

Lab 3

Simon Jorstedt

2024-11-29

```
library(ade4)
```

```
## Warning: package 'ade4' was built under R version 4.4.2
```

```
library(ape)
```

```
## Warning: package 'ape' was built under R version 4.4.2
```

```
library(dplyr)
```

```
##
```

```
## Attaching package: 'dplyr'
```

```
## The following object is masked from 'package:ape':
```

```
##
```

```
##      where
```

```
## The following objects are masked from 'package:stats':
```

```
##
```

```
##      filter, lag
```

```
## The following objects are masked from 'package:base':
```

```
##
```

```
##      intersect, setdiff, setequal, union
```

```
library(magrittr)
```

```
library(mvMORPH)
```

```
## Warning: package 'mvMORPH' was built under R version 4.4.2
```

```
## Loading required package: phytools
```

```
## Warning: package 'phytools' was built under R version 4.4.2
```

```
## Loading required package: maps
```

```
## Warning: package 'maps' was built under R version 4.4.2
```

```
## Loading required package: corpcor

## Loading required package: subplex

## ##
## ## mvMORPH package (1.2.1)

## ## Multivariate evolutionary models

## ##
## ## See the tutorials: browseVignettes("mvMORPH")

## ##
## ## To cite package 'mvMORPH': citation("mvMORPH")
## ##

library(mvSLOUCH)

## Warning: package 'mvSLOUCH' was built under R version 4.4.2

## Loading required package: abind

data(carni70)
```

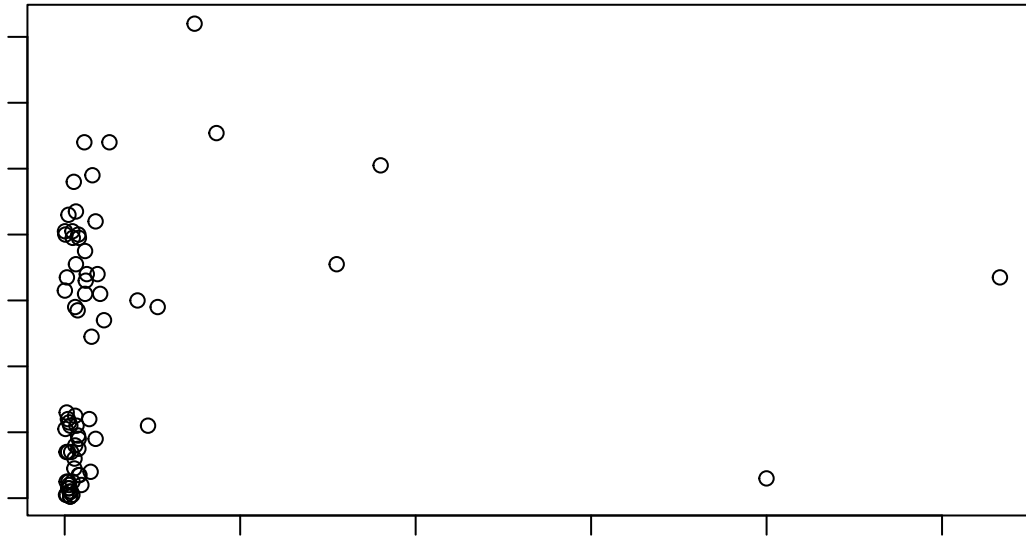
Q 2

Q 2.1

Explore the data set and report what can be found in it. Provide some plots

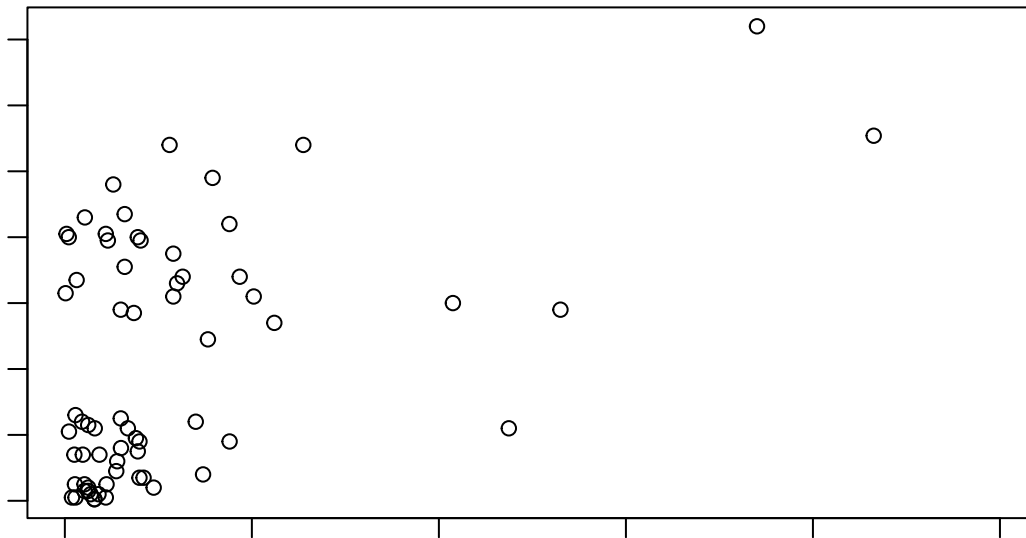
The `carni70` dataset describes the phylogeny, as well as geographic range (km) and body size (kg) of 70 carnivorous animals. In Figure 1 and 2 below we find that a majority of the animals are relatively small/light (under 10kg), with some outliers in the 20-50 kg range, and just two in the range of 200-260 kg range. Most of the animals belong to either a cluster with low range (up to about 7 km), or a cluster with longer range (around 12-27 km). In Figure 3 we see a phylogenetic tree of the animals

```
# Plot the range vs the size
plot(carni70$tab$size, carni70$tab$range,
      xlab="Body size (kg)",
      ylab="Geographical range (km)",
      main="Fig. 1: Geographical range vs body size")
```

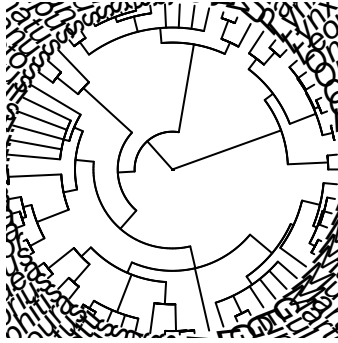


```
# Plot range vs size of small animals
small_carni <- carni70$tab %>%
  filter(size < 50)

plot(small_carni$size, small_carni$range,
     xlab="Body size (kg)",
     ylab="Geographical range (km)",
     main="Fig. 2: Geographical range vs body size of small animals (< 50kg)",
     xlim = c(0,50))
```



```
# Plot the phylogeny
carni_tree <- ape::read.tree(text = carni70$tre)
plot(carni_tree, type="fan",
     main="Fig. 3: Species phylogeny")
```



```
# Change carni70 names, since names are separated with "." in the tree
rownames(carni70$tab) <- gsub("_", replacement = ".", rownames(carni70$tab))
```

Q 2.2

Analyze the two traits (size and range) with a number of different phylogenetic comparative models. Look at the R packages *ape*, *mvMORPH*, *mvSLOUCH*, *ouch* and *slouch* (the last one is NOT on CRAN and can be downloaded from <https://github.com/kopperud/slouch>). We will analyse the data under five different models, described in the code chunk below.

Below we train the models, and then take some interesting results (mainly the loglikelihood and AIC scores) and display them in a dataframe. We find that both the Brownian motion models are practically the same, while the two Ornstein-Uhlenbeck models are slightly better, but the mixed model achieves the best fit, measured in the AIC score, but by a small margin.

```
# Both traits evolving as independent Brownian motions
bm_indep <- mvMORPH::mvBM(carni_tree,
                          data = carni70$tab,
                          model="BM1",
                          param = list(constaint="diagonal"))
```

```
## successful convergence of the optimizer
## a reliable solution has been reached
##
## -- Summary results for multiple rate BM1 model --
## LogLikelihood:   -588.7853
## AIC:             1187.571
## AICc:            1188.018
## 5 parameters
##
## Estimated rate matrix
## -----
##           size      range
## size 73.703348  3.579341
## range 3.579341 13.545242
##
## Estimated root state
## -----
##           size      range
## theta: 38.43947 13.78439
```

```
# The traits evolve as a correlated Brownian motion
bm_dep <- mvMORPH::mvBM(carni_tree,
                        data = carni70$tab,
                        model="BM1")
```

```
## successful convergence of the optimizer
## a reliable solution has been reached
##
## -- Summary results for multiple rate BM1 model --
## LogLikelihood:    -588.7853
## AIC:              1187.571
## AICc:             1188.018
## 5 parameters
##
## Estimated rate matrix
## -----
##           size      range
## size 73.703348 3.579341
## range 3.579341 13.545240
##
## Estimated root state
## -----
##           size      range
## theta: 38.43947 13.78439
```

```
# Both traits evolving as independent Ornstein-Uhlenbeck processes
ou_indep <- mvMORPH::mvOU(carni_tree,
                          data=carni70$tab,
                          model="OU1",
                          param = list(constaint="diagonal"))
```

```
## successful convergence of the optimizer
## a reliable solution has been reached
##
## -- Summary results --
## LogLikelihood:    -573.7985
## AIC:              1163.597
## AICc:             1164.696
## 8 parameters
##
## Estimated theta values
## -----
##           size      range
## OU1 37.13047 11.41715
##
## ML alpha values
## -----
##           size      range
## size 0.006381987 -0.003730754
## range -0.003730754 0.234973814
##
## ML sigma values
## -----
```

```
##           size      range
## size  79.979667  6.127908
## range  6.127908 38.501723
```

```
# Traits evolving as bivariate Ornstein-Uhlenbeck process
```

```
ou_dep <- mvMORPH::mvOU(carni_tree,
                        data=carni70$tab,
                        model="OU1")
```

```
## successful convergence of the optimizer
## a reliable solution has been reached
```

```
##
## -- Summary results --
## LogLikelihood:   -572.6063
## AIC:             1161.213
## AICc:            1162.312
## 8 parameters
```

```
##
## Estimated theta values
```

```
## -----
##           size      range
## OU1  37.55833 11.42602
```

```
##
## ML alpha values
```

```
## -----
##           size      range
## size   8.345549e-05 -0.003859286
## range -3.859286e-03  0.233577603
```

```
##
## ML sigma values
```

```
## -----
##           size      range
## size   73.766441  5.859783
## range  5.859783 38.247492
```

```
mixed_mod <- mvSLOUCH::mvslouchModel(carni_tree,
                                     as.matrix(carni70$tab[c(2,1)]),
                                     kY=1)
```

```
## Atype is at the default "Invertible" setting. This is a highly inefficient and unrecommended setting
```

```
# mvSLOUCH is an... interesting package
```

```
if (mixed_mod$MaxLikFound == "Same as final found"){
  mixed_mod$MaxLikFound <- mixed_mod$FinalFound
}
```

```
# Format results of the analyses
```

```
list("BM indep"=c(bm_indep$LogLik,
                  bm_indep$AIC,
                  bm_indep$AICc,
                  bm_indep$convergence,
                  bm_indep$hess.values),
```

```

"BM dep"=c(bm_dep$LogLik,
            bm_dep$AIC,
            bm_dep$AICc,
            bm_dep$convergence,
            bm_dep$hess.values),

"OU indep"=c(ou_indep$LogLik,
              ou_indep$AIC,
              ou_indep$AICc,
              ou_indep$convergence,
              ou_indep$hess.values),

"OU dep"=c(ou_dep$LogLik,
            ou_dep$AIC,
            ou_dep$AICc,
            ou_dep$convergence,
            ou_dep$hess.values),

"Mixed"=c(mixed_mod$MaxLikFound$LogLik,
           mixed_mod$MaxLikFound$ParamSummary$aic,
           mixed_mod$MaxLikFound$ParamSummary$aic.c,
           NA,
           NA)) %>%
do.call(rbind, .) %>%
set_colnames(c("LogLikelihood", "AIC", "AICc", "convergence", "hess.values"))

```

##	LogLikelihood	AIC	AICc	convergence	hess.values
## BM indep	-588.7853	1187.571	1188.018	0	0
## BM dep	-588.7853	1187.571	1188.018	0	0
## OU indep	-573.7985	1163.597	1164.696	0	0
## OU dep	-572.6063	1161.213	1162.312	0	0
## Mixed	-576.1675	1164.335	1164.967	NA	NA