Section: Ordination analysis

Explained variation and Monte Carlo permutation test (constrained ordination)

Theory R functions Examples **Exercise** 🔒

Exercise 1

Use vegetation data from an experimental study on wet meadow, which tried to answer the question how are abundance and species composition of seedlings of herb species on wet meadow influenced by experimental removal of dominant clonal plant species (*Nardus stricta*), plant litter (remnants of plant biomass from the previous season in case that the meadow was not mown) and removal of litter+mosses (by raking). Before analysis, please get familiar with the data you will be using. Data are from completely randomized block design with four blocks, each with four plots (one per treatment, including control). The block design will need to be taken into consideration when testing the significance of explained variation using Monte Carlo permutation test.

1. Import datasets `seedlings.spe` and `seedlings.env` - the first containing species composition of seedlings per plot, the second contain an assignment of the plot to the block and experimental treatment.
2. First, calculate DCA on compositional data (no transformation) to decide whether to use linear (RDA) or unimodal (CCA) constrained ordination method.
3. According to the result of the previous analysis, use either RDA or CCA, where you will explain the species composition by treatment. Since the experiment design is a block design (each block contains one replication of each treatment), you need to specify the variable `seedlings.env$blocks` as a covariable in the model (the vegetation within individual blocks may slightly differ because the experimental site (meadow) is not perfectly homogeneous, but for us, this variation is not relevant - we are not interested in it, so we will remove it as covariable).
4. Draw the resulting ordination diagram.
5. Test the significance of the variation explained by treatment (use model-based permutation test).
6. Test the significance of individual ordination axes. Which of them is the most important, and to which level of the treatment it corresponds?

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1. `read.delim`;
2. check the length of the first axis in `decorana` results. If over 4, use CCA, if less then 3, use RDA, 3-4 -both are fine;
3. the formula will look like this: `seedlings.spe ~ treatment + Condition (block), data = seedlings.env`;
4. `ordiplot`
5. `anova` without any other arguments; since the `blocks` are defined as covariable, the function will test the significance of variation after removal of their variation;
6. `anova` with argument `by = "axis"`.

Solution

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:expl_var_exercise

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