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Exercise 1

(This exercise is based on *Case study 4* from Šmilauer & Lepš 2014, and the coding was partly inspired by the [blog post of Gavin Simpson](#), analysing this data - I recommend it for checking on more details.)

Use vegetation data from an [experimental study on wet meadow](#), which tried to answer the question how is 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 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 previous analysis, use either RDA or CCA, where you will explain the species composition by treatment. Since the experiment design is a block design, you need to specify the variable `seedlings.env$blocks` as covariable in the model.
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?

```
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, he will test the significance of variation after removal of their variation;  
6. anova with argument by = "axis".
```

[Solution](#)

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

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