R Project Part 2

Make an R notebook to reproduce the analyses for the Community Ecology analyses on the grassland data in the links.

(1) In addition to the analysis changes below, look up the purpose of all the analyses and use the R notebook markup language to explain the purpose of each analysis and the meaning of each result to the best of your ability. NMDS, Ordiplot, Adonis…etc.

(2) You may have to change some tests (e.g., t-test).

(3) RENAME your notebook, *__YourLastName__RProjectPt2__* and load the finished project to Canvas.

(4) *Let me repeat that*: TURN IN THE ".Rmd" FILE, the text file itself. Not a pdf or anything else.

NOTE: You will have to read in multiple files from the grassland dataset for this exercise. To do so, you can use paths to the grassland folder like this:
comm <- read.csv("grassland_data/grassland.community.csv", header = TRUE, row.names = 1)
I will have this folder on my drive to test your code. Each dataset only needs to be read in once to a dataframe.
Do the same for the other files in the folder and DO NOT CHANGE THE NAMES OF THE FILES.
Otherwise I will have to change all your code and I do not want to have to do that.
**Do NOT USE read.table(file.choose()) – Use the filenames. If you use this function, I will have to find the files every single time I run this function and this is highly annoying.

Instructions
Follow the protocol of this workshop/tutorial in the link with one major change (see below):
http://kembellab.ca/r-workshop/biodivR/SK_Biodiversity_R.html

The data for the tutorial can be found here:

http://kembellab.ca/r-workshop/

Instead of examining the effect of habitat (metadata$habitat) do an analysis of rel.moisture (metadata$rel.moisture). All the code that examine habitat should be changed to examine rel.moisture

For example,
boxplot(specnumber(comm) ~ metadata$habitat, ylab = "# of species")
should be:
boxplot(specnumber(comm) ~ metadata$rel.moisture, ylab = "# of species")
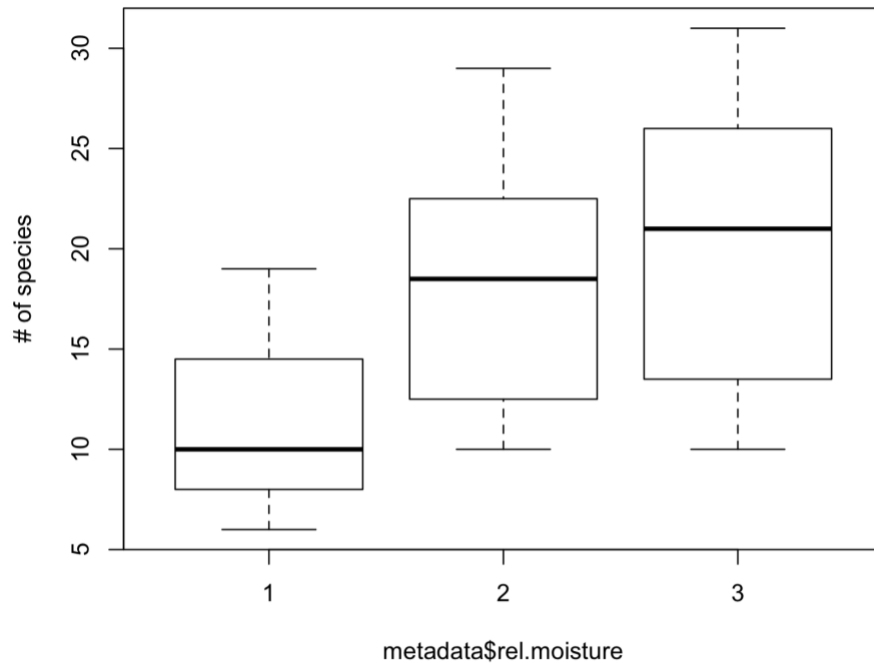
NOTE:
If you are having trouble installing the picante code try the code below. I had to use the this because it would not connect to the CRAN mirror for some reason:

install.packages('picante', dependencies=TRUE, repos='http://cran.rstudio.com/')