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Unconstrained ordination

Distance-based ordination methods (PCoA & NMDS)

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R functions

- **capscale** (library vegan) - without environmental variables, the function calculates PCoA, while with environmental variables it calculates distance-based RDA. Input could be either species composition matrix (samples x species) or distance matrix (in that case, the species scores will not be available, unless the original species composition matrix is provided as argument comm). By default distance = "euclidean", which returns results identical to PCA. Note that even if no environmental variables are included, the formula structure is still required (e.g. capscale (spe ~ 1, distance = 'bray')).
- **cmdscale** (basic library stats) - calculates PCoA on matrix of distances among samples (this could be calculated e.g. by function vegdist from library vegan). Use function ordiplot to project the ordination diagram.
- **wcmdscale** (library vegan) - based on cmdscale function, but allows to weight the importance of samples in the PCoA. If arguments eig = TRUE or x.ret = TRUE, the function returns an object of class "wcmdscale" with print, plot, scores, eigenvals and stressplot methods.
- **pcoa** (library ape) - another way how to achieve PCoA analysis. Use biplot.pcoa function (or simply generic biplot) to project ordination diagram. Does not work with vegan's functions ordiplot or scores.
- **metaMDS** (library vegan) - rather advanced function, composed of many subroutine steps. See example below for details.
- **stressplot** (library vegan) - draws Shepards stress plot, which is the relationship between real distances between samples in resulting *m* dimensional ordination solution, and their particular compositional dissimilarities expressed by selected dissimilarity measure.
- **goodness** (library vegan) - returns goodness-of-fit of particular samples. See example how can be this result visualized (inspired by Borcard et al. 2011).