Details

Fix Me! (this is an old ordijuice version)

For quick exploratory analysis of vegetation data, JUICE can handle three basic methods of unconstrained ordination analysis - Detrended Correspondence Analysis (DCA), Principal Component Analysis (PCA) and Non-metric Multidimensional Scaling (NMDS). Calculations and drawing of the ordination diagrams are run in the environment of R software, using package vegan written by Oksanen et al. (2008).

JUICE offers following options:

- two and three dimensional ordination diagrams with sites and/or species (as points or labels),
- projection of Ellenberg indicator values (if available and initialized) as vectors,
- projection of factor stored in 'Short header' as a vector or surface (using GAM smoother function),
- projection of selected header data as vectors or factors,
- separation of relevé groups in ordination diagram using envelopes and spider plots,
- various options of species data transformation,
- various formats of figure export files.

Short overview of unconstrained ordination methods available in JUICE:

DCA (Detrended Correspondence Analysis) - definitely the most popular and also the most problematic unconstrained ordination method used in vegetation ecology. It has been introduced as an improvement of classical Correspondence Analysis (CA) method and its algorithm contains two problematic moments - detrending and rescaling of axes. Some scientists like DCA for its ecologically meaningful results; others hate it for somehow unclear and twisted nature. For more technical details about this function, see help page of function decorana implemented in vegan package. Default setting of DCA as used in JUICE are: detrending by segments, without any standardization or centering.

PCA (Principal Component Analysis) - linear ordination method, assuming linear species response to environment. One of well known artifacts of this method is horseshoe effect, similar to arch effect in CA and occurring in case of unimodal response of species along gradient. As PCA doesn't contain detrending and rescaling, this method could be satisfactory alternative to DCA in case you have data from vegetation on rather short environmental gradient. Default setting of PCA as used in JUICE: no standardization, no centering.

NMDS (Non-metric dimensional scaling) - is a non-metric method of ordination. It is using different strategy for ordination from metric methods (DCA, PCA etc.) - it analyzes the matrix of dissimilarities between samples and tries to find configuration of these samples in k-dimensional ordination space, so as distances between samples in this ordination space correspond as much as possible to dissimilarities between samples. Interpretation of resulting diagram is less intuitive than those of metric ordination methods, but according some studies (e.g. Minchin 1987) is NMDS considered to be most robust unconstrained ordination methods used in vegetation ecology. Various dissimilarity measure indexes can be used. Method implemented in R package vegan represents sophisticated combination of several algorithms, including search for the stable solution from random starts, axis scaling and projection of species scores into ordination diagram. For more technical details about used computation algorithm, see vegan help tutorial, section Details. Default setting of NMDS in JUICE is: dissimilarity measure - Bray-Curtis, k=2 dimensions, no random starts (it was too time demanding), axis scaling and orientation of main gradient axis in data using principal component analysis.