

# Module 5 Lab Submission

Nora Quick

Again we consider the Brain size data in the data set `case0902` from the `Sleuth3` library. You can read more about this data set by viewing the help file:

```
help(case0902)
head(case0902)
```

```
##           Species Brain   Body Gestation Litter
## 1      Aardvark    9.6    2.20         31    5.0
## 2      Acouchis    9.9    0.78         98    1.2
## 3 African elephant 4480.0 2800.00        655    1.0
## 4      Agoutis    20.3    2.80        104    1.3
## 5      Axis deer  219.0   89.00        218    1.0
## 6      Badger    53.0    6.00         60    2.2
```

In Lecture 2 of this Module, we considered modeling all four variables on the log scale, and we compared two models: a full model with log-Body, log-Gestation, and log-Litter as predictors, and a reduced model with only log-Body as a predictor.

1. Fit the two models described above (and as shown on slide 15 of Lecture 2).

```
full_model <- lm(log(Brain) ~ log(Body) + log(Gestation) + log(Litter), data = case0902)
reduced_model <- lm(log(Brain) ~ log(Body), data = case0902)
```

Now suppose we have four new species, with the following values of Body, Gestation, and Litter:

Species	Body	Gestation	Litter
A	1	50	1
B	1	50	2
C	1	150	1
D	50	50	1

2. Create a new data frame with these values, and use the `predict()` function to predict the log-brain size for these new species.

```
same_gest <- data.frame(
  Species = rep(c('A', 'B', 'C', 'D'), 4),
  Body = rep(c(1, 1, 1, 50), each = 4),
  Gestation = rep(c(50, 50, 150, 50), each = 4),
  Litter = rep(c(1, 2, 1, 1), each = 4)
)

# same_gest
```

```
cbind(same_gest, pred_log_energy = predict(full_model, newdata = same_gest))
```

```
##      Species Body Gestation Litter pred_log_energy
## 1      A      1      50      1      2.489821
## 2      B      1      50      1      2.489821
## 3      C      1      50      1      2.489821
## 4      D      1      50      1      2.489821
## 5      A      1      50      2      2.274896
## 6      B      1      50      2      2.274896
## 7      C      1      50      2      2.274896
## 8      D      1      50      2      2.274896
## 9      A      1     150      1      2.948977
## 10     B      1     150      1      2.948977
## 11     C      1     150      1      2.948977
## 12     D      1     150      1      2.948977
## 13     A     50      50      1      4.739513
## 14     B     50      50      1      4.739513
## 15     C     50      50      1      4.739513
## 16     D     50      50      1      4.739513
```

```
cbind(same_gest, pred_log_energy = predict(reduced_model, newdata = same_gest))
```

```
##      Species Body Gestation Litter pred_log_energy
## 1      A      1      50      1      2.332351
## 2      B      1      50      1      2.332351
## 3      C      1      50      1      2.332351
## 4      D      1      50      1      2.332351
## 5      A      1      50      2      2.332351
## 6      B      1      50      2      2.332351
## 7      C      1      50      2      2.332351
## 8      D      1      50      2      2.332351
## 9      A      1     150      1      2.332351
## 10     B      1     150      1      2.332351
## 11     C      1     150      1      2.332351
## 12     D      1     150      1      2.332351
## 13     A     50      50      1      5.145825
## 14     B     50      50      1      5.145825
## 15     C     50      50      1      5.145825
## 16     D     50      50      1      5.145825
```

3. Obtain confidence intervals for the mean log-brain size of the new species above, using the `interval = "confidence"` argument in the `predict()` function.

```
ci_full_model <- predict(full_model, newdata = same_gest, interval = "confidence")
ci_full_model
```

```
##      fit      lwr      upr
## 1 2.489821 2.208628 2.771014
## 2 2.489821 2.208628 2.771014
## 3 2.489821 2.208628 2.771014
## 4 2.489821 2.208628 2.771014
```

```
## 5  2.274896 2.116014 2.433778
## 6  2.274896 2.116014 2.433778
## 7  2.274896 2.116014 2.433778
## 8  2.274896 2.116014 2.433778
## 9  2.948977 2.732987 3.164968
## 10 2.948977 2.732987 3.164968
## 11 2.948977 2.732987 3.164968
## 12 2.948977 2.732987 3.164968
## 13 4.739513 4.312767 5.166260
## 14 4.739513 4.312767 5.166260
## 15 4.739513 4.312767 5.166260
## 16 4.739513 4.312767 5.166260
```

```
ci_reduced_model <- predict(reduced_model, newdata = same_gest, interval = "confidence")
ci_reduced_model
```

```
##      fit      lwr      upr
## 1  2.332351 2.186921 2.477782
## 2  2.332351 2.186921 2.477782
## 3  2.332351 2.186921 2.477782
## 4  2.332351 2.186921 2.477782
## 5  2.332351 2.186921 2.477782
## 6  2.332351 2.186921 2.477782
## 7  2.332351 2.186921 2.477782
## 8  2.332351 2.186921 2.477782
## 9  2.332351 2.186921 2.477782
## 10 2.332351 2.186921 2.477782
## 11 2.332351 2.186921 2.477782
## 12 2.332351 2.186921 2.477782
## 13 5.145825 5.008289 5.283360
## 14 5.145825 5.008289 5.283360
## 15 5.145825 5.008289 5.283360
## 16 5.145825 5.008289 5.283360
```

4. Obtain prediction intervals for the log-brain size of the new species above, using the `interval = "prediction"` argument in the `predict()` function.

```
pi_full_model <- predict(full_model, newdata = same_gest, interval = "prediction")
pi_full_model
```

```
##      fit      lwr      upr
## 1  2.489821 1.505881 3.473761
## 2  2.489821 1.505881 3.473761
## 3  2.489821 1.505881 3.473761
## 4  2.489821 1.505881 3.473761
## 5  2.274896 1.318700 3.231092
## 6  2.274896 1.318700 3.231092
## 7  2.274896 1.318700 3.231092
## 8  2.274896 1.318700 3.231092
## 9  2.948977 1.981651 3.916303
## 10 2.948977 1.981651 3.916303
## 11 2.948977 1.981651 3.916303
```

```
## 12 2.948977 1.981651 3.916303
## 13 4.739513 3.704535 5.774492
## 14 4.739513 3.704535 5.774492
## 15 4.739513 3.704535 5.774492
## 16 4.739513 3.704535 5.774492
```

```
pi_reduced_model <- predict(reduced_model, newdata = same_gest, interval = "prediction")
pi_reduced_model
```

```
##          fit      lwr      upr
## 1  2.332351 1.175408 3.489294
## 2  2.332351 1.175408 3.489294
## 3  2.332351 1.175408 3.489294
## 4  2.332351 1.175408 3.489294
## 5  2.332351 1.175408 3.489294
## 6  2.332351 1.175408 3.489294
## 7  2.332351 1.175408 3.489294
## 8  2.332351 1.175408 3.489294
## 9  2.332351 1.175408 3.489294
## 10 2.332351 1.175408 3.489294
## 11 2.332351 1.175408 3.489294
## 12 2.332351 1.175408 3.489294
## 13 5.145825 3.989847 6.301802
## 14 5.145825 3.989847 6.301802
## 15 5.145825 3.989847 6.301802
## 16 5.145825 3.989847 6.301802
```

5. Compare the reduced model to the full model using the AIC and BIC measures.

```
AIC_comp <- AIC(full_model, reduced_model)
AIC_comp
```

```
##          df      AIC
## full_model    5 135.3188
## reduced_model  3 171.1866
```

```
BIC_comp <- BIC(full_model, reduced_model)
BIC_comp
```

```
##          df      BIC
## full_model    5 148.1405
## reduced_model  3 178.8796
```