

R course exercises Kiefer/Schmidt WS 2021/22 part 3

Phylogenetic Reconstruction

Exercise 1 (optional):

Use the functions of `seqinr` to download matk-sequences from the genus *Isaris*. Write a fasta-file saved in your working directory. Use `readDNAStringSet()` to read in the data as a DNA stringset.

Use `muscle` to generate a multi-alignment. Transform the alignment into DNABin by using `DNABin()`.

Generate a distance matrix using `dist.dna()`. Generate a NJ-tree and plot it accordingly.

Exercise 2:

Use `phyDat()` and `optim.parsimony()` to calculate a parsimonious tree. Use the NJ-tree from exercise 1 as a starting tree.

User defined functions

Exercise 3:

Write a function in R to add a given value to every n-th element of a numeric vector. The output of the function should be (1) the original vector, (2) the values of n used for multiplication, and (3) the new vector. In case (1) is not a vector an error message should be shown.

Exercise 4:

Write a function in R that deletes a certain word out of a longer character string. The function should take (1) the original longer string and (b) the word to be deleted as an input and output the new string.

Exercise 5:

Write a function in R that takes two strings as an input, e.g. X and O, and a numeric length of the edges and outputs a matrix that looks as follows:

```
XXXX
XOOX
XOOX
XXXX
```

GIS

Exercise 6:

Write an R-function that downloads distribution data from GBIF and plots it on a basic world wide map. The function should take the search term as an argument. Restrict the number of downloaded entries to a maximum of 1000.

Exercise 7:

Plot the distribution of *Isatis tinctoria* on a map of Germany, Switzerland and Austria. Apply the functions `map()` and `points()`. (The outputs of both functions need to be connected with a +)!