Chapter 2

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```
library(Stat2Data)
data("MetabolicRate")
head (MetabolicRate)
```

```
##   Computer BodySize LogBodySize Instar CO2ppm      Mrate   LogMrate
## 1        1   0.0021   −2.677781      1  2.875 0.18652543 −0.7292620
## 2        1   0.0096   −2.017729      1  2.201 0.20399768 −0.6903748
## 3        1   0.0060   −2.221849      1  0.965 0.08952349 −1.0480630
## 4        1   0.0059   −2.229148      1  3.820 0.35107971 −0.4545943
## 5        1   0.0061   −2.214670      1  6.106 0.36291150 −0.4401993
## 6        1   0.0076   −2.119186      1  2.449 0.17659516 −0.7530212
```

Let us create a model as asked in 2.24:

```
model = lm (LogBodySize ~ LogMrate, data=MetabolicRate)
summary (model)
```

```
##
## Call:
## lm(formula = LogBodySize ~ LogMrate, data = MetabolicRate)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## −0.53362 −0.12886  0.00303  0.11205  0.52210
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) −1.38990    0.01381  −100.7   <2e-16 ***
## LogMrate     1.03429    0.01394    74.2   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1861 on 303 degrees of freedom
## Multiple R-squared:  0.9478, Adjusted R-squared:  0.9477
## F-statistic:  5505 on 1 and 303 DF,  p-value: < 2.2e-16
```

1.1

2.24 A) LogBodySize = -1.39 + 1.03 LogMrate 2.24 B) The slope parameter is significant! Generally speaking, I'd calculate t-stat, then p-val of that t-stat from DF. However, R provides 'Signif Codes', and the summary of the model inidicates that the slope parameter is significant. 2.24 D) Model sum of squares is SSM and the Total sum of squares is SST. Since R^2 is SSM/SST, then the answer is 0.9478. The larger this value, the better the model explains the relationship between the Y and X variables.

2.1

2.50 A) When LogBodySize is 0 then LogMrate is (139/103). Got the LogMrate value by solving for 0 = -1.39 + 1.03 LogMrate. Then, Mrate = 22.36 μW 2.50 B) Predicted interval = -1.38 (+/-) (-100.7*0.01381) The 95% PI will be (-2.781334, 0)

[Confused about the 2.50 B answer, suspect it is incorrect: trying to understand the process from 2.4]

2.2

Index of comments

1.1 You should have the order of this switched. We are trying to predict Log(MRate) from Log(BodySize). -1

2.1 2.50a. When any log is equal to 0, we know that the input is 1. So a log of 0 corresponds with a body size of 1. -1

2.2 Dr. Phil typically always gives you an outline r markdown file with most of the code in it that you can use for your assignments. You should use those for the future.