

Exploring Niches on Phylogenies Practical

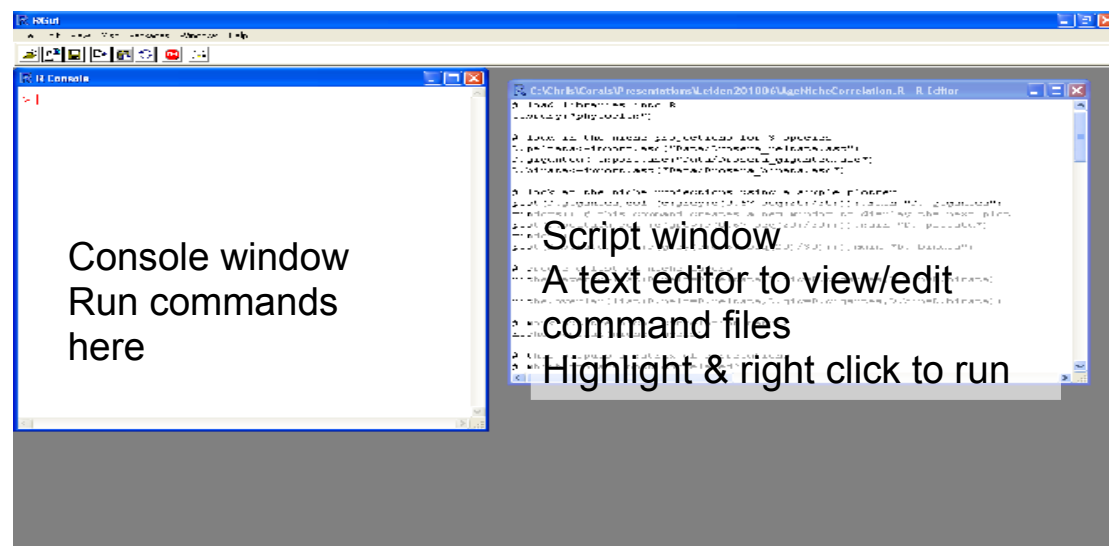


R is a free software environment for statistical computing and graphics (<http://www.r-project.org/>). R is primarily a command driven environment, and we will be using command scripts to run our analyses. R has multiple package libraries, developed by many different people for particular applications. We require the phylogenetics package “ape”, the niche modelling package “adehabitat” and the phyloclimatic modelling package “phyloclim”. R packages can be installed using the `install.packages` command. Type the following commands into an R console window to install these packages.

```
install.packages(c("phyloclim", "ape", "adehabitat",
"SDMTtools"))
```

A quick note on using R

This is not a tutorial about R, but we are doing some examples with R. When you open R you will see a command window, you can type instructions here to run analyses. Generally it is a good idea to store your commands in a text file (called a script file and given a .R extension). Use File-Open to open script files. This creates a script window (essentially just a text editor). Run lines of code by right-clicking then and selecting run-line-section. You must run each line in order as later commands may depend on earlier ones. Any line starting with # is a comment, please read the comments as they describe what is going on. **To run the example script files you must set the current directory to the folder with our test files. Use File-Change dir and select the directory with the R scripts.**



The practicals using R will involve opening script files and running one line at a time. Data can be downloaded from via the link to the phyloclimatic modelling workshop at <http://www.zsl.org/chrisyesson/>. For this practical you will need `PhyloclimaticModellingPracticalData.zip`

Niche comparison

Given 2 or more niches we can compare their projected surfaces by performing a correlation analysis. Remember to use File-Change dir and select the data directory "PCMDData"

In R open the file NicheCorrelation.R and run the following lines one step at a time.

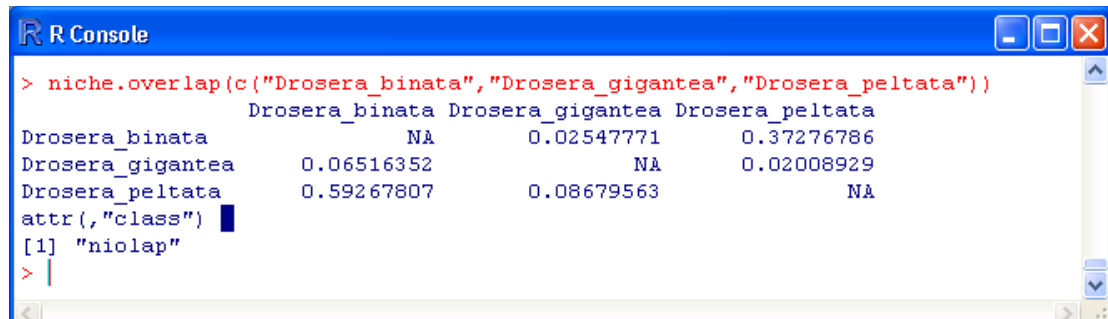
```
# load libraries into R
library("phyloclim")
library("adehabitat")
```

```
# load in the niche projections for 3 Australian sundews
Drosera_peltata<-import.asc("Drosera_peltata.asc")
Drosera_gigantea<-import.asc("Drosera_gigantea.asc")
Drosera_binata<-import.asc("Drosera_binata.asc")
```

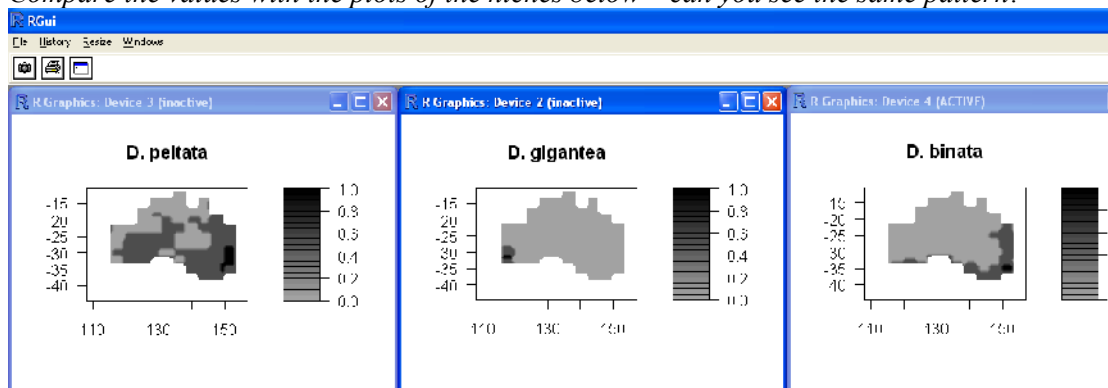
We can look at any of these maps using the plot command # for example this will give you a rough grid of Australia, dark areas are stronger predictions
plot(Drosera_gigantea,col=(c(grey(c(0.67-seq(20)/30))))),main="D. gigantea")

```
# Use this line to perform the niche overlap analysis
niche.overlap(c("Drosera_binata","Drosera_gigantea","Drosera_peltata"))
# Note: niche.overlap() runs the analysis
# Note: the list() command converts the individual layers into a list of layers, which is the
format required by the niche.overlap function.
```

the output will look like this – which two niches are most correlated?



Compare the values with the plots of the niches below – can you see the same pattern?



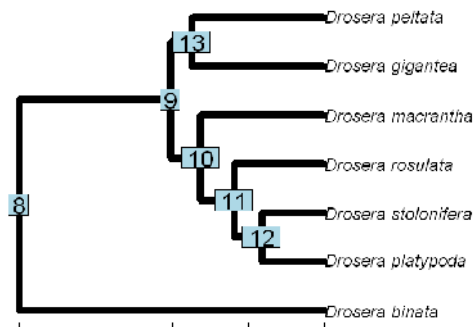
If you saved any projected niches from you openmodeller practical, why not try repeating the correlation with these (note the maps you compare must be the same size)

Age and Niche correlation

```
# open the file AgeNicheCorrelation.R
# to get age to most recent common ancestor we need a phylogeny
# load in tree example tree file and turn into a chronogram
t<-read.nexus("YessonCulham2006Subtree.tre")
```

```
# this tree is not ultrametric, convert to
ultrametric using NPRS smoothing
t.dated<-chronopl(t,age.min=20,lambda=1)
```

```
# plot the tree using the following command
plot(t.dated)
nodelabels() # add node numbers
axisPhylo() # add a scale axis
```



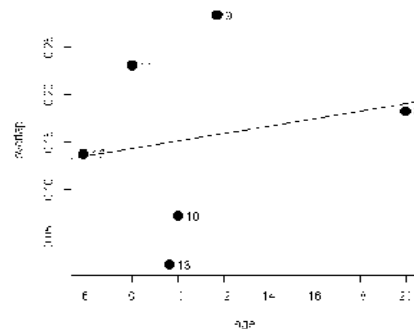
```
# this tree has 7 terminal taxa
# we must repeat the niche correlation analysis
species.models.no<-niche.overlap( c("Drosera_peltata", "Drosera_binata",
"Drosera_gigantea", "Drosera_macrantha", "Drosera_platypoda", "Drosera_rosulata",
"Drosera_stolonifera"))
```

```
# now parse the tree and the niche overlap results to the final analysis
arc<-age.range.correlation(t.dated,species.models.no)
```

```
# plot the age to mrca and niche overlap
```

```
plot(arc$age.range.correlation, cex=2,pch=19)
```

```
# add node numbers and a regression
text(arc$age.range.correlation, labels =
labels(arc$age.range.correlation)[[1]],pos=4)
abline(arc$linear.regression$coefficients)
```



```
# display regression statistics
summary(arc$linear.regression)
```

```
# Does niche overlap correlate
with age to MRCA for sundews?
```

```
# Run the example from the help
to see a correlated example
help(age.range.correlation)
```

```
R Console
> summary(arc$linear.regression)

Call:
lm(formula = overlap ~ age)

Residuals:
    8      9     10     11     12     13 
-0.007003  0.121907 -0.073044  0.007163  0.002741 -0.123104 

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  0.111352   0.116178   0.958   0.392
age          0.003934   0.009875   0.398   0.711

Residual standard error: 0.1078 on 4 degrees of freedom
Multiple R-squared:  0.03816,    Adjusted R-squared: -0.02023 
F-statistic: 0.1587 on 1 and 4 DF,  p-value: 0.7107

> |
```