

Lab 3 - Gr. 14 - Bioinformatics (732A93)

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Assignment 1

Using the script <http://ape-package.ird.fr/APER/APER2/SylviaWarblers.R> obtain the Sylvia warblers phylogeny (the script saves in the file `sylvia_nj_k80.tre`). The geographical range data can be found in http://ape-package.ird.fr/APER/APER2/sylvia_data.txt and in the script is referenced as `DF$geo.range`. Notice that one tip is removed due to missing data.

```
tr <- drop.tip(tr, "Chamaea_fasciata")
```

and the data has to be ordered by the tips of the phylogeny

```
DF <- sylvia.eco[tr$tip.label, ]
```

WARNING: Running the script bare might result in errors and very long running times.

Choose only the lines that you actually need!

Question 1.1

Question: Explain all the steps in the script required to obtain the phylogeny and trait data.

The keep it clean we keep track of everything as a bullet point list:

Setup

- We moved all library imports to the top of our RMarkdown file
- Install ClustalW from <http://www.clustal.org/download/current/>
- Add ClustalW to the PATH variable of your system
- Install phyloch with `install_github("fmichonneau/phyloch")`
- <http://www.christophheibl.de/Rpackages.html>
- Install 'MAFFT' from <https://mafft.cbrc.jp/alignment/software/>
- Use the `path` parameter to point to the executable OR
- Add to PATH
- PhyML 3.0 must be installed
- <http://www.atgc-montpellier.fr/phyml/download.php>
- Point to the executable in the `execpath` arguments or add to PATH

Script

```
# -----  
# Question 1.1  
# -----  
  
#source("SylviaWarblers.R")  
# As we have to explain the code line by line we will not source it but paste it  
# here do add comments.
```

```

###
### Chapter 3
###

# These line create a vector whioch contains 'Z73494' followed by 'AJ5345' with
# ascending numbers at the end ranging from 26 to 49. Then the GenBank database
# is searched and the result saved in 'sylvia.seq' which holds 25 results.
x <- paste("AJ5345", 26:49, sep = "")
x <- c("Z73494", x)
sylvia.seq <- read.GenBank(x)

# 'clustal()' alignes a set of nucletotide sequences. The programm ClustalW must
# be installed locally for this to work.
sylvia.clus <- clustal(sylvia.seq)

# MAFFT must be installed. For windows the easiest way is to point to the exe-
# cutable. As it's > 60MB of size, it's not included in the git repository.
# On Linux or macOS this might work out of the box, simply remove the 'path'
# argument.
# MAFFT is used for sequence and profile aligning. It seems like that both
# clustal and mafft return the same result.
sylvia.maff <- mafft(sylvia.seq)
# This function checks if two R objects are equal, which retruns TRUE, so our
# guess was correct.
#identical(sylvia.clus[x, ], sylvia.maff[x, ])

# Add's the attribute 'species' to a new object.
taxa.sylvia <- attr(sylvia.seq, "species")
# The names we mentioned above are assigned to this new object.
names(taxa.sylvia) <- names(sylvia.seq)
# This removes the previous object read from the GenBank.
rm(sylvia.seq)
# The first and the 24th entry get names.
taxa.sylvia[1] <- "Sylvia_atricapilla"
taxa.sylvia[24] <- "Sylvia_abyssinica"

# Now we read from the text file which was provided via a link.
# It holds the geographical range data.
# Note that we changed the name of the file.
sylvia.eco <- read.table("SylviaData.txt")
# Shows the structure of the importet data.frame. It has 26 obveruations and 3
# variables.
#str(sylvia.eco)
# Displays the rownames of the data.frame which are a bunch of names 'Sylvia_*'.
#rownames(sylvia.eco)
# We save the three objects to the file called 'sylvia.RData'.
# Note that we added an 'S' to 'sylvia.cluS' as it was misspelled.
save(sylvia.clus, taxa.sylvia, sylvia.eco,
     file = "sylvia.RData")

###
### Chapter 5
###

```

```

# These functions create a matrix of pairwise distances from DNA sequences using
# a model of DNA evolution (taking from Help file).
# The calls also have the argument 'pairwise.deletion' which is set to TRUE.
# This deletes the sites with missing data in a pairwise way.
# The model parameter specifies which model is to be used. As 'K80' is the
# default model, this parameter is not specified for the first call.
# A description of the models can be found in the Help file.
syl.K80 <- dist.dna(sylvia.clus, pairwise.deletion = TRUE)
syl.F84 <- dist.dna(sylvia.clus, model = "F84", p = TRUE)
syl.TN93 <- dist.dna(sylvia.clus, model = "TN93", p = TRUE)
syl.GG95 <- dist.dna(sylvia.clus, model = "GG95", p = TRUE)

# This just plots a distance matrix and is not needed for saving the tree.
#round(cor(cbind(syl.K80, syl.F84, syl.TN93, syl.GG95)), 3)

syl.JC69 <- dist.dna(sylvia.clus, model = "JC69", p = TRUE)
syl.raw <- dist.dna(sylvia.clus, model = "raw", p = TRUE)

# The following code is used for more plotting which we don't need for obtaining
# the tree.
#layout(matrix(1:2, 1))
#plot(syl.JC69, syl.raw)
#abline(b = 1, a = 0) # draw x = y line
#plot(syl.K80, syl.JC69)
#abline(b = 1, a = 0)

#layout(matrix(1:3, 1))
#for (i in 1:3) {
#  s <- logical(3); s[i] <- TRUE
#  x <- sylvia.clus[, s]
#  d <- dist.dna(x, p = TRUE)
#  ts <- dist.dna(x, "Ts", p = TRUE)
#  tv <- dist.dna(x, "Tv", p = TRUE)
#  plot(ts, d, xlab = "Number of Ts or Tv", col = "blue",
#        ylab = "K80 distance", xlim = range(c(ts, tv)),
#        main = paste("Position", i))
#  points(tv, d, col = "red")
#}

#y <- numeric()
#for (i in 1:3) {
#  s <- logical(3); s[i] <- TRUE
#  y <- c(y, dist.dna(sylvia.clus[, s], p = TRUE))
#}
#g <- gl(3, length(y) / 3)

# Plots the histogram
#histogram(~ y | g, breaks = 20)

# The function nj is doing a neighbor-joining tree estimation
nj.sylvia.K80 <- nj(syl.K80)
nj.sylvia.GG95 <- nj(syl.GG95)

```

```

# dist.topo calculates the topological distance between two trees (12 here).
# It's not needed for saving the tree, so we uncomment it.
#dist.topo(nj.sylvia.K80, nj.sylvia.GG95)

# Just the unix command getting "Chamaea_fasciata"
#grep("Chamaea", taxa.sylvia, value = TRUE)
f <- function(xx) root(nj(dist.dna(xx, p=TRUE)), "AJ534526")
tr <- f(sylvia.clus)
## same than: tr <- root(nj.sylvia.K80, "AJ534526")
# nj.phylo analyse bipartitions found in series of trees (from documntation)
nj.boot.sylvia <- boot.phylo(tr, sylvia.clus, f, 200,
                           rooted = TRUE)
nj.boot.codon <- boot.phylo(tr, sylvia.clus, f, 200, 3,
                           rooted = TRUE)

nj.est <- tr
nj.est$tip.label <- taxa.sylvia[tr$tip.label]

# The plot is not needed
#plot(nj.est, no.margin = TRUE)
#odelabels(round(nj.boot.sylvia / 200, 2), bg = "white")
#add.scale.bar(length = 0.01)

# Saves the tree to the file
write.tree(nj.est, "sylvia_nj_k80.tre")

# Writes 25 sequences to a file. Length is 1143.
write.dna(sylvia.clus, "sylvia.txt")

# Calls PhyML and fits 28 models of DNA evolution. They're saved to disk and
# in R returned as a vector. The log-likelihood is saved in this vector.
phyml.sylvia <- phymltest("sylvia.txt")

# Again not needed for obtaining the tree
#summary(phyml.sylvia)
#plot(phyml.sylvia, col = "black")

# Read the tree from the txt.
TR <- read.tree("sylvia.txt_phyml_tree.txt")

# Adding some labels and descriptions to the tree
mltr.sylvia <- TR[[28]]
mltr.sylvia$tip.label <- taxa.sylvia[mltr.sylvia$tip.label]
mltr.sylvia <- root(mltr.sylvia, "Chamaea_fasciata")
#plot(mltr.sylvia, no.margin = TRUE)
#add.scale.bar(length = 0.01)

# The tip is dropped as explained in the exercise
tr.ml <- drop.tip(mltr.sylvia, "Chamaea_fasciata")
res <- vector("list", 9)

# The for loop takes some time. chronopl estimates the node ages of trees by
# using a semi-parametric method based on penalized likelihood (see docu-
# mentation).

```

```

for (L in -4:4)
  res[[L + 5]] <- chronopl(tr.ml, 10^L, 12, 16, CV = TRUE)
Lambda <- 10^(-4:4)
CV <- sapply(res, function(x) sum(attr(x, "D2")))
#plot(Lambda, CV / 1e5, log = "x")

# Add the attribute "rates" to the tree with 24 tips and 23 internal nodes
sylvia.chrono <- res[[2]]
rts <- attr(sylvia.chrono, "rates")
#summary(rts)

# Not needed for obtaining the tree
#par(mar = c(2, 0, 0, 0))
#plot(sylvia.chrono, edge.width = 100*rts, label.offset = .15)
#axisPhylo()

# Finally writes the tree to the file.
write.tree(sylvia.chrono, "sylvia.chrono.tre")

###
### Chapter 6
###

# Load the RData
load("sylvia.RData")
# Read the tree
nj.est <- read.tree("sylvia_nj_k80.tre")
# Drop the tip as mentioned in the exercise
nj.est <- drop.tip(nj.est, "Chamaea_fasciata")

# Get mig.dist, mig.behav and geo.range and save if to DF
DF <- sylvia.eco[nj.est$tip.label, ]

# Create a table with the range and the behav, so its long, resid, short against
# temp, temptrop and trop
table(DF$geo.range, DF$mig.behav)

# Ace ist used to estimate the ancestral character states and the corresponding
# uncertainty (traits), the "d" defines that we're handling discrete
# characters. Seond call changes the model, which is a numeric matrix
syl.er <- ace(DF$geo.range, nj.est, type = "d")
syl.sym <- ace(DF$geo.range, nj.est, type="d", model="SYM")
# Variance/Deviance for the fitted models (incl. Likelihood) and Chi Testing
#anova(syl.er, syl.sym)

mod <- matrix(0, 3, 3)
mod[2, 1] <- mod[1, 2] <- 1
mod[2, 3] <- mod[3, 2] <- 2

# Now we use the creates model to estimate again
syl.mod <- ace(DF$geo.range, nj.est, type="d", model=mod)

sapply(list(syl.er, syl.sym, syl.mod), AIC)

```

```

#Q <- syl.mod$index.matrix
#diag(Q) <- 0
#Q[1, 2] <- Q[2, 1] <- syl.mod$rates[1]
#Q[2, 3] <- Q[3, 2] <- syl.mod$rates[2]

#Q[] <- c(0, syl.mod$rates)[Q + 1]
#diag(Q) <- -rowSums(Q)

# THIS IS NOT WORKING AS WE HAVE NAs IN THE MATRIX
#P <- mategpo(0.05 * Q)
#rownames(P) <- c("temp", "temptrop", "trop")
#colnames(P) <- rownames(P)

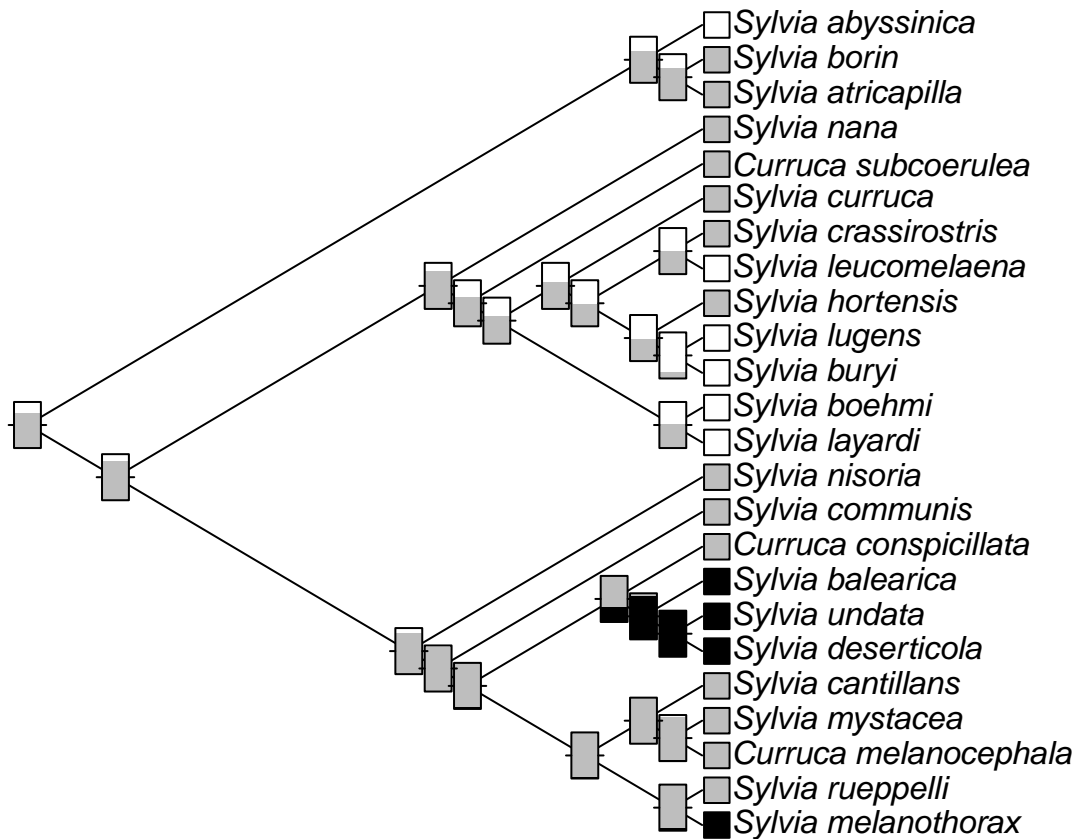
# This works but do we need this?
#sylvia.chrono <- read.tree("sylvia.chrono.tre")
#yule(sylvia.chrono)
#birthdeath(sylvia.chrono)
#1 - pchisq(2*(-1.034112 - -1.113822), 1)

#x <- sylvia.eco[sylvia.chrono$tip.label, "geo.range"]
#ANC <- ace(x, sylvia.chrono, type = "d", model = mod)
#ANC$lik.anc[1:3, ]
#anc <- apply(ANC$lik.anc, 1, which.max)
#X <- factor(c(x, anc))
# This breaks as we have NAs!
#yule.cov(sylvia.chrono, ~ X)
#1 / (1 + exp(-(-0.0535529)))
#1 / (1 + exp(-(-0.0535529 -1.4608019)))
#1 / (1 + exp(-(-0.0535529 -0.9775966)))

#fsamp <- function(x) sample(length(x), size = 1, prob = x)
#nrep <- 1e3
#Puls <- numeric(nrep)
#for (i in 1:nrep) {
#  anc <- apply(ANC$lik.anc, 1, fsamp)
#  X <- factor(c(x, anc))
#  Puls[i] <- yule.cov(sylvia.chrono, ~ X)$Pval
#}
#hist(Puls, freq = FALSE, main = "")
#lines(density(Puls))

```

Here we have the phylogenetic tree of Sylvia:



Question 1.2

Question: Analyze the discrete (`type=discrete`) geographical range variable (`DF$geo.range`) using `ape::ace`. Consider different models (parameter `model`). Report on the results and interpret the estimated rates and their standard errors.

Function `ape::ace` Ancestral Character Estimation, estimates ancestral character states, and the associated uncertainty, for continuous or discrete characters. For this question, we are analyzing the discrete geographical range variable, there are 3 available model for `type=discrete` : “ER”, “ARD”, “SYM”. - “ER” is an equal-rates model

- “ARD” is an all-rates-different model
- “SYM” is a symmetrical model

From the phylogenetic tree of *Sylvia* above, we were able to figure out how the given *Sylvia* data end up in three features - trop(white), temp(black), temptrop(grey) and their phylogenetic relations. *Sylvia* from “trop” consists 6/24(0.25%), from “temp” consists 4/24(0.17%), and for temptrop 14/24(0.58). After we fitted the data into 3 available model : “ER”, “ARD”, “SYM”, we were able to figure out that three models shows the same result - temptrop shows the highest likelihood. For “ER” method and “SYM”, trop shows the seconde highest likelihood, followed by temp. We can also check similiar probability from the phylogenetic tree so we can conclude that “ER” method and “SYM” method is reliable. For “ER” method only one(1) rate index is used and estimatd value 5.9888, For “SYM” method three rate index(1,2,3) is used and estimated value is 3.9839, 0, 11.8850 which we can interpret second rate index is meaningless. The standard error for the first rate index for those two plots are similar.

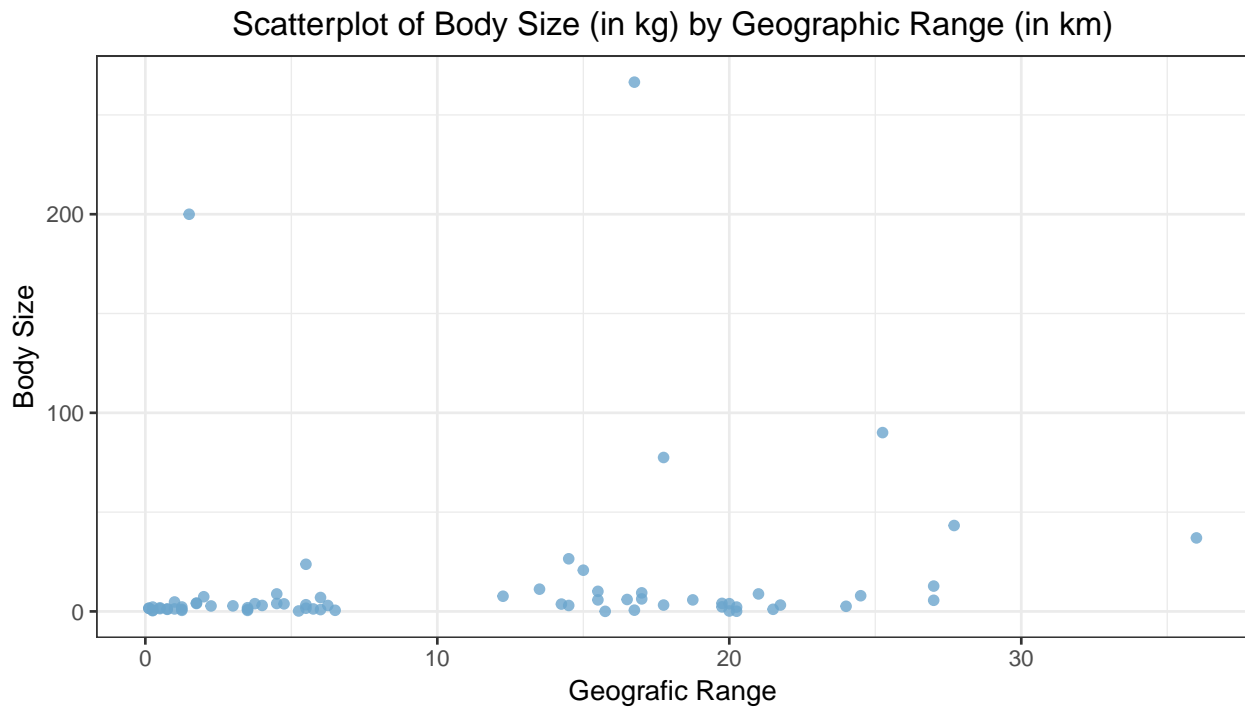
Assignment 2

Question 2.1

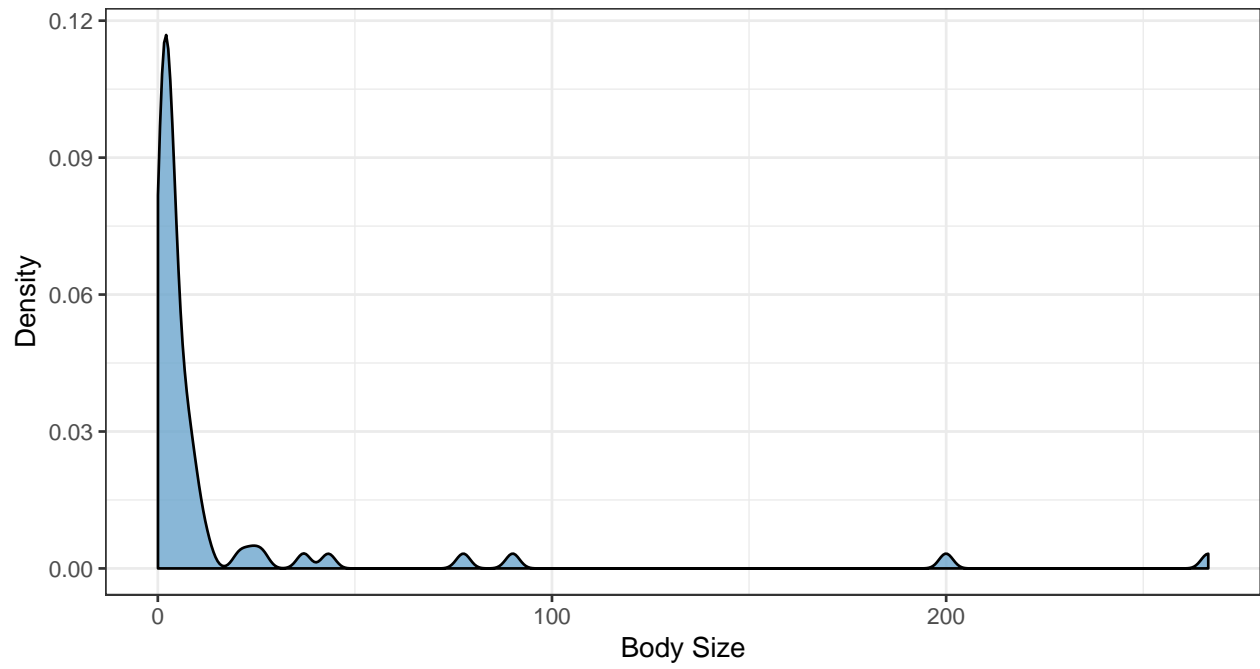
We are given a data set about carnivores. The first task is to explore this data set. Overall, it is a list consisting of a) a phylogenetic tree in Newick format and b) quantitative traits of the species in the tree. The quantitative traits consist of two variables, **size** (body size) and **range** (geographic range in km). There are 70 species in total. The exploratory analysis follows after the visualizations below.

Table 1: Descriptive Statistics of Quantitative Traits

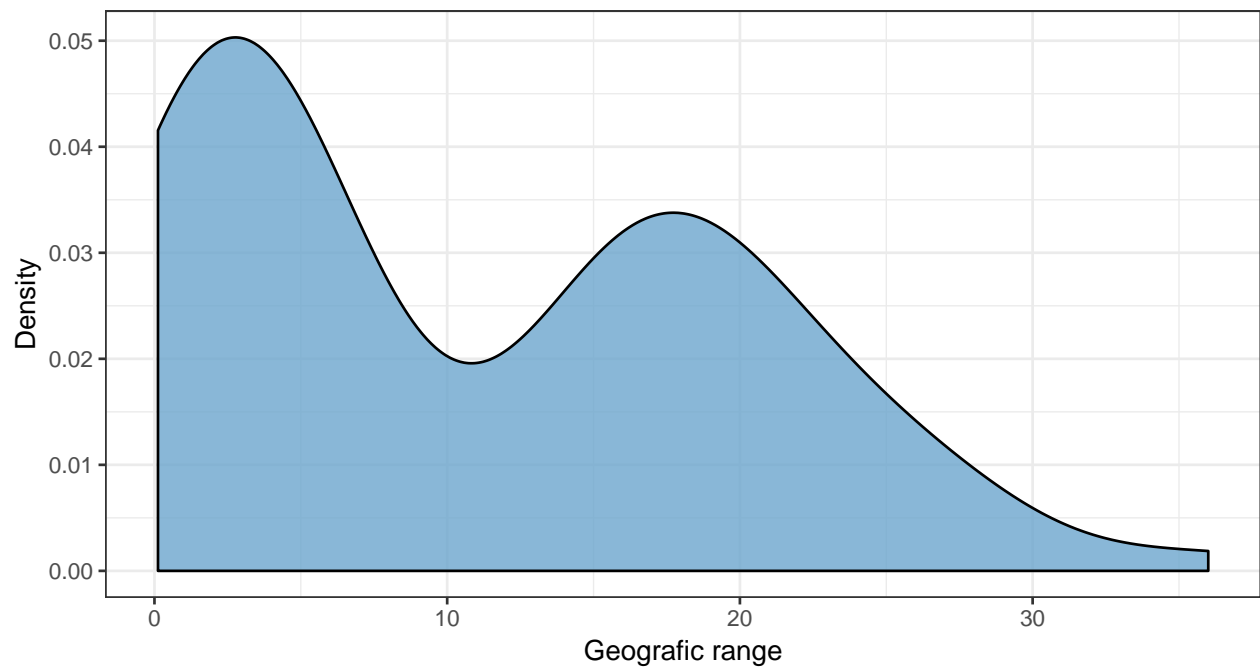
	vars	n	mean	sd	median	trimmed	mad	min	max	range	skew	kurtosis	se
size	1	70	14.29	41.19	3.20	4.60	3.35	0.04	266.5	266.46	4.72	23.23	4.92
range	2	70	10.72	9.20	6.12	9.95	8.81	0.12	36.0	35.88	0.50	-0.91	1.10



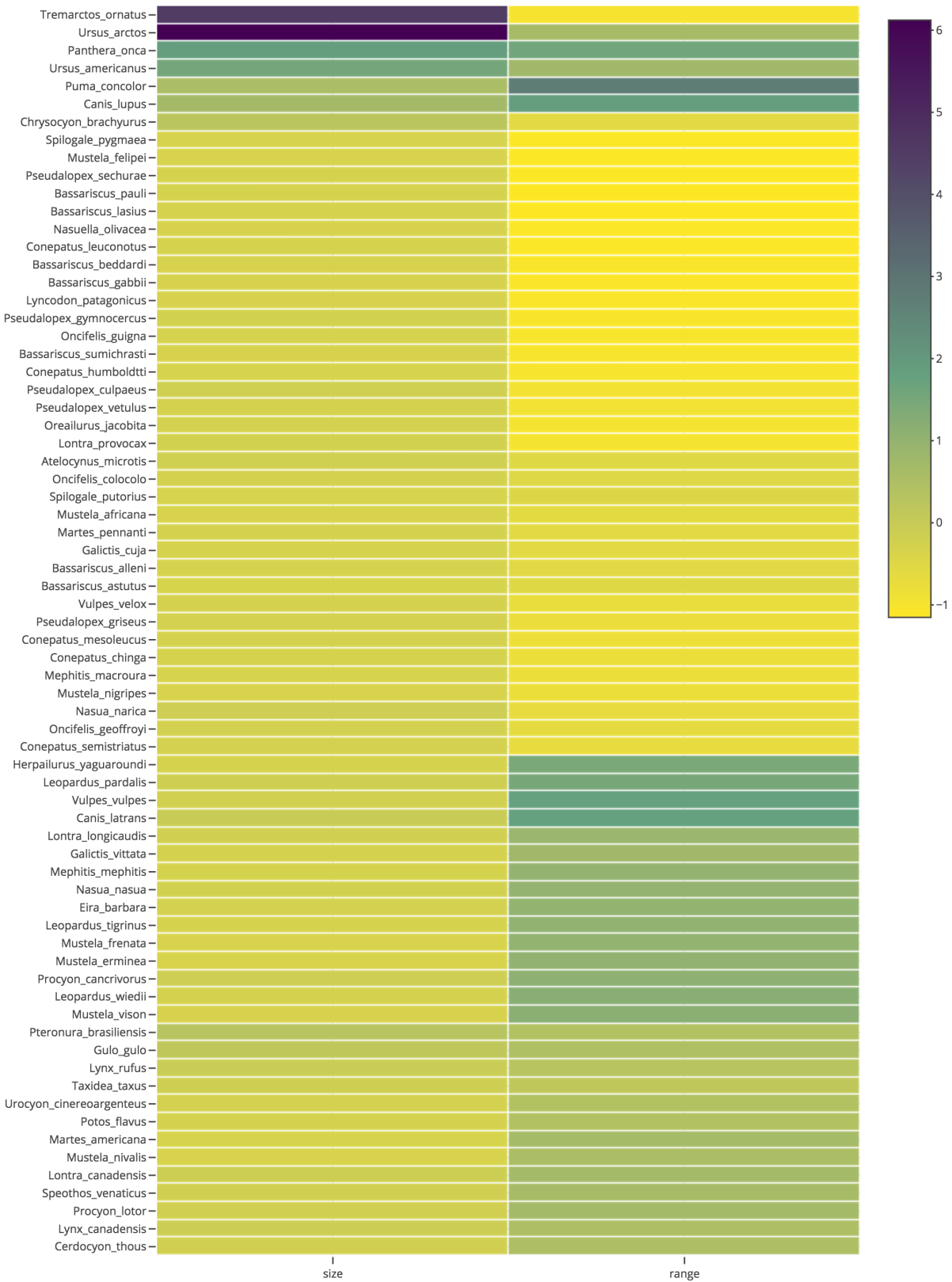
Density Plot of Body Size (in kg)

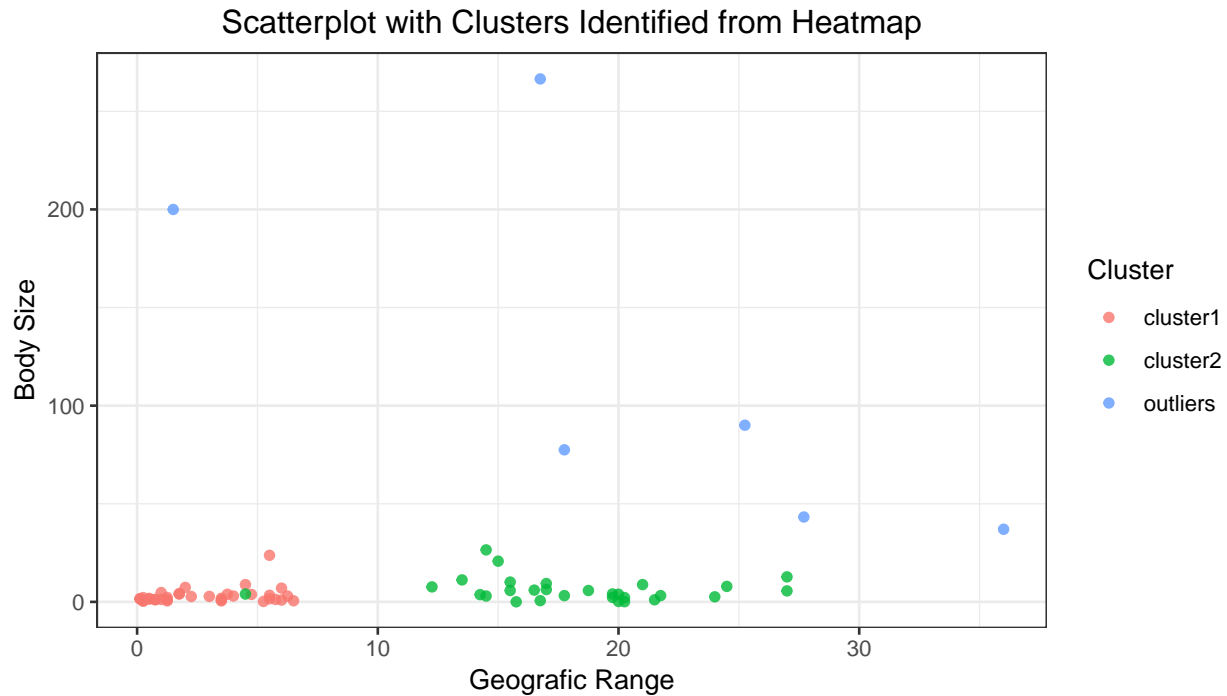


Density Plot of Geographic Range (in km)



Heatmap: Body Size and Geographic Range by Species [normalized]





Exploratory Analysis: Main Findings [Quantitative Variables]

Scatterplot

- It does not seem like **size** and **range** are correlated or non-linearly related.
- There is one upper-side outlier w.r.t. geographic range: *Puma_concolour*.
- There are two upper-side outliers w.r.t. body size: *Ursus_arctos* and *Tremarctos_ornatus*.

Density Plot

- Both quantitative variables, **size** and **range** are highly skewed to the right.
- **size** is much more skewed to the right than **range**.

Heatmap

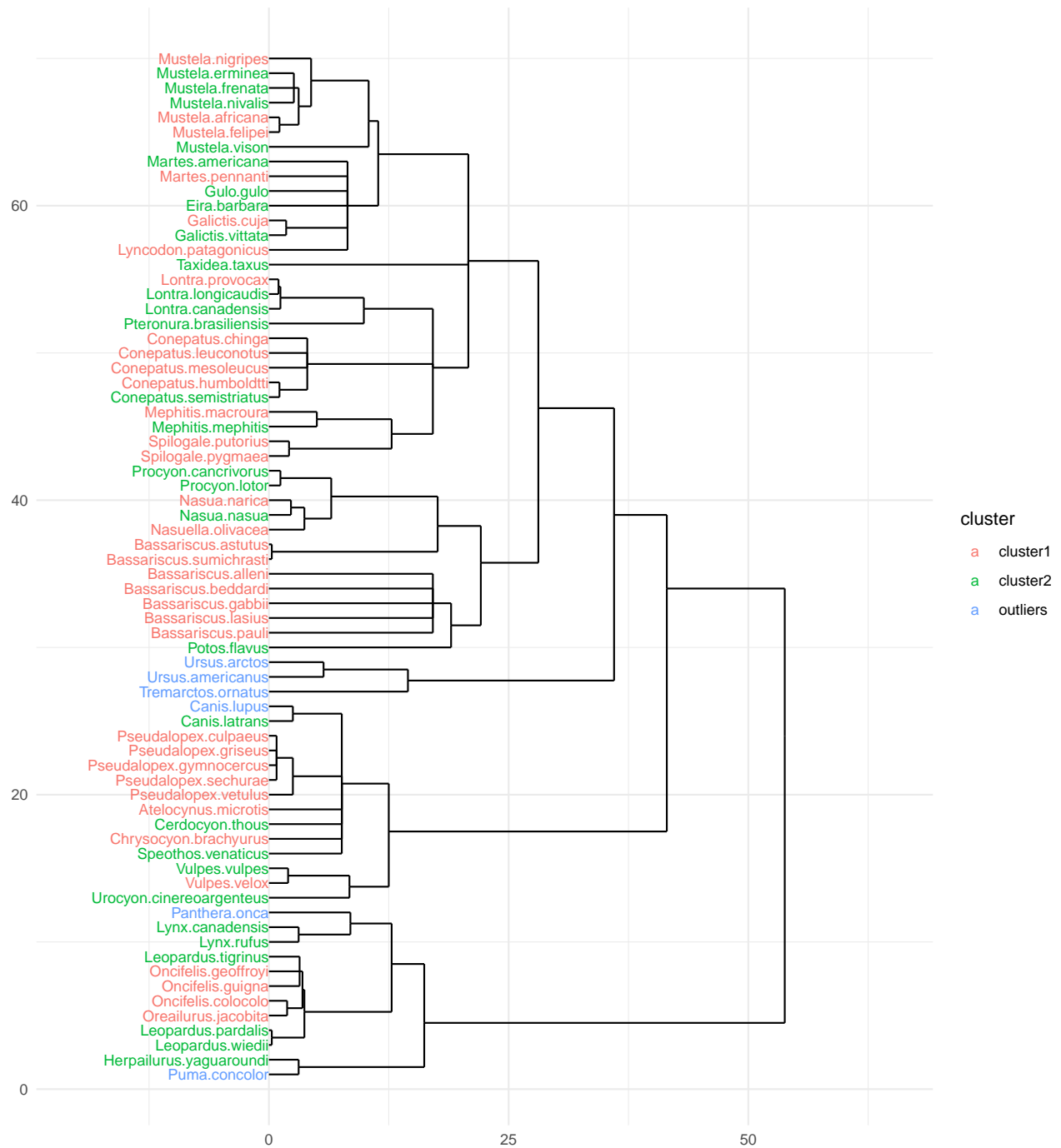
- Two clusters can be identified. The species not belonging to these clusters are described as here.
 - Cluster 1: from *Chrysocyon_brachyurus* to *Conepatus_semistriatus*
 - Cluster 2: everything below *Conepatus_semistriatus*
 - Outliers: everything above *Chrysocyon_brachyurus*
- The clusters are mainly based on the **range** since both clusters have similar values w.r.t. **size**.
- The clusters found in the heatmap are visualized in a scatterplot again (using the color aesthetic). We can see, that they are also cluster in the scatterplot.

Exploratory Analysis: Main Findings [Tree]

Dendrogram

- The clusters identified in the heatmap do not (!) actually correspond to different branches in the dendrogram.
- We can conclude that different species can have very similar traits w.r.t. **size** and **range** but still be different species.

Dendrogram (Colored by Clusters identified from Heatmap)



Question 2.2

Here, we analyze the two quantitative traits (**size** and **range**) with five different phylogenetic comparative models.

Comparison Strategy:

Different packages and functions needed to be used. All of them provided the metrics AIC, AICc and log likelihood. Therefore, we choose these metrics to compare the five models.

AIC is supposed to be minimized and the log likelihood is supposed to be maximized. Note that AICc is a modified version AIC that corrects for a small sample size. AICc may be more accurate for small sample sizes and we may consider 70 species a small sample.

Best Model:

Overall, we see that the smallest AIC and AICc as well as largest log likelihood is issued by the 4th model (traits evolve as a bivariate Ornstein–Uhlenbeck process).

This model estimated an asymptotic mean $\theta_{size} = 37.55482$ and $\theta_{range} = 11.42832$

The estimated alpha values can be found below. Note that in OU, alpha indicates how strongly the system reacts to movements (“perturbations”) away from the asymptotic mean.

$$\begin{bmatrix} & size & range \\ size & 0.0000701675 & -0.003902526 \\ range & -0.0039025258 & 0.235597609 \end{bmatrix}$$

The estimated sigma values can be found below. They indicate the variation of the noise.

$$\begin{bmatrix} & size & range \\ size & 73.691771 & 5.944651 \\ range & 5.944651 & 38.594288 \end{bmatrix}$$

It’s important to notice, however, that using a different function, specifically `ouchModel` from the package `mvSLOUCH`, leads to different results, where the asymptotic mean $\theta_{size} = 14.28806$ differs substantially from the model found through `mvOU` of the library `mvMORPH`. Moreover the AICc would then be equal to 1233.058, making the independent Brownian motions model the best one. The results appear to be confusing.

1. Both traits evolve as independent Brownian motions.

Results after Successful Convergence:

AIC: 1186.475 AICc: 1186.771 Log-Likelihood: -589.2373

2. The traits evolve as a correlated Brownian motion.

Results after Successful Convergence:

AIC: 1187.571 AICc: 1188.018 Log-Likelihood: -588.7853

3. Both traits evolve as independent Ornstein–Uhlenbeck processes.

Results after Successful Convergence:

AIC: 1225.225 AICc: 1225.857 Log-Likelihood: -606.6126

4. The traits evolve as a bivariate Ornstein–Uhlenbeck process

Results after Successful Convergence:

AIC : 1161.211 AICc: 1162.311 Log-Likelihood: -572.6057

5. Size evolves as Brownian motion, range as Ornstein–Uhlenbeck process adapting to it

Results after Successful Convergence:

AIC : 1313 AICc: 1296 Log-Likelihood: -643

Problems we encountered:

We found it quite difficult to find the correct functions with the correct parameters for the five models. Mainly this was based on lack of examples and explanation in the documentations of the packages online. Maybe it would be possible to provide sample codes to the students when the course is offered next time so that they can focus on interpretation and understanding (instead of debugging and getting the functions to work).

Appendix

```
knitr::opts_chunk$set(fig.width = 7, fig.height = 4.5, echo = FALSE,
                        warning = FALSE, message = FALSE)

library(ape)
library(knitr)
library(lattice)

# The easiest way to get "phyloch" package is via
# install_github("fmichonneau/phyloch") more information can be found at
# http://www.christophheibl.de/Rpackages.html
# if you got the error saying incomplete final line blah blah
# open the file .Rprofile and put the curser at the very end and type enter,
# save the file and try installing them again.

library(phyloch)

# Use this if BiocManager is not installed
#if (!requireNamespace("BiocManager", quietly = TRUE))
#   install.packages("BiocManager")
#library("BiocManager")

# BiocManager packages

#####
# IMPORTANT
# Install ClustalW from http://www.clustal.org/download/current/
# Don't forget to add it to your PATH!
# Install MAFFT version 7 from https://mafft.cbrc.jp/alignment/software/
#####

# For all -----

library(dplyr)
library(tidyr)
library(magrittr)

# Question 2.1 -----
library(ade4)      # carni70 data set
```

```

library(plotly)      # Heatmap
library(seriation)   # Ordering heatmap
library(ggplot2)     # All other plots
library(phylogram)   # Phylogenetic tree visualization
library(ggdendro)    # Phylogenetic tree visualization

# Question 2.2 -----
library(ape)
library(mvMORPH)
library(mvSLOUCH)
library(ouch)
library(slouch) # devtools::install_github("https://github.com/kopperud/slouch")

# -----
# Question 1.1
# -----

#source("SylviaWarblers.R")
# As we have to explain the code line by line we will not source it but paste it
# here do add comments.

###
### Chapter 3
###

# These line create a vector whioch contains 'Z73494' followed by 'AJ5345' with
# ascending numbers at the end ranging from 26 to 49. Then the GenBank database
# is searched and the result saved in 'sylvia.seq' which holds 25 results.
x <- paste("AJ5345", 26:49, sep = "")
x <- c("Z73494", x)
sylvia.seq <- read.GenBank(x)

# 'clustal()' alignes a set of nucletotide sequences. The programm ClustalW must
# be installed locally for this to work.
sylvia.clus <- clustal(sylvia.seq)

# MAFFT must be installed. For windows the easiest way is to point to the exe-
# cutable. As it's > 60MB of size, it's not included in the git repository.
# On Linux or macOS this might work out of the box, simply remove the 'path'
# argument.
# MAFFT is used for sequence and profile aligning. It seems like that both
# clustal and mafft return the same result.
sylvia.maff <- mafft(sylvia.seq)
# This function checks if two R objects are equal, which retruns TRUE, so our
# guess was correct.
#identical(sylvia.clus[x, ], sylvia.maff[x, ])

# Add's the attribute 'species' to a new object.
taxa.sylvia <- attr(sylvia.seq, "species")
# The names we mentioned above are assigned to this new object.
names(taxa.sylvia) <- names(sylvia.seq)
# This removes the previous object read from the GenBank.
rm(sylvia.seq)

```

```

# The first and the 24th entry get names.
taxa.sylvia[1] <- "Sylvia_atricapilla"
taxa.sylvia[24] <- "Sylvia_abyssinica"

# Now we read from the text file which was provided via a link.
# It holds the geographical range data.
# Note that we changed the name of the file.
sylvia.eco <- read.table("SylviaData.txt")
# Shows the structure of the imported data.frame. It has 26 observations and 3
# variables.
#str(sylvia.eco)
# Displays the rownames of the data.frame which are a bunch of names 'Sylvia_*'.
#rownames(sylvia.eco)
# We save the three objects to the file called 'sylvia.RData'.
# Note that we added an 'S' to 'sylvia.cluS' as it was misspelled.
save(sylvia.clus, taxa.sylvia, sylvia.eco,
     file = "sylvia.RData")

###
### Chapter 5
###

# These functions create a matrix of pairwise distances from DNA sequences using
# a model of DNA evolution (taking from Help file).
# The calls also have the argument 'pairwise.deletion' which is set to TRUE.
# This deletes the sites with missing data in a pairwise way.
# The model parameter specifies which model is to be used. As 'K80' is the
# default model, this parameter is not specified for the first call.
# A description of the models can be found in the Help file.
syl.K80 <- dist.dna(sylvia.clus, pairwise.deletion = TRUE)
syl.F84 <- dist.dna(sylvia.clus, model = "F84", p = TRUE)
syl.TN93 <- dist.dna(sylvia.clus, model = "TN93", p = TRUE)
syl.GG95 <- dist.dna(sylvia.clus, model = "GG95", p = TRUE)

# This just plots a distance matrix and is not needed for saving the tree.
#round(cor(cbind(syl.K80, syl.F84, syl.TN93, syl.GG95)), 3)

syl.JC69 <- dist.dna(sylvia.clus, model = "JC69", p = TRUE)
syl.raw <- dist.dna(sylvia.clus, model = "raw", p = TRUE)

# The following code is used for more plotting which we don't need for obtaining
# the tree.
#layout(matrix(1:2, 1))
#plot(syl.JC69, syl.raw)
#abline(b = 1, a = 0) # draw x = y line
#plot(syl.K80, syl.JC69)
#abline(b = 1, a = 0)

#layout(matrix(1:3, 1))
#for (i in 1:3) {
#  s <- logical(3); s[i] <- TRUE
#  x <- sylvia.clus[, s]
#  d <- dist.dna(x, p = TRUE)

```



```

#   ts <- dist.dna(x, "Ts", p = TRUE)
#   tv <- dist.dna(x, "Tv", p = TRUE)
#   plot(ts, d, xlab = "Number of Ts or Tv", col = "blue",
#         ylab = "K80 distance", xlim = range(c(ts, tv)),
#         main = paste("Position", i))
#   points(tv, d, col = "red")
#}

#y <- numeric()
#for (i in 1:3) {
#   s <- logical(3); s[i] <- TRUE
#   y <- c(y, dist.dna(sylvia.clus[, s], p = TRUE))
#}
#g <- gl(3, length(y) / 3)

# Plots the histogram
#histogram(~ y | g, breaks = 20)

# The function nj is doing a neighbor-joining tree estimation
nj.sylvia.K80 <- nj(syl.K80)
nj.sylvia.GG95 <- nj(syl.GG95)

# dist.topo calculates the topological distance between two trees (12 here).
# It's not needed for saving the tree, so we uncomment it.
#dist.topo(nj.sylvia.K80, nj.sylvia.GG95)

# Just the unix command getting "Chamaea_fasciata"
#grep("Chamaea", taxa.sylvia, value = TRUE)
f <- function(xx) root(nj(dist.dna(xx, p=TRUE)), "AJ534526")
tr <- f(sylvia.clus)
## same than: tr <- root(nj.sylvia.K80, "AJ534526")
# nj.phylo analyse bipartitions found in series of trees (from documntation)
nj.boot.sylvia <- boot.phylo(tr, sylvia.clus, f, 200,
                           rooted = TRUE)
nj.boot.codon <- boot.phylo(tr, sylvia.clus, f, 200, 3,
                           rooted = TRUE)
nj.est <- tr
nj.est$tip.label <- taxa.sylvia[tr$tip.label]

# The plot is not needed
#plot(nj.est, no.margin = TRUE)
#modelabels(round(nj.boot.sylvia / 200, 2), bg = "white")
#add.scale.bar(length = 0.01)

# Saves the tree to the file
write.tree(nj.est, "sylvia_nj_k80.tre")

# Writes 25 sequences to a file. Length is 1143.
write.dna(sylvia.clus, "sylvia.txt")

# Calls PhyML and fits 28 models of DNA evolution. They're saved to disk and
# in R returned as a vector. The log-likelihood is saved in this vector.
phymL.sylvia <- phymLtest("sylvia.txt")

```

```

# Again not needed for obtaining the tree
#summary(phyml.sylvia)
#plot(phyml.sylvia, col = "black")

# Read the tree from the txt.
TR <- read.tree("sylvia.txt_phyml_tree.txt")

# Adding some labels and descriptions to the tree
mltr.sylvia <- TR[[28]]
mltr.sylvia$tip.label <- taxa.sylvia[mltr.sylvia$tip.label]
mltr.sylvia <- root(mltr.sylvia, "Chamaea_fasciata")
#plot(mltr.sylvia, no.margin = TRUE)
#add.scale.bar(length = 0.01)

# The tip is dropped as explained in the exercise
tr.ml <- drop.tip(mltr.sylvia, "Chamaea_fasciata")
res <- vector("list", 9)

# The for loop takes some time. chronopl estimates the node ages of trees by
# using a semi-parametric method based on penalized likelihood (see docu-
# mentation).
for (L in -4:4)
  res[[L + 5]] <- chronopl(tr.ml, 10^L, 12, 16, CV = TRUE)
Lambda <- 10^(-4:4)
CV <- sapply(res, function(x) sum(attr(x, "D2"))))
#plot(Lambda, CV / 1e5, log = "x")

# Add the attribute "rates" to the tree with 24 tips and 23 internal nodes
sylvia.chrono <- res[[2]]
rts <- attr(sylvia.chrono, "rates")
#summary(rts)

# Not needed for obtaining the tree
#par(mar = c(2, 0, 0, 0))
#plot(sylvia.chrono, edge.width = 100*rts, label.offset = .15)
#axisPhylo()

# Finally writes the tree to the file.
write.tree(sylvia.chrono, "sylvia.chrono.tre")

###
### Chapter 6
###

# Load the RData
load("sylvia.RData")
# Read the tree
nj.est <- read.tree("sylvia_nj_k80.tre")
# Drop the tip as mentioned in the exercise
nj.est <- drop.tip(nj.est, "Chamaea_fasciata")

# Get mig.dist, mig.behav and geo.range and save it to DF
DF <- sylvia.eco[nj.est$tip.label, ]

```

```

# Create a table with the range and the behav, so its long, resid, short against
# temp, temptrop and trop
table(DF$geo.range, DF$mig.behav)

# Ace ist used to estimate the ancestral character states and the corresponding
# uncertainty (traits), the "d" defines that we're handling discrete
# characters. Seond call changes the model, which is a numeric matrix
syl.er <- ace(DF$geo.range, nj.est, type = "d")
syl.sym <- ace(DF$geo.range, nj.est, type="d", model="SYM")
# Variance/Deviance for the fitted models (incl. Likelihood) and Chi Testing
#anova(syl.er, syl.sym)

mod <- matrix(0, 3, 3)
mod[2, 1] <- mod[1, 2] <- 1
mod[2, 3] <- mod[3, 2] <- 2

# Now we use the creates model to estimate again
syl.mod <- ace(DF$geo.range, nj.est, type="d", model=mod)

sapply(list(syl.er, syl.sym, syl.mod), AIC)

#Q <- syl.mod$index.matrix
#diag(Q) <- 0
#Q[1, 2] <- Q[2, 1] <- syl.mod$rates[1]
#Q[2, 3] <- Q[3, 2] <- syl.mod$rates[2]

#Q[] <- c(0, syl.mod$rates)[Q + 1]
#diag(Q) <- -rowSums(Q)

# THIS IS NOT WORKING AS WE HAVE NAs IN THE MATRIX
#P <- mtepo(0.05 * Q)
#rownames(P) <- c("temp", "temptrop", "trop")
#colnames(P) <- rownames(P)

# This works but do we need this?
#sylvia.chrono <- read.tree("sylvia.chrono.tre")
#yule(sylvia.chrono)
#birthdeath(sylvia.chrono)
#1 - pchisq(2*(-1.034112 - -1.113822), 1)

#x <- sylvia.eco[sylvia.chrono$tip.label, "geo.range"]
#ANC <- ace(x, sylvia.chrono, type = "d", model = mod)
#ANC$lik.anc[1:3, ]
#anc <- apply(ANC$lik.anc, 1, which.max)
#X <- factor(c(x, anc))
# This breaks as we have NAs!
#yule.cov(sylvia.chrono, ~ X)
#1 / (1 + exp(-(-0.0535529)))
#1 / (1 + exp(-(-0.0535529 -1.4608019)))
#1 / (1 + exp(-(-0.0535529 -0.9775966)))

#fsamp <- function(x) sample(length(x), size = 1, prob = x)
#nrep <- 1e3

```

```

#Puls <- numeric(nrep)
#for (i in 1:nrep) {
#  anc <- apply(ANC$lik.anc, 1, fsamp)
#  X <- factor(c(x, anc))
#  Puls[i] <- yule.cov(sylvia.chrono, ~ X)$Pval
#}
#hist(Puls, freq = FALSE, main = "")
#lines(density(Puls))

# That's the plot which is nice so we should leave it :)
co <- rep("grey", 24)
co[DF$geo.range == "temp"] <- "black"
co[DF$geo.range == "trop"] <- "white"
plot(nj.est, "c", FALSE, no.margin = TRUE, label.offset = 1)
tiplabels(pch = 22, bg = co, cex = 2, adj = 1)
nodelabels(thermo = syl.mod$lik.anc, cex = 0.8,
            piecol = c("black", "grey", "white"))
ace(DF$geo.range, nj.est, type="discrete", model="ER")
#check R console
ace(DF$geo.range, nj.est, type="discrete", model="ARD")
#check R console
ace(DF$geo.range, nj.est, type="discrete", model="SYM")
#check R console

```

```

# -----
# Question 2, Task 1
# -----

```

```

# Data import -----

```

```

data("carni70")
df = carni70$tab # quantitative traits
tree = carni70$tre # phylogenetic tree
rm(carni70)

```

```

# Create Plots -----

```

```

# Descriptive Statistics -----

```

```

knitr::kable(as.data.frame(round(psych::describe(df), 2)),
             caption = "Descriptive Statistics of Quantitative Traits")

```

```

# Scatterplot of size by range -----

```

```

ggplot(df, aes(range, size)) + geom_point(color = "skyblue3", alpha = 0.8) +
  labs(title = "Scatterplot of Body Size (in kg) by Geographic Range (in km)",
       y = "Body Size", x = "Geografic Range") +
  theme_bw() + theme(plot.title = element_text(hjust = 0.5))

```

```

# Density plots of size and range -----

```

```

ggplot(df, aes(size)) + geom_density(fill = "skyblue3", alpha = 0.8) +
  labs(title = "Density Plot of Body Size (in kg)",
       y = "Density", x = "Body Size") +
  theme_bw() + theme(plot.title = element_text(hjust = 0.5))

```

```

cat("\n\n\n")

ggplot(df, aes(range)) + geom_density(fill = "skyblue3", alpha = 0.8) +
  labs(title = "Density Plot of Geografic Range (in km)",
       y = "Density", x = "Geografic range") +
  theme_bw() + theme(plot.title = element_text(hjust = 0.5))

# Heatmap of observation by size and range -----
library(plotly)
library(seriation)
df_scaled = scale(df)
rowdist=dist(df_scaled)
set.seed(12345)
order=seriate(rowdist, "HC")
ord=get_order(order)
reordmatr=df_scaled[rev(ord),]

p = plot_ly(x=colnames(reordmatr), y=rownames(reordmatr), z=reordmatr,
            type="heatmap", colors = ~rev(scales::viridis_pal(option = "viridis")(3)),
            xgap = 1, ygap = 1) %>%
  layout(title = "Heatmap: Body Size and Geografic Range by Species [normalized]",
         font = list(size = 8))

# CONVERTING PLOTLY OBJ. TO PNG (MAPBOX_TOKEN + orca INSTALLATION REQUIRED)
# Sys.setenv("MAPBOX_TOKEN" = "YOURTOKEN")
# plotly::orca(p, file = "images/heatmap.png", scale = 3, height = 950, width = 700)

knitr::include_graphics("images/heatmap.png")

# Scatterplot colored by clusters identified by heatmap -----
df_cluster = data.frame(species = rev(rownames(reordmatr)),
                        cluster = rep("outliers", nrow(reordmatr)),
                        stringsAsFactors = FALSE)
df_cluster[7:41, "cluster"] = "cluster1"
df_cluster[42:nrow(df_cluster), "cluster"] = "cluster2"

df_plot = df
df_plot$species = rownames(df_plot)
df_plot %<>% left_join(df_cluster, by = "species")

# Scatterplot of size by range -----
ggplot(df_plot, aes(range, size)) + geom_point(aes(color = cluster), alpha = 0.8)+
  labs(title = "Scatterplot with Clusters Identified from Heatmap",
       y = "Body Size", x = "Geografic Range", color = "Cluster") +
  theme_bw() + theme(plot.title = element_text(hjust = 0.5))

# Tree Visualization -----

# For reference:
# https://cran.r-project.org/web/packages/phylogram/vignettes/phylogram-vignette.html
# http://www.sthda.com/english/wiki/beautiful-dendrogram-visualizations-in-r-5-must-known-methods-unsup

```

```

# converting tree to dendrogram (required for all alternatives below)
dnd = phylogram::read.dendrogram(text = tree)

# # ALTERNATIVE 1: Ugly
# plot(dnd, yaxt = "n")

# # ALTERNATIVE 2: Okay
# dnd %>% dendextend::set("labels_cex", 0.5) %>% plot

# ALTERNATIVE 3: Nice
# gg dendrogram(dnd, rotate = TRUE, theme_dendro = FALSE)

# ALTERNATIVE 4: Nice + Cluster Colors Specified
dnd_data = gg dendro::dendro_data(dnd) # converting dendrogram to data.frame
df_cluster$species = gsub("_", ".", df_cluster$species) # replace "_" by "."
dnd_data$labels %<>% left_join(df_cluster, by = c("label" = "species")) # join

gg dendrogram(dnd, rotate = TRUE, theme_dendro = FALSE, labels = FALSE) +
  geom_text(data = dnd_data$labels, aes(x, y, label = label, color = cluster),
            hjust = 1, angle = 0, size = 3) + labs(x = "", y = "",
            title = "Dendrogram (Colored by Clusters identified from Heatmap)") +
  theme(plot.title = element_text(hjust = 0.5)) + theme_minimal() +
  scale_y_continuous(limits = c(-20, 65))

# -----
# Question 2, Task 2
# -----

# Data import -----

data("carni70")
df = carn70
rm(carni70)

# For reference:
# mvSLOUCH: https://cran.r-project.org/web/packages/mvSLOUCH/mvSLOUCH.pdf
# mvMORPH: https://cran.r-project.org/web/packages/mvMORPH/mvMORPH.pdf
# https://cran.r-project.org/web/packages/mvMORPH/vignettes/tutorial\_mvMORPH.pdf
# ouch: https://cran.r-project.org/web/packages/ouch/ouch.pdf
# slouch: https://cran.r-project.org/web/packages/slouch/slouch.pdf

# -----
# 1. Both traits evolve as independent Brownian motions. -----
tree = ape::read.tree(text = df$tre)
BM_independent = mvMORPH::mvBM(tree, df$stab, model="BM1",
                                param=list(constraint="diagonal"))
summary(BM_independent)

# -----
# 2. The traits evolve as a correlated Brownian motion. -----
tree = ape::read.tree(text = df$tre)
BM_correlated = mvMORPH::mvBM(tree, df$stab, model="BM1",

```

```

                                param=list(constraint="correlation"))
summary(BM_correlated)

# -----
# 3. Both traits evolve as independent Ornstein-Uhlenbeck proc. -----

## Kryzstof: ouchModel and specify Atype = "Diagonal", Syytype = "Diagonal"
tree = ape::read.tree(text = df$tre)
tre_ouch = ouch::ape2ouch(tree = tree)

# TAKES TIME
OU_indep = mvSLOUCH::ouchModel(tre_ouch, as.matrix(df$tab),
                                Atype = "Diagonal", Syytype = "Diagonal")
OU_indep

# -----
# 4. The traits evolve as a bivariate Ornstein-Uhlenbeck process -----

# For reference, see page 5 from here:
# https://cran.r-project.org/web/packages/mvMORPH/vignettes/tutorial_mvMORPH.pdf
set.seed(12345)
tree = ape::read.tree(text = df$tre)
OU_bivariate = mvMORPH::mvOU(tree, df$tab, model="OU1")
summary(OU_bivariate)
# Alternative solution (different result)
# multiOU = ouchModel(tree_ouch, data_matrix)

# -----
# 5. Size evolves as a Brownian motion and range as an Ornstein-Uhlenbeck process
# adapting to it -----
tree = ape::read.tree(text = df$tre)
phyltree = ouch::ape2ouch(tree = tree)

# TAKES TIME
BM_OU = mvSLOUCH::mvslouchModel(phyltree, as.matrix(df$tab[, c(2, 1)]), kY = 1)
BM_OU

# 2.2.3 Output -----

# > OU_indep
# $FinalFound
# $FinalFound$HeuristicSearchPointFinalFind
#      Astart      Aend      Syystart      Syyend      LogLik
#      3.753733      2.279597      5.938614      3.704447 -606.612614
#
# $FinalFound$ParamsInModel
# $FinalFound$ParamsInModel$A
#      size      range
# size 42.6801 0.000000
# range 0.0000 9.772741
#
# $FinalFound$ParamsInModel$mPsi

```

```

#           reg.1
# size  14.51679
# range 11.11718
#
# $FinalFound$ParamsInModel$mPsi0
#           [,1]
# size      0
# range     0
#
# $FinalFound$ParamsInModel$uY0
#           [,1]
# size  14.51679
# range 11.11718
#
# $FinalFound$ParamsInModel$Syy
#           size      range
# size  379.4088  0.00000
# range  0.0000 40.62757
#
#
# $FinalFound$ParamSummary
# $FinalFound$ParamSummary$phyl.halflife
# $FinalFound$ParamSummary$phyl.halflife$directions
#           [,1] [,2]
# [1,]    -1    0
# [2,]     0   -1
#
# $FinalFound$ParamSummary$phyl.halflife$halflives
#           [,1]      [,2]
# eigenvalues 42.68009601 9.77274147
# halflife    0.01624053 0.07092659
# %treeheight 1.62405253 7.09265852
#
# $FinalFound$ParamSummary$phyl.halflife$halflifeLowerbounds
# [1] 0.01321467
#
#
# $FinalFound$ParamSummary$expmtA
#           size      range
# size      0 0.000000e+00
# range     0 5.698392e-05
#
# $FinalFound$ParamSummary$mPsi.rotated
#           reg.1
# size  14.51679
# range 11.11654
#
# $FinalFound$ParamSummary$mPsi0.rotated
#           [,1]
# size      0
# range     0
#
# $FinalFound$ParamSummary$cov.matrix

```



```

#           size    range
# size 1686.395 0.00000
# range 0.000 84.44917
#
# $FinalFound$ParamSummary$corr.matrix
#           size range
# size      1      0
# range     0      1
#
# $FinalFound$ParamSummary$stationary.cov.matrix
#           size    range
# size 1686.395 0.00000
# range 0.000 84.44917
#
# $FinalFound$ParamSummary$stationary.corr.matrix
#           size range
# size      1      0
# range     0      1
#
# $FinalFound$ParamSummary$StS
#           size range
# size 143951 0.0
# range      0 1650.6
#
# $FinalFound$ParamSummary$LogLik
# [1] -606.6126
#
# $FinalFound$ParamSummary$dof
# [1] 6
#
# $FinalFound$ParamSummary$m2loglik
# [1] 1213.225
#
# $FinalFound$ParamSummary$aic
# [1] 1225.225
#
# $FinalFound$ParamSummary$aic.c
# [1] 1225.857
#
# $FinalFound$ParamSummary$sic
# [1] 1242.875
#
# $FinalFound$ParamSummary$bic
# [1] 1242.875
#
# $FinalFound$ParamSummary$RSS
# $FinalFound$ParamSummary$RSS$RSS
#           [,1]
# [1,] 140.0022
#
# $FinalFound$ParamSummary$RSS$R2
#           [,1]
# [1,] -4.440892e-16

```

```

#
#
# $FinalFound$ParamSummary$trait.regression
# $FinalFound$ParamSummary$trait.regression[[1]]
#   range
# size    0
#
# $FinalFound$ParamSummary$trait.regression[[2]]
#   size
# range    0
#
#
# $FinalFound$ParamSummary$confidence.interval
# $FinalFound$ParamSummary$confidence.interval$regression.summary
# $FinalFound$ParamSummary$confidence.interval$regression.summary$mPsi.regression.confidence.interval
#   Lower.end Estimated.Point Upper.end
# size  4.468074      14.51679  24.56551
# range  8.338613      11.11718  13.89574
#
#
#
# $FinalFound$ParamSummary$limiting.trait.regression
# $FinalFound$ParamSummary$limiting.trait.regression[[1]]
#   range
# size    0
#
# $FinalFound$ParamSummary$limiting.trait.regression[[2]]
#   size
# range    0
#
#
#
# $FinalFound$LogLik
# [1] -606.6126
#
#
# $MaxLikFound
# [1] "Same as final found"

# 2.2.5 Output -----

# $FinalFound
# $FinalFound$HeuristicSearchPointFinalFind
#   A      Syy  LogLik
# 2.34  3.71 -641.80
#
# $FinalFound$ParamsInModel
# $FinalFound$ParamsInModel$A
#   range
# range 10.4
#

```

```

# $FinalFound$ParamsInModel$B
#      size
# range -0.689
#
# $FinalFound$ParamsInModel$mPsi
#      reg.1
# range 10.2
#
# $FinalFound$ParamsInModel$mPsi0
#      [,1]
# range 0
#
# $FinalFound$ParamsInModel$uY0
#      [,1]
# range 10.7
#
# $FinalFound$ParamsInModel$uX0
#      [,1]
# size 8.43
#
# $FinalFound$ParamsInModel$Syy
#      range
# range 41
#
# $FinalFound$ParamsInModel$Syx
#      size
# range 0
#
# $FinalFound$ParamsInModel$Sxy
#      range
# size 0
#
# $FinalFound$ParamsInModel$Sxx
#      size
# size 171
#
#
# $FinalFound$ParamSummary
# $FinalFound$ParamSummary$phyl.halflife
# $FinalFound$ParamSummary$phyl.halflife$directions
#      [,1]
# [1,] 1
#
# $FinalFound$ParamSummary$phyl.halflife$halflives
#      [,1]
# eigenvalues 10.3893
# halflife 0.0667
# %treeheight 6.6717
#
# $FinalFound$ParamSummary$phyl.halflife$halflifeLowerbounds
# [1] 0.0667
#
#

```

```

# $FinalFound$ParamSummary$expmtA
#       range
# range 0.0000308
#
# $FinalFound$ParamSummary$optimal.regression
#       size
# range 0.0663
#
# $FinalFound$ParamSummary$mPsi.rotated
#       reg.1
# range 10.2
#
# $FinalFound$ParamSummary$mPsi0.rotated
#       [,1]
# range 0
#
# $FinalFound$ParamSummary$cov.matrix
#       range size
# range 191 1761
# size 1761 29383
#
# $FinalFound$ParamSummary$corr.matrix
#       range size
# range 1.000 0.743
# size 0.743 1.000
#
# $FinalFound$ParamSummary$conditional.cov.matrix
#       range
# range 85.9
#
# $FinalFound$ParamSummary$conditional.corr.matrix
#       range
# range 1
#
# $FinalFound$ParamSummary$stationary.cov.matrix
#       range
# range 87.1
#
# $FinalFound$ParamSummary$stationary.corr.matrix
#       range
# range 1
#
# $FinalFound$ParamSummary$optima.cov.matrix
#       range
# range 129
#
# $FinalFound$ParamSummary$optima.corr.matrix
#       range
# range 1
#
# $FinalFound$ParamSummary$cov.with.optima
#       range
# range 117

```

```

#
# $FinalFound$ParamSummary$corr.with.optima
#     range
# range 0.743
#
# $FinalFound$ParamSummary$evolutionary.regression
#     size
# range 0.0599
#
# $FinalFound$ParamSummary$StS
#     range size
# range 1681    0
# size      0 29383
#
# $FinalFound$ParamSummary$LogLik
# [1] -642
#
# $FinalFound$ParamSummary$dof
# [1] 6
#
# $FinalFound$ParamSummary$m2loglik
# [1] 1284
#
# $FinalFound$ParamSummary$aic
# [1] 1296
#
# $FinalFound$ParamSummary$aic.c
# [1] 1296
#
# $FinalFound$ParamSummary$sic
# [1] 1313
#
# $FinalFound$ParamSummary$bic
# [1] 1313
#
# $FinalFound$ParamSummary$RSS
# $FinalFound$ParamSummary$RSS$RSS
#     [,1]
# [1,]  140
#
# $FinalFound$ParamSummary$RSS$R2
#     [,1]
# [1,] 0.0178
#
#
# $FinalFound$ParamSummary$trait.regression
# $FinalFound$ParamSummary$trait.regression[[1]]
#     size
# range 0.0599
#
#
# $FinalFound$ParamSummary$confidence.interval
# $FinalFound$ParamSummary$confidence.interval$regression.summary

```

```

# $FinalFound$ParamSummary$confidence.interval$regression.summary$B.regression.confidence.interval
#       Lower.end Estimated.Point Upper.end
# range   -1.89          -0.689    0.512
#
# $FinalFound$ParamSummary$confidence.interval$regression.summary$mPsi.regression.confidence.interval
#       Lower.end Estimated.Point Upper.end
# range     6.95          10.2    13.4
#
#
#
#
# $FinalFound$LogLik
# [1] -642
#
#
# $MaxLikFound
# $MaxLikFound$HeuristicSearchPointMaxLik
#       A      Syy LogLik
#  2.33   3.71 -641.80
#
# $MaxLikFound$ParamsInModel
# $MaxLikFound$ParamsInModel$A
#       range
# range 10.3
#
# $MaxLikFound$ParamsInModel$B
#       size
# range -0.658
#
# $MaxLikFound$ParamsInModel$mPsi
#       reg.1
# range 10.1
#
# $MaxLikFound$ParamsInModel$mPsi0
#       [,1]
# range 0
#
# $MaxLikFound$ParamsInModel$uY0
#       [,1]
# range 10.7
#
# $MaxLikFound$ParamsInModel$uX0
#       [,1]
# size 8.43
#
# $MaxLikFound$ParamsInModel$Syy
#       range
# range 40.8
#
# $MaxLikFound$ParamsInModel$Syx
#       size
# range 0
#

```

```

# $MaxLikFound$ParamsInModel$Sxy
#     range
# size      0
#
# $MaxLikFound$ParamsInModel$Sxx
#     size
# size    171
#
#
# $MaxLikFound$ParamSummary
# $MaxLikFound$ParamSummary$phyl.halflife
# $MaxLikFound$ParamSummary$phyl.halflife$directions
#     [,1]
# [1,]    1
#
# $MaxLikFound$ParamSummary$phyl.halflife$halflives
#     [,1]
# eigenvalues 10.2826
# halflife    0.0674
# %treeheight 6.7410
#
# $MaxLikFound$ParamSummary$phyl.halflife$halflifeLowerbounds
# [1] 0.0674
#
#
# $MaxLikFound$ParamSummary$expmtA
#     range
# range 0.0000342
#
# $MaxLikFound$ParamSummary$optimal.regression
#     size
# range 0.064
#
# $MaxLikFound$ParamSummary$mPsi.rotated
#     reg.1
# range 10.1
#
# $MaxLikFound$ParamSummary$mPsi0.rotated
#     [,1]
# range    0
#
# $MaxLikFound$ParamSummary$cov.matrix
#     range size
# range  184 1697
# size   1697 29383
#
# $MaxLikFound$ParamSummary$corr.matrix
#     range size
# range  1.00 0.73
# size   0.73 1.00
#
# $MaxLikFound$ParamSummary$conditional.cov.matrix
#     range

```

```

# range 85.8
#
# $MaxLikFound$ParamSummary$conditional.corr.matrix
# range
# range 1
#
# $MaxLikFound$ParamSummary$stationary.cov.matrix
# range
# range 86.9
#
# $MaxLikFound$ParamSummary$stationary.corr.matrix
# range
# range 1
#
# $MaxLikFound$ParamSummary$optima.cov.matrix
# range
# range 120
#
# $MaxLikFound$ParamSummary$optima.corr.matrix
# range
# range 1
#
# $MaxLikFound$ParamSummary$cov.with.optima
# range
# range 109
#
# $MaxLikFound$ParamSummary$corr.with.optima
# range
# range 0.73
#
# $MaxLikFound$ParamSummary$evolutionary.regression
# size
# range 0.0578
#
# $MaxLikFound$ParamSummary$StS
# range size
# range 1667 0
# size 0 29383
#
# $MaxLikFound$ParamSummary$LogLik
# [1] -642
#
# $MaxLikFound$ParamSummary$dof
# [1] 6
#
# $MaxLikFound$ParamSummary$m2loglik
# [1] 1284
#
# $MaxLikFound$ParamSummary$aic
# [1] 1296
#
# $MaxLikFound$ParamSummary$aic.c
# [1] 1296

```



```

#
# $MaxLikFound$ParamSummary$sic
# [1] 1313
#
# $MaxLikFound$ParamSummary$bic
# [1] 1313
#
# $MaxLikFound$ParamSummary$RSS
# $MaxLikFound$ParamSummary$RSS$RSS
#      [,1]
# [1,] 140
#
# $MaxLikFound$ParamSummary$RSS$R2
#      [,1]
# [1,] 0.0177
#
#
# $MaxLikFound$ParamSummary$trait.regression
# $MaxLikFound$ParamSummary$trait.regression[[1]]
#      size
# range 0.0578
#
#
# $MaxLikFound$ParamSummary$confidence.interval
# $MaxLikFound$ParamSummary$confidence.interval$regression.summary
# $MaxLikFound$ParamSummary$confidence.interval$regression.summary$B.regression.confidence.interval
#      Lower.end Estimated.Point Upper.end
# range      -1.82      -0.658      0.505
#
# $MaxLikFound$ParamSummary$confidence.interval$regression.summary$mPsi.regression.confidence.interval
#      Lower.end Estimated.Point Upper.end
# range      6.72      10.1      13.5
#
# $MaxLikFound$LogLik
# [1] -642

```