Lab3 Q2

Milda Poceviciute, Fanny Karelius, Rab Nawaz Jan Sher and Saman Zahid

10 December 2018

```
#install.packages("ade4")
#install.packages("mvMORPH")
#install.packages("mvSLOUCH")
#install.packages("adephylo")
library(ade4)
library(mvMORPH)
```

```
## Loading required package: phytools

## Loading required package: ape

## Loading required package: maps

## Loading required package: corpcor

## Loading required package: subplex

## ##
## ## mvMORPH package (1.1.0)

## ## Multivariate evolutionary models

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

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

```
library(mvSLOUCH)
```

```
## Loading required package: ouch

## Loading required package: numDeriv

## Loading required package: mvtnorm
```

```
library(ape)
#devtools::install_github("kopperud/slouch")
# install.packages("rlang")
# install.packages("tibble")
library(tibble)
library(rlang)
```

Questions 2

Q2.1

In this question we analyse the data from *ade4* package. It contains the phylogeny of 70 carnivora as reported by Diniz-Filho and Torres (2002), and provides the geographic range size and body size corresponding to them.

```r
data(carni70)
carni70_tree <- newick2phylog(carni70$tre)


size <- scalewt(log(carni70$tab))[,1] # scaled log body size in kg
names(size) <- row.names(carni70$tab)
yrange <- scalewt(carni70$tab[,2])# scaled geographic range in km
names(yrange) <- row.names(carni70$tab)
plot_data <- data.frame(spieces = row.names(carni70$tab), size = size, range =yrange )
```
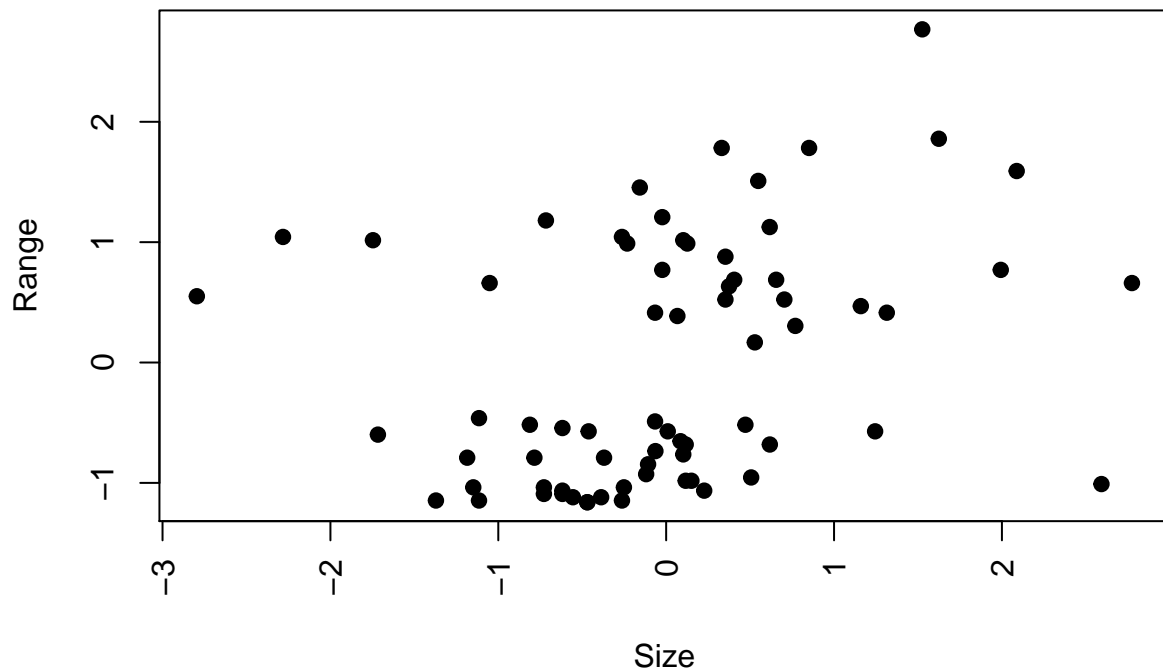
Plots below show the body sizes (scaled log), the ranges (scaled), as well as size and range dependencies that correspond to the different species. There seem to be no obvious linear relation between these two traits.

```r
par(mfrow=c(1,1),las=3)


plot(plot_data$spieces, plot_data$size, cex.axis=0.6,ylab = "Size", pch = 19,
     col = rgb(0, 0, 0, 0.1))
```



```r
plot(plot_data$spieces, plot_data$range, cex.axis=0.6, ylab = "Range", pch = 19,
     col = rgb(0, 0, 0, 0.1))
```
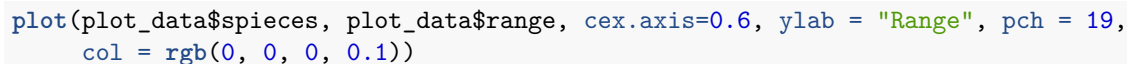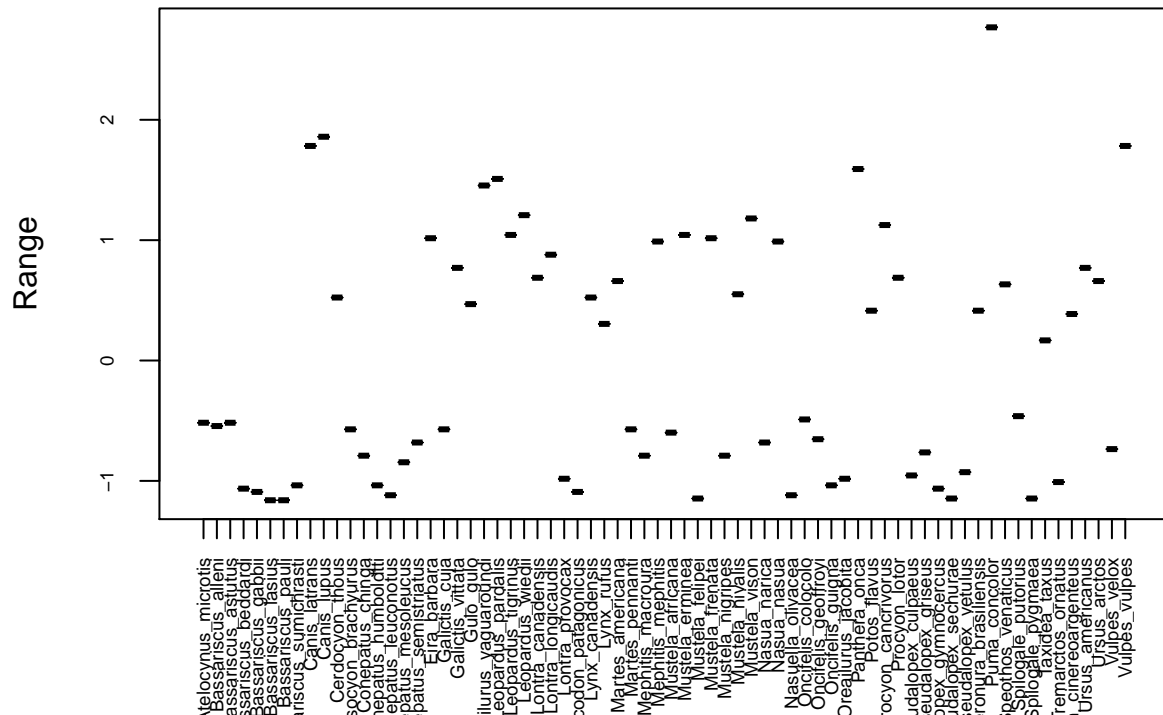
```
plot(plot_data$size, plot_data$range, xlab = "Size", ylab = "Range", pch = 19)
```
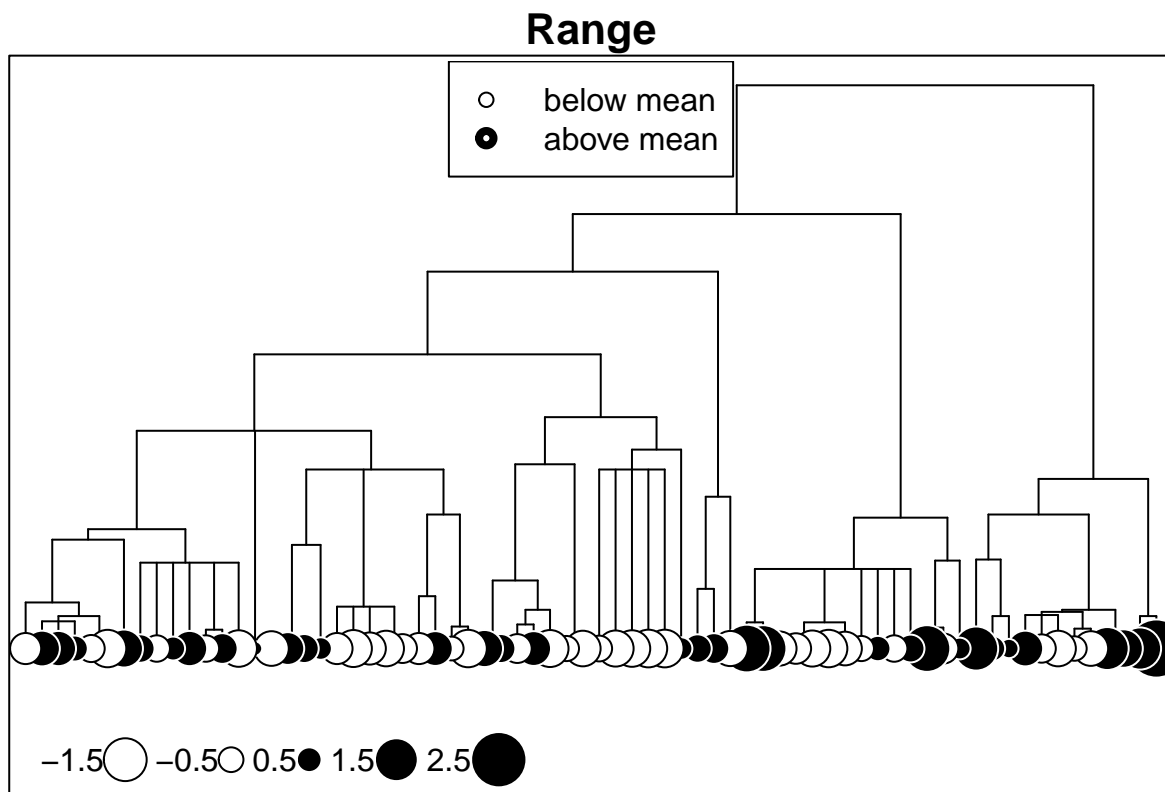
The plots below shows the phylogenetic tree. The first plot shows how the size trait evolved for different species. The white nodes represent the size below the mean while the black ones represent the body sizes above the mean. Similarly, the second tree plot shows the phylogenetic tree with respect to range.

```
tre <- as.phylo(carni70_tree)
carni70_tree <- newick2phylog(carni70$tre)

par(mfrow = c(1, 1), oma = c(1, 1, 2, 1))
symbols.phylog(carni70_tree,size)
mtext("Size", side = 3, line = 0, outer = TRUE, font = 2, cex = 1.3)
par(fig = c(0, 1, .1, .9), oma = c(0, 0, 0, 0), mar = c(0, 0, 0, 0), new = TRUE)
plot(0, 0, type = "n", bty = "n", xaxt = "n", yaxt = "n")
legend("top", c("below mean", "above mean"), col = c("black", "black"), lty=c(NA, NA),pch = c(1, 1), lw
```

Size


```
par(mfrow = c(1, 1), oma = c(1, 1, 2, 1))
symbols.phylog(carni70_tree,yrange)
mtext("Range", side = 3, line = 0, outer = TRUE, font = 2, cex = 1.3)
par(fig = c(0, 1, .1, .9), oma = c(0, 0, 0, 0), mar = c(0, 0, 0, 0), new = TRUE)
plot(0, 0, type = "n", bty = "n", xaxt = "n", yaxt = "n")
legend("top", c("below mean", "above mean"), col = c("black", "black"), lty=c(NA, NA),pch = c(1, 1), lw
```
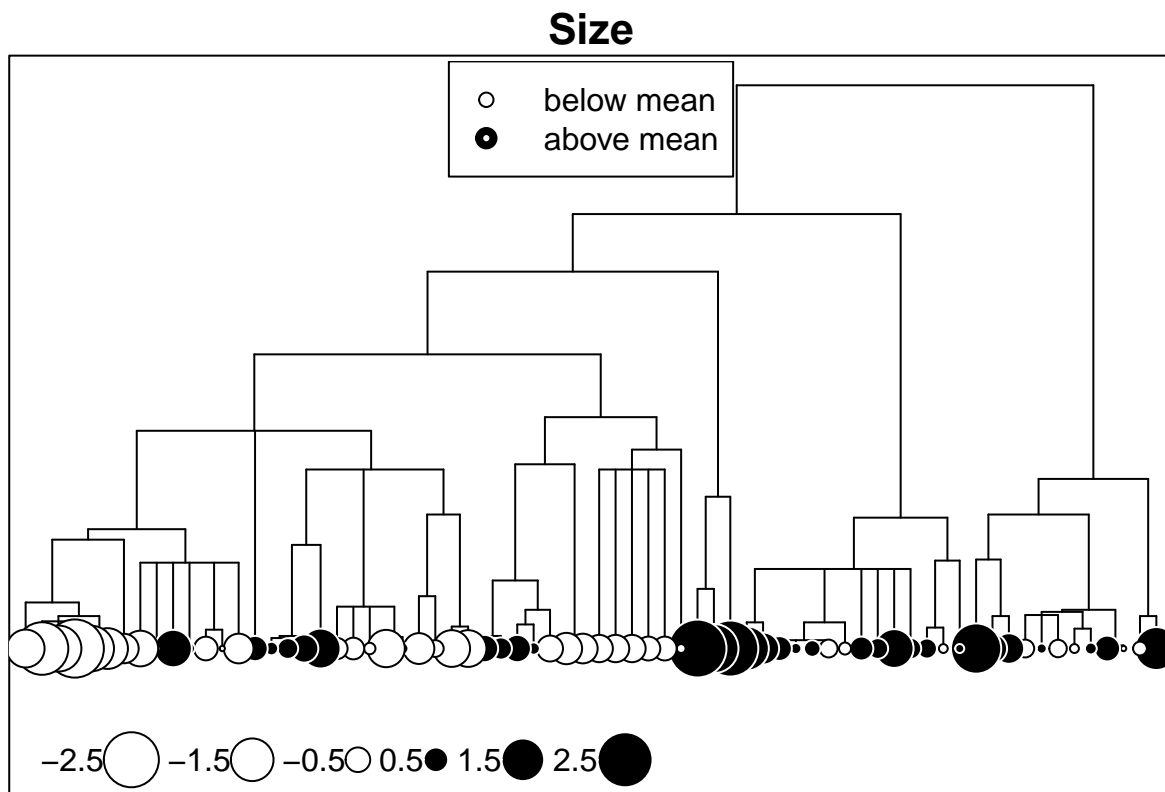
Range

Q2.2

Both traits evolve as independent Brownian motions

The parameter list of the function *mvBM* allows user to control if the traits evolved independently or not. Here we set constraint="diagonal" to make a model based on a joint likelihood of two independent traits.

```
fit1 <- mvBM(tre, data = carni70$tab, model="BM1", param=list(constraint="diagonal"))
```

```
## successful convergence of the optimizer
## a reliable solution has been reached
##
## -- Summary results for constrained rate  BM1 model --
## LogLikelihood:    -589.2373
## AIC:       1186.475
## AICc:      1186.771
## 4 parameters
##
## Estimated rate matrix
## _____
##           size     range
## size   73.70335  0.00000
## range   0.00000 13.54524
##
## Estimated root state
```

```
## -----------------------
##         size    range
## theta: 38.43947 13.78439
```

The model above is independent BMs for the size and range traits. The model estimated two parameters: *
Evolutionary rate matrix: is related to the variance (and covariances which are 0). We can see that the trait
size has much higher variance than the range trait:

```
fit1$sigma
```

```
##         size    range
## size  73.70335  0.00000
## range  0.00000 13.54524
```

- Estimated ancestral states: this shows that the expected value of the body size is higher than the
  expected value of the range.

```
fit1$theta
```

```
##         size    range
## theta: 38.43947 13.78439
```

The traits evolve as a correlated Brownian motion.

```
fit2 <- mvBM(tre, 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
```

The same parameters are estimated when both traits are assumed to have correlation between them:

```
cat(" Evolutionary rate matrix:")
```

```
##  Evolutionary rate matrix:
```

```
cat("\n")
```

```
fit2$sigma
```

```
##         size    range
## size  73.703348  3.579341
```

```
## range   3.579341 13.545240
```

```
cat(" Estimated ancestral states:")
```

```
##  Estimated ancestral states:
```

```
cat("\n")
```

```
fit2$theta
```

```
##               size     range
## theta: 38.43947 13.78439
```

We see that range and size has a positive covariance under this model. The variances and the ancestral states are very close to the ones estimated by the univariate models.

Both traits evolve as independent Ornstein-Uhlenbeck processes

```
phyltree = ape2ouch(tre)
# fit3_size <- mvOU(tre, data = carni70$tab[,1], model="OU1")
# fit3_range <- mvOU(tre, data = carni70$tab[,2], model="OU1")
fit3 <- ouchModel(phyltree, data = carni70$tab, Atype="Diagonal", Syytype="Diagonal")
```

```
## [1] "Starting point of heuristic search procedure : "
##      Astart         Aend   Syystart      Syyend
##   0.4140874 -0.3129726 -0.4184968   0.3397672
```

The two model is the independent Ornstein-Uhlenbeck processes (each trait is independent). The parameters estimated are:

```
cat("Alpha: strength of selection - low alpha favours a random change during the time step \n")
```

```
## Alpha: strength of selection - low alpha favours a random change during the time step
```

```
fit3$FinalFound$ParamsInModel$A
```

```
##               size     range
## size   2.316904e-07   0.00000
## range 0.000000e+00 12.35429
```

```
cat("Sigma: evolutionary rate matrix \n")
```

```
## Sigma: evolutionary rate matrix
```

```
fit3$FinalFound$ParamsInModel$Syy
```

```
##            size     range
## size   62.97915   0.00000
## range   0.00000 45.25617
```

```
cat("Theta: estimated ancestral states \n")
```

```
## Theta: estimated ancestral states
```

```
fit3$FinalFound$ParamsInModel$vY0
```

```
##             [,1]
## size   38.43947
## range  11.08612
```

It seems that the size trait is more likely to change over time than the range trait due to lower alpha value of size. The theta values are quite similar to the ones from the independent Brownian motion models, however sigma values are more different.

The traits evolve as a bivariate Ornstein-Uhlenbeck process

```
## [1] "Starting point of heuristic search procedure : "
##      Astart         A_2         A_3        Aend    Syystart       Syy_2
## -0.45195809 -0.03554628  0.05199015  0.56413103 -0.48047355 -0.79239801
##      Syyend
## -1.37870345
```

The bivariate OU model estimated parameters:

```
## A: strength of selection
```

```
##               size     range
## size    0.1736793 11.15741
## range  -0.4074014 13.28148
```

```
## vY0: estimated ancestral state
```

```
##           [,1]
## size  39.08738
## range 11.67291
```

```
## Syy is the sigma value
```

```
##            size     range
## size   64.84504 16.87674
## range   0.00000 46.35857
```

We can see that again the most visible difference is in the sigma values - they changes considerably in comparison to the first two models, also the estimated ancestral states changed. This is reasonable as we introduced dependencies in the model.

***size* evolves as a Brownian motion and *range* as an Ornstein-Uhlenbeck process adapting to it**

```
## [1] "Starting point of heuristic search procedure : "
##          A        Syy
## -0.5969451 -0.6544833
```

The bivariate OUBM model estimated these parameters:

```
## A: strength of selection
```

```
##         range
## range 12.89067
```

```
## vY0: estimated ancestral state for range (OU part)
```

```
##          [,1]
## range 11.64507
```

```
## vX0: estimated ancestral state for size (BM part)
```

```
##          [,1]
## size 38.43947
```

```
## Syy is the sigma value for range
```

```
##          range
## range 45.78095
```

```
## Sxx is the sigma value for size
```

```
##          size
## size 62.97015
```

Comparison

All 5 models above tried to fit the parameters based on the given phylogenetic tree, and the observed trait values for the 70 species. We compare the models based on the AICc criterion:

```
## Comparison of the AICc values:
```

```
## Both traits evolve as independent Brownian motions
```

```
## [1] 1186.771
```

```
## The traits evolve as a correlated Brownian motion
```

```
## [1] 1188.018
```

```
## Both traits evolve as independent Ornstein-Uhlenbeck processes
```

```
## [1] 1159.138
```

```
## The traits evolve as a bivariate Ornstein-Uhlenbeck process
```

```
## [1] 1165.83
```

```
## size evolves as a Brownian motion and range as an Ornstein-Uhlenbeck process
```

```
## [1] 1158.363
```

To compare the models, we printed out all the AICc criterions, and found that the smallest AICc value has model 5 (where size evolves as a Brownian motion and range as an Ornstein-Uhlenbeck process). Hence, it seems the bivariate OUBM model is the best fit.

```r
knitr::opts_chunk$set(echo = TRUE)


#install.packages("ade4")
#install.packages("mvMORPH")
#install.packages("mvSLOUCH")
#install.packages("adephylo")
library(ade4)
library(mvMORPH)
library(mvSLOUCH)
library(ape)
#devtools::install_github("kopperud/slouch")
# install.packages("rlang")
# install.packages("tibble")
library(tibble)
library(rlang)
data(carni70)
carni70_tree <- newick2phylog(carni70$tre)



size <- scalewt(log(carni70$tab))[,1] # scaled log body size in kg
names(size) <- row.names(carni70$tab)
yrange <- scalewt(carni70$tab[,2])# scaled geographic range in km
```

```
names(yrange) <- row.names(carni70$tab)
plot_data <- data.frame(spieces = row.names(carni70$tab), size = size, range =yrange )
par(mfrow=c(1,1),las=3)

plot(plot_data$spieces, plot_data$size, cex.axis=0.6,ylab = "Size", pch = 19,
     col = rgb(0, 0, 0, 0.1))

plot(plot_data$spieces, plot_data$range, cex.axis=0.6, ylab = "Range", pch = 19,
     col = rgb(0, 0, 0, 0.1))

plot(plot_data$size, plot_data$range, xlab = "Size", ylab = "Range", pch = 19)

tre <- as.phylo(carni70_tree)
carni70_tree <- newick2phylog(carni70$tre)

par(mfrow = c(1, 1), oma = c(1, 1, 2, 1))
symbols.phylog(carni70_tree,size)
mtext("Size", side = 3, line = 0, outer = TRUE, font = 2, cex = 1.3)
par(fig = c(0, 1, .1, .9), oma = c(0, 0, 0, 0), mar = c(0, 0, 0, 0), new = TRUE)
plot(0, 0, type = "n", bty = "n", xaxt = "n", yaxt = "n")
legend("top", c("below mean", "above mean"), col = c("black", "black"), lty=c(NA, NA),pch = c(1, 1), lw

par(mfrow = c(1, 1), oma = c(1, 1, 2, 1))
symbols.phylog(carni70_tree,yrange)
mtext("Range", side = 3, line = 0, outer = TRUE, font = 2, cex = 1.3)
par(fig = c(0, 1, .1, .9), oma = c(0, 0, 0, 0), mar = c(0, 0, 0, 0), new = TRUE)
plot(0, 0, type = "n", bty = "n", xaxt = "n", yaxt = "n")
legend("top", c("below mean", "above mean"), col = c("black", "black"), lty=c(NA, NA),pch = c(1, 1), lw


fit1 <- mvBM(tre, data = carni70$tab, model="BM1", param=list(constraint="diagonal"))
fit1$sigma
fit1$theta

fit2 <- mvBM(tre, data = carni70$tab, model="BM1")
cat(" Evolutionary rate matrix:")
cat("\n")
fit2$sigma
cat(" Estimated ancestral states:")
cat("\n")
fit2$theta
phyltree = ape2ouch(tre)
# fit3_size <- mvOU(tre, data = carni70$tab[,1], model="OU1")
# fit3_range <- mvOU(tre, data = carni70$tab[,2], model="OU1")
fit3 <- ouchModel(phyltree, data = carni70$tab, Atype="Diagonal", Syytype="Diagonal")

cat("Alpha: strength of selection - low alpha favours a random change during the time step \n")
fit3$FinalFound$ParamsInModel$A
cat("Sigma: evolutionary rate matrix \n")
fit3$FinalFound$ParamsInModel$Syy
cat("Theta: estimated ancestral states \n")
fit3$FinalFound$ParamsInModel$vY0
```

```r
fit5 <- ouchModel(phyltree = phyltree, data = carni70$tab)

cat("A: strength of selection")
cat("\n")
fit5$FinalFound$ParamsInModel$A
cat("vY0: estimated ancestral state")
cat("\n")
fit5$FinalFound$ParamsInModel$vY0
cat("Syy is the sigma value")
cat("\n")
fit5$FinalFound$ParamsInModel$Syy


traits <-  data.frame(range=carni70$tab[,2],size=carni70$tab[,1])
row.names(traits) <- row.names(carni70$tab)


fit6 <-mvslouchModel(phyltree, traits,kY=1)
#
cat("A: strength of selection")
cat("\n")
fit6$FinalFound$ParamsInModel$A
cat("vY0: estimated ancestral state for range (OU part)")
cat("\n")
fit6$FinalFound$ParamsInModel$vY0
cat("vX0: estimated ancestral state for size (BM part)")
cat("\n")
fit6$FinalFound$ParamsInModel$vX0
cat("Syy is the sigma value for range")
cat("\n")
fit6$FinalFound$ParamsInModel$Syy
cat("Sxx is the sigma value for size")
cat("\n")
fit6$FinalFound$ParamsInModel$Sxx
cat("Comparison of the AICc values:\n")
cat("Both traits evolve as independent Brownian motions \n")
fit1$AICc
cat("The traits evolve as a correlated Brownian motion \n")
fit2$AICc
cat("Both traits evolve as independent Ornstein-Uhlenbeck processes \n")
fit3$`FinalFound`$ParamSummary$aic.c
cat("The traits evolve as a bivariate Ornstein-Uhlenbeck process \n")
fit5$`FinalFound`$ParamSummary$aic.c
cat("size evolves as a Brownian motion and range as an Ornstein-Uhlenbeck process \n")
fit6$`FinalFound`$ParamSummary$aic.c
```