Cheat Sheet : : **VEGAN**

What is VEGAN?

The **vegan** package provides tools for descriptive community ecology. It has basic functions of **community ordination**, **diversity analysis** and **dissimilarity analysis**. Most of its multivariate tools can be used for other data types as well.

Examples using : **data**(dune)

Unconstrained Ordination

metaMDS(data, …) `Nonmetric Multidimensional Scaling`

All ordination results can be displayed with

plot(data, type = "")

type = "p" results with points of black circles to indicate sites and red pluses to show species

type = "t" results with text
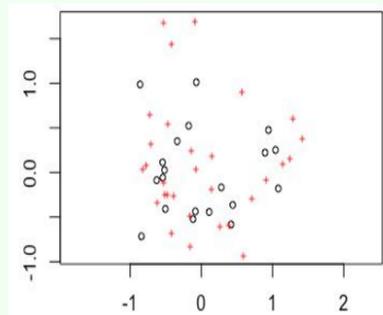
ordihull() adds convex hulls

ordiellipse() adds ellipses of standard deviation, standard error or confidence areas

ordispider() draws items to their center
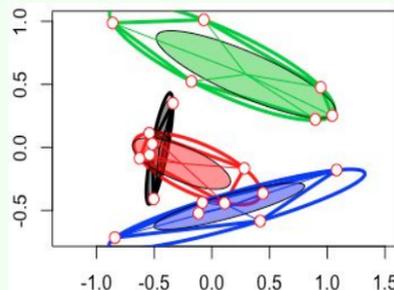
Constrained Ordination

cca(formula, data, …) `Constrained Correspondence Analysis Displays only the variation that can be explained by used constraints`

rda(formula, data, scale=FALSE, …) `Redundancy Analysis`

capscale(formula, data, distance = "", …) `Distance based Redundancy Analysis`

formula( ) Model formula must be either community data matrix or dissimilarity matrix

OR

distance = "name of dissimilarity index**"** if formula is not specified

Analysis of constraints

anova.cca(object, permutations = "", …) `Permutation Test for CCA & RDA to assess the significance of constraints`

object specifies one or several result objects from cca, rda, or capscale

permutations = control values, or permutation index

Diversity Analysis of Eco Communities

diversity(data, index = " ", MARGIN = 1, base = exp(1), …) `Shannon, Simpson, and Fisher diversity indices and species richness.`

renyi(data, scale = c(), raw = FALSE, …) `Rényi Diversity index`
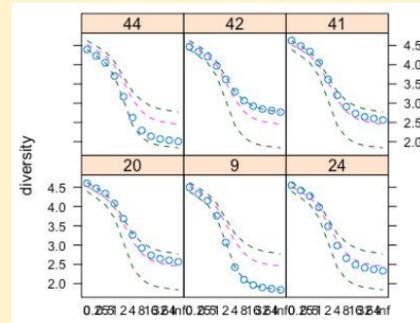
scale = c() Scales of Rényi diversity

raw = FALSE summary stats of permutations

raw = TRUE individual permutations

rarefy(data, sample, …) `Rarefied Species Richness results in expected species richness of subsample`

Taxonomic Diversity

taxondive(data, distance, match.force = FALSE) `Taxonomic diversity indices`

taxa2dist(data, varstep = FALSE, check = TRUE, …) `Converts class tables to taxonomic distances`

Ranked Abundance Distribution

radfit(data, …) `Fits the most popular model to data using maximum likelihood estimation`

rad.null(data, family = poisson) `Fits broken stick model to expected abundance of species`

type = "b" Plots both observed points and fitted lines

family = Error distribution; poisson default is used for counts, gaussian may be appropriate for abundance
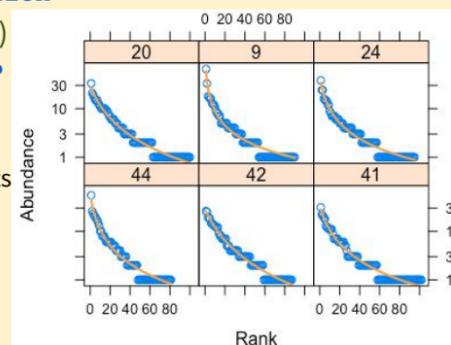
Beta Diversity

betadiver(data, method = NA, …) `Estimates beta diversity`

method = "" can specify which beta index to use (24 options)

betadiver(help=TRUE) list all 24 indices available

Analysis of Diversity in Groups

anosim(data**,** grouping, permutations = "", distance = " ", …) `Analysis of similarities between two or more groups`
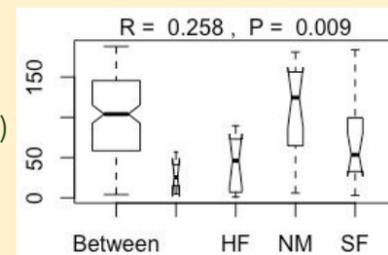
Dissimilarity Analysis

vegdist(data, method=" ", na.rm = FALSE, …) `Dissimilarity indices`

method = "dissimilarity index "
➤ "manhattan", "euclidean", "canberra", "clark", "bray", "kulczynski", "jaccard", "gower", "altGower", "morisita", "horn", "mountford", "raup", "binomial", "chao", "cao" or "mahalanobis".

Other Fun Features

vegemite(data, use, scale, sp.ind = "", site.ind = "", select , …) `Creates a compact ordered community tree in text format`
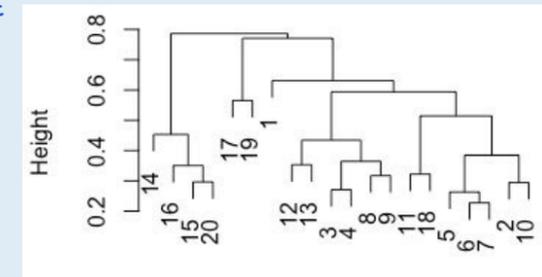
tabasco(data, use, sp.ind = "", site.ind = "", select, Rowv = TRUE, Colv = TRUE, scale, col = heat.colors(12), …) `Creates a community table using heat map, abundances are coded by color`

use is either a vector or object

sp.ind / site.ind species and site indices

select a subset of plots

**Rowv / Colv =** reorder rows and columns, if TRUE it is ordered by correspondence analysis
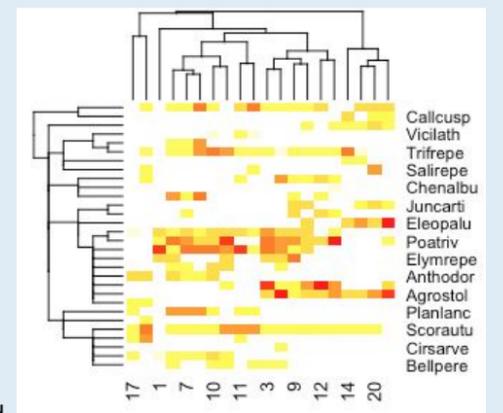
beals(data, species = NA, reference = data, include = TRUE) `Beals Smoothing and Degree of Absence Analysis determines probability of a species occurring in a site based on joint occurrences with other species`

species = NA will compute for all species, or can specify single

**reference =** data to be used to compare for joint analysis

include = TRUE to include target species in computations

VEGAN uses quantitative data but setting **binary = TRUE will make data presence/absence******