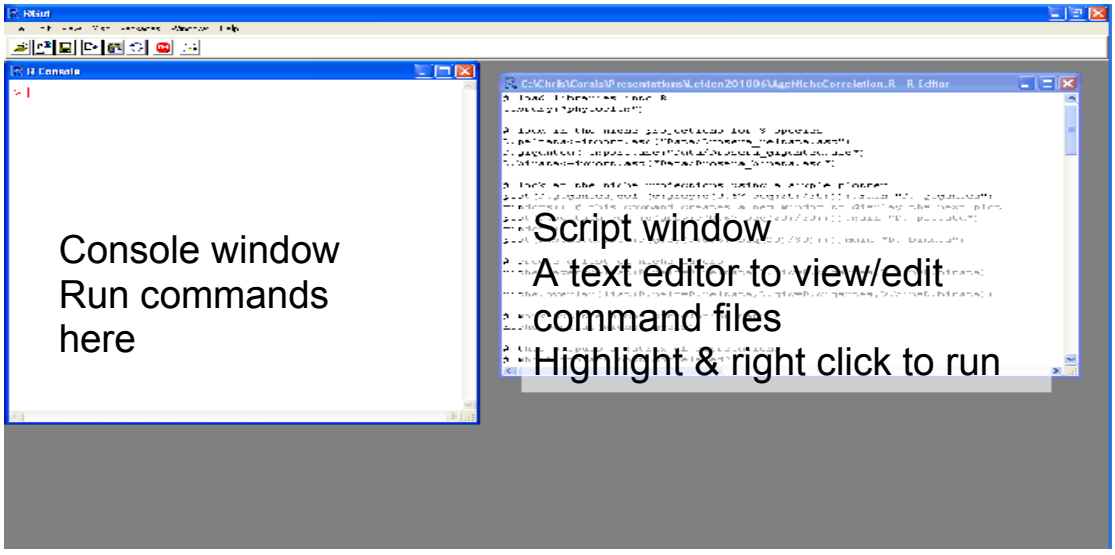
Phyloclimatic Modelling Practical

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",
"SDMTools"))
```

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

Ancestral state reconstruction a simple example

 # Use the file AncestralStateReconstruction.R

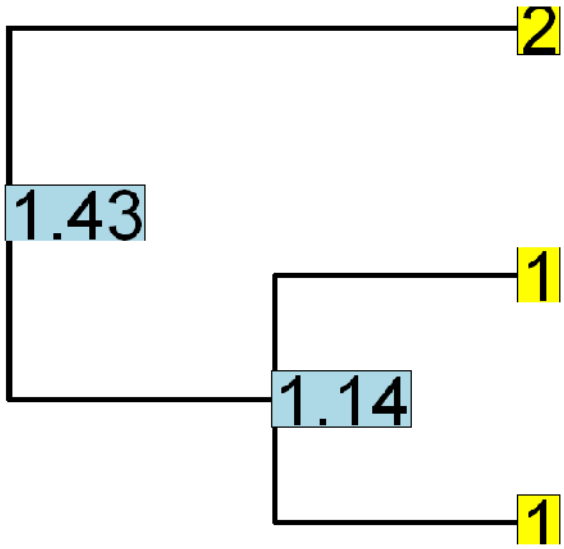
 # Get a tree
T<-read.tree(text="((A:1,B:1):1,C:2);")

 # Make a data set
M<-c(1,1,2)

 # calculate niche overlap between species
TM <-ace(M,T)

 # show tree
plot(T,show.tip.labels=F)

 # add node labels
nodelabels(round(TM$ace,2))
tiplabels(M,adj=1)



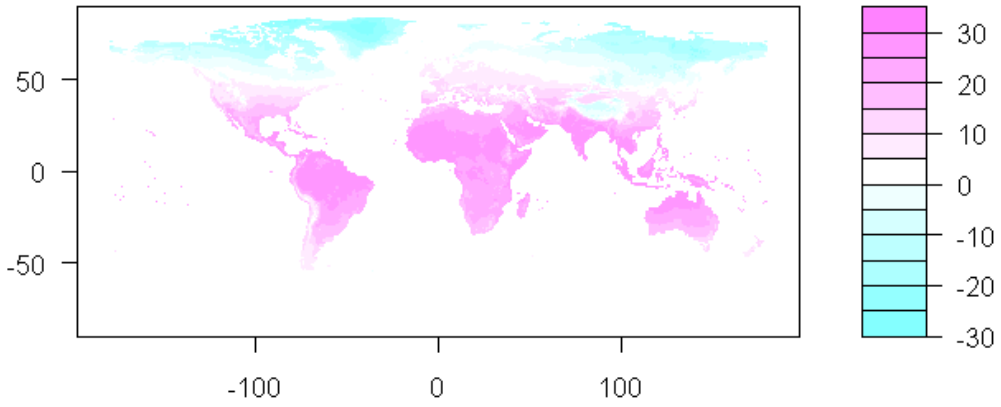
Phyloclimatic modelling

 # putting gether niche models and ancestral state reconstruction is a tricky process
 # here is a walk-through of a simple example that you could build upon

 # Build a phyloclimatic model
 # start by loading libraries
require("adehabitat")
require("ape")
require("SDMTools")

 # fetch environmental layers
 # for now we will pick one layer
temp.mean<-import.asc("Climate/CRUCL1Present/Mean_temperature.asc")

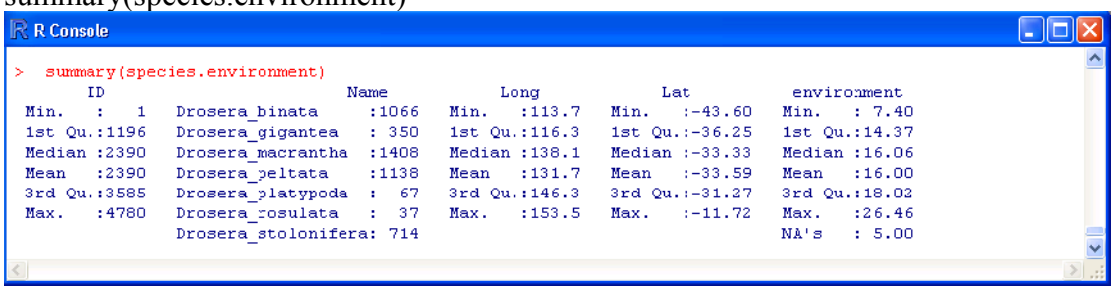
 # have a look at the data
plot(temp.mean)



 # load species data
species.locs <- read.table("YessonCulham2006Localities.txt", sep="\t",
col.names=c("ID","Name","Long","Lat"))

 # extract environmental data for the species locations
species.environment <-
cbind(species.locs,environment=extract.data(species.locs[,3:4],temp.mean))

 # view a summary of the data
summary(species.environment)

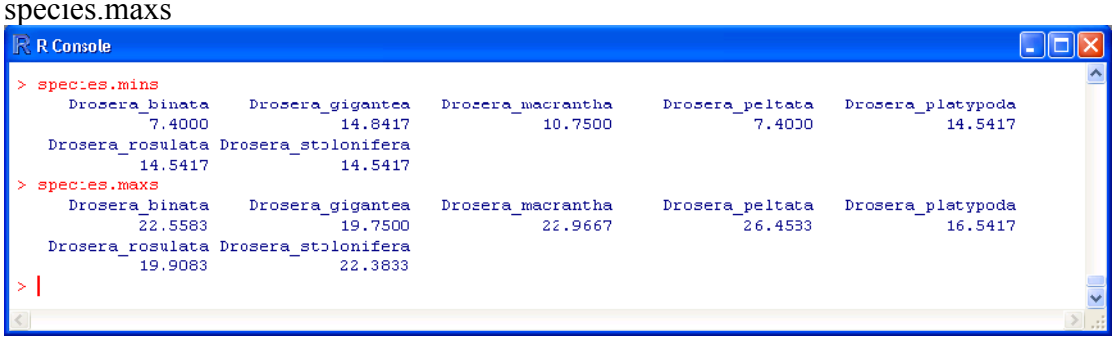


```
## fetch the phylogeny
t<-read.nexus("YessonCulham2006Subtree.tre")
t.dated<-chronopl(t,lambda=1,age.min=20)

# create a store for the min and max values for each species
species.mins<-vector()
species.maxs<-vector()

# fetch the min/max/mean for each species in the phylogeny
for(i in unique(t.dated$tip.label))
{
    mySubset<-subset(species.environment,Name==i)
    species.mins[i]<-min(mySubset$environment,na.rm=T)
    species.maxs[i]<-max(mySubset$environment,na.rm=T)
 }

# view the results
species.mins
species.maxs
```



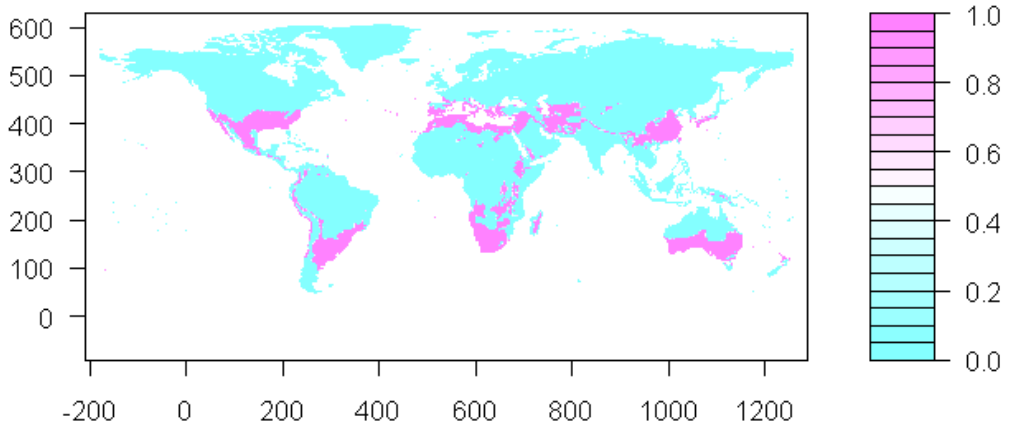

```
## do ancestral state reconstruction with continuous characters
species.mins.ace<-ace(species.mins,t.dated,method="ML")

## look at values on tree
plot(t.dated)
tiplabels(round(species.mins,2),adj=1)
nodelabels(adj=2,font=3)
nodelabels(round(species.mins.ace$ace,2),adj=0,bg="yellow")
axisPhylo()

## we want to focus on node 10 as this lineage was around at 8Ma
## which is the date of our palaeo environmental layer
## the reconstructed value is 12.35 degrees C

## now get max value
species.maxs.ace<-ace(species.maxs,t.dated,method="ML")
plot(t.dated)
tiplabels(round(species.maxs,2),adj=1)
nodelabels(adj=2,font=3)
nodelabels(round(species.maxs.ace$ace,2),adj=0,bg="yellow")
axisPhylo()
## This time the max value is 21.47 degrees C
```

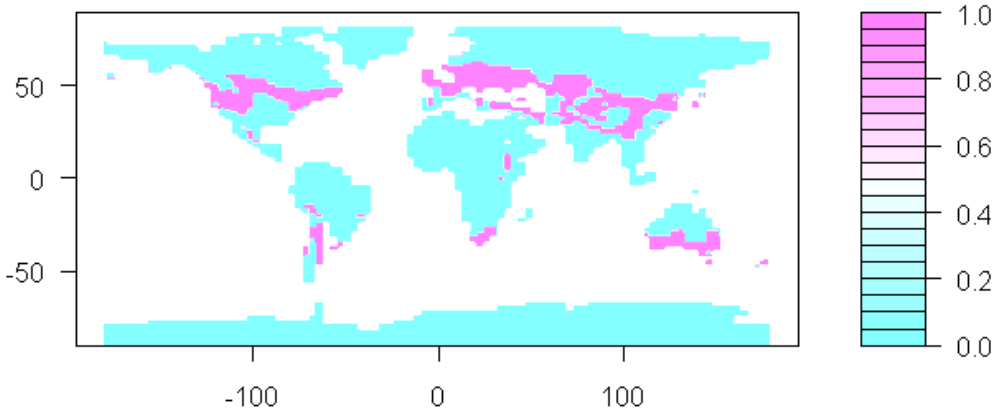
Look at the area bounded by these values in the present climate
reclassify map to 1 for within range and 0 for outside range
temp.mean.masked<-as.asc((temp.mean<21.47)*(temp.mean>12.35)*1, xll=-180, yll=-90)
plot(temp.mean.masked)



Open the environmental layer for 8Ma
temp.mean.8ma<-import.asc("Climate/Bridge8Ma/Mean_temperature.asc")
reclassify map to 1 for within range and 0 for outside range
temp.mean.8ma.masked<-
as.asc((temp.mean.8ma<21.47)*(temp.mean.8ma>12.35)*1,xll=-180,yll=-90)

now look at the projected image
plot(temp.mean.8ma.masked)

export to an ascii grid file
export.asc(temp.mean.8ma.masked,"Node10Temp.asc")



Using multiple layers and given time we can produce more complicated analyses

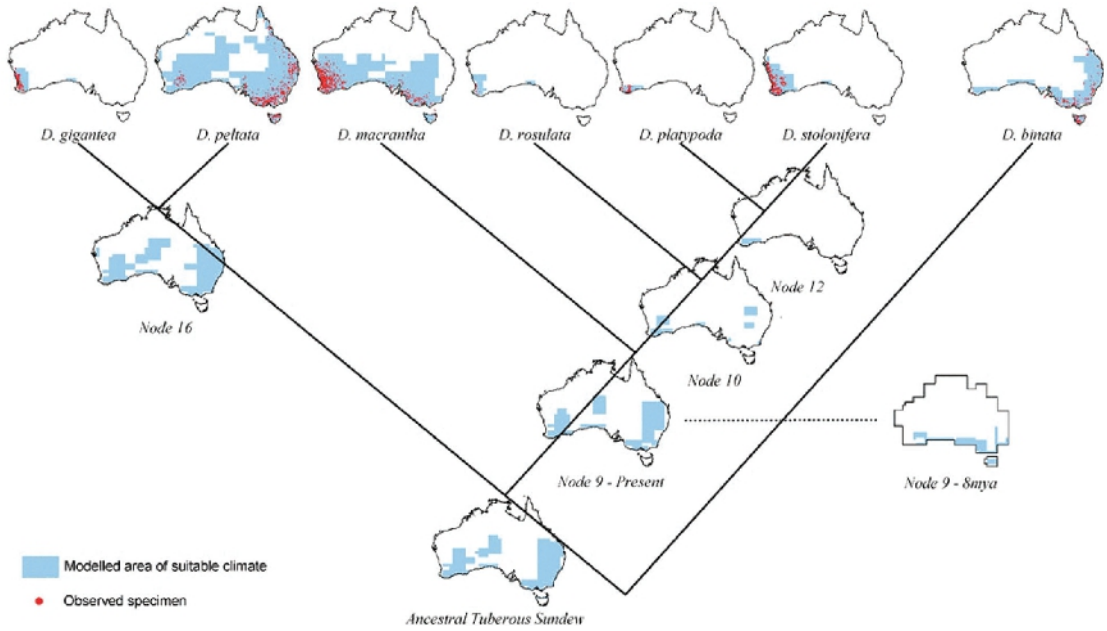


FIGURE 5. Bioclimatic models projected into modeled present-day climate of Australia. Full extent of bioclimatic range marked blue. Red dots show locality data used to construct models. Internal nodes projected into the same present climate to demonstrate model similarity. (Node 9 also projected into model of 8 Mya.) (From Yesson & Culham 2006)

This is the end of the practical

A note on environmental layer selection

The Bioclim modelling algorithm can be sensitive the to number of environmental layers that you select. Each additional layer restricts the potential suitable area by imposing additional environmental constraints. It is advisable to restrict the environmental layers you select for modelling.

One way to do this is to test for phylogenetic conservancy of an environmental layer, and only model with environmental data that is displaying significant phylogenetic pattern. This involves a replication test by randomising all observed data on the phylogeny, performing ancestral state reconstruction on the randomised data and recoding total likelihood then comparing the observed to the randomised likelihoods. If the observed is outside the majority of the randomised replicates (say 1st/99th percentile) then we have significant phylogenetic conservancy.

The file PhylogeneticConservancy.R gives an example how to do this in R.