

R Markdown Test

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21 September, 2020

EBIO 3080 Selection Lab (Week 4)

Setting Up the Code

Calculating mean beak size from the data:

```
setwd("E:/Documents/GitHub/EBIO-R-Code/EBIO 3080/Lab/Week 4")
heritability <- read.csv(file.choose(), header = T)
mid_parent <- (heritability$father_beak + heritability$mother_beak) / 2
model <- lm(heritability$offspring ~ mid_parent)
h2 <- summary(model)$coeff[2, 1]
p <- summary(model)$coeff[2, 4]
```

Pre-Quiz

