(1) A precise description of the role and mathematical contribution of each member of the group. An indication of which components of the nal presentation are completed by which group members. This item should be identical for all members of the same group, the proceeding items, below, are individualized.

Cody's contribution: After the variable analysis done by Rachel i used the data set that had no NA values and set up a for loop with the suggested variables. This for loop was pre-transformation, and created 16 different combinations of variables coupled with predation being constant in all combinations. The loop then spat out the sorted standard error value for all combinations and the lowest standard error was then chosen for our model to work with.

Rachel's Contribution: I will present the initial data analysis, including the first observations of the data, narrowing of the variables used for our possible models, decisions regarding omission of particular data points, as well as the assessment of the missing values within the data set.

Ryan's Contribution: Presenting on transformations to biological predictors based on research from allometric scaling. Checked for potential transformation of the response variable using the box cox method.

Nate's contribution: Presenting which mammals most greatly effect the standard error of predation and why we choose to keep them in the data set. Also showing the difference between base and final model with PRESS to evaluate the magnitude our manipulations had on the model.

Jonothan's Contribution: Investigation and validation of the model assumptions regarding residual normality and constant variance as well as creation of some visual descriptive statistics. As with the other members I was also heavily involved with discussions involving choosing the final model and transformation considerations.

Note: In addition to the individual contributions discussed previously, all group members were heavily involved in discussions regarding model changes and assessment. Through this process a lot of work was completed, but sometimes became irrelevant and as a consequence was subsequently discarded.

(3) An indication of the statistical software commands and outputs used to create your individual contribution to the group project presentation.

```
mammalsleep1 <- mammalsleep[complete.cases(mammalsleep),]
mams <- mammalsleep1
summary_pred_mams <- mams %>% group_by(predation) %>% summarize(n = n(), sd = sd(sleep),
          mean = mean(sleep))
ggplot(summary_pred_mams) + geom_bar( aes(x=predation, y=mean), stat="identity", fill="blue",
      alpha=0.7) + geom_errorbar( aes(x=predation, ymin=mean-sd, ymax=mean+sd), width=0.4,
      colour="orange", alpha=0.9, size=1.3) + ggtitle("Average Amount of Sleep for Each Predation
      Level") + geom_text(aes(label=n, x=predation, y=1), position=position_dodge(width=0.9),
      size=4) + geom_text(aes(label="n =", x=.8, y=1), position=position_dodge(width=0.9), size=4)
      + xlab("Predation Level") + ylab("Mean Hours of Sleep") + labs(stat = "Standard Deviation")

# ^ Commands were used to create and interpret the graphic in slide #4

hist(mams$body, main = "Histogram of Body", xlab = "body")
hist(log(mams$body), col= "red", main = "Histogram of log(body)", xlab = "log(body)")
text(x=5, y=12, labels = "*color added to illustrate
    excitment of transformation")

hist(mams$nondream, main = "Histogram of Dream", xlab = "dream")
hist(log(mams$nondream), col = "blue")
text(x=1, y=15, labels = "*color added to illustrate
    excitment of transformation")

hist(mams$gestation, main = "Histogram of Gestation", xlab="gestation")
hist(log(mams$gestation), col = "pink", main = "Histogram of log(gestation)", xlab="log(gestation)")
text(x=2.8, y=8, labels = "*color added to illustrate
    excitment of transformation")

hist(mams$sleep, main = "Histogram of Sleep", xlab = "sleep")
hist(log(mams$sleep), col= "black", main = "Histogram of log(sleep)", xlab = "log(sleep)")
text(x=1.5, y=6, labels = "*black added to illustrate
    sadness of transformation")

hist(test.lm$residuals, breaks = 20, main = "Histogram of Residuals", xlab = "residuals")

ggplot(data=test.lm, aes(fitted(test.lm), resid(test.lm))) +geom_point() +
  xlab("Fitted") + ylab("Residuals")

qqnorm(residuals(test.lm), pch = 1, frame = TRUE)
qqline(residuals(test.lm),
    col = "blue")

# ^ These commands were used to create the transformation explanation, and model assumption
# validation graphics in slide #13

# Note: Many more commands and graphics were performed through the process of cleaning,
# transforming, and evaluating the data and linear model. However, I believe they do not need to be
```

explicitly listed here as they are either no longer relevant to the chosen final model, or are implicitly
demonstrated through the slide presentation.

(4) Your description of the final conclusions of the analysis in terms of the real world problem.

We estimate that for every increased change in predation level that mammals will tend to receive 16.2 less minutes of sleep per night when holding all other predictor variables constant. Our final model sought to give the most precise explanation of the relationship between sleep and predation in the simplest way possible. In other terms, adding an additional predictor, interaction, or transformation to our model was only seriously considered if it's inclusion substantially improved the model. In conclusion, we reject the null hypothesis that the likelihood an animal is to be preyed upon does not significantly affect it's amount of sleep per night with a p-value of .025.