TMA4315: Project 2

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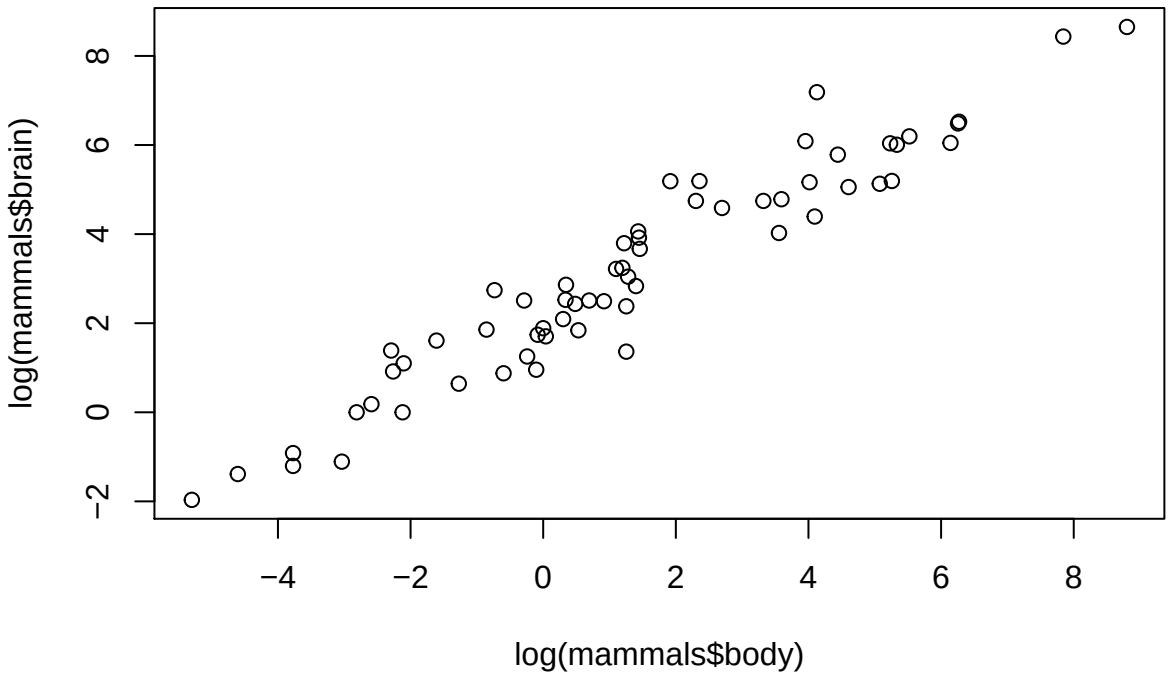
Problem 1

```
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)
summary(mod1)
```

```
##
## Call:
## lm(formula = log(brain) ~ log(body) + is.human, data = mammals)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.68392 -0.46764 -0.02398  0.47237  1.64949
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  2.11500    0.09030  23.421  < 2e-16 ***
## log(body)    0.74228    0.02687  27.622  < 2e-16 ***
## is.human1    2.00691    0.66083   3.037  0.00356 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.6511 on 59 degrees of freedom
## Multiple R-squared:  0.9315, Adjusted R-squared:  0.9292
## F-statistic: 401.1 on 2 and 59 DF,  p-value: < 2.2e-16
```

Let $\hat{\boldsymbol{\beta}} = [\hat{\beta}_0, \hat{\beta}_1, \hat{\beta}_2]^T$ be the coefficient estimates given in the summary above. Then the estimated effect on brain mass from being a human is $\hat{\beta}_2 \approx 2.0069072$. Since we have used a log-transform on both the brain mass and body mass, humans will according to the model be larger by a factor of $e^{\hat{\beta}_2} = 7.4402704$.

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, $\boldsymbol{\varepsilon} \sim \mathcal{N}(\mathbf{0}, \sigma^2 I_n)$. This (along with the other usual assumptions how much detail is required here??) gives the well known result:

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

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 (we also index from 0 in the design matrix)

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

Combining this with the fact that

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

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

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

under H_0. We perform the calculations in R:

```
n <- nrow(mammals)
p <- 3
beta.2 <- mod1$coefficients[3]
s <- sqrt(deviance(mod1)/(n-p))
X <- model.matrix( ~ log(body) + is.human, data = mammals)
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
## 0.001777696
```

The calculated p-value is 0.0017777.

c)

We now consider the linear model with only two parameters, β_0 and β_1. Let $Y_h = \beta_0 + \beta_1 x_h$ be the stochastic variable from which the log of the human brain mass is realized and $\widehat{Y}_h = \hat{\beta}_0 + \hat{\beta}_1 x_h$ be the corresponding estimator. Then we can find the pivotal quantity

$$T = \frac{Y_h - \widehat{Y}_h}{s\sqrt{1 + 1/n + \frac{(x_h - \bar{x})^2}{\sum_{i=1}^n (x_i - \bar{x})^2}}} \sim t_{n-2}.$$

We refer to the good old subject-pages (simple linear regression/prediction and prediction intervals in simple linear regression) for this result. Thus, we can find the one-sided prediction interval:

$$P(T \leq U) = 1 - \alpha \implies U = t_{n-2,\alpha}.$$

Since there are $n = 61$ rows in the dataset (excluding humans), the exact prediction interval is $(-\infty, t_{61,\alpha})$