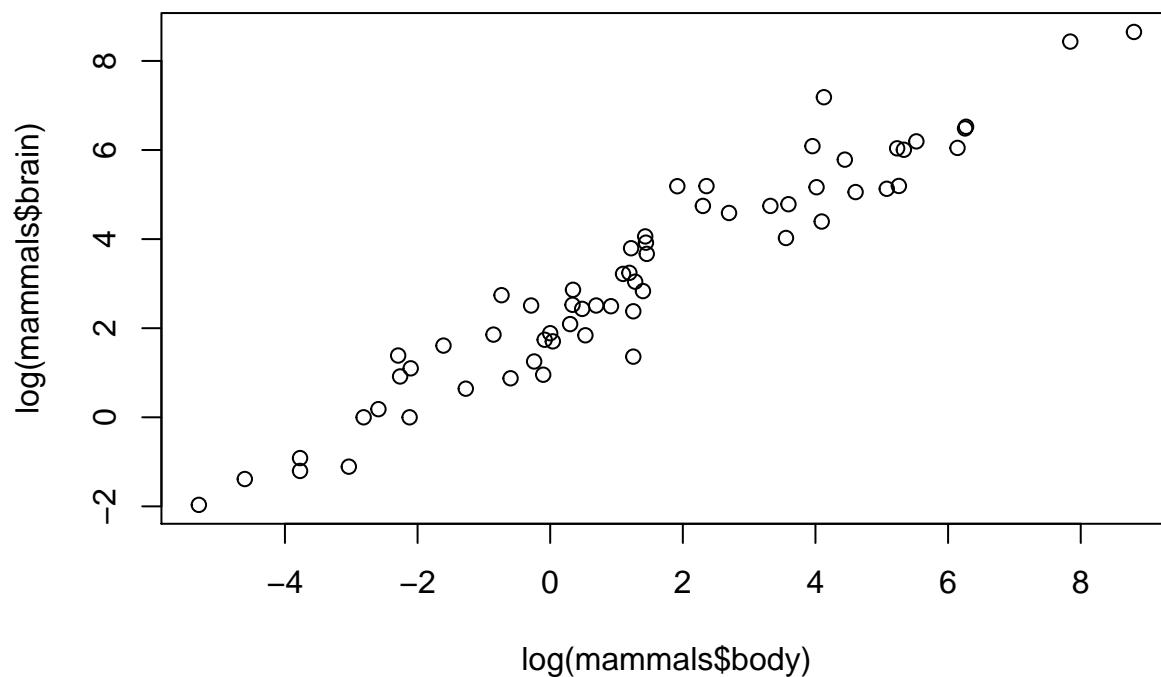# TMA4315: Project 2

jototlan@stud.ntnu.no (10018), martigtu@stud.ntnu.no (10037)

## Problem 1

```
mammals <- read.table(
  "https://www.math.ntnu.no/~jarlet/statmod/mammals.dat",
  header=T)
```

### a)

```
plot(log(mammals$body), log(mammals$brain)) # Seems pretty linear.
```



A log-log plot of the brain mass against body mass seems to reveal a linear trend. We thus fit the following model:

```
mod0 <- lm(log(brain) ~ log(body), data = mammals)
summary(mod0)
```

```
##
## Call:
## lm(formula = log(brain) ~ log(body), data = mammals)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
```

```
## -1.71550 -0.49228 -0.06162  0.43597  1.94829
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   2.13479    0.09604   22.23   <2e-16 ***
## log(body)     0.75169    0.02846   26.41   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.6943 on 60 degrees of freedom
## Multiple R-squared:  0.9208, Adjusted R-squared:  0.9195
## F-statistic: 697.4 on 1 and 60 DF,  p-value: < 2.2e-16
```

## b)

```
is.human = ifelse(mammals$species == "Human", 1, 0)
mammals$is.human = as.factor(is.human)

mod1 <- lm(log(brain) ~ log(body) + is.human, data = mammals)
sum1 <- summary(mod1)
```

We use the notation $\boldsymbol{y} = X\boldsymbol{\beta} + \boldsymbol{\varepsilon}$ to represent the linear model. Here, $X$ is the $n \times p$ design matrix, where $n$ is the number of observations and $p$ is the number of parameters used in the model. As usual, $\boldsymbol{\varepsilon} \sim \mathcal{N}(\boldsymbol{0}, \sigma^2 I_n)$. This (along with the other usual assumptions how much detail is required here??) gives the well known result:

$$\hat{\boldsymbol{\beta}} \sim \mathcal{N}(\boldsymbol{\beta}, \sigma^2(X^T X)^{-1}).$$

We let $\hat{\boldsymbol{\beta}} = [\hat{\beta}_0, \hat{\beta}_1, \hat{\beta}_2]^T$, where $\hat{\beta}_2$ estimates the effect of being a human (we also index from 0 in the design matrix). Now we want to perform the hypothesis test

$$H_0 : \beta_2 = 0 \quad \text{vs.} \quad H_1 : \beta_2 > 0.$$

Under $H_0$, we obtain that

$$\frac{\hat{\beta}_2}{\sigma\sqrt{(X^T X)_{2,2}^{-1}}} \sim \mathcal{N}(0, 1).$$

Combining this with the fact that

$$\frac{(n-p)s^2}{\sigma^2} \sim \chi_{n-p}^2,$$

where $s^2 = RSS/(n-p)$, we obtain the test statistic

$$\frac{\hat{\beta}_2}{s\sqrt{(X^T X)_{2,2}^{-1}}} \sim t_{n-p},$$

under $H_0$. We perform the calculations in R:

```
n <- nrow(mammals)
p <- 3
beta.2 <- mod1$coefficients[3]
s <- sqrt(deviance(mod1))
X <- model.matrix( ~ log(body) + is.human, data = mammals)
```

2

```
XtX.inv <- solve(t(X) %*% X)


T.stat <- beta.2/(s*sqrt(XtX.inv[3,3]))
p.val <- pt(T.stat, n - p, lower.tail = F)
p.val
```

```
## is.human1
## 0.3469957
```

The calculated p-value is 0.3469957, which suggest that. . .