

tp-batman

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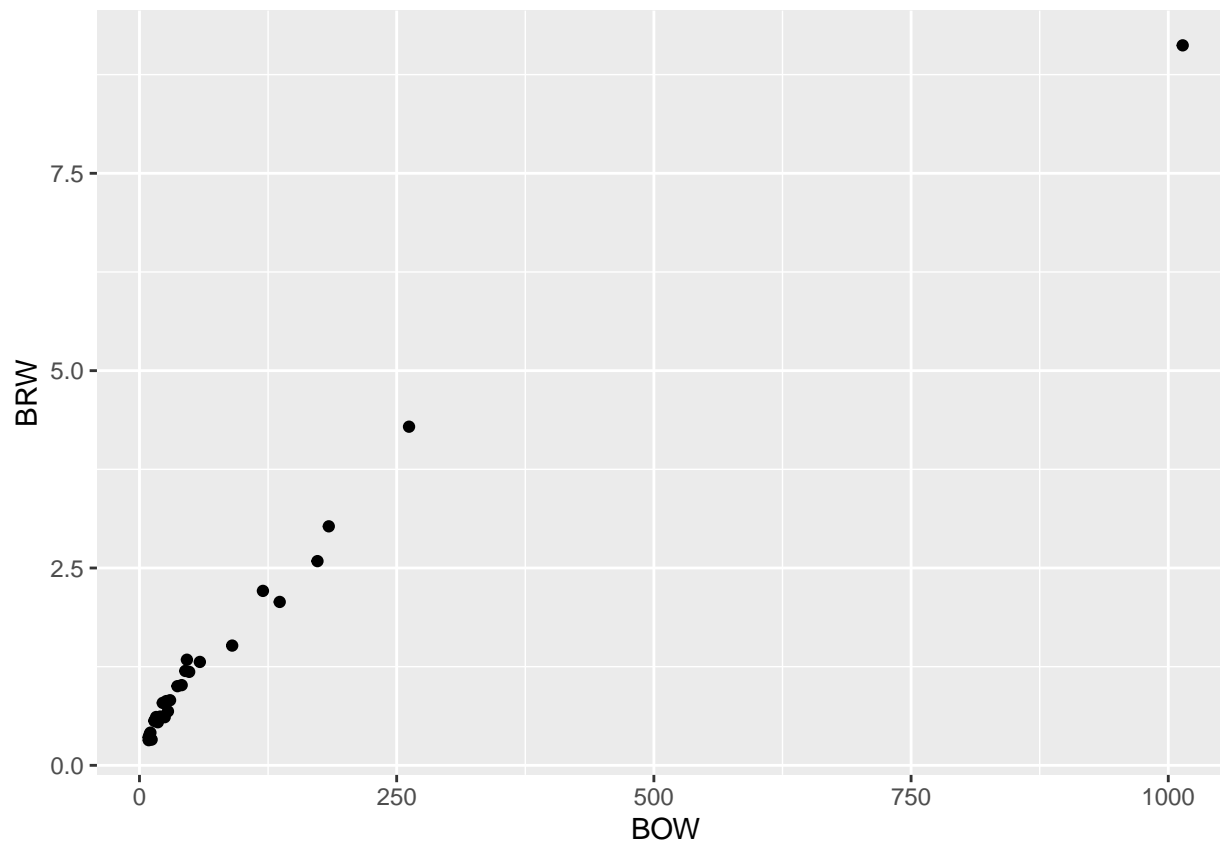
R Markdown

```
mydata <- read.csv("bats.csv", sep = ";", skip = 3, header = T)
mydata$BRW <- mydata$BRW/1000
names(mydata)
```

```
## [1] "Species" "Diet"      "Clade"      "BOW"      "BRW"      "AUD"      "MOB"
## [8] "HIP"
```

Study of the relationship between brain weight and body mass

```
phyto = mydata[(mydata$Diet==1),]
ggplot(data = phyto, aes(x = BOW, y = BRW)) + geom_point()
```



```
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
```

$BRW = 0.6234469 + 0.0089999 * BOW$ $BRW = a_1 + a_2 * BOW$

The estimate of the intercept is 623.4469, the p-value is less than $2e-16$ for the slope and equal to $3.14e-08$ for the intercept. H_0 hypothesis says that $a_1 = a_2 = 0$. We can say the brain weight is linearly dependent of

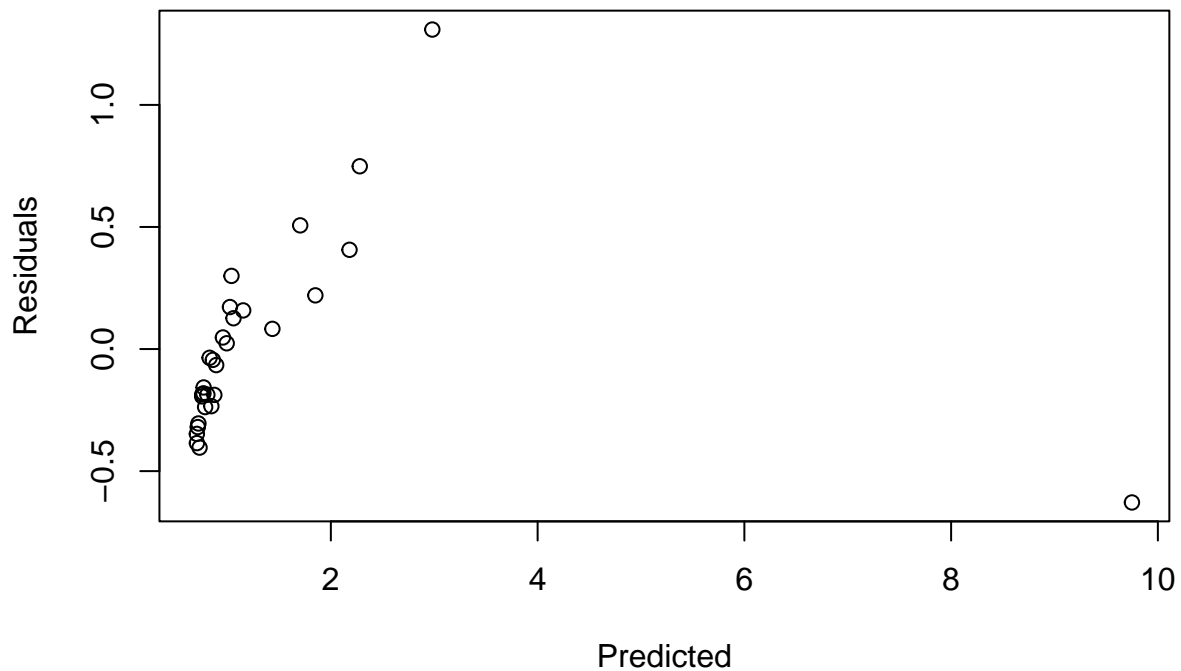
the body mass, the coefficient of determination is 0.95

```
anova(reg1)
```

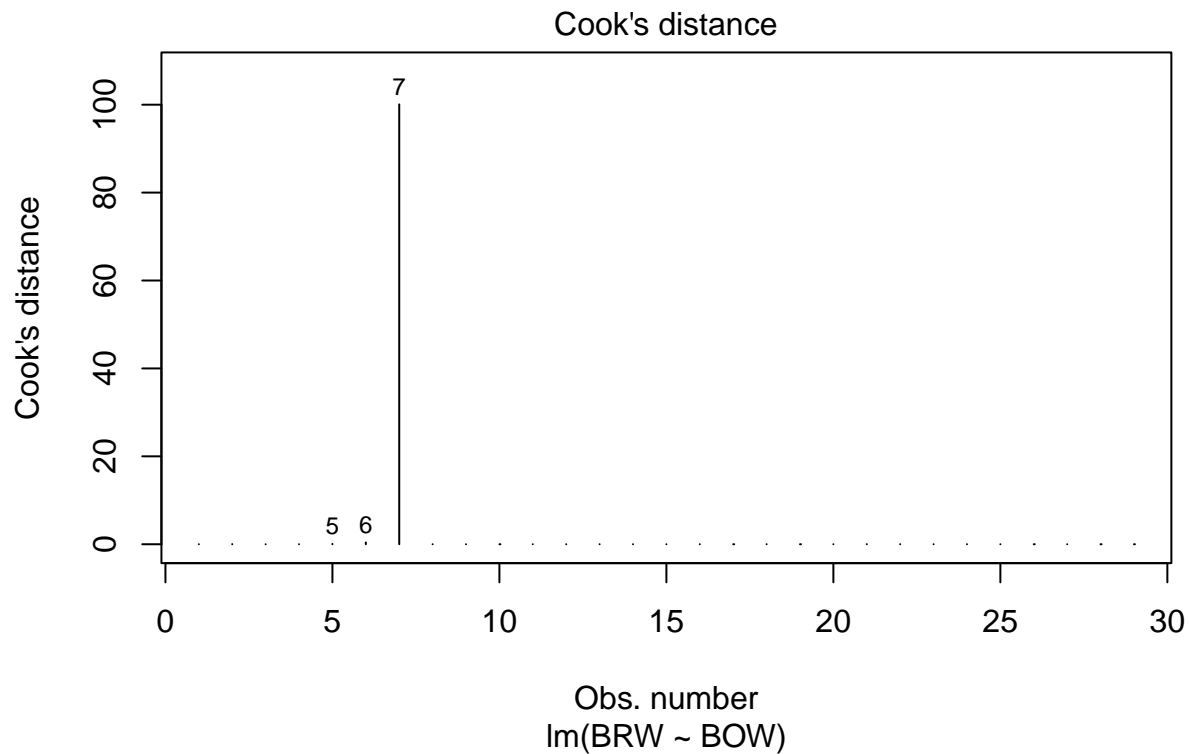
```
## Analysis of Variance Table
##
## Response: BRW
##           Df Sum Sq Mean Sq F value    Pr(>F)
## BOW         1  80.888   80.888   513.42 < 2.2e-16 ***
## Residuals   27   4.254    0.158
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Additional information : the residuals and statistics about the impact of BOW on BRW, the sum of residual is 4.4254

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



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



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

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

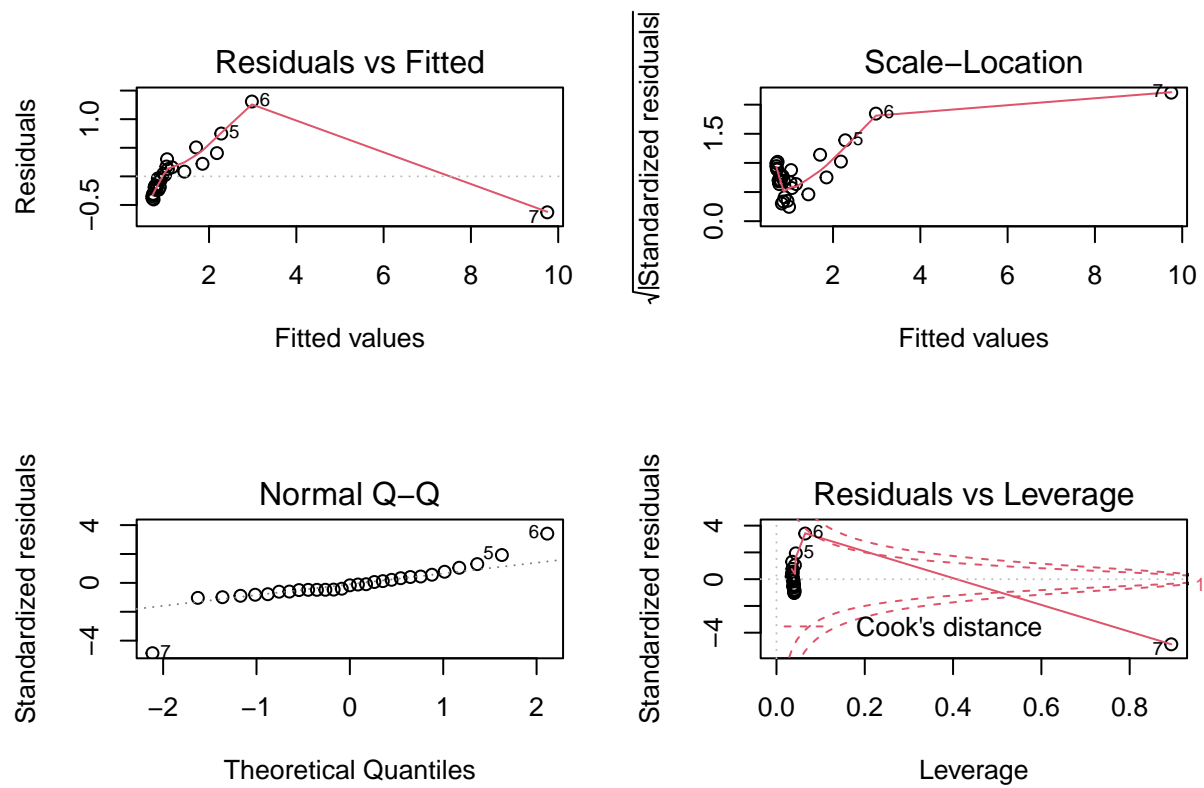
```
phytobis = phyto[which(phyto$BRW<8),]
```

```
reg2 = lm(BRW ~ BOW, data = phytobis)
summary(reg2)
```

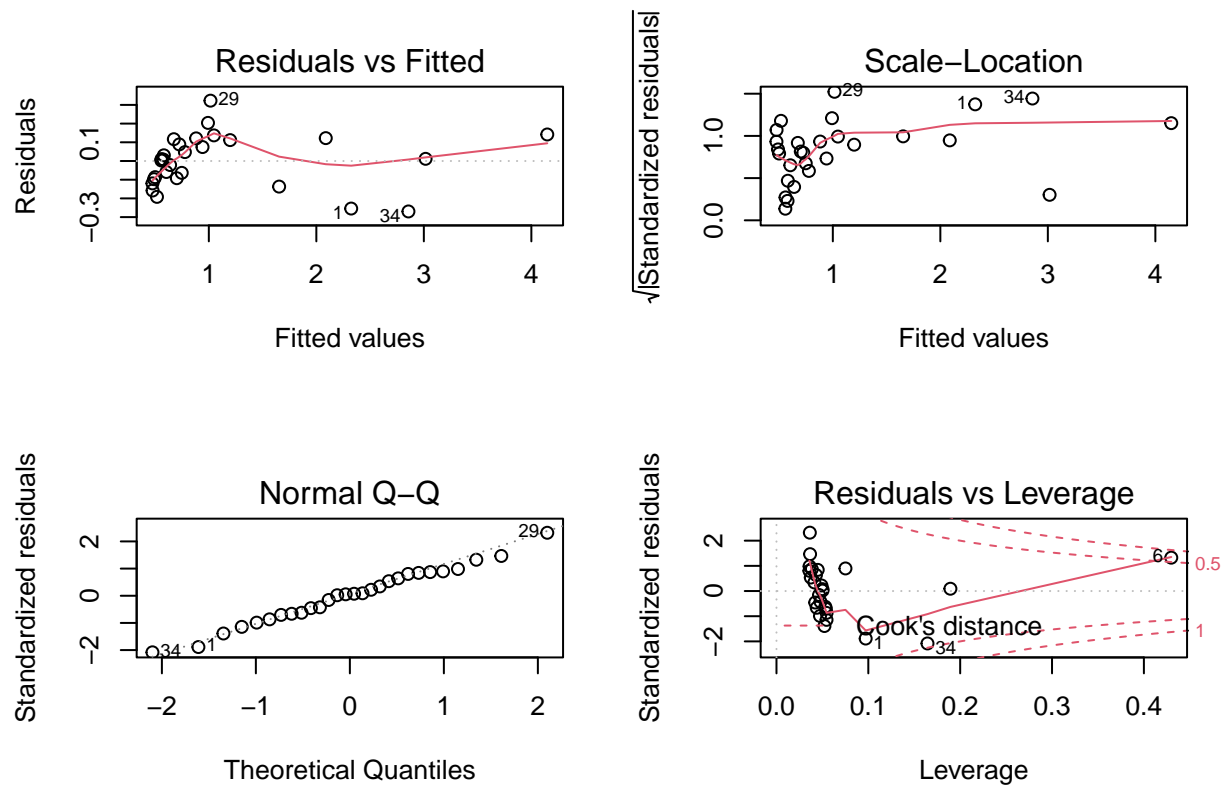
```
##
## Call:
## lm(formula = BRW ~ BOW, data = phytobis)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.26976 -0.09333  0.00873  0.11293  0.32255
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.3465452  0.0354920   9.764 3.48e-10 ***
## 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)
```

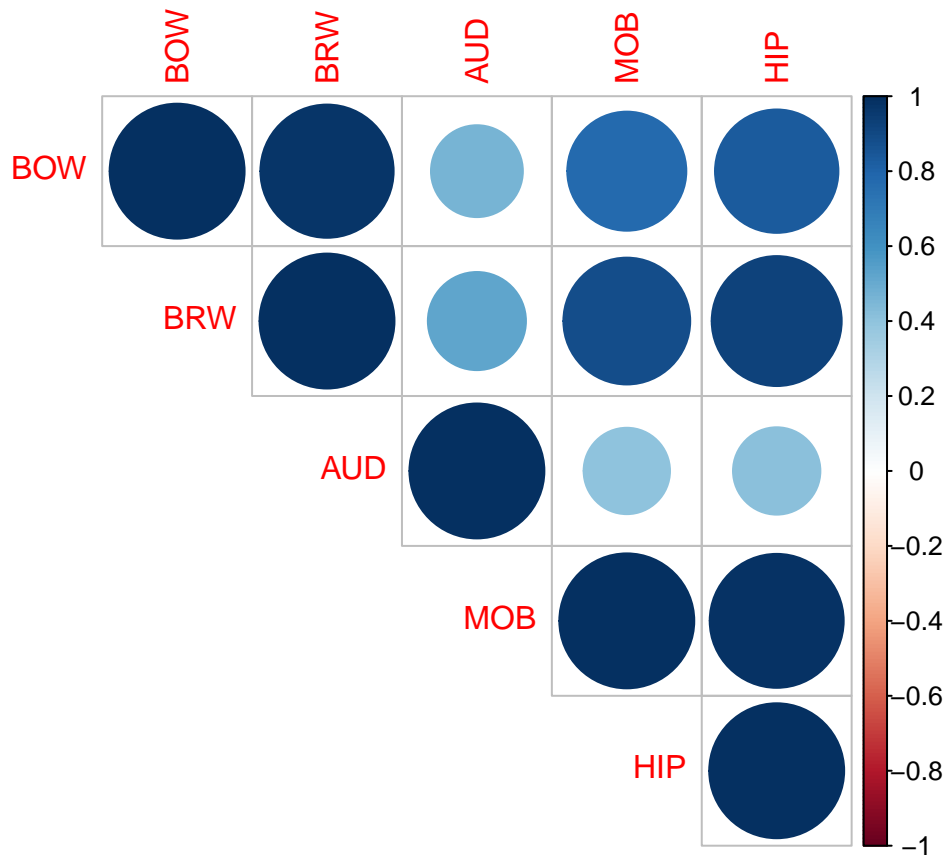


```
plot(reg2)
```



Study of the contribution of the total weight of each part of the brain

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



```
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
```

```
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
```

```
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
```

We can conclude that the BRW is correlated with HIP, MOB and not with AUD

```
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
```