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Section: [Ordination analysis](#)

## PCoA & NMDS (distance-based unconstrained ordination)

Theory **R functions** Examples Exercise 

### 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 Shepard's 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](#)).

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

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