Cheat Sheet:: vegan

What is VFGAN?

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 = "")

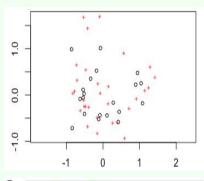
type = "p" results with points of black circles to indicate sites and red pluses to show species

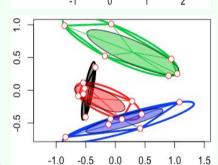
type = "t" results with text

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

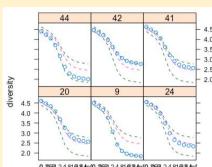
object specifies one or several result objects from cca, rda, or capscale

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

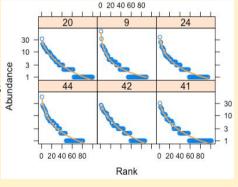
Ranked Abundance Distribution

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

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

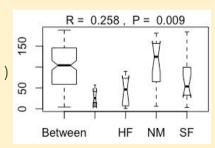
betadiver(data, method = NA, ...) Estimates beta diversity

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

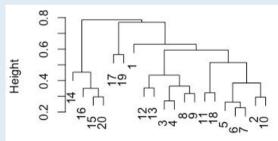
method = "dissimilarity index"

➤ "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,

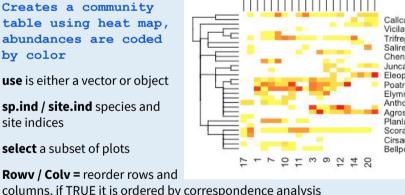
Colv = TRUE, scale, col = heat.colors(12), ...) Creates a community table using heat map, abundances are coded by color

use is either a vector or object

sp.ind / site.ind species and site indices

select a subset of plots

Rowy / Coly = reorder rows and



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