Homework 3

Denis Ostroushko

2022-10-01

Problem 6.3

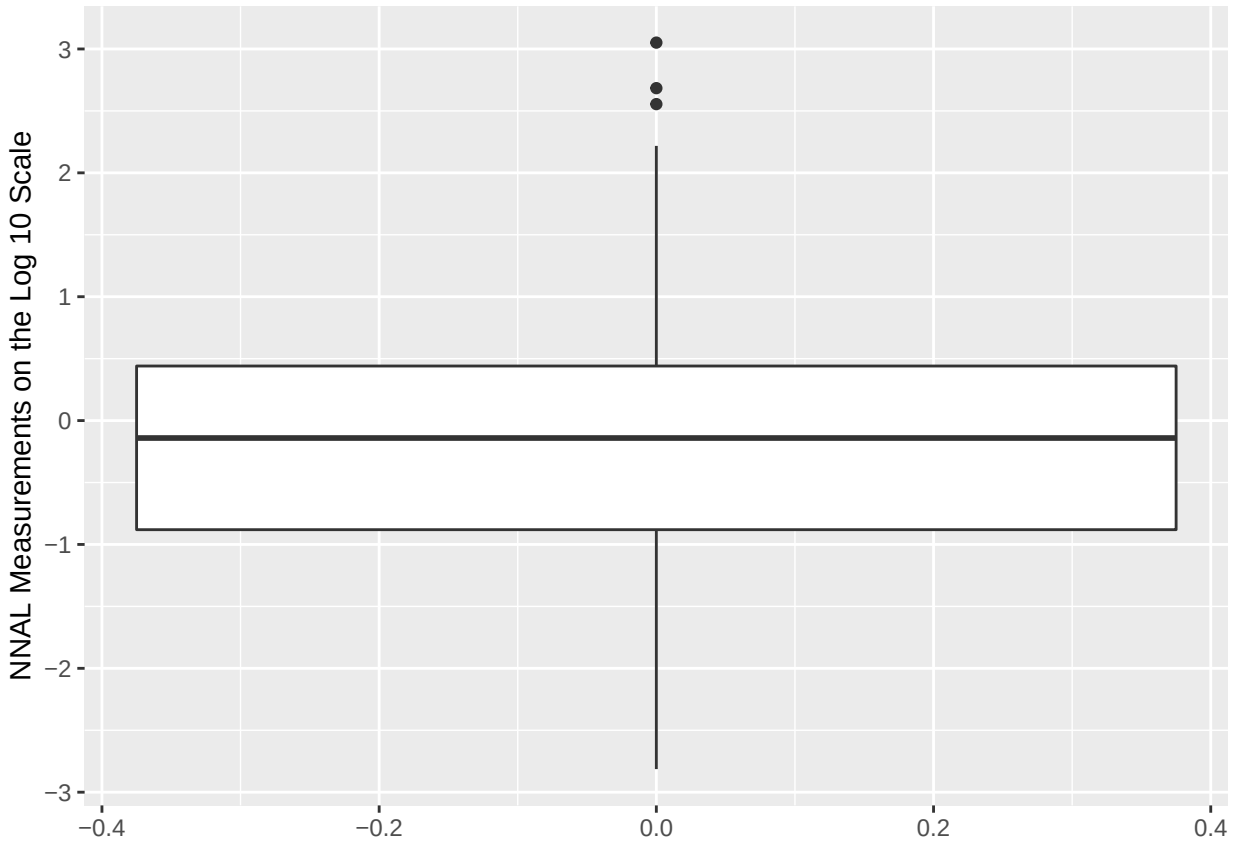
Problem 7.1

```
cig <- read_xls("/Users/denisostroushko/Desktop/UofM MS/MS Fall 2022/Puhb 7405/Data Sets/Cigarettes.xls

original_names <- colnames(cig)

colnames(cig) <- c("age", "gender", "cpd", "carbon_mono", "cotinine", "nnal")

cig$log_nnal <- log(cig$nnal)
```

7.1 - A

Simple box plot of NNAL measurements on the natural base logarithmic scale is given below:

```
ggplot(data = cig,
       aes(y = log_nnal)) + geom_boxplot() +

  ylab("NNAL Measurements on the Log 10 Scale")
```



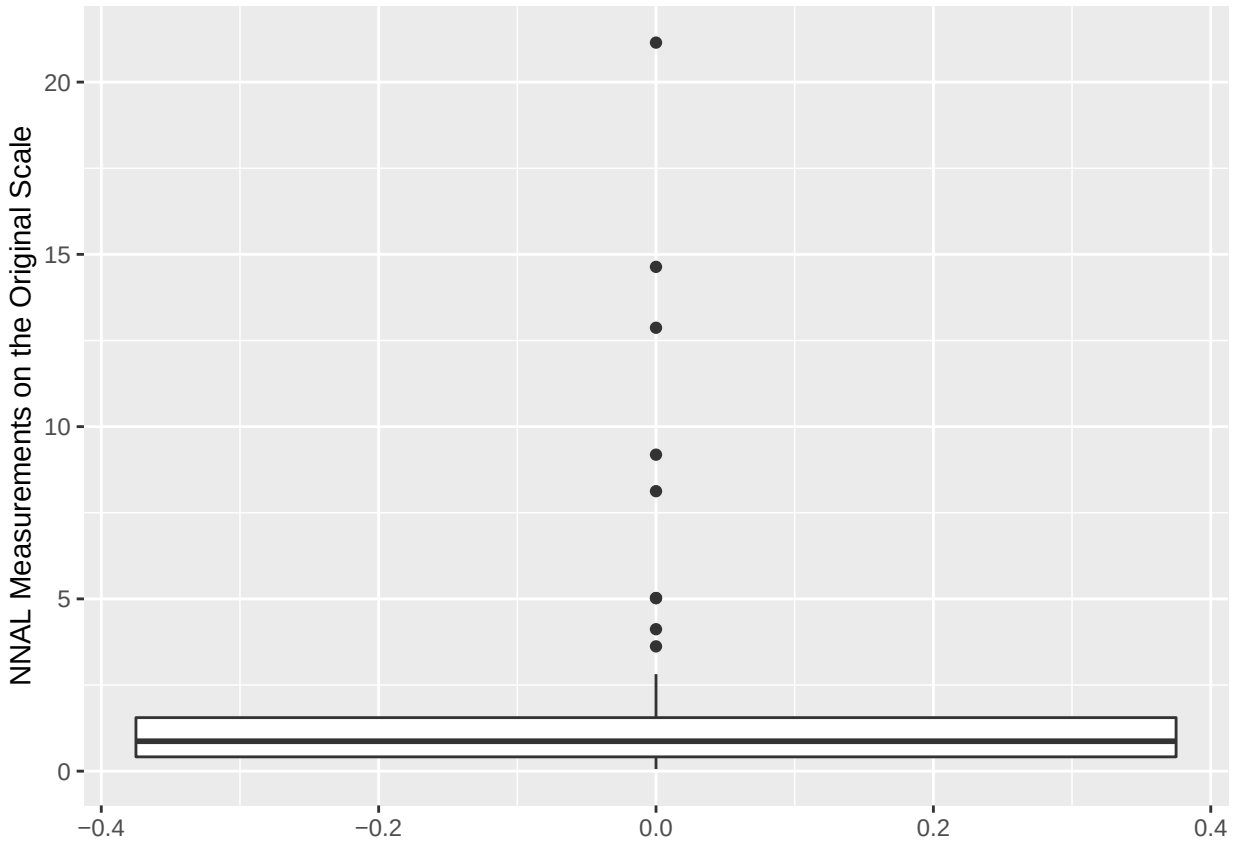
Section (i) There are extreme measurements on NNAL on the natural base logarithmic scale. They are located on the higher end of the distribution. These values are identified as potential outliers in the data. Values above above the threshold given by $1.5 \times UpperIQR$, which is 1.7616.

There are 5 values of Log NNAL measurements that are above that range.

Section (ii) This plot is symmetric. The main body of the box is almost evenly distributed around zero, with a slight bias towards negative values. Same applies to maximum values withing the 1.5 IQR range. Lower whisker extends to values close to negative three, while the upper whisker goes to 1.7616, as we saw previously.

If the get a box plot for values of NNAL on the original scale, we can why we need a transformation.

```
ggplot(data = cig,
       aes(y = nnal)) + geom_boxplot() +

  ylab("NNAL Measurements on the Original Scale")
```

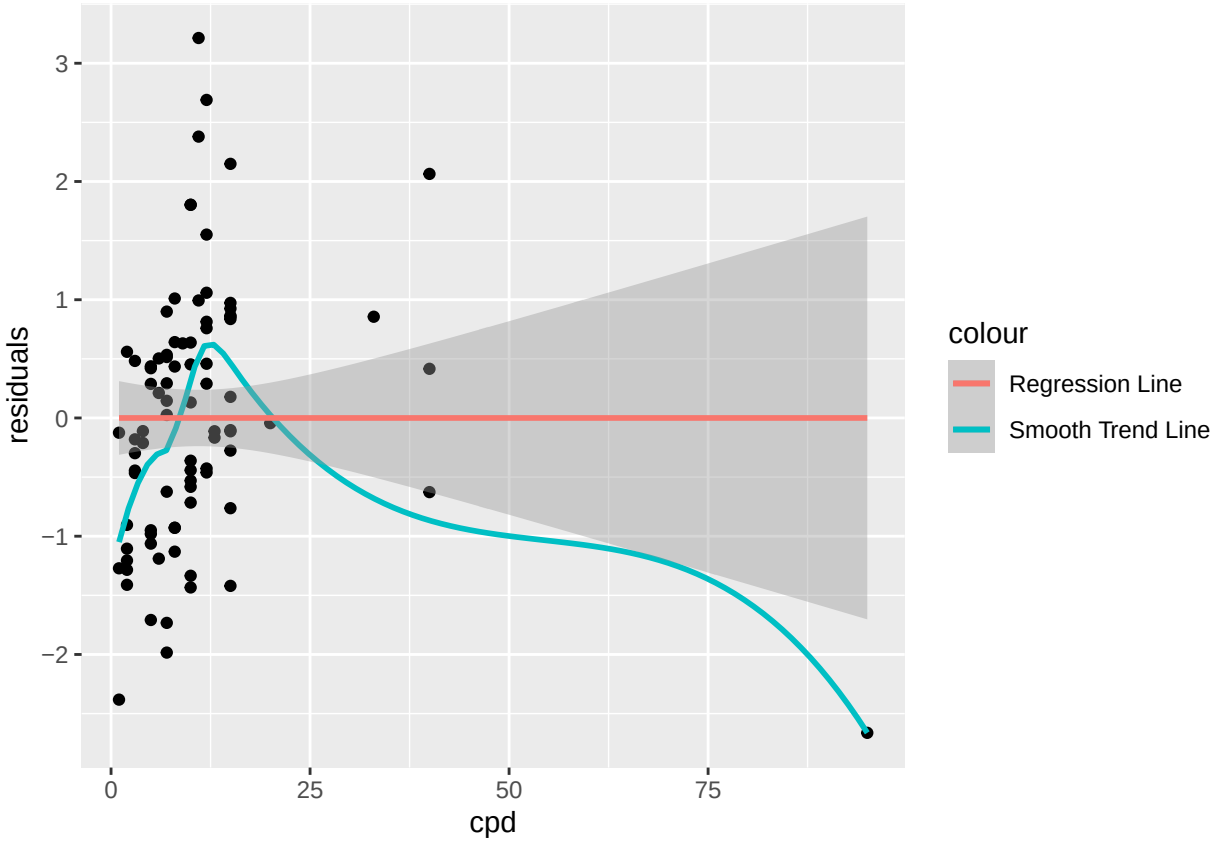


This type of plot reveal almost no information about the variance of NNAL values, other than there are heavy outliers on the upper end. Usually, this type of distribution suggests that the measurements are in fact log-normally distributed, which is why we performed a transformation in the first place.

7.1 - B

We showed how to fit a linear model and obtain $\hat{\beta}_i$ estimates using least squares method in the previous homework, so we will skip manual calculation this time. We will use R function to fit the model and obtain fitted, or predicted, values as well as residuals. Code below obtains all needed data, and shows the plot of residuals against corresponding values of predictor variable - the number of cigarettes per day.

```
lm_7_1 <- lm(log_nnal ~ cpd, data = cig)

cig$residuals <- lm_7_1$residuals

# obtain studentized residuals
cig$student_residuals <- studres(lm_7_1)

cig$y_hat <- lm_7_1$fitted.values

ggplot(data = cig,
       aes(x = cpd,
           y = residuals)) + geom_point() +

  geom_smooth(aes(colour = "Smooth Trend Line"), se = F) +
  geom_smooth(aes(colour = "Regression Line"), method = "lm", se = T)
```



There is a number of departures from the normal error regression that we can study.

- **Non-constant variance**

Right away we can see that the variance of residuals may not be constant. However, it is hard to tell if that is true, because we have some outliers in terms of cigarette consumption. However, due to the shape of the cluster of residuals and values of predictor variable where residuals are concentrated, more tests are required to say more about the constant variance assumption.

- **Linearity of Regression Function and Residual Independence**

We can see that the regression line against residuals in flat at zero, so residuals are independent from the predictor variable.

The model clearly does not fit the outliers very well. We can see that a person who consumes more than 75 cigarettes per day has values of NNAL much lower than expected under this mode, while one person who consumes around 35 cigarettes per day has values of NNAL that are much larger than expected.

- **Outliers and Important Variables**

The reason for outliers, as Chap explained, might be the proportion of a cigarette that these people consume. A person who consumers over 75 cigarettes per day might start it, have some of it, and throw most of it away. While someone who smokes around 35 per day consumer all 35 in full. This is, of course, just a speculation, but if we include more data and construct a multiple linear regression model we may be able to explain these outliers better.

- **Normality of Residual Distribution**

In order to test outliers for normality we plot the residuals against expected values of residuals in a normally distributed random sample.

We can calculate these expected values using the formula:

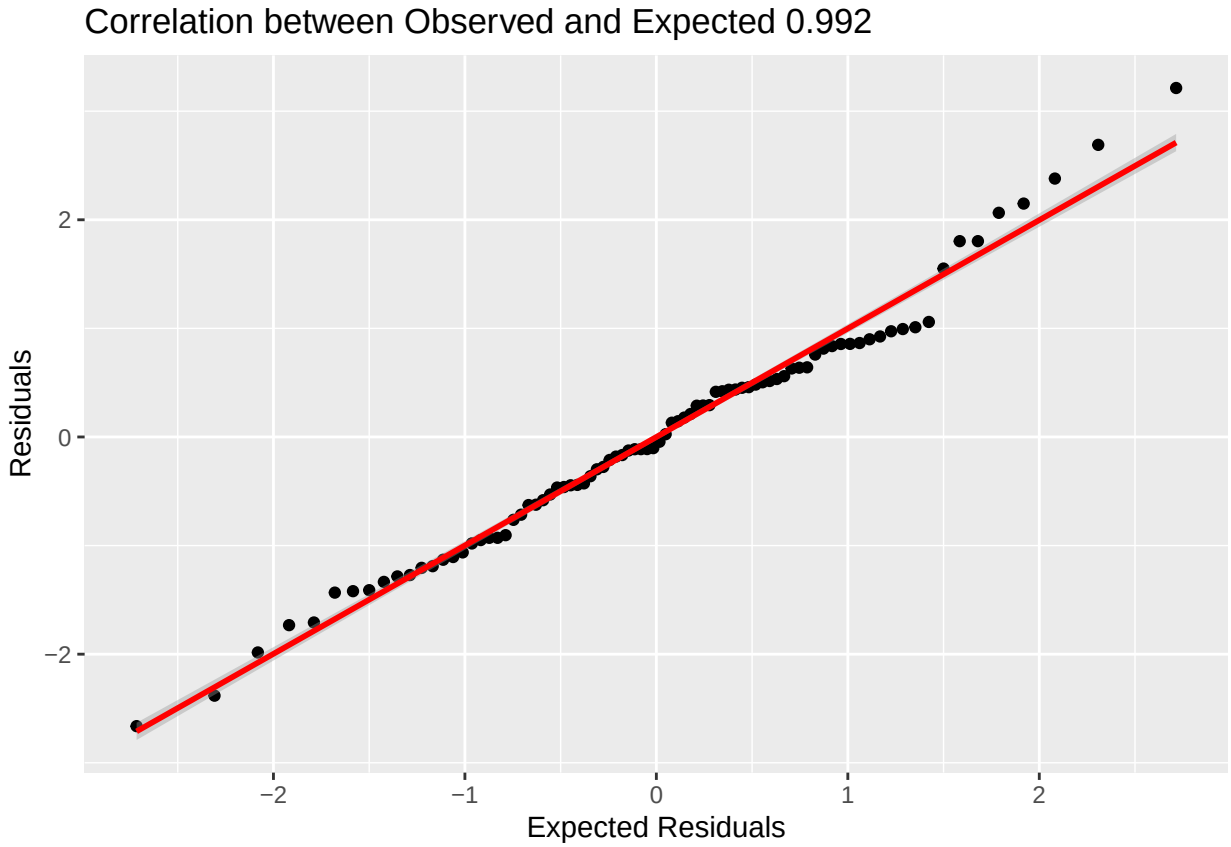
$$\sqrt{MSE} \times z(\frac{Residual - .375}{N + .25})$$

Where $z()$ is the quartile of the standard normal distribution.

We plot this relationship below:

```
mse <- sum(lm_7_1$residuals^2)/lm_7_1$df.residual

cig <- cig %>% arrange(residuals)

cig$resid_rank <- as.numeric(rownames(cig))

N <- nrow(cig)

cig$expected_resid <- sqrt(mse) * qnorm((cig$resid_rank - .375)/(N + .25))

corr <- cor(cig$residuals, cig$expected_resid)

crit_value_80 <- .985
crit_value_90 <- .986
```

```
ggplot(data= cig,
       aes(x = expected_resid, y = residuals)) + geom_point() +
  geom_smooth(method = "lm", color = "red") +
  ylab("Residuals") +
  xlab("Expected Residuals") +
  ggtitle(paste("Correlation between Observed and Expected", round(cor(cig$residuals, cig$expected_resi
```



We can see that observed and expected residuals are very strongly linearly correlated. So, we do not have heavy tails and residuals do not deviate from normality. Correlation coefficient is 0.992. Our sample has 86 observations, so we can find a critical value for 95% confidence level for this correlation coefficient. With 80 observations, the critical level is 0.985, while with 90 observations the critical level is 0.986. Estimated correlation coefficient is above both of those values, so out residuals are normally distributed.

7.1 - C

In order to perform a Brown-Forsythe test we need to complete a number of data transformation steps. We begin by saving residuals into its own data frame, and splitting them into two groups. We have a total of 86 observations, so we will assign 43 lowest values of residuals into "Lower" groups, and the rest into "Upper" group.

```
resid_df <- data.frame(residuals = cig$residuals)

# sort data by residuals and split into two groups.
resid_df <- resid_df %>% arrange(residuals)

resid_df$rank <- seq(from = 1, to = nrow(resid_df), by  = 1)

resid_df$group <-
  as.factor(
    case_when(
      resid_df$rank <= nrow(resid_df)/2 ~ "Lower",
      TRUE ~ "Upper"
    )
  )
paste("Observation in each groups")
```

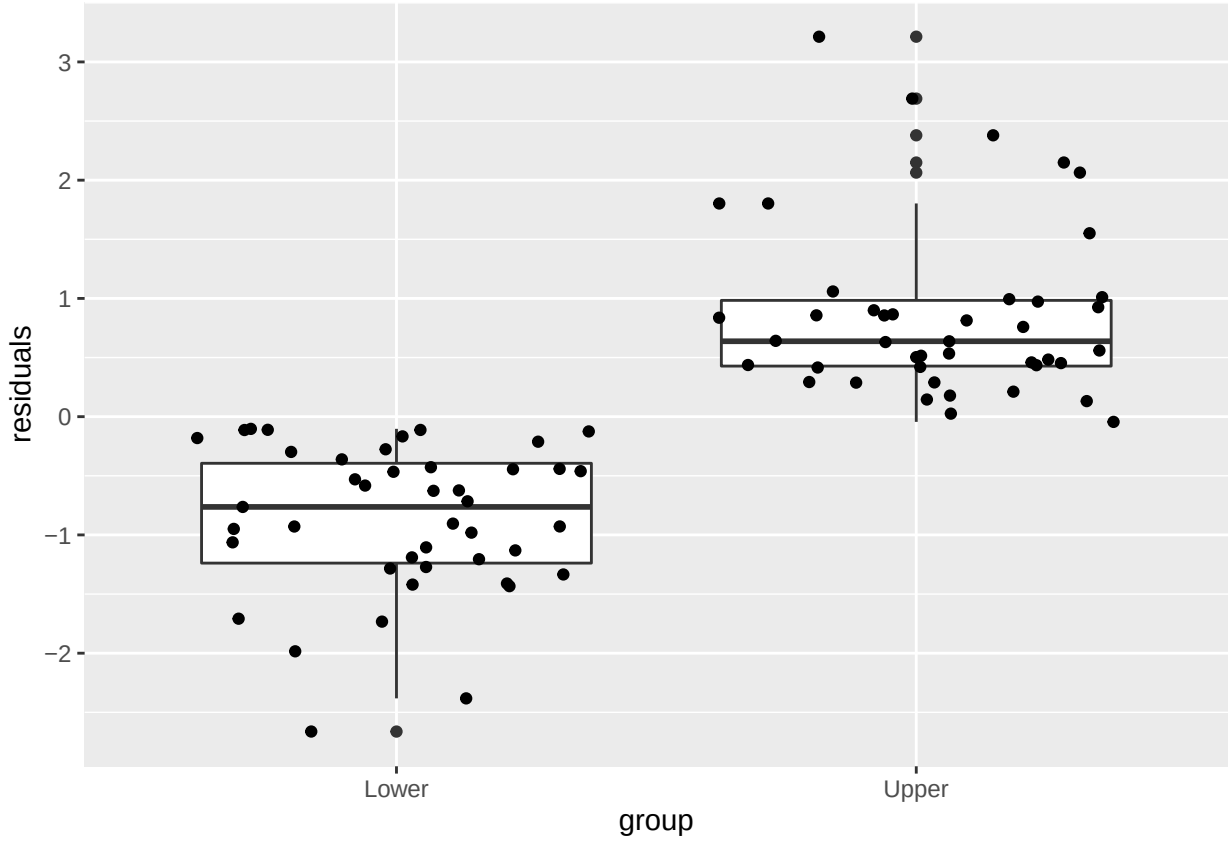
```
## [1] "Observation in each groups"
```

```
summary(resid_df$group)
```

```
## Lower Upper
##    43    43
```

Let's examine variance of residuals in each group using boxplots

```
ggplot(
  data = resid_df,
  aes(x = group,
      y = residuals)
) + geom_boxplot() + geom_jitter()
```



So far, we can see that the median and values of residuals in the upper group are greater than those in the lower group, however, their variance might not differ that much. While residuals in the lower group tend to be below the median of their group, and residuals in the upper group tend t be above the median in their respective group, absolute deviations do not appear so different in the two groups, at least visually.

So, we continue to perform transformations of residual data, mainly we find the median residual value in each group, and calculate absolute deviations. Median residual values for two groups is given below:

```
medians <-
  resid_df %>%
  group_by(group) %>%
  summarize(
    median = median(residuals))

medians
```

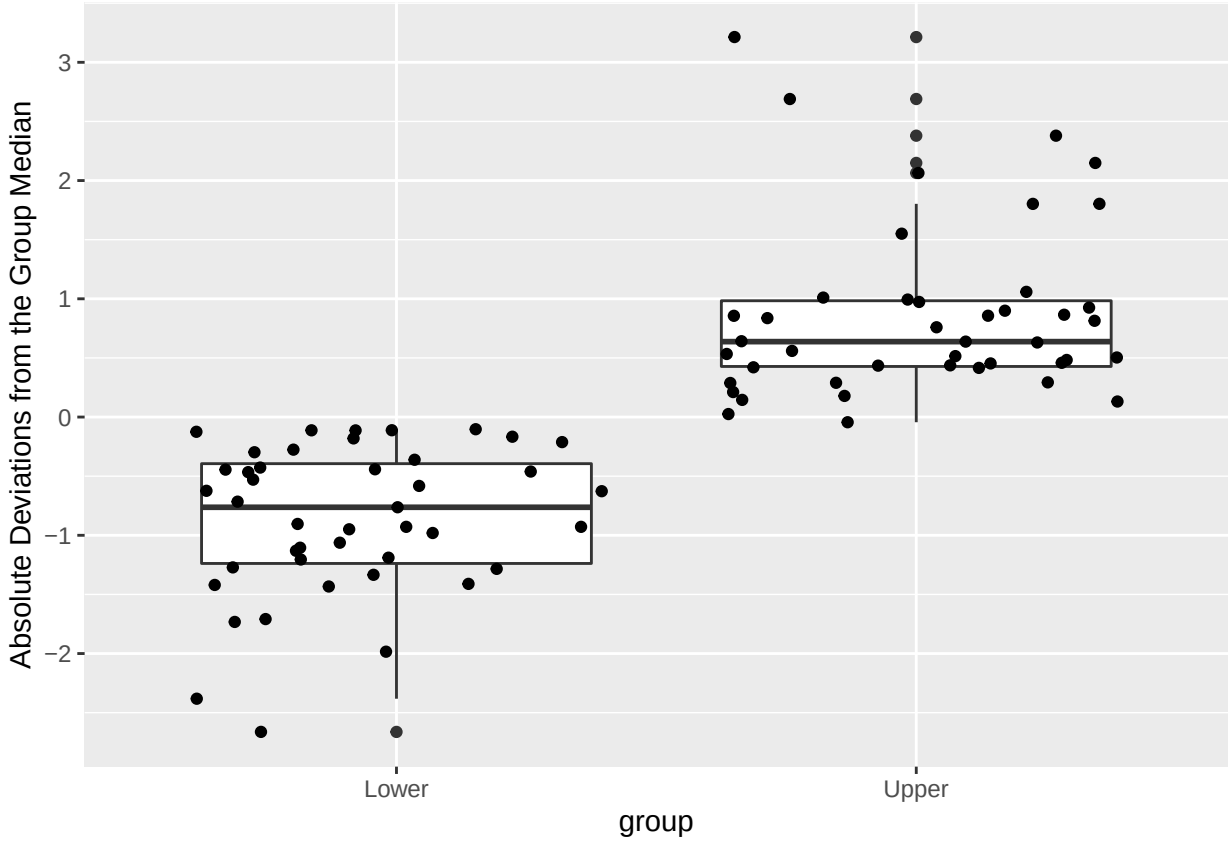
```
## # A tibble: 2 x 2
##   group median
##   <fct>  <dbl>
## 1 Lower -0.763
## 2 Upper  0.638
```

Now we take these values and apply them to resiuals data frame:

```
resid_df$absolute_deviation <-
  case_when(
    resid_df$group == "Lower" ~ abs(resid_df$residuals - medians$median[1]),
    TRUE ~ abs(resid_df$residuals - medians$median[2])
  )
```

Let's visually examine the absolute deviations:

```
ggplot(
  data = resid_df,
  aes(x = group,
      y = residuals)
) + geom_boxplot() + geom_jitter() +
  ylab("Absolute Deviations from the Group Median")
```



Same conclusion as before, while the values themselves are quite different for the two groups, dispersion of values does not seem to differ between the two groups.

Next we find the T statistic. We need average deviations, sample sizes, and pooled variance. All calculations are given in code below, we formally defined all equations in previous homework assignments.

```r
n_lower <- nrow(resid_df[resid_df$group == "Lower", ])
n_upper <- nrow(resid_df[resid_df$group == "Upper", ])

avg_lower <- mean(resid_df[resid_df$group == "Lower", ]$absolute_deviation)
avg_upper <- mean(resid_df[resid_df$group == "Upper", ]$absolute_deviation)

pooled_var <-
  (sum((resid_df[resid_df$group == "Lower", ]$absolute_deviation  - avg_lower)^2 ) +
      sum((resid_df[resid_df$group == "Upper", ]$absolute_deviation  - avg_upper)^2 ) ) /
  (nrow(resid_df) - 2)

t_stat <-
  abs(
  (avg_lower - avg_upper)/
  (sqrt(pooled_var) * sqrt(1/n_lower + 1/n_upper) )
    )
```

We now have all needed data to state the hypotheses and give the conclusion.

- Null Hypothesis: $H_0 : \bar{d_1} = \bar{d_2}$
- Alternative Hypothesis: $H_0 : \bar{d_1} \neq \bar{d_2}$
- Test T statistic: 0.032
- Cutoff T statistic value under $n - 2 = 84$ degrees of freedom
- Test statistic does not exceed cutoff so we do not have enough statistical evidence to reject the null hypothesis. Therefore, we can not conclude that the variance of residuals differs between the two groups. Therefore, there must be no deviation from the assumption of constant variance.