# Is batman somewhere ?

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First we get the data.

```
data_path = "bats.csv"
mydata = read.table(file = data_path, sep=";", skip=3, header= T)
mydata
```

```
##                          Species Diet Clade     BOW     BRW   AUD    MOB
## 1         Rousettus aegyptiacus     1     I  136.30 2070.00  9.88 105.77
## 2             Epomops franqueti     1     I  120.00 2210.00 10.44 107.80
## 3            Eonycteris spelaea     1     I   58.70 1310.00  5.48  67.00
## 4             Cynopterus sphinx     1     I   48.30 1184.33  4.77  65.27
## 5           Dobsonia praedatrix     1     I  184.00 3028.00  7.09 213.43
## 6                Eidolon helvum     1     I  262.00 4290.00 12.77 208.70
## 7             Pteropus vampyrus     1     I 1014.00 9121.00 16.93 243.54
## 8         Macroglossus miniumus     1     I   14.60  561.00  2.40  30.05
## 9        Syconycteris australis     1     I   14.70  570.00  2.13  31.40
## 10         Nyctimene albiventer     1     I   29.70  825.00  4.56  68.93
## 11          Rhinolophus landeri     2     I    6.30  208.00  4.88   4.83
## 12     Hipposideros commersoni     2     I  101.90  750.00  8.79   9.50
## 13      Aselliscus stoiczkanus     2     I    4.90  150.00  2.72   1.88
## 14          Triaenops persicus     2     I   13.70  271.00  4.07   5.22
## 15            Megaderma spasma     3     I   22.60  644.00 10.56  14.25
## 16            Macroderma gigas     3     I  119.80 1704.00 22.36  21.60
## 17             Cardioderma cor     3     I   26.00  670.00 10.81   8.07
## 18                 Lavia frons     3     I   23.40  644.00 10.92   4.35
## 19           Nycteris thebaica     3     I    8.90  323.00  5.79   3.65
## 20        Rhinopoma hardwickei     3     I   12.90  275.00  5.20   7.48
## 21 Craseonycteris thonglongyai     3     I    2.56   87.00  1.84   0.66
## 22           Desmodus rotundus     4    II   36.30  999.00  9.77  33.00
## 23           Diphylla ecaudata     4    II   30.90  798.00  8.30  36.20
## 24     Brachyphylla cavernarum     1    II   44.50 1196.00  8.63  42.20
## 25       Lionycteris spurrelli     1    II    9.90  393.00  3.71  10.30
## 26        Glossophaga soricina     1    II   10.60  414.00  3.74  12.20
## 27      Leptonycteris curasoae     1    II   24.50  610.00  5.57  18.60
## 28             Anoura geofroyi     1    II   16.00  586.00  5.20  14.15
## 29         Phylloderma stenops     1    II   46.10 1338.00 10.20  87.40
## 30      Phyllostomus haustatus     1    II   90.10 1517.00 12.74  34.33
## 31            Mimon crenulatum     1    II   11.80  326.00  5.92   7.30
## 32          Trachops cirrhosus     1    II   36.90 1003.00 16.34  23.50
## 33             Tonatia bidens     1    II   27.67  684.67 13.37  17.96
## 34           Vampyrum spectrum     1    II  173.00 2587.00 27.60  92.00
## 35    Micronycteris brachyotis     1    II    8.98  319.00  4.19  13.85
## 36      Carollia perspicillata     1    II   17.80  546.00  5.27  23.55
```

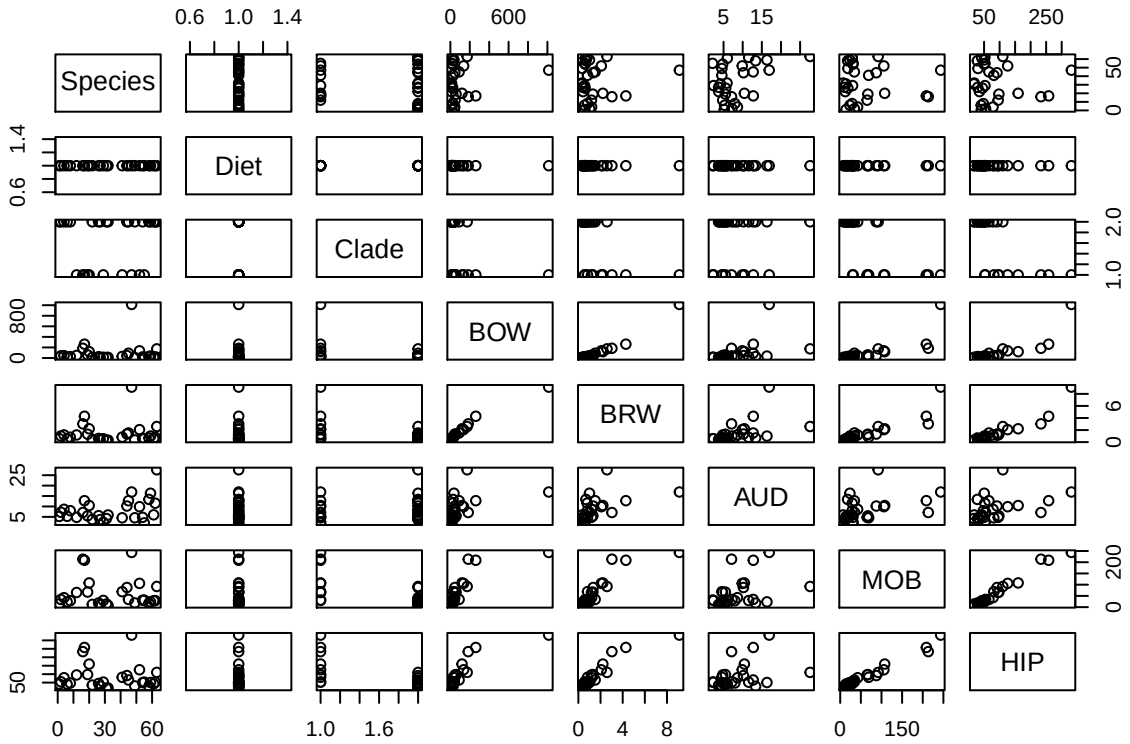
```
## 37         Rhinophlylla pumilio     1    II    8.90  356.00  4.57  18.80
## 38              Sturnira lilium     1    II   20.20  618.00  4.77  30.77
## 39           Artibeus lituratus     1    II   41.00 1016.00  7.21  34.38
## 40           Uroderma bilobatum     1    II   16.20  612.00  5.98  28.70
## 41           Vampyrops vittatus     1    II   22.60  791.00 11.56  29.22
## 42          Chiroderma villosum     1    II   26.10  814.00  7.95  28.75
## 43          Pteronotus parnelli     2    II   20.20  543.00  5.52   7.98
## 44        Mormoops megalophylla     3    II   15.70  386.00  4.19   6.66
## 45         Noctilio albiventris     3   III   32.70  597.00 11.59  13.54
## 46        Natalus tumidirostris     3    IV    6.90  245.00  3.28   3.58
## 47           Furipterus horrens     3    IV    3.43  127.00  2.78   1.37
## 48                Molossus ater     3    IV   33.60  526.00  7.07  10.26
## 49           Tadarida condylura     3    IV   20.27  367.78  4.94   9.75
## 50            Molossops abrasus     3    IV   19.35  301.00  5.38   6.93
## 51         Otomops martiensseni     3    IV   41.50  756.00 11.41  14.30
## 52        Cheiromeles torquatus     3    IV  167.00 1362.00 13.20  40.50
## 53          Saccopteryx leptura     3    IV    7.80  228.00  3.48   1.49
## 54             Cyttarops alecto     3    IV    5.30  175.00  3.51   0.74
## 55         Cormura brevirostris     3    IV    8.20  219.00  4.37   2.28
## 56        Peropteryx trinitatus     3    IV    5.00  149.50  2.81   1.47
## 57         Rhynchonycteris naso     3    IV    3.80  118.00  2.34   0.91
## 58        Emballonura monticola     3    IV    5.30  166.00  3.16   1.30
## 59                Coleura afra     3    IV   11.50  257.00  4.08   3.98
## 60        Taphozous saccolaimus     3    IV   43.00  671.00  9.65  10.92
## 61           Kerivoula papilosa     3    IV    5.73  209.67  4.47   2.52
## 62                Myotis myotis     3    IV    7.00  190.00  7.50   5.23
## 63           Miniopterus medius     3    IV   11.71  271.22  4.77   5.31
##       HIP
## 1  125.97
## 2  159.80
## 3   97.70
## 4   95.40
## 5  233.30
## 6  258.10
## 7  331.29
## 8   52.95
## 9   53.10
## 10  81.40
## 11  20.89
## 12  27.68
## 13  11.60
## 14  17.40
## 15  35.85
## 16  68.90
## 17  32.30
## 18  25.80
## 19  21.65
## 20  20.95
## 21   4.80
## 22  42.40
## 23  41.00
## 24  78.80
## 25  29.50
## 26  35.00
```

```
## 27  44.95
## 28  41.40
## 29  91.70
## 30  65.60
## 31  18.20
## 32  50.60
## 33  28.30
## 34 110.40
## 35  17.10
## 36  40.75
## 37  30.30
## 38  49.73
## 39  54.90
## 40  42.70
## 41  52.46
## 42  47.58
## 43  22.23
## 44  27.50
## 45  36.00
## 46  27.10
## 47   9.46
## 48  20.13
## 49  18.60
## 50  15.87
## 51  30.60
## 52  61.20
## 53   9.21
## 54   7.96
## 55  11.20
## 56   7.54
## 57   5.48
## 58   8.93
## 59  12.40
## 60  26.38
## 61  19.02
## 62  16.24
## 63  17.28
```

# 1. Study of the relationship between brain weight and body mass

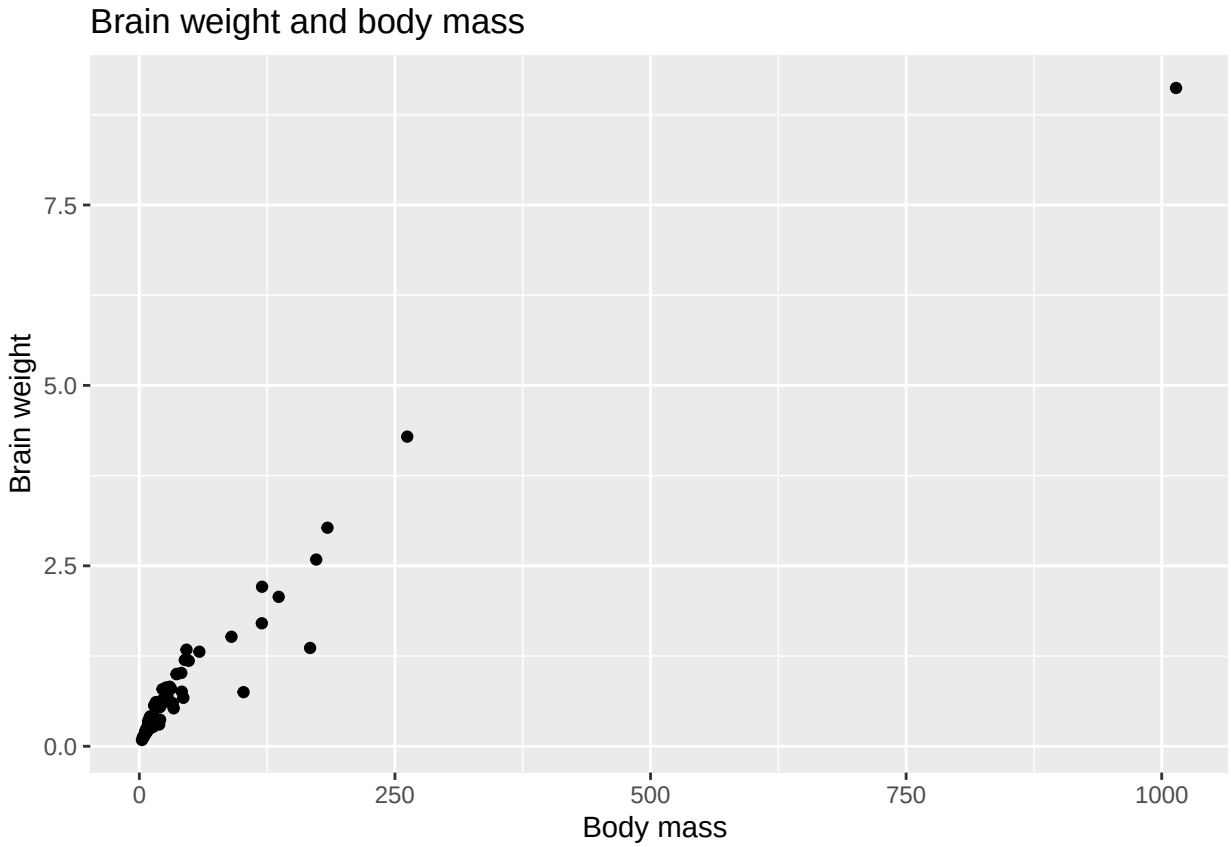
Because, BRW and BOW variable s don't have the same order of magnitude, we divide the column of BRW by 1000.

```
mydata$BRW <- mydata$BRW/1000
phyto = mydata[(mydata$Diet == 1),]
plot(phyto)
```




Then We can plot a figure showing the dependence of body mass and brain weight.

```
library(ggplot2)
ggplot(mydata, aes(x=BOW,y=BRW)) +
  geom_point() +
  #geom_line() +
  ggtitle("Brain weight and body mass") +
  xlab("Body mass ") +
  ylab("Brain weight")
```




Then we obtain the mathematical form of the model based on a **simple regression model**.

```
reg1 = lm(BRW~BOW, data = phyto)
summary(reg1)
```

```
##
## Call:
## lm(formula = BRW ~ BOW, data = phyto)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.62832 -0.23394 -0.06574  0.15826  1.30859
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.6234469  0.0814762   7.652 3.14e-08 ***
## BOW         0.0089999  0.0003972  22.659  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3969 on 27 degrees of freedom
## Multiple R-squared:   0.95,  Adjusted R-squared:  0.9482
## F-statistic: 513.4 on 1 and 27 DF,  p-value: < 2.2e-16
```

The estimate of the intercept is **0.6234**. The coefficient of determination is **alpha1 = 0.0089**. **BRW = alpha1 * BOW + intercept**

The **H0 hypothesis is : alpha1 = intercept = 0**. So we reject it. Brain weight depends strongly on body mass.

Now we analyse the variance.

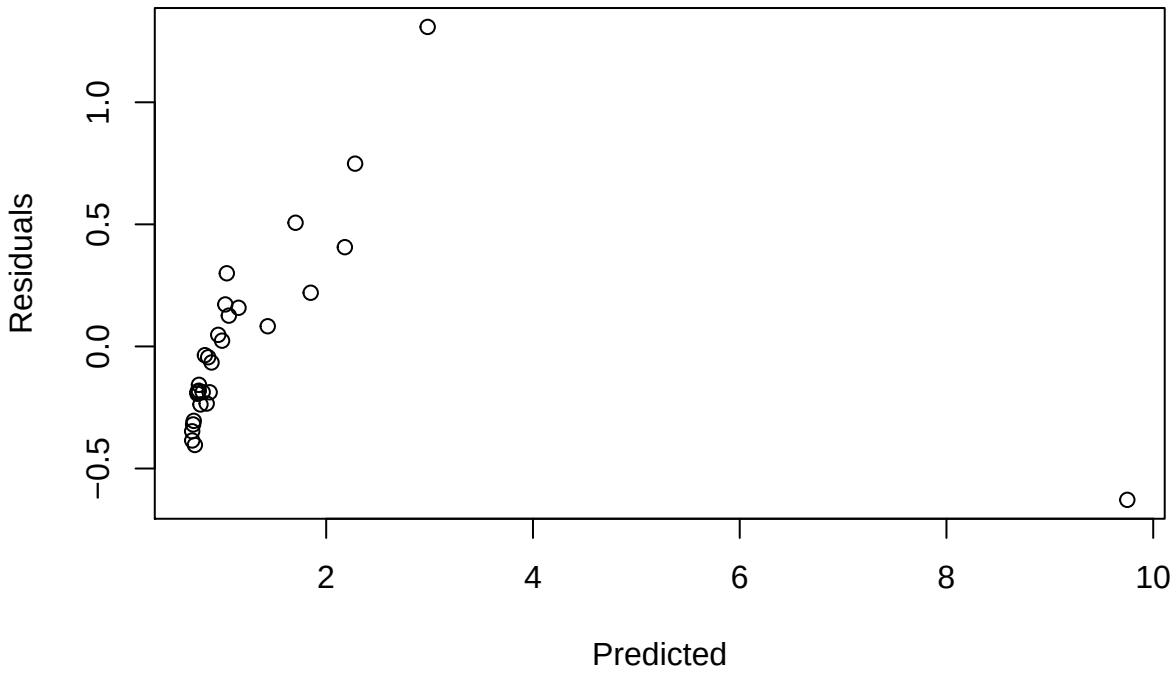
```
anova(reg1)
```

```
## Analysis of Variance Table
##
## Response: BRW
##           Df Sum Sq Mean Sq F value    Pr(>F)
## BOW        1 80.888  80.888  513.42 < 2.2e-16 ***
## Residuals 27  4.254   0.158
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

We can see the MSM, MSE, Degree of freedom. The sum of residual squares is **MSE = 4.254**

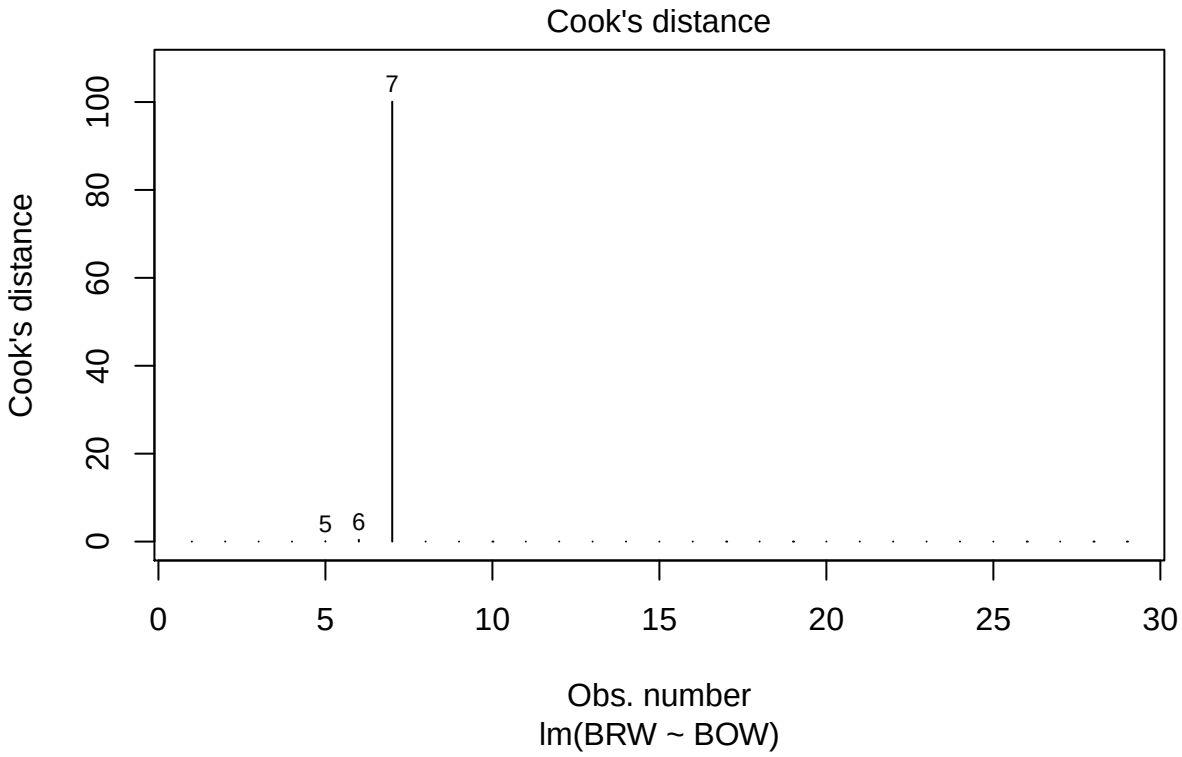
Now we plot the graph of the residuals.

```
plot(reg1$fitted.values, reg1$residuals, xlab = "Predicted", ylab = "Residuals")
```




It appears to this graph one very distant point.

```
plot(reg1,4)
```




```
which(phyto$BRW>8)
```

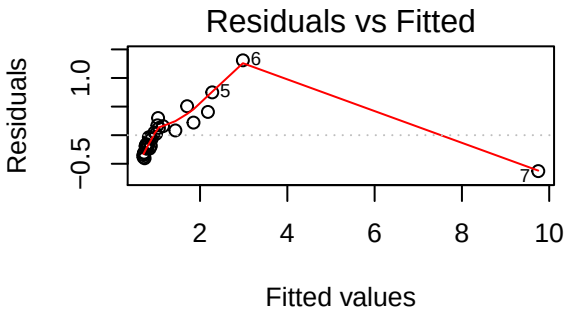
```
## [1] 7
```

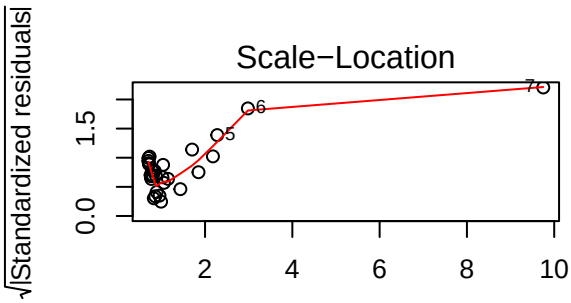
So we have one individual point. We redo the analysis by removing this point.

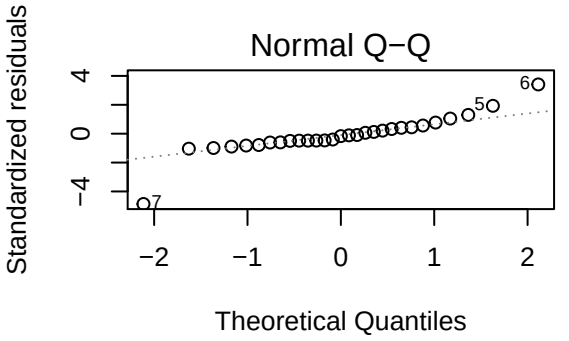
```
phytobis = phyto[which(phyto$BRW < 8),]
reg2 = lm(BRW ~ BOW, data = phytobis)
summary(reg2)
```

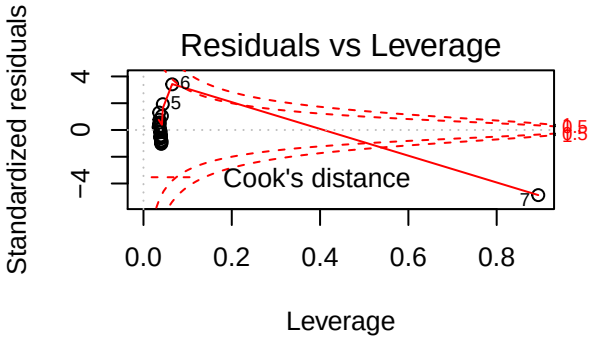
```
##
## Call:
## lm(formula = BRW ~ BOW, data = phytobis)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.26976 -0.09333  0.00873  0.11293  0.32255
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.3465452  0.0354920   9.764 3.48e-10 ***
## BOW         0.0145099  0.0004285  33.860  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1418 on 26 degrees of freedom
## Multiple R-squared:  0.9778, Adjusted R-squared:  0.977
## F-statistic:  1147 on 1 and 26 DF,  p-value: < 2.2e-16
```

```
par(mfcol = c(2,2))
plot(reg1)
```

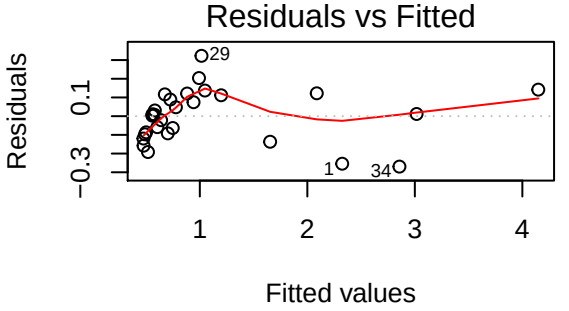


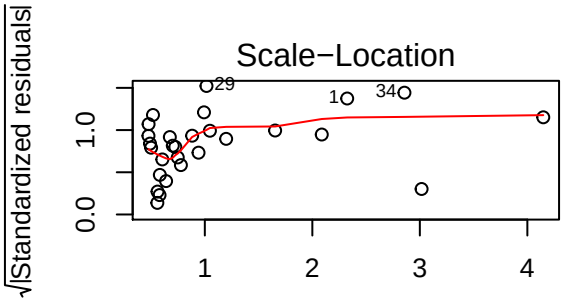



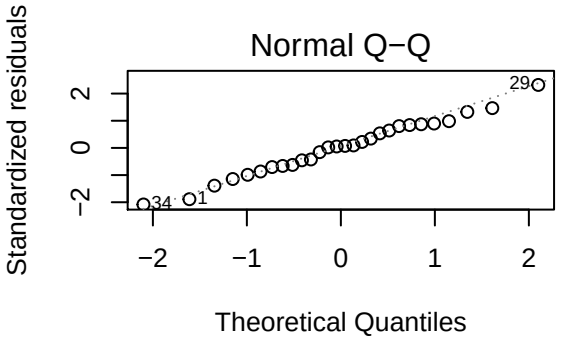



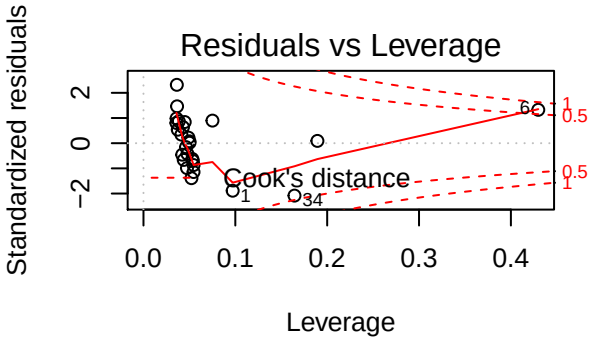




```
plot(reg2)
```




Discussion :

## 2. Study of the contribution to the total weight od each part of the brain

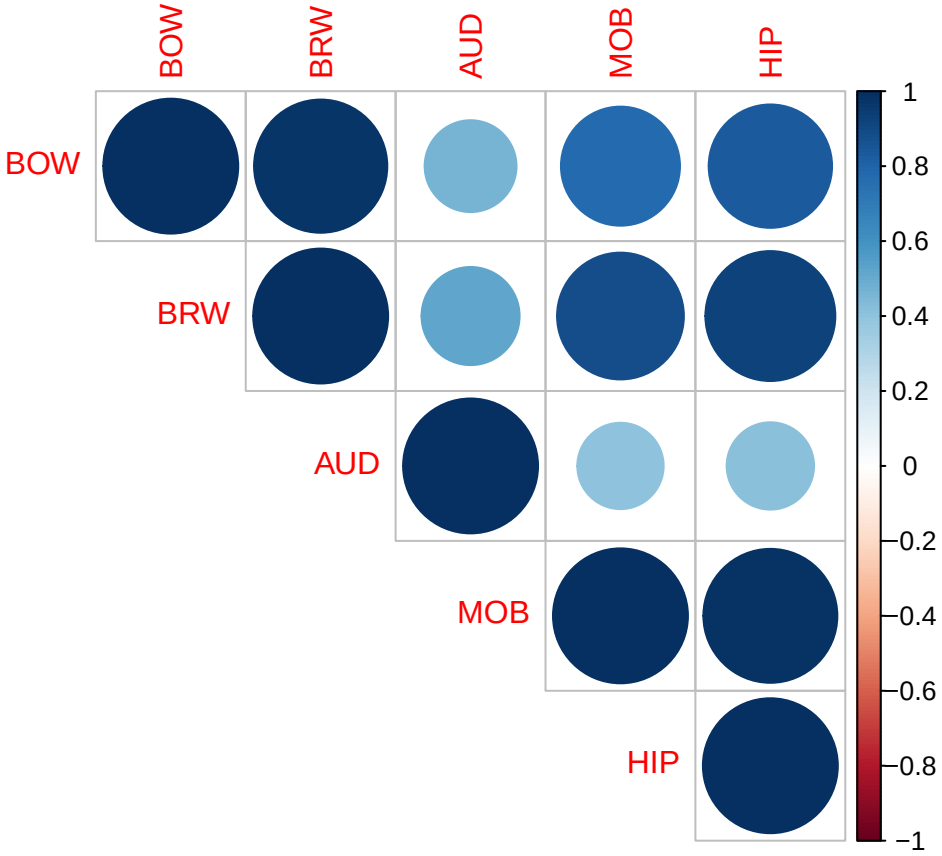
```
library(corrplot)
```

```
## corrplot 0.92 loaded
```

```
phytoNum = phyto[, c(4:8)]
mat.cor = cor(phytoNum)
corrplot(mat.cor, type = "upper")
```

```
## Warning in data.row.names(row.names, rowsi, i): some row.names duplicated:
## 2,4,5,7,8,9,11,12,13,14 --> row.names NOT used
```

```
## Warning in data.row.names(row.names, rowsi, i): some row.names duplicated:
## 2,4,5,7,8,9,11,12,13,14 --> row.names NOT used
```




```
cor.test(phyto$BRW, phyto$HIP)
```

```
##
##  Pearson's product-moment correlation
##
## data:  phyto$BRW and phyto$HIP
## t = 12.91, df = 27, p-value = 4.574e-13
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.8502663 0.9658107
```

```
## sample estimates:
##       cor
## 0.9276811
```

BRW variable depend on HIP variable.

```
cor.test(phyto$BRW, phyto$MOB)
```

```
##
##  Pearson's product-moment correlation
##
## data:  phyto$BRW and phyto$MOB
## t = 9.7964, df = 27, p-value = 2.203e-10
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.7644185 0.9442114
## sample estimates:
##       cor
## 0.8834215
```

BRW variable depend on MOB variable.

```
cor.test(phyto$BRW, phyto$AUD)
```

```
##
##  Pearson's product-moment correlation
##
## data:  phyto$BRW and phyto$AUD
## t = 3.2338, df = 27, p-value = 0.003215
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.2007495 0.7497021
## sample estimates:
##       cor
## 0.5283792
```

BRW variable doesn't depend enough on AUD variable.

Now we run some multiple regression model.

```
regm = lm(BRW~AUD+MOB+HIP, data = phytobis)
summary(regm)
```

```
##
## Call:
## lm(formula = BRW ~ AUD + MOB + HIP, data = phytobis)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.26855 -0.06884  0.00988  0.06166  0.37534
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.312692   0.076628  -4.081  0.00043 ***
## AUD          0.047989   0.006067   7.910 3.85e-08 ***
## MOB         -0.002444   0.003257  -0.750  0.46034
## HIP          0.015981   0.002960   5.399 1.52e-05 ***
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1585 on 24 degrees of freedom
## Multiple R-squared:  0.9744, Adjusted R-squared:  0.9712
## F-statistic: 304.5 on 3 and 24 DF,  p-value: < 2.2e-16
```

The estimate of the intercept is **-0.3126**. The coefficients of determination are **alpha1 = 0.048**, **alpha2 = -0.0024** and **alpha3 = 0.016**.

**BRW = alpha1 * AUD + alpha2 * MOB + alpha3 * HIP + intercept**

The **H0 hypothesis is : alpha1 = alpha2 = alpha3 = intercept = 0**. So we reject it. Brain weight (BRW) depends strongly on the volume of the auditory part of the brain (AUD) and the hippocampus (HIP). But it doesn't depend a lot on the volume of the olfactory zone (MOB). So we can remove the variable MOB in the model.

Now we analyse the variance.

```
anova(regm)
```

```
## Analysis of Variance Table
##
## Response: BRW
##           Df  Sum Sq Mean Sq F value    Pr(>F)
## AUD        1  6.8171  6.8171 271.210 1.397e-14 ***
## MOB        1 15.4094 15.4094 613.040 < 2.2e-16 ***
## HIP        1  0.7327  0.7327  29.148 1.519e-05 ***
## Residuals 24  0.6033  0.0251
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
reg0 = lm(BRW ~ 1, data = phyto)
step(reg0, scope=BRW~AUD + MOB + HIP, discretion = "forward")
```

```
## Start:  AIC=33.23
## BRW ~ 1
##
##        Df Sum of Sq    RSS     AIC
## + HIP   1    73.273 11.869 -21.906
## + MOB   1    66.448 18.694  -8.733
## + AUD   1    23.770 61.372  25.740
## <none>              85.142  33.234
##
## Step:  AIC=-21.91
## BRW ~ HIP
##
##        Df Sum of Sq    RSS     AIC
## + MOB   1     2.847  9.023 -27.860
## + AUD   1     2.014  9.856 -25.298
## <none>              11.869 -21.906
## - HIP   1    73.273 85.142  33.234
##
## Step:  AIC=-27.86
## BRW ~ HIP + MOB
##
##        Df Sum of Sq     RSS     AIC
## + AUD   1    1.9101  7.1124 -32.758
```

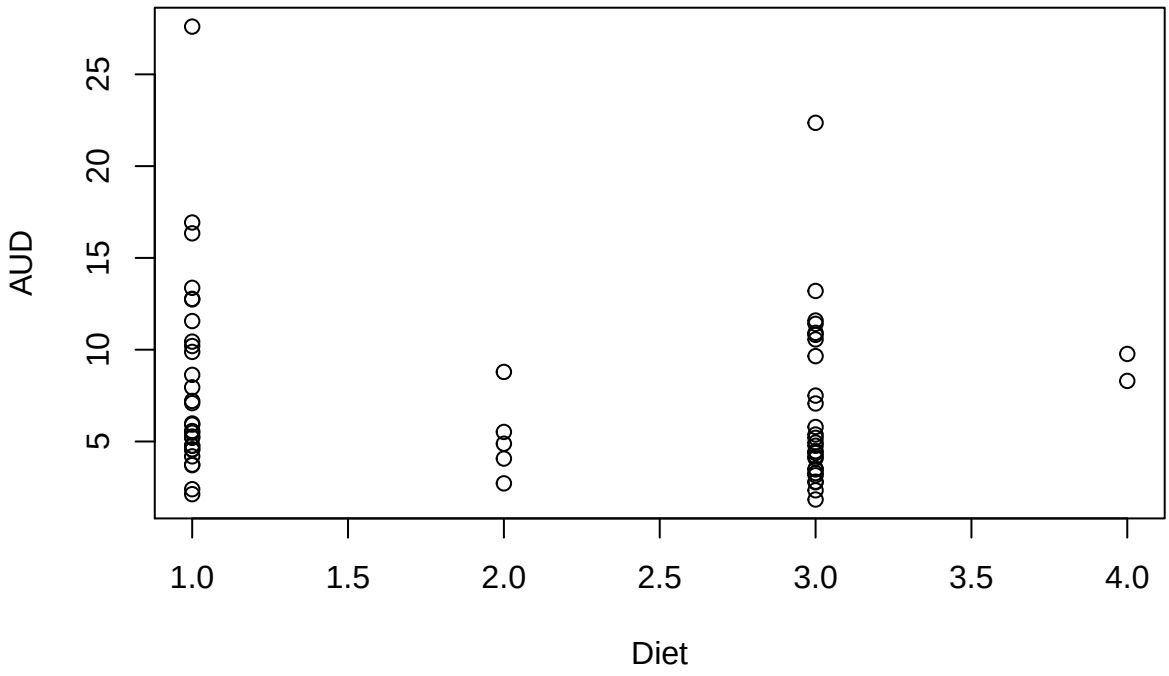
```
## <none>               9.0225 -27.860
## - MOB   1    2.8469 11.8695 -21.906
## - HIP   1    9.6718 18.6944  -8.733
##
## Step:  AIC=-32.76
## BRW ~ HIP + MOB + AUD
##
##        Df Sum of Sq     RSS     AIC
## <none>               7.1124 -32.758
## - AUD   1    1.9101  9.0225 -27.860
## - MOB   1    2.7433  9.8557 -25.298
## - HIP   1    8.7453 15.8577 -11.506
```

```
##
## Call:
## lm(formula = BRW ~ HIP + MOB + AUD, data = phyto)
##
## Coefficients:
## (Intercept)          HIP          MOB          AUD
##    -1.00395      0.04435     -0.02924      0.05282
```

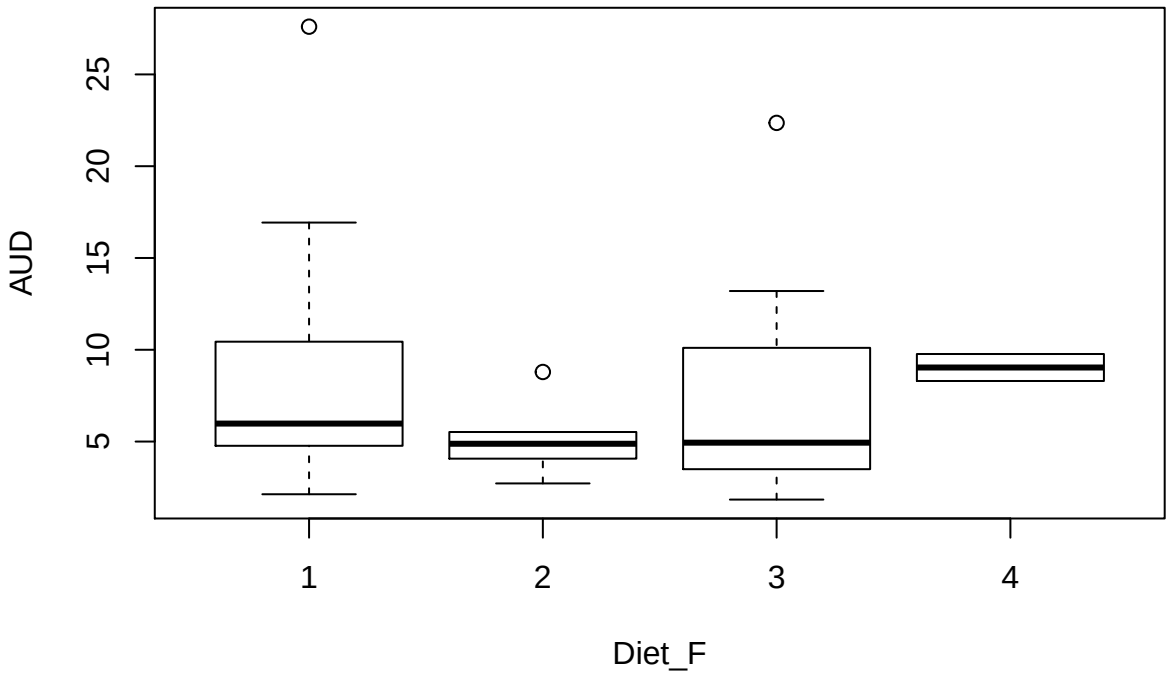
The purpose of this test is

## 3. Link between volume of the auditory part and diet.

```
mydata$Diet_F = as.factor(mydata$Diet)
with(mydata, plot(AUD~Diet))
```




```
with(mydata, plot(AUD~Diet_F))
```




Now we do the regression analysis.

```
lm = lm(AUD~Diet_F, data = mydata)
anova(lm)
```

```
## Analysis of Variance Table
##
## Response: AUD
##           Df  Sum Sq Mean Sq F value Pr(>F)
## Diet_F     3   66.07  22.023  0.9293 0.4323
## Residuals 59 1398.26  23.699
```

So we can conclude that auditory brain volume (AUD) and diet (Diet) are not really linked.