Analyses of species distributions in peatlands

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Contents

Load the R packages that you will use

If you do not have the R packages installed, you need to install them.

```
library(tidyverse)
library(readxl)
library(knitr)
library(ggeffects)
library(car)
library(glmmTMB)
library(ggplot2)
library(BiodiversityR)
library(vegan)
```

Data preparation

Read data from Excel file

Note that you need to change the path to the folder where you have the Excel file

```
data_peat<-read_excel("data/raw/Modelling_SDM_species_data_Updated.xlsx",
                      sheet="Sheet1")
data_peat<-data_peat[1:29] # This is to remove some columns that we do not need!
```

Have a look at the data

This shows the first rows of your data file in "tibble" format. You can also see the variable type for each variable (double or character).

```
data_peat
```

```
## # A tibble: 115 x 29
##    n_samples depth depth_corrected fen   tot_Sphagnum  Erio Carex Erica
##        <dbl> <chr>           <dbl> <chr>        <dbl> <dbl> <dbl> <dbl>
##  1         1 0                   0 N              100     0     0     0
##  2         2 14-15              14 N               87     3     2     8
##  3         3 20-21              20 N               74     6     6    14
##  4         4 30-31              30 N               87     5     4     4
##  5         5 40-41              40 N               90     2     3     5
##  6         6 50-51              50 N               41    46     9     4
##  7         7 55-56              55 N               74    19     6     1
##  8         8 60-61              60 N               94     4     1     1
##  9         9 65-66              65 N               95     3     1     1
## 10        10 70-71              70 N               90     3     4     3
##    other_veg Balticum Medium Cuspidata Austinii Fuscum Rubellum Acutifolia
##        <dbl>    <dbl>  <dbl>     <dbl>    <dbl>  <dbl>    <dbl>      <dbl>
##  1         0    0.32  0.68      0             0      0    0         0
##  2         0    0.724 0.253     0.0230        0      0    0         0
##  3         0    0.324 0.649     0             0      0    0         0.0270
##  4         0    0.264 0.276     0             0      0    0.368     0.0920
##  5         0    0.189 0.0556    0.0333        0      0    0         0.722
##  6         0    0.171 0.415     0.220         0      0    0.195     0
##  7         0    0.568 0.216     0.216         0      0    0         0
##  8         0    0.489 0.383     0.128         0      0    0         0
##  9         0    0.589 0.263     0.147         0      0    0         0
## 10         0    0.544 0.111     0.344         0      0    0         0
##    'Diseased Acutifolia' Angustifolium Tenellum Papillosum Fallax Stems   age
##                    <dbl>         <dbl>    <dbl>      <dbl>  <dbl> <dbl> <dbl>
##  1                     0             0        0          0      0     0     0
##  2                     0             0        0          0      0     0    75
##  3                     0             0        0          0      0     0   136
##  4                     0             0        0          0      0     0   244
##  5                     0             0        0          0      0     0   352
##  6                     0             0        0          0      0     0   452
##  7                     0             0        0          0      0     0   505
##  8                     0             0        0          0      0     0   555
##  9                     0             0        0          0      0     0   606
## 10                     0             0        0          0      0     0   643
##     temp imp_temp moist nutrient  fire   dry
##    <dbl>    <dbl> <chr>    <dbl> <dbl> <dbl>
##  1  6.35        0 NA           0     0     0
##  2  6.92        1 NA           0     0     0
##  3  7.39        1 NA           0     0     0
##  4  8.21        0 NA           0     0     0
##  5  8.00        1 -0.38        1     0     0
##  6  7.81        1 -0.3         1     0     0
##  7  7.71        1 0.01         1     0     0
##  8  7.62        1 -0.26        1     0     0
```

```
##  9  7.52        1 0.22         1     0     0
## 10  7.45        1 -0.25        1     0     0
## # i 105 more rows
```

Convert some variables to factors

It is better to convert some variables (those that are Y/N or 0/1) to factors.

```
data_peat<-data_peat%>%
  mutate(fen=as.factor(fen),imp_temp=as.factor(imp_temp),
         nutrient=as.factor(nutrient),fire=as.factor(fire),dry=as.factor(dry))
# with mutate you create new variables that are equal to the old variables
# but are coded as factors
```

Convert moist to numeric

For some reason, moist appears as a character variable. It should be numeric, so we convert it.

```
data_peat<-data_peat%>%
  mutate(moist=as.numeric(moist))
```

Ordinations (vegan package)

Suggested reading: https://www.davidzeleny.net/anadat-r/doku.php/en:ordination

(lots of info on this webpage!)

Chapter 10 in this pdf: https://apps.worldagroforestry.org/downloads/Publications/PDFS/b13695.pdf

Using the vegan package.

I performed some ordinations with Sphagnum species. I tried different methods, but if I would need to choose one, I would do a constrained ordination, specifically a Distance-based redundancy analysis (db-RDA) with Bray-Curtis distance. You can read about all types in the webpage above if you feel like it.

Data for ordination:

```
data_ordi2<-data_peat %>%
  filter_at(vars(Balticum:Fallax),
            all_vars(!is.na(.)))%>% # Remove rows with all NAs
  filter_at(vars(Balticum:Fallax),
            any_vars(.>0))%>% # Remove rows with all zeros - WHY?
  filter(!is.na(age)&!is.na(temp)&!is.na(moist)&!is.na(nutrient)&!is.na(fire)&
           !is.na(dry))%>%
  rename(Diseased_Acutifolia=`Diseased Acutifolia`) #Rename to avoid problems
```

Distance-based redundancy analysis (db-RDA) with Bray-Curtis distance.

See https://www.davidzeleny.net/anadat-r/doku.php/en:similarity for info on distances.

Calculate ordination:

```
ordi6<-capscale(data_ordi2[10:21]~ # species data matrix
             age+temp+moist+nutrient+fire+dry, # Environmental variables
             data = data_ordi2, distance="bray") # Bray-Curtis distance
```

Result of the ordination:

```
ordi6
```

```
## Call: capscale(formula = data_ordi2[10:21] ~ age + temp + moist +
## nutrient + fire + dry, data = data_ordi2, distance = "bray")
##
##               Inertia Proportion Rank
## Total         31.0246     1.0000
## Constrained    8.3892     0.2704    6
## Unconstrained 26.3948     0.8508   34
## Imaginary     -3.7594    -0.1212   38
## Inertia is squared Bray distance
## Species scores projected from '[' 'data_ordi2' '10:21'
##
## Eigenvalues for constrained axes:
##  CAP1  CAP2  CAP3  CAP4  CAP5  CAP6
## 4.886 2.239 0.760 0.276 0.138 0.090
##
## Eigenvalues for unconstrained axes:
##  MDS1  MDS2  MDS3  MDS4  MDS5  MDS6  MDS7  MDS8
## 7.438 4.231 3.328 2.484 2.345 2.009 1.230 0.598
## (Showing 8 of 34 unconstrained eigenvalues)
```

"Intertia" is the total variance - your environmental variables explain 0.2704 of this variance ("constrained" part).

Proportion explained by each ordination axis. CAP1-CAP6 are the "constrained" axes, explained by your environmental variables. MDS1-MDS34 are the "unconstrained" axes.

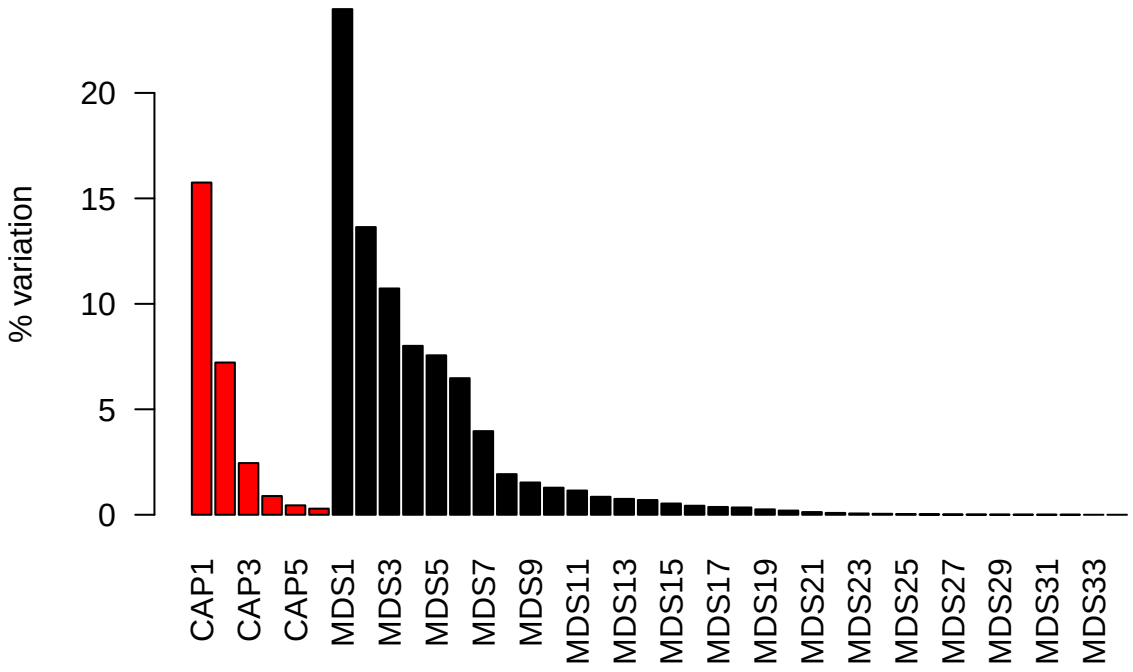
```
eigenvals(ordi6) %>%
  summary()
```

```
## Importance of components:
##                           CAP1    CAP2    CAP3     CAP4     CAP5     CAP6   MDS1
## Eigenvalue            4.8863 2.23908 0.76030 0.275526 0.138265 0.089651 7.4376
## Proportion Explained  0.1405 0.06437 0.02186 0.007921 0.003975 0.002577 0.2138
## Cumulative Proportion 0.1405 0.20485 0.22671 0.234627 0.238602 0.241179 0.4550
##                           MDS2    MDS3    MDS4    MDS5    MDS6    MDS7    MDS8
## Eigenvalue            4.2314 3.32835 2.48447 2.34511 2.00855 1.23007 0.59751
## Proportion Explained  0.1216 0.09569 0.07143 0.06742 0.05774 0.03536 0.01718
## Cumulative Proportion 0.5766 0.67234 0.74376 0.81118 0.86892 0.90429 0.92147
##                           MDS9   MDS10   MDS11    MDS12    MDS13    MDS14
## Eigenvalue            0.47443 0.39821 0.35601 0.264468 0.233343 0.216337
## Proportion Explained  0.01364 0.01145 0.01023 0.007603 0.006708 0.006219
## Cumulative Proportion 0.93510 0.94655 0.95679 0.964391 0.971099 0.977319
##                          MDS15    MDS16    MDS17   MDS18    MDS19    MDS20
## Eigenvalue            0.165074 0.132727 0.114648 0.10713 0.079384 0.061005
```

```
## Proportion Explained  0.004746 0.003816 0.003296 0.00308 0.002282 0.001754
## Cumulative Proportion 0.982065 0.985880 0.989176 0.99226 0.994538 0.996292
##                          MDS21     MDS22     MDS23     MDS24     MDS25
## Eigenvalue            0.039707 0.0272079 0.0186386 0.0140238 0.0100911
## Proportion Explained  0.001142 0.0007822 0.0005358 0.0004032 0.0002901
## Cumulative Proportion 0.997434 0.9982159 0.9987517 0.9991549 0.9994450
##                          MDS26     MDS27     MDS28     MDS29     MDS30
## Eigenvalue            0.0072677 0.0045643 3.108e-03 1.815e-03 1.313e-03
## Proportion Explained  0.0002089 0.0001312 8.935e-05 5.217e-05 3.774e-05
## Cumulative Proportion 0.9996539 0.9997851 9.999e-01 9.999e-01 1.000e+00
##                          MDS31     MDS32     MDS33     MDS34
## Eigenvalue            7.435e-04 4.026e-04 9.116e-05 9.039e-07
## Proportion Explained  2.138e-05 1.157e-05 2.621e-06 2.599e-08
## Cumulative Proportion 1.000e+00 1.000e+00 1.000e+00 1.000e+00
```

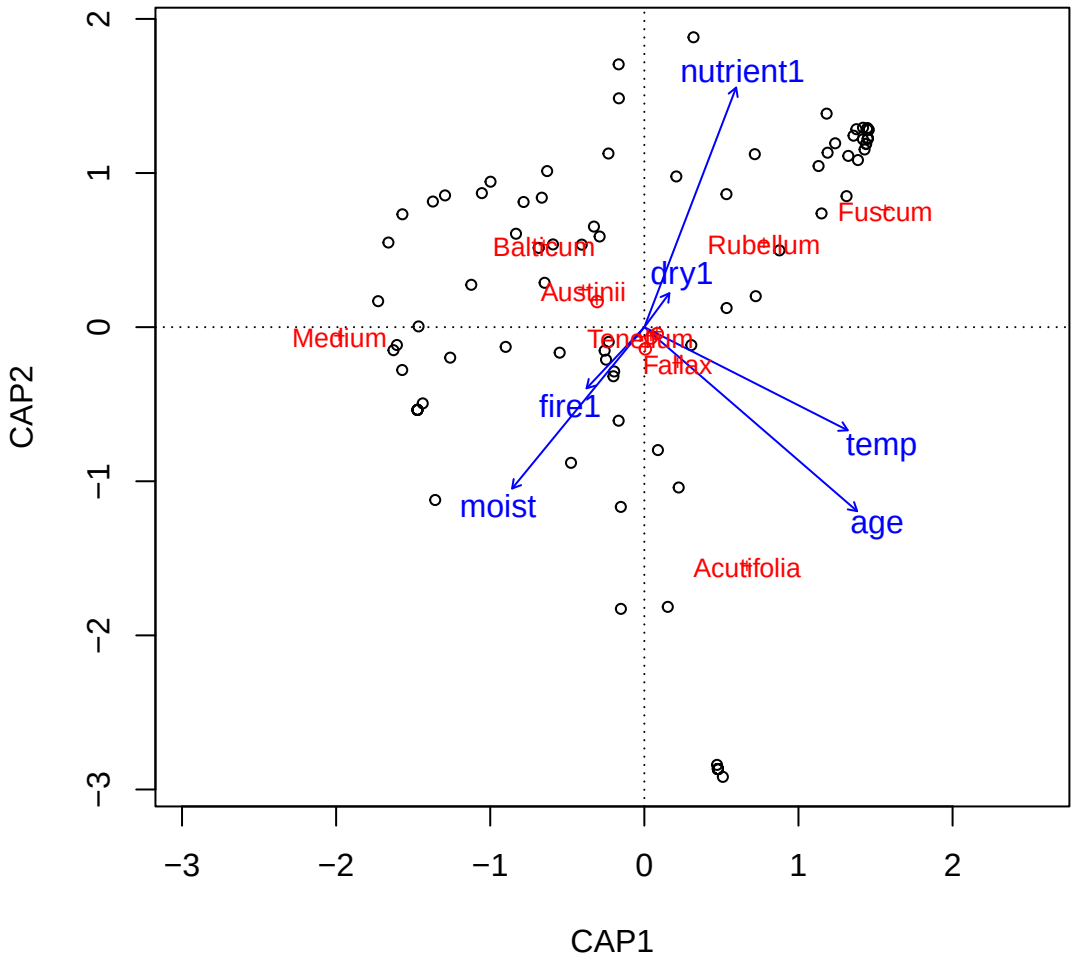
Barplot of percentage variance explained by individual axes

```
expl_var_ordi6 <- c(ordi6$CCA$eig/ordi6$tot.chi*100,
                    ordi6$CA$eig/ordi6$tot.chi*100)
barplot (expl_var_ordi6, col = c(rep ('red',
                                      length (ordi6$CCA$eig/ordi6$tot.chi*100)),
                                 rep ('black',
                                      length (ordi6$CA$eig/ordi6$tot.chi*100))),
         las = 2, ylab = '% variation')
```



Plot of the ordination (species in red and sites-samples in black):

```
vegan::ordiplot(ordi6,display = c('species', 'sites', 'bp'))
orditorp(ordi6,display="species",cex=0.8,col="red")
```



This shows the two first constrained axes of the ordination. You can see how the sites and species distribute along these axes.

Test significance of the ordination with Monte Carlo permutation test.

For the whole model:

```
anova (ordi6, permutations = 999)
```

```
## Permutation test for capscale under reduced model
## Permutation: free
## Number of permutations: 999
##
## Model: capscale(formula = data_ordi2[10:21] ~ age + temp + moist + nutrient + fire + dry, data = data
```

```
##          Df SumOfSqs      F Pr(>F)
## Model     6   8.3892 4.2378  0.001 ***
## Residual 80  26.3948
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The model is significant.

For each explanatory variable (with all the others used as covariables, independently from their order in the model):

```
anova (ordi6, by = 'margin', permutations = 999)
```

```
## Permutation test for capscale under reduced model
## Marginal effects of terms
## Permutation: free
## Number of permutations: 999
##
## Model: capscale(formula = data_ordi2[10:21] ~ age + temp + moist + nutrient + fire + dry, data = data
##          Df SumOfSqs      F Pr(>F)
## age       1   1.2989 3.9369  0.002 **
## temp      1   0.3226 0.9778  0.411
## moist     1   0.8304 2.5168  0.024 *
## nutrient  1   1.1292 3.4226  0.005 **
## fire      1   0.1146 0.3472  0.948
## dry       1   0.8159 2.4728  0.025 *
## Residual 80  26.3948
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Age, moist, nutrient and dry show significant effects.

For each axis:

```
anova (ordi6, by = 'axis', permutations = 999)
```

```
## Permutation test for capscale under reduced model
## Forward tests for axes
## Permutation: free
## Number of permutations: 999
##
## Model: capscale(formula = data_ordi2[10:21] ~ age + temp + moist + nutrient + fire + dry, data = data
##          Df SumOfSqs       F Pr(>F)
## CAP1      1   4.8863 14.8100  0.001 ***
## CAP2      1   2.2391  6.7864  0.002 **
## CAP3      1   0.7603  2.3044  0.315
## CAP4      1   0.2755  0.8351  0.972
## CAP5      1   0.1383  0.4191  0.997
## CAP6      1   0.0897  0.2717  0.989
## Residual 80  26.3948
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Axis 1 and 2 are significant.

Ordination plot with ggplot2.

Install ggord package (you only need to do this once):

```
# Enable the r-universe repo
options(repos = c(
    fawda123 = 'https://fawda123.r-universe.dev',
    CRAN = 'https://cloud.r-project.org'))

# Install ggord
install.packages('ggord')
```

```
## package 'ggord' successfully unpacked and MD5 sums checked
##
## The downloaded binary packages are in
##  C:\Users\alici\AppData\Local\Temp\RtmpMTfBdL\downloaded_packages
```

Load ggord package:

```
library(ggord)
```

```
ggord(ordi6,ptslab=T,repel=T,labcol="red",veccol="red",size=NA,addsize=3,
      xlims=c(-1.1,1.1),ylims=c(-1.1,1.1))+
  geom_point(size=3,shape=20,color="black",alpha=0.2)
```