

Group 1. plant traits

Aurele Toussaint (aurele.toussaint@cnrs.fr)

Autumn 2024

Contents

```
## step 1. load the data.
library(readxl)
data_plant <- read_excel("data_plant.xlsx", sheet = "TRAITdata")

## step 2. data exploration
# Here we use common R function to explore the files
# Getting some statistics
ncol(data_plant) # number of columns
nrow(data_plant) # ... rows
dim(data_plant)  # dimensions
names(data_plant) # names of columns (colnames works as well)
row.names(data_plant) # if there are row names
str(data_plant)
head(data_plant) # just upper rows
summary(data_plant) # short summary of each variable

# it is possible to make graphics too
hist(data_plant$LDMCstd)

## We can do the same for community environmental data
## HERE ITS JUST AN OVERVIEW, Feel free to add/remove/update with your favorite functions

## Step 2: set a problematic

## Step 3. Design analyses
library(funspace)
# Community plot
comm = matrix(0, nrow = length(unique(data_plant$Plot)), ncol = length(unique(data_plant$Species)),
              dimnames = list(unique(data_plant$Plot), unique(data_plant$Species)))

envirVar = c("ET(mm)", "Rad(w/m2)", "Tc", "ele(m)", "precip(mm)", "rain", "temp")
envir = matrix(0, nrow = length(unique(data_plant$Plot)), ncol = length(envirVar),
              dimnames = list(unique(data_plant$Plot), envirVar))
for(i in rownames(comm)){
  comm[i, unique(data_plant[which(data_plant$Plot == i),]$Species)] = 1

  envir[i,] = as.matrix(data_plant[which(data_plant$Plot == i), envirVar][1,])
}
```

```

envir = as.data.frame(envir)
## species richness in each comm
SR = apply(comm,1,sum)

# traits
traitSelected = c("LDMCstd","AREAst","SLAst","Ldensstd","height(m)","Wdensity","seedmass(g)","%N","%C")
trait = data_plant[, c("Species", traitSelected)]
# We can average the values per species
traitMean = matrix(0, ncol = ncol(trait)-1, nrow = length(unique(data_plant$Species)),
                    dimnames = list(unique(data_plant$Species), colnames(trait)[-1]))
for(i in unique(trait$Species)){
  traitMean[i,] = apply(trait[which(trait$Species %in% i),-1],2,mean,na.rm=T)
}

logscale.traits = scale(log10(traitMean[,!colnames(traitMean)%in%c("Wdensity","seedmass(g)")]+1))
table(is.na(logscale.traits)) # there are no NA

# Run PCA
pca.trait = princomp(logscale.traits, cor = TRUE)
# Building the functional trait space (using the first two PCs)
trait_space_global = funspace(x = pca.trait, PCs = c(1, 2), n_divisions = 300)
plot(x = trait_space_global, type = "global", quant.plot = TRUE, arrows = TRUE, arrows.length = 0.5)

library(FD)
resFunDivIndex = dbFD(pca.trait$scores[, c(1, 2)], comm)

## NULL MODEL

## plots
plot(resFunDivIndex$nbsp,resFunDivIndex$FRic)

## environmental variable
resCWM = functcomp(logscale.traits, comm, CWM.type = "all")

boxplot(resCWM$LDMCstd~envir$rain)
plot(resCWM$LDMCstd~envir$`precip(mm)`)

#

```