

Scientific Computing :: Drop In

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Session: 10

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Activity: R Coding

Internal loops

The following `for` loop is used to assign different colours to different species for plotting colour maps of spatial species distribution:

```
1 myData$colour <- NA # initialisation
2 for (i in 1 : length(myData$Species)) {
3   if(myData$Species[i] == 1)
4     myData$colour[i] <- c("blue")
5   else if (myData$Species[i] == 2)
6     myData$colour[i] <- c("green")
7   else
8     myData$colour[i] <- c("orange")
9 }
```

Read the code and try to understand what happens in the `for` loop. The small example data set `Plot1.txt` can be downloaded from <https://github.com/apommerening/Session10>. The ASCII file has 101 observations relating to the data of research plot 1 in Lligwy Woods on the Isle of Anglesey in North Wales. The data are from a natural woodland of ash (*Fraxinus excelsior* L.) and sycamore (*Acer pseudoplatanus* L.), where I studied the question of species alternation.

Your task is to write an R script avoiding **for** loops by using so-called internal loops and conditional assignments.

References

Pommerening, A., Zhao, Z. and Grabarnik, P., 2018. Considering allometric relationships in the analysis of spatial tree patterns. *Russian Journal of Ecosystem Ecology* 3, DOI 10.21685/2500-0578-2018-2-1 (available on www.pommerening.org).