

Vegan unconstrained ordination functions (Shiny app)

I developed a simple [interactive online tool](#) visualizing the use of all unconstrained ordination methods in vegan package discussed on this website, using a set of example datasets ([why?](#)). Scroll down for a short manual [how to use the app](#).

Unconstrained ordination in vegan

Dataset:

simul1

[simul1](#) - simulated community data along one environmental gradient, very heterogeneous; plots: 500, species: 296, species data: presence-absence.

Ordination method:

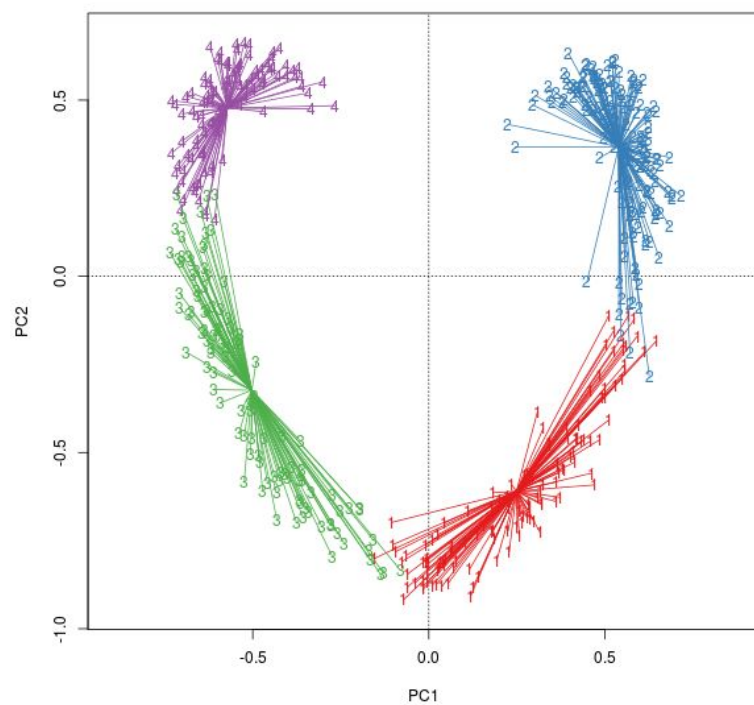
PCA CA DCA tb-PCA
 PCoA NMDS

Transformation of species data:

none sqrt log
 presence-absence

Display in ordination diagram:

species sites groups
 ordispider ordihull



```
# The R code which can be used to reproduce the ordination
library(vegan) # uploading vegan library

# Import of data from GitHub repository:
spe <- read.delim('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/data/simul1')
env <- read.delim('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/data/simul1')
groups <- env$groups

# Calculating ordination:
ordi <- rda(spe)
```

How to use the app

The app comes with two parts: clickable input (where you can choose dataset, ordination method, transformation etc.), and then the output (ordination diagram, reproducible R code and numerical output of analysis). At this screen, the input is above the output; if you open the app in the new window, the input is at the right and the output is in the main panel).

Input

Datasets

Currently five example community datasets are provided. Vltava is rather heterogeneous forest vegetation dataset (sample across wide range of habitat conditions and forest types on the slopes of deep Vltava river valley). Grasslands is rather homogeneous grassland vegetation dataset representing narrow range of habitat conditions (acidophilous grasslands on shallow soils). Simul* datasets were generated artificially using simulation model, in which species response to one (simul1) or two (simul.short and simul.long) environmental gradients. Simul1 is the most heterogeneous dataset, structured by only a single “environmental” gradient, and is good to inspect the shape of artifacts it can produce in various ordination methods. Simul.short and simul.long are structured by two uncorrelated gradients (with gradient2 being shorter than gradient1); simul.short represents relatively homogeneous community (both gradients are rather short), while simul.long is highly heterogeneous.

Below the drop-down menu for selecting the dataset, the brief description together with the link to detailed online description appears. Click through to see what the dataset represents, and what is the meaning of groups and environmental variables (these appear in the ordination diagram if selected in the menu “Display in ordination diagram”).

Ordination method:

Set of ordination methods is provided: PCA (linear method), CA and DCA (unimodal methods), tb-PCA (transformation-based PCA, with pre-transformation of species data by either Hellinger or chord distance sensu Legendre & Gallagher 2001), and PCoA with NMDS (distance-based methods, with several choices of distance coefficient). When tb-PCA is selected, another menu (Pre-transformation of data for tb-PCA) appears below, in which one may select the pre-transformation method for the compositional data. When PCoA or NMDS are selected, Distance index for PCoA menu will appear, offering several distance indices which are first applied on compositional data before PCoA or NMDS are calculated.

Transformation of species data:

Some datasets may need to transform the data; e.g. vltava and grasslands contains percentage species estimations with strongly right-skewed distribution and species with high cover will have too high influence in the analysis. Transformation of species data is a way how to reduce this effect.

Display in ordination diagram

Choose items to be displayed in the ordination diagram. *Groups* refer to classification of samples into several clusters (the method of classification differs among datasets, e.g. cluster analysis in case of vltava dataset, or manual classification into vegetation associations in case of grasslands dataset). *Ordispider* and *ordihull* are yet other methods how to visualize groups of samples. *Envfit* fits selected environmental variables onto ordination diagram using multiple regression; you can choose between displaying all environmental variables or just those which are significant (the significance here is

considered without correcting for multiple testing issue). Numerical results of envfit could be checked at the bottom window in the main panel.

Output

Contains ordination diagram and R output (set of functions which can be used to draw the diagram). Below the box with R functions is result of ordination (object "ordi"), and in case that "envfit" option was selected in "Display in ordination diagram" option, another box reporting the results of environmental variables fitting will appear.

Note one difference: the color palette in the application is modified (it is not using the standard colors, but colors from palette "Set1" in "RColorBrewer"). This is why the ordination diagram reproduced by the provided R script will appear in different colors.

Known bugs

- None reported right now (but there will be some for sure)

From:

<https://www.davidzeleny.net/anadat-r/> - **Analysis of community ecology data in R**

Permanent link:

<https://www.davidzeleny.net/anadat-r/doku.php/en:uncordi>

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