitioning the temporal changes in abundance-based beta diversity into loss and gain components

Shinichi Tatsumi[1,2] | Ryosuke Iritani[3] | Marc W. Cadotte[1,4]



Total change in beta diversity ($\Delta\beta$)

$= \beta' - \beta$

$= \Delta\beta_{L+} + \Delta\beta_{G+} + \Delta\beta_{L-} + \Delta\beta_{G-}$

Differentiation by abundance loss ($\Delta\beta_{L+}$)

Differentiation by abundance gain ($\Delta\beta_{G+}$)

Homogenization by abundance loss ($\Delta\beta_{L-}$)

Homogenization by abundance gain ($\Delta\beta_{G-}$)