

# 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

**vegemit**(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\*\*