# TP: Is Batman Somewhere

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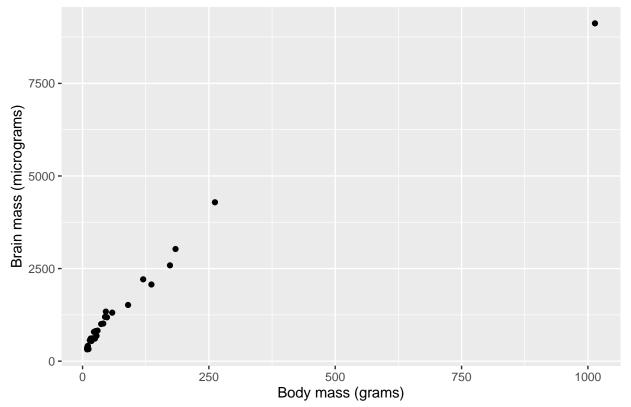
```
library(ggplot2)
myData <- read.table(file="bats.csv", sep=";", skip=3, header=T)</pre>
names(myData)
                                                                        "MOB"
## [1] "Species" "Diet"
                             "Clade"
                                        "BOW"
                                                   "BRW"
                                                              "AUD"
## [8] "HIP"
dim(myData)
```

### ## [1] 63 8

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

phyto=myData[(myData\$Diet==1),]

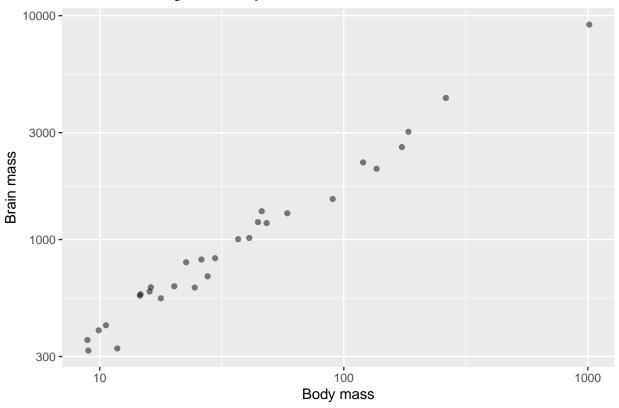
# Total brain weight vs Body mass



The initial graph shows a linear relationship between the brain mass and body mass. The data also appear

to be clustered as 95% of the data points have a body mass below 250. In the following graph, we try to observe a more spreadout representation by taking the logarithm of the data.

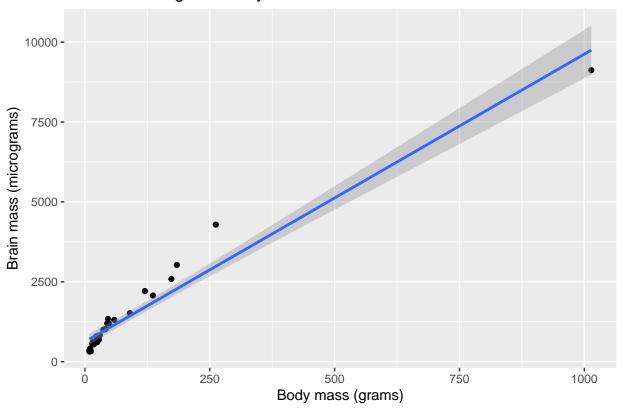




We can also include fit regression lines to both graphs as below:

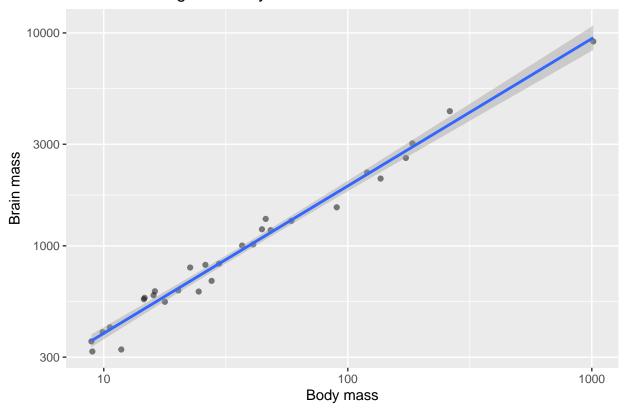
## `geom\_smooth()` using formula 'y ~ x'

# Total brain weight vs Body mass



##  $geom_smooth()$  using formula 'y ~ x'

# Total brain weight vs Body mass



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

#### Mathematical form

In general, the expression of the model estimated for linear regression is:  $Y = \hat{\beta}_1 + \hat{\beta}_2 X + \epsilon$  R. Specifically, R computes

$$BRW = \hat{\beta}_1 + \hat{\beta}_2 BOW + \epsilon$$

#### Regression summary

#### summary(reg1)

```
##
## Call:
## lm(formula = BRW ~ BOW, data = phyto)
## Residuals:
##
               1Q Median
  -628.32 -233.94 -65.74 158.26 1308.59
##
##
## Coefficients:
##
              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 623.4469
                          81.4762
                                    7.652 3.14e-08 ***
## BOW
                8.9999
                           0.3972 22.659 < 2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
```

```
## Residual standard error: 396.9 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
```

- 1. Intercept:  $\hat{\beta}_1 = 623.4469$ .
- 2.  $\hat{\beta}_2 = 8.9999$ .
- 3. Test statistics:  $T_{\hat{\beta}_1} = 7.652$  and  $T_{\hat{\beta}_2} = 22.659$ .
- 4. The p-value  $< 2.2 \times 10^{-16}$  « 0.05 showing that BOW has an influence on BRW.
- 5. The null hypothesis H0 is  $\hat{\beta}_1 = \hat{\beta}_2 = 0$ . In this case it is rejected as  $\hat{\beta}_2 \neq 0$  and the p-value is also very small
- 6. Based on the above observations, we can say that body mass has an effect on brain weight and the relationship is linear.
- 7. Coefficient of determination:  $R^2 = 0.95$  which tells that almost all the variation is explained by the model.

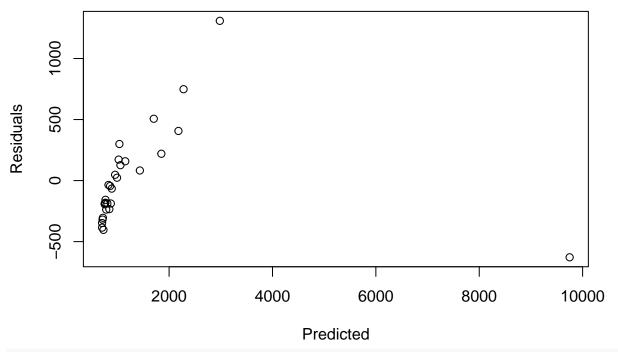
#### Analysis of variance (ANOVA)

# anova(reg1)

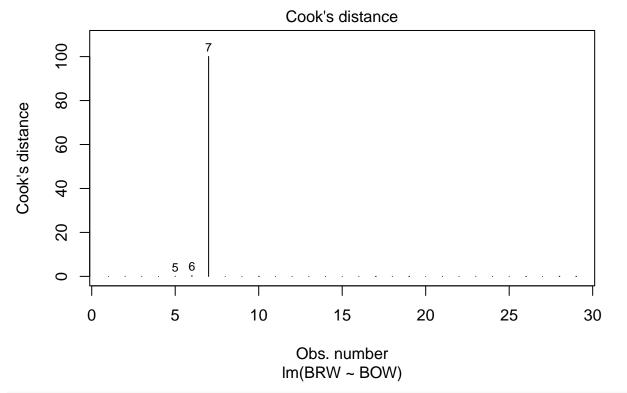
The analysis of variance provides additional information such as Sum of Squared Explained (SSE) = 80888380 and Sum of Residual Squares (SRS) = 4253838.

#### Graph of residuals

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



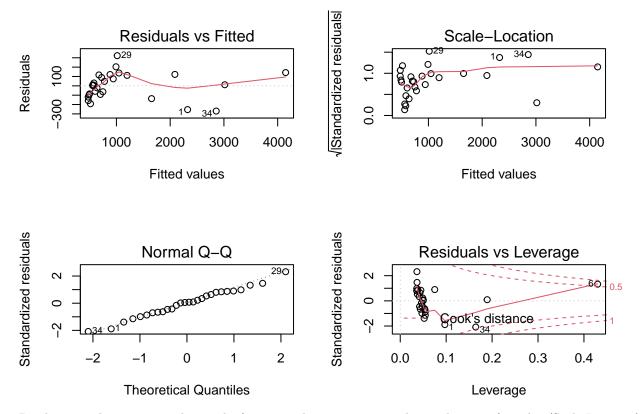
plot(reg1,4)



```
which(phyto$BRW>8000)
```

```
## [1] 7
phytobis=phyto[which(phyto$BRW<8000),]
reg2 = lm(BRW ~ BOW, data=phytobis)
summary(reg2)</pre>
```

```
##
## Call:
## lm(formula = BRW ~ BOW, data = phytobis)
##
## Residuals:
##
       Min
                 1Q Median
                                   3Q
                                           Max
##
   -269.76 -93.33
                        8.73
                              112.93
                                       322.55
##
## Coefficients:
##
                Estimate Std. Error t value Pr(>|t|)
   (Intercept) 346.5452
                             35.4920
                                         9.764 3.48e-10 ***
                                       33.860 < 2e-16 ***
## BOW
                 14.5099
                               0.4285
##
                    0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Signif. codes:
## Residual standard error: 141.8 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)
                                                 /Standardized residuals
                                                                   Scale-Location
                Residuals vs Fitted
     1000
Residuals
                                                      1.5
     -200
                                                      0.0
             2000
                    4000
                          6000
                                 8000
                                                              2000
                                                                     4000
                                                                            6000
                                                                                   8000
                    Fitted values
                                                                      Fitted values
Standardized residuals
                                                 Standardized residuals
                   Normal Q-Q
                                                               Residuals vs Leverage
                                         60
              0
     0
                                                      4
                                                                  Cook's distance
     4
          -2
                          0
                                         2
                                                           0.0
                                                                  0.2
                                                                         0.4
                                                                                0.6
                                                                                       8.0
                Theoretical Quantiles
                                                                       Leverage
par(mfcol=c(2,2))
plot(reg2)
```



By observing diagnostic graphs 2 and 3 for reg1 and reg2, we can see that in the case of graph 2 (Scale-Location), the data points are grouped describe a pattern.

graph 3 comparison: More symetric wrt zero (reg2). reg1 not that symetric.

# 3. Study of the contribution to the total weight of each part of the $\frac{1}{2}$