Can we detect AI Reviews versus Human Reviews

Title and Introduction

Data Sets:

The data set we have is provided by DataHack 2022 which describes reviews given to products on Amazon. These reviews are either given by a human or an AI (Chat GPT3 generated). (https://drive.google.com/file/d/1S8teNBz0I1eH6g3k4CIGi0Z06k0mxoMy/view?usp=sharing (https://drive.google.com/file/d/1S8teNBz0I1eH6g3k4CIGi0Z06k0mxoMy/view?usp=sharing))

Observations:

This dataset has 10000 entries, 5000 of which are AI-generated, and the rest are Human Generated.

Row: Each row represents a given review.

Column: We have the following columns: reviewerId, ASIN, reviewerName, helpful, reviewText, overall, summary, unixReviewTime, reviewTime, and llm.

- **reviewerId**: An unique ID given to the review.
- **ASIN**: The product identification number which Amazon assigns.
- **reviewerName**: Name of the reviewer.
- **helpful**: Formatted as such: “[x, y]” where x is the number of helpful upvotes the review received and “y” is the number of total upvotes and downvotes the review received.
- **reviewText**: The full review the reviewer wrote.
- overall: The review value given to the product from the reviewer summary: The summary of the review given.
- **unixReviewTime**: The time review was posted since January 1st, 1970, at 00:00:00 UTC.
- **reviewTime**: Human readable time the review is made.
- **llm**: Boolean represents whether the review is AI-generated (True) or Human (False).

This dataset interests me because AI-generated reviews are a severe problem in today’s world. I check the reviews before purchasing products; if those reviews are fake, I will lose trust in companies such as Amazon. Hence I am curious if this issue can be solved, which I plan to explore using this dataset.

How will I make this dataset usable and clean:

Currently, the data I have is not directly usable without quantifying it. I plan to make the following columns in the following process so that I can use this dataset to explore the research question:

- **grammar_score**: In order to get a grammar score I will use a python library called multiprocessing and language_tool_python, and then assign a score to the reviewText and import the dataset into R.
- **helpful_vote_reviews/total_vote_reveiws**: I will make two columns from helpful where **helpful_vote_reviews** = “X” and total_vote_reveiws = “Y”.
- **Review_freq**: This is the number of reviews the reviewerId has made, this can be done using group_by and summarize with the TidyVerse library.
- **mean_timing**: This represents the average time they take between multiple reviews posted by the same reviewerId. If there is only 1 post, the default value is 0.
- **llm_result**: This is the numeric value of the boolean value llm, done using tidyverse.
- **length**: This represents the length of the reviewText, which I can get using tidyverse and the nchar function.

Expectations:

Given my changes, there will likely be a high correlation between grammar_score and AI-generated reviews. To make it more human-like, the AI would use lower-quality grammar; hence we should be able to see that a lower grammar score will indicate AI.

Another trend I think we might see is that the review’s helpfulness will tend to be near 0 for the AI since I think most humans only rate a review if the review is personal and detailed, which the AI model may not be able to generate.

The last trend I think we may notice is that the review length will be shorter for AI since I think it’s attempting to show that the product is good, but it would not be able to describe or share a personal anecdote making the review shorter on average.

Research Question: Is it possible to distinguish between AI and Human generated reviews? If so how good is the accuracy? What are some other way Amazon can further improve this accuracy?

Data Set Cleaning and Set Up:

Python Code to Assign Crammer Score:

```
 import pandas as pd
 from multiprocessing import Pool, cpu_count
 from language_tool_python import LanguageTool

# Load the dataset
 url = "Amazon_reviews_plus_LLM.csv"
 data = pd.read_csv(url)

# Trims the dataset to have a balanced dataset
 df_false = data[data['llm'] == False].sample(n=5000)
 df_true = data[data['llm'] == True].sample(n=5000)
 data = pd.concat([df_false, df_true])

# Initialize LanguageTool with default language (English)
 tool = LanguageTool('en-US')

# Define a function to check grammar for a given text
 def get_grammar_score(text):
    matches = tool.check(text)
    return len(matches)

# Use multiprocessing to parallelize the grammar checking process
 with Pool(processes=cpu_count()) as pool:
    grammar_scores = pool.map(get_grammar_score, data['reviewText'])

# Add the grammar scores as a new column in the dataset
 data['grammar_score'] = grammar_scores


# Display first few rows of the dataset
 data.head()
```

a. Import Data Set with Grammar

```
# Impports Data Set
reviews <- read_csv("Amazon_reviews_plus_LLM_with_grammar_scores.csv")

# Displays Part of the DataSet
head(reviews)
```

```
## # A tibble: 6 × 11
##   reviewerID asin  revie…¹ helpful revie…² overall summary unixR…³ revie…⁴ llm
##   <chr>      <chr> <chr>   <chr>   <chr>     <dbl> <chr>     <dbl> <chr>   <lgl>
## 1 acde75b2-… 235e… S. Bohn [0, 0]  It has…       5 I love…  1.37e9 05 1, … FALSE
## 2 92c283f1-… 7c34… L. Haw… [0, 0]  These …       4 work m…  1.40e9 04 18,… FALSE
## 3 ee564575-… ce51… Antigo… [0, 0]  Patien…       3 Color …  1.40e9 05 20,… FALSE
## 4 115d1af4-… d0e6… Zombie… [0, 0]  This w…       1 Didn't…  1.37e9 05 3, … FALSE
## 5 219de8a5-… ac5e… Cute C… [0, 0]  This s…       4 Great …  1.40e9 06 27,… FALSE
## 6 c74a551f-… d998… Steven… [2, 2]  I am u…       5 My Fav…  1.38e9 08 20,… FALSE
## # … with 1 more variable: grammar_score <dbl>, and abbreviated variable names
## #   ¹reviewerName, ²reviewText, ³unixReviewTime, ⁴reviewTime
```

b. Cleaning and Mutating

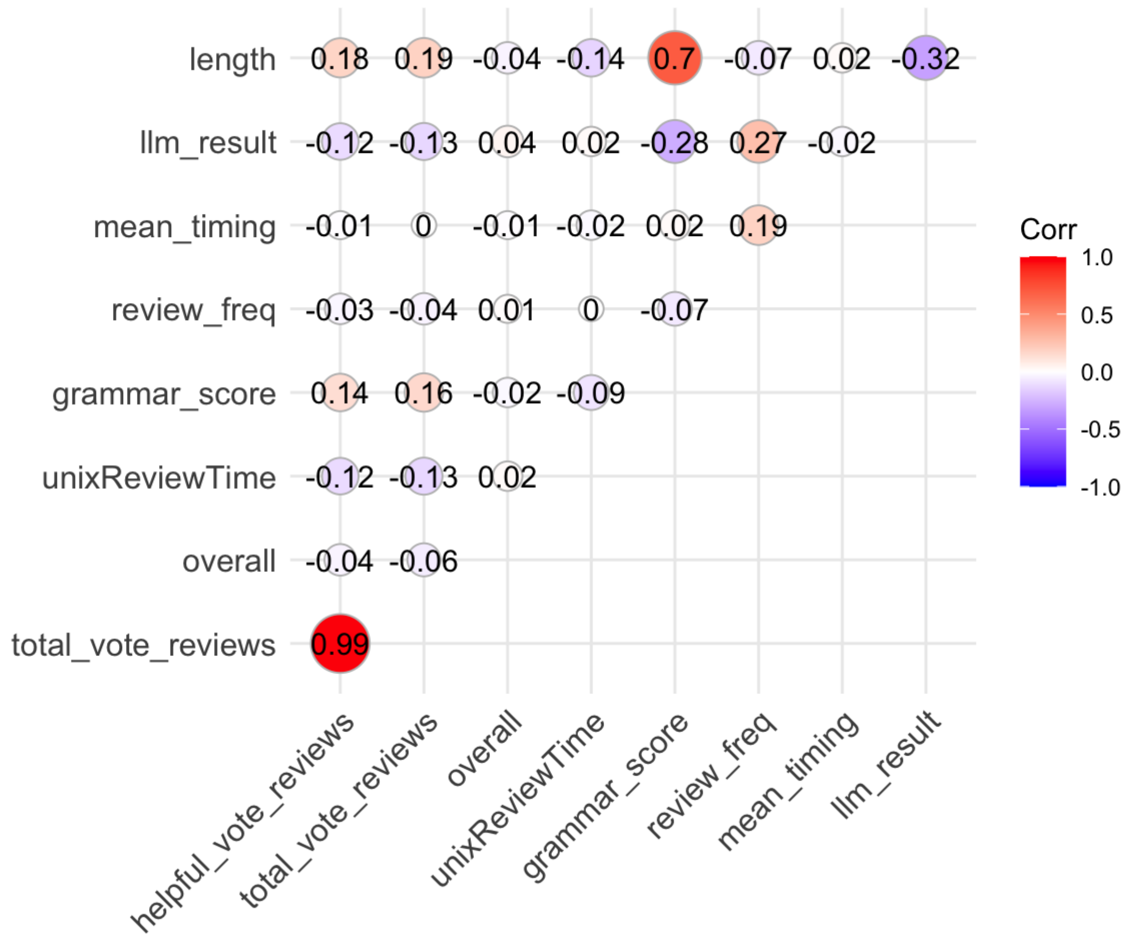
```
# Get the number of reviews the reviewer has made
reviews_num_reviews <- reviews %>%
  group_by(reviewerID) %>%
  summarize(review_freq = n())

# Combines the datasets to add the number of reviews the reviewer has made to the o
rgial dataset
reviews <- left_join(reviews, reviews_num_reviews, by = "reviewerID")

# Finds the average time the reviewer takes between makinf reviews
reviews_mean_timing <- reviews %>%
  group_by(reviewerID) %>%
  arrange(unixReviewTime) %>% # Sorting to find average in an accending order
  summarize(mean_timing = ifelse(review_freq > 1, mean(diff(as.POSIXct(unixReviewTi
me, origin = "1970-01-01", tz = "UTC")
), na.rm = TRUE), 0))

# Joining the datasets so we can add the mean_timing to the orginal dataset
reviews_mean_timing <- inner_join(reviews, reviews_mean_timing, by = "reviewerID")

# Droping all duplicate rows
reviews <- distinct(reviews_mean_timing)

# Spliting the helful [x, y] -> helpful_vote_reviews = x and total_vote_reviews = y
reviews <- reviews %>%
  extract(helpful, c("helpful_vote_reviews", "total_vote_reviews"), "\\[(\\d+),
(\\d+)\\]", convert = TRUE)

# Making a numerical representation of the boolean llm
reviews <- reviews %>% mutate(llm_result = ifelse(llm == FALSE, 0, 1))

# Adds the length of the review as a column to the dataset
reviews <- reviews %>% mutate(length = nchar(reviewText))

# Displays the new modifed  dataset
head(reviews)
```

```
## # A tibble: 6 × 16
##   review…¹ asin  revie…² helpf…³ total…⁴ revie…⁵ overall summary unixR…⁶ revie…⁷
##   <chr>    <chr> <chr>     <int>   <int> <chr>     <dbl> <chr>     <dbl> <chr>
## 1 acde75b… 235e… S. Bohn       0       0 It has…       5 I love…  1.37e9 05 1, …
## 2 92c283f… 7c34… L. Haw…       0       0 These …       4 work m…  1.40e9 04 18,…
## 3 ee56457… ce51… Antigo…       0       0 Patien…       3 Color …  1.40e9 05 20,…
## 4 115d1af… d0e6… Zombie…       0       0 This w…       1 Didn't…  1.37e9 05 3, …
## 5 219de8a… ac5e… Cute C…       0       0 This s…       4 Great …  1.40e9 06 27,…
## 6 c74a551… d998… Steven…       2       2 I am u…       5 My Fav…  1.38e9 08 20,…
## # … with 6 more variables: llm <lgl>, grammar_score <dbl>, review_freq <int>,
## #   mean_timing <dbl>, llm_result <dbl>, length <int>, and abbreviated variable
## #   names ¹reviewerID, ²reviewerName, ³helpful_vote_reviews,
## #   ⁴total_vote_reviews, ⁵reviewText, ⁶unixReviewTime, ⁷reviewTime
```

Exploratory Data Analysis:

Correlation Matrix:

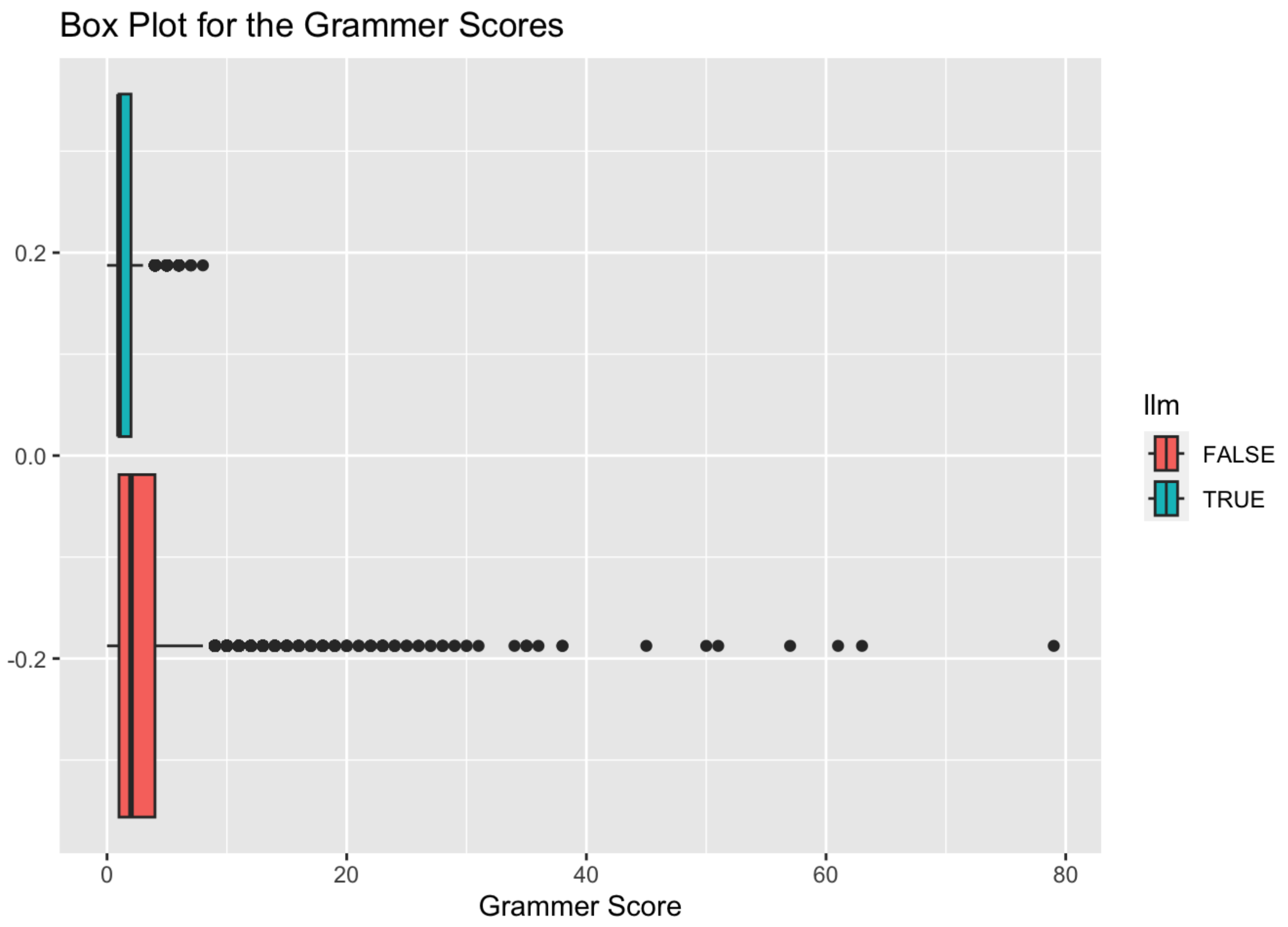
```
# Makes a Correlation Matrix
ggcorrplot(cor(reviews %>% select_if(is.numeric)),
           type = "upper", # upper diagonal
           lab = TRUE, # print values
           method = "circle") # use circles with different sizes
```



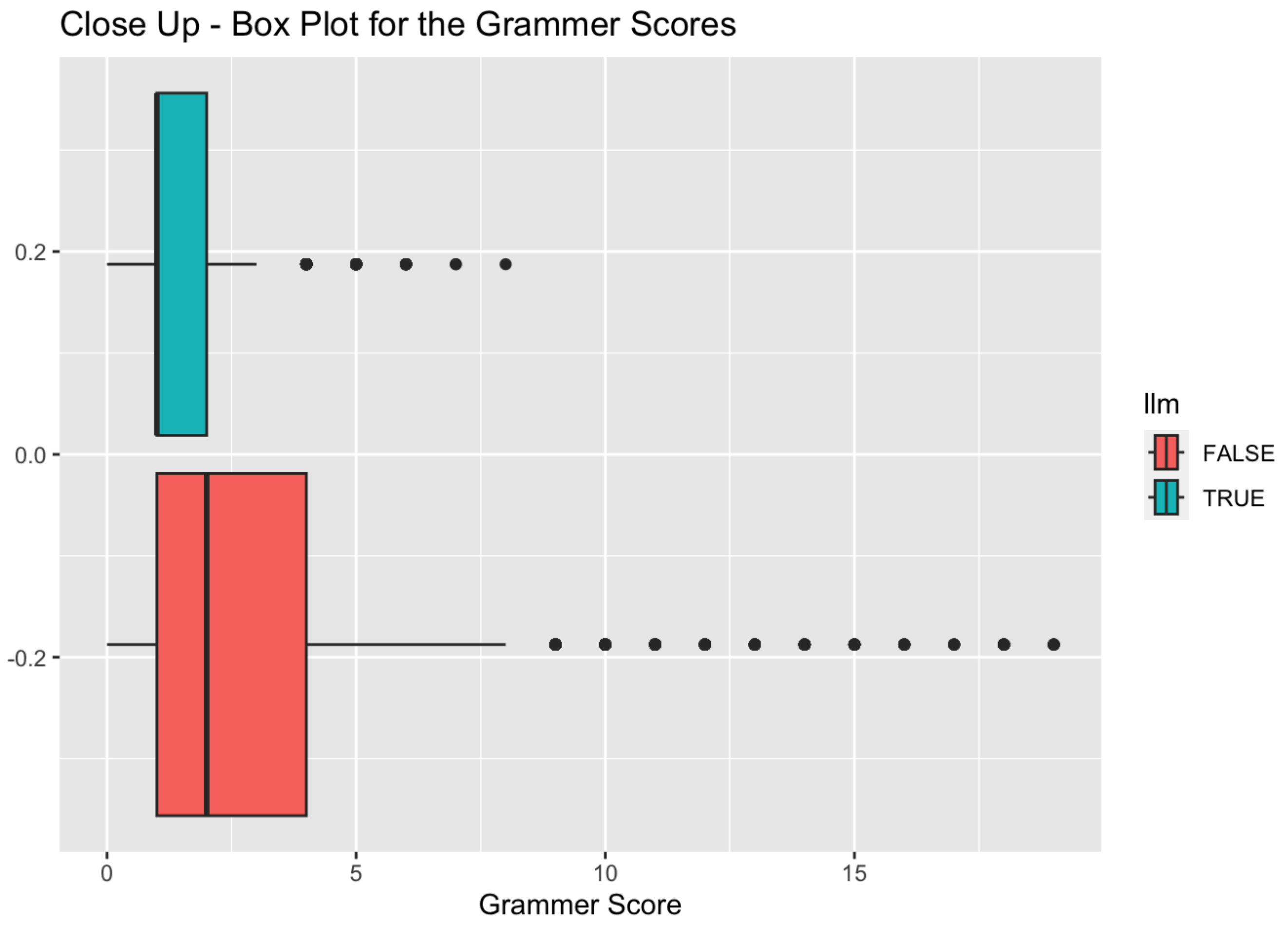
Looking at the Correlation Matrix we can see that here is a high correlation between helpful_vote_reviews and total_vote_reviews with a value of .99. This makes sense the higher number helpful_vote_reviews the higher the number of total_vote_reviews. An interesting correlation can be seen between grammar_score and length of the review with the value of .7. This makes sense since the longer the sentence the higher the chance that the grammar is formal, instead of “its great” the longer reviews would be “This product is amazing!” We see that review_freq and unixReviewTime have no correlation. This makes since the frequency of someone posting a review has no logical connection with the time they post it.

Now lets explore the data sets:

```
# Makes a box_plot for the grammer scores given its AI or Human
reviews %>%
  ggplot(aes(grammar_score, group = llm)) +
  geom_boxplot(aes(fill = llm)) +
  labs(x = "Grammer Score", title = "Box Plot for the Grammer Scores", color = "LL
M")
```

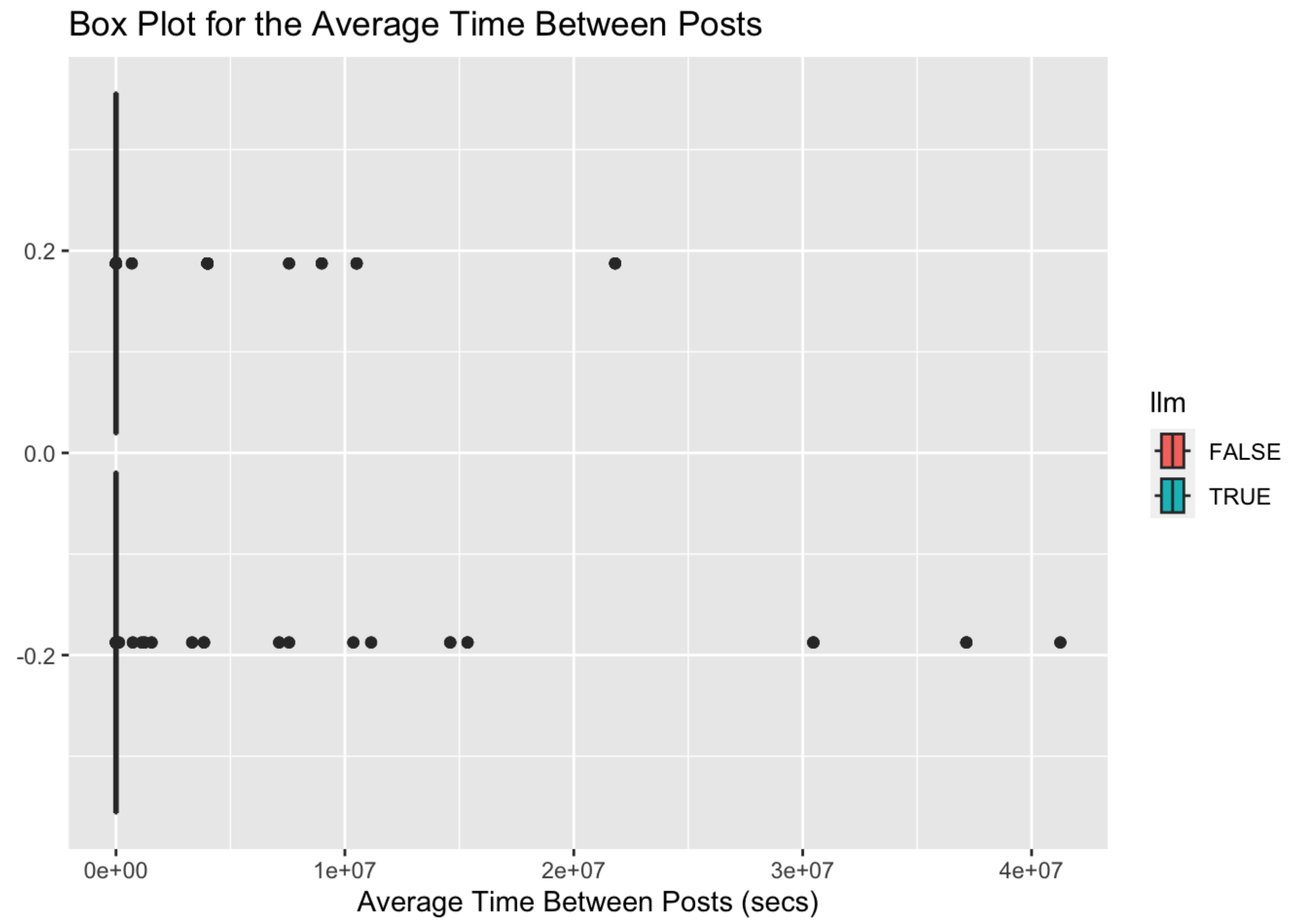


```
# Makes a close up of the box_plot above
reviews %>%
  filter(grammar_score < 20) %>%
  ggplot(aes(grammar_score, group = llm)) +
  geom_boxplot(aes(fill = llm)) +
  labs(x = "Grammer Score", title = "Close Up - Box Plot for the Grammer Scores", c
olor = "LLM")
```

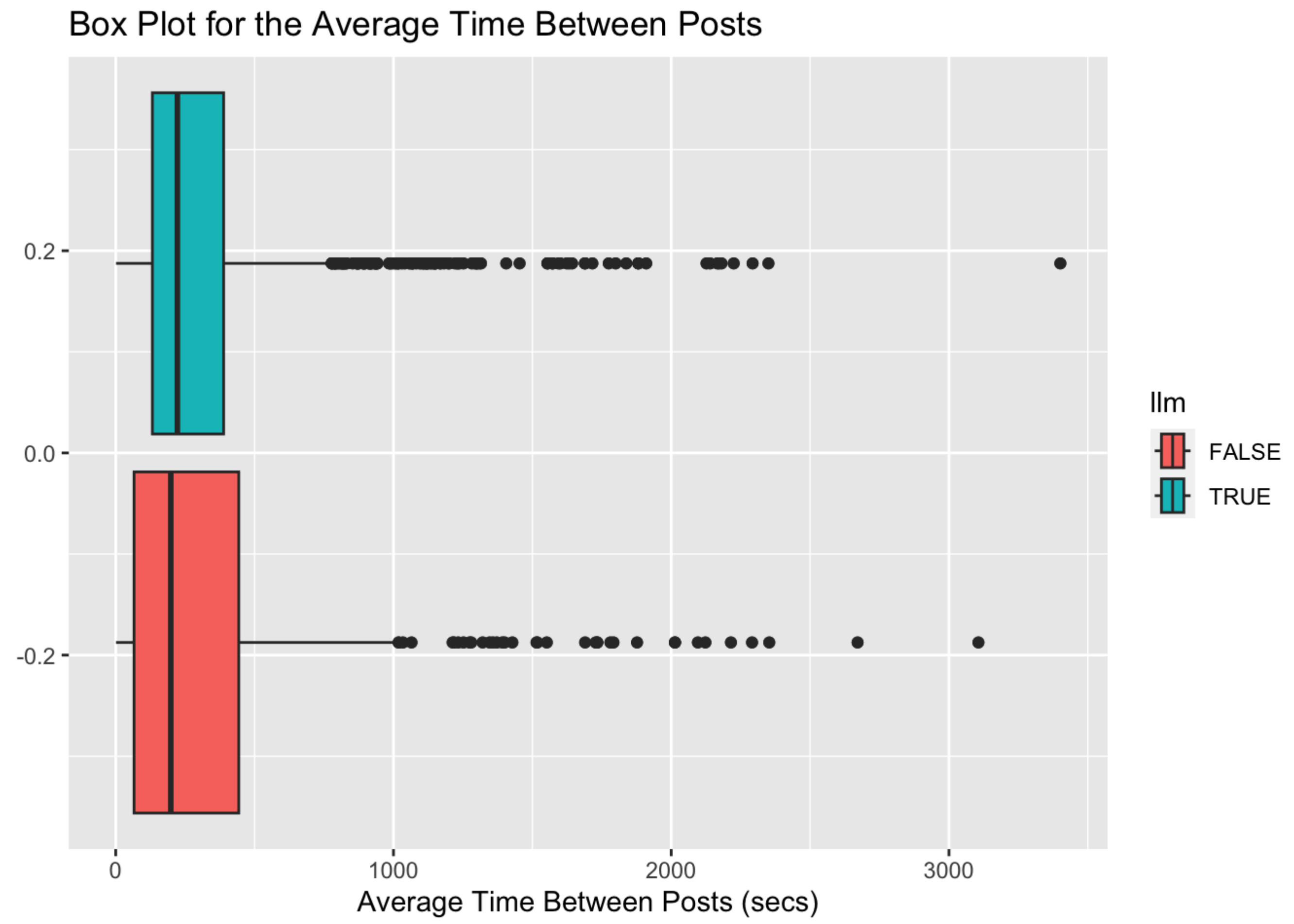


In this box plot we can see that that the humans tend to have a higher grammar score compared to the AI generated ones. This could be a good predictor to use to see if the review is AI generated or Human generated. We can also see that the range for the Human generated reviews is much higher than the AI generated ones. Also as to what I predicted the grammar score for the AI generated reviews is low in general. We can also see that the upper qaurtile value of the Grammar is the mean for the Humans which indictaes this is a good predictor. Also we can see in the close up version that the difference between the two is significant enough to be used a predictor, as its clear the AI model has a lower range of values within its IQR.

```
# Makes a box_plot for the average time reviewers take between posts
reviews %>%
  filter(mean_timing != 0) %>%
  ggplot(aes(mean_timing, group = llm)) +
  geom_boxplot(aes(fill = llm)) +
  labs(x = "Average Time Between Posts (secs)", title = "Box Plot for the Average T
ime Between Posts", color = "LLM")
```

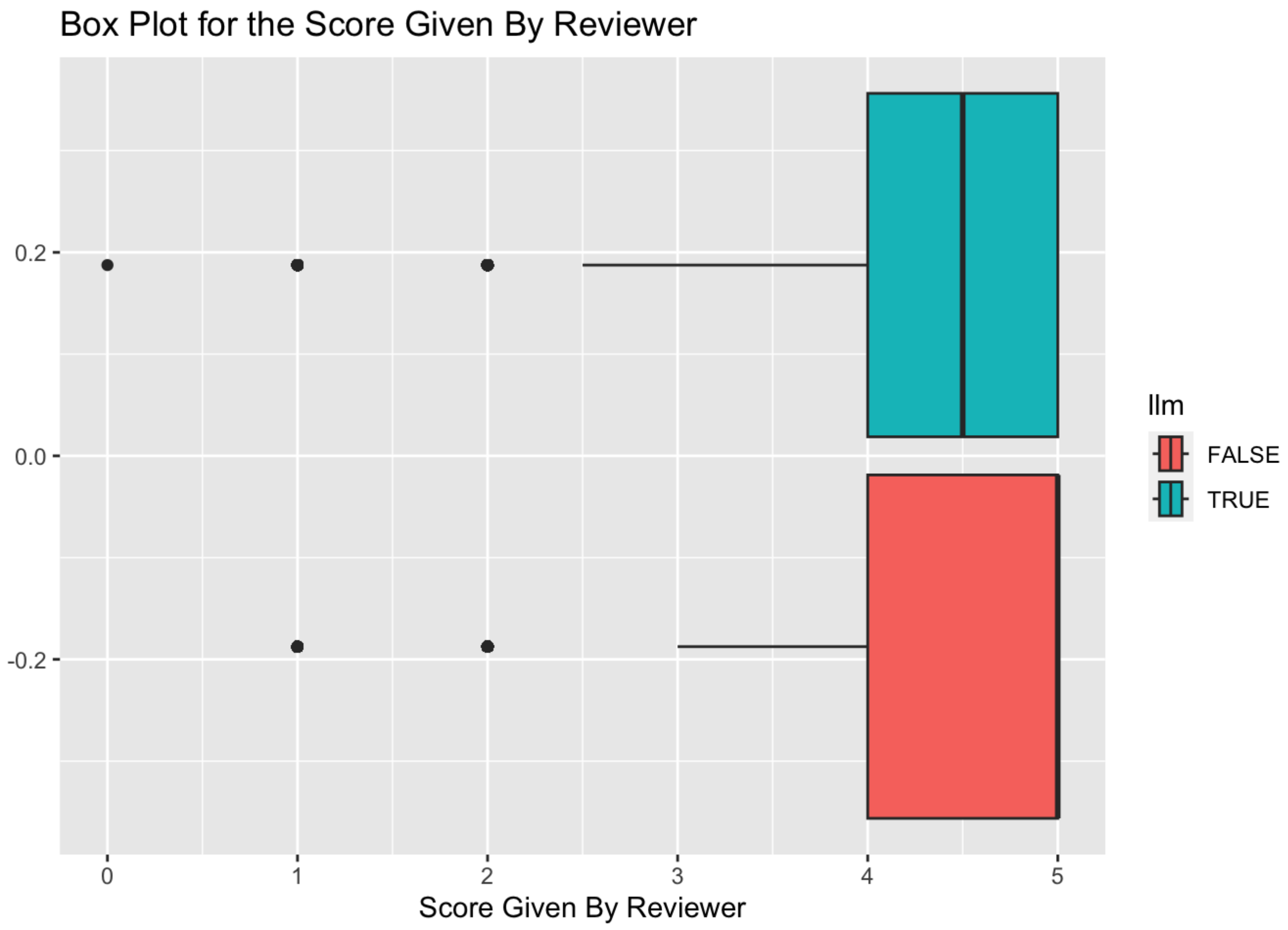


```
# Makes a box_plot for the average time reviewers take between posts removing some
of
# the outliers
reviews %>%
  filter(mean_timing != 0 & mean_timing < 10000) %>%
  ggplot(aes(mean_timing, group = llm)) +
  geom_boxplot(aes(fill = llm)) +
  labs(x = "Average Time Between Posts (secs)", title = "Box Plot for the Average T
ime Between Posts", color = "LLM")
```



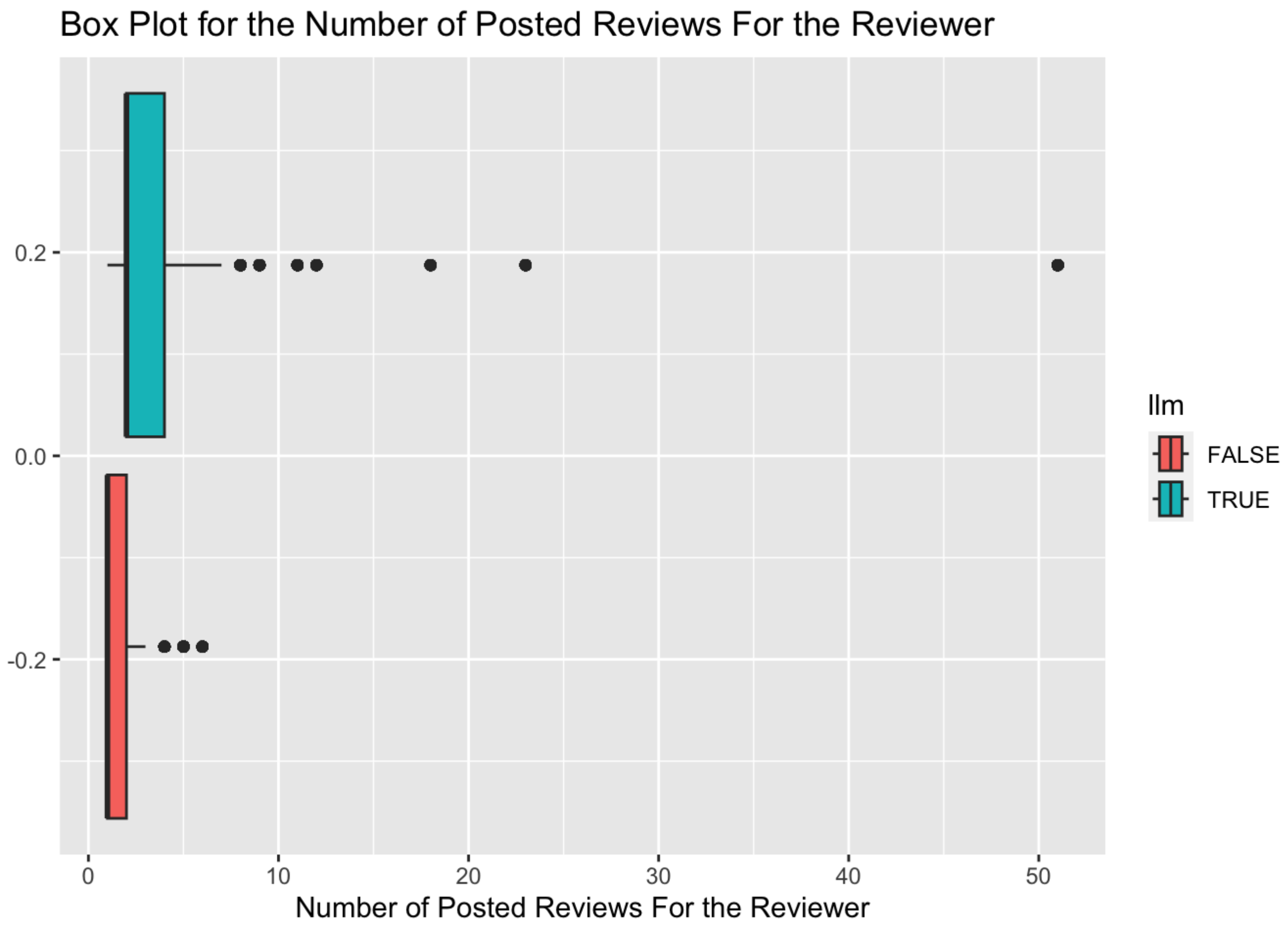
In this box plot we can see that that the humans tend to have much higher valued outliers. Looking at the close up version we can say that this is not a good predictor since the mean seems to be the same between the AI and Human generated reviews. This goes against my expectation, I thought that the AI would post more frequently than Human at a faster pace. This however makes sense since if the AI posted too much too fast the companies such as Amazon would easily be able to pick up on them. We can still use this as a predictor, but it won’t be a good predictor which provides much insight.

```
# Makes a box_plot for the overall review the reviews give
reviews %>%
  ggplot(aes(overall, group = llm)) +
  geom_boxplot(aes(fill = llm)) +
  labs(x = "Score Given By Reviewer", title = "Box Plot for the Score Given By Revi
ewer", color = "LLM")
```

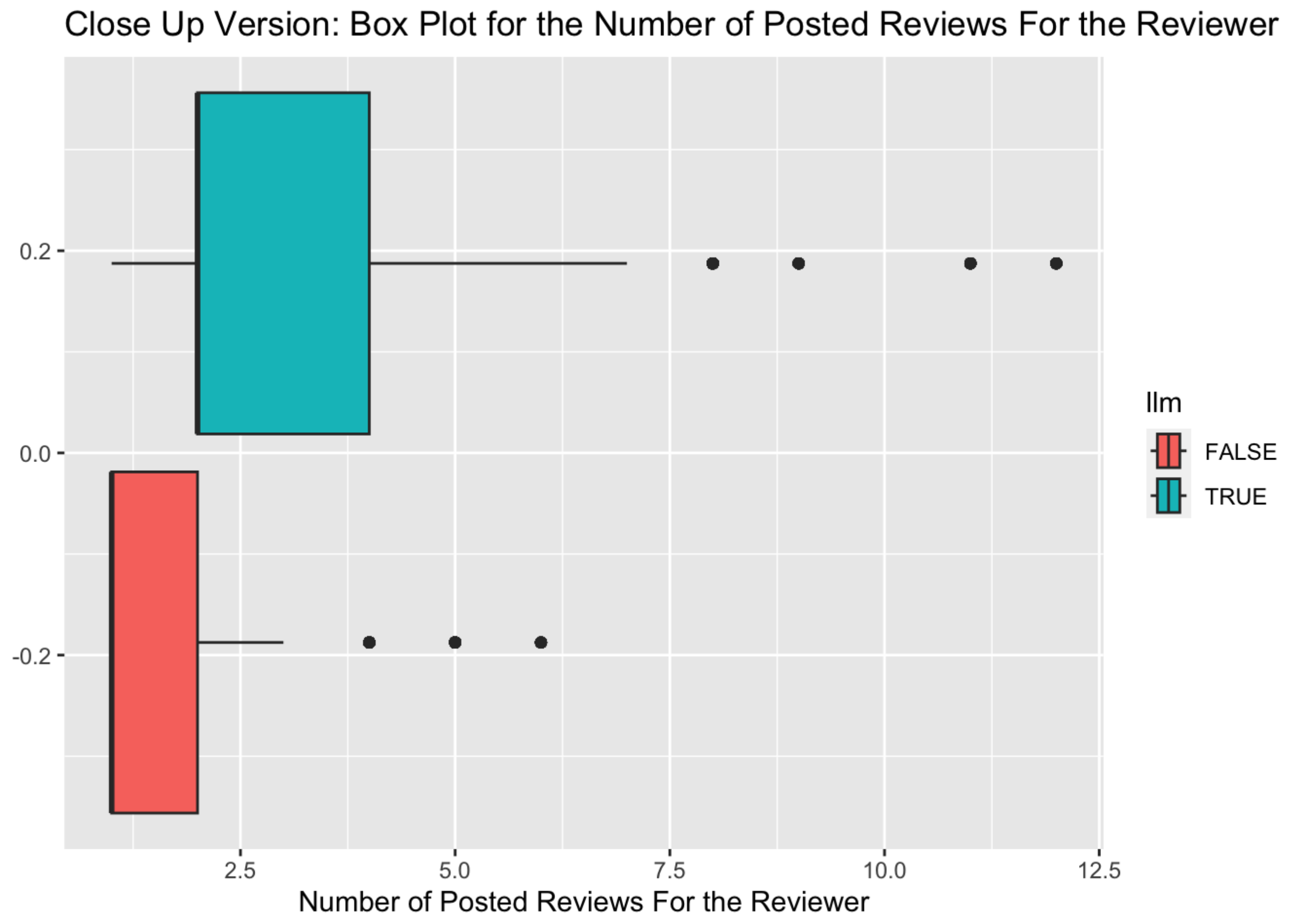


In this box plot we can see that that the humans on average give a rating of 5. This would also be not a good (~ok predictor) predictor since both Humans and AI tend to give a score between 4 and 5, and the means are close for them: AI is 4.5 on average and Humans are 5. One interesting thing that we can see is that the AI tends to give a higher range of values, and I wonder if this is to seem “Human Like” ? This can still be used a predictor as a tipping point, however the insight this provides is little. However Amazon could preform a further analysis to see if there is a pattern in which a reviewer gives a review, or if the overall review they gave seems to be a random number? Perhaps that would give more insight.

```
# Makes a box_plot for the Number of Posted Reviews For the Reviewer
reviews %>%
  ggplot(aes(review_freq, group = llm)) +
  geom_boxplot(aes(fill = llm)) +
  labs(x = "Number of Posted Reviews For the Reviewer", title = "Box Plot for the N
umber of Posted Reviews For the Reviewer", color = "LLM")
```

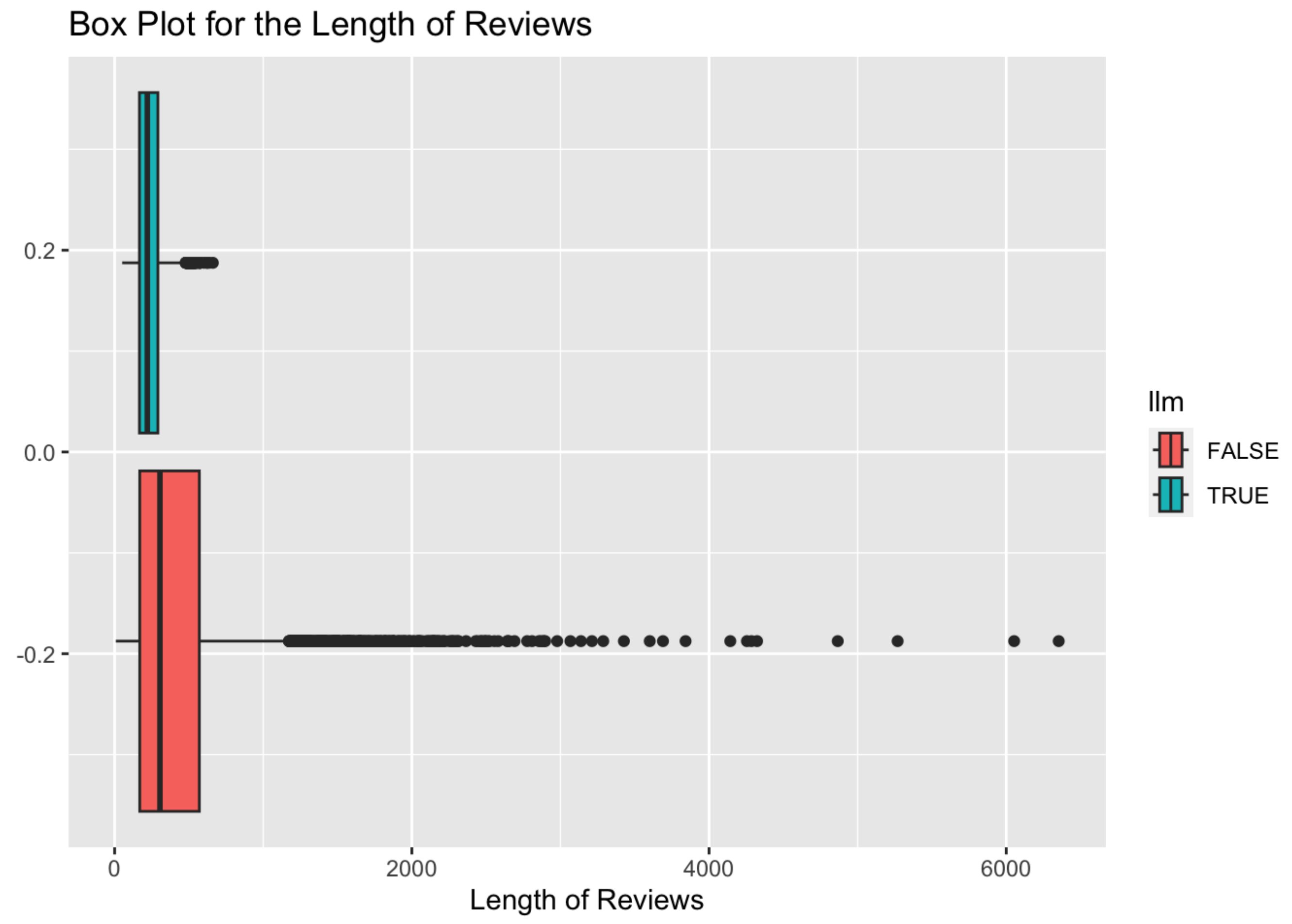


```
# Makes a box_plot for the Number of Posted Reviews For the Reviewer - Close Up Ver
sion
reviews %>%
  filter(review_freq < 15) %>%
  ggplot(aes(review_freq, group = llm)) +
  geom_boxplot(aes(fill = llm)) +
  labs(x = "Number of Posted Reviews For the Reviewer", title = "Close Up Version:
Box Plot for the Number of Posted Reviews For the Reviewer", color = "LLM")
```

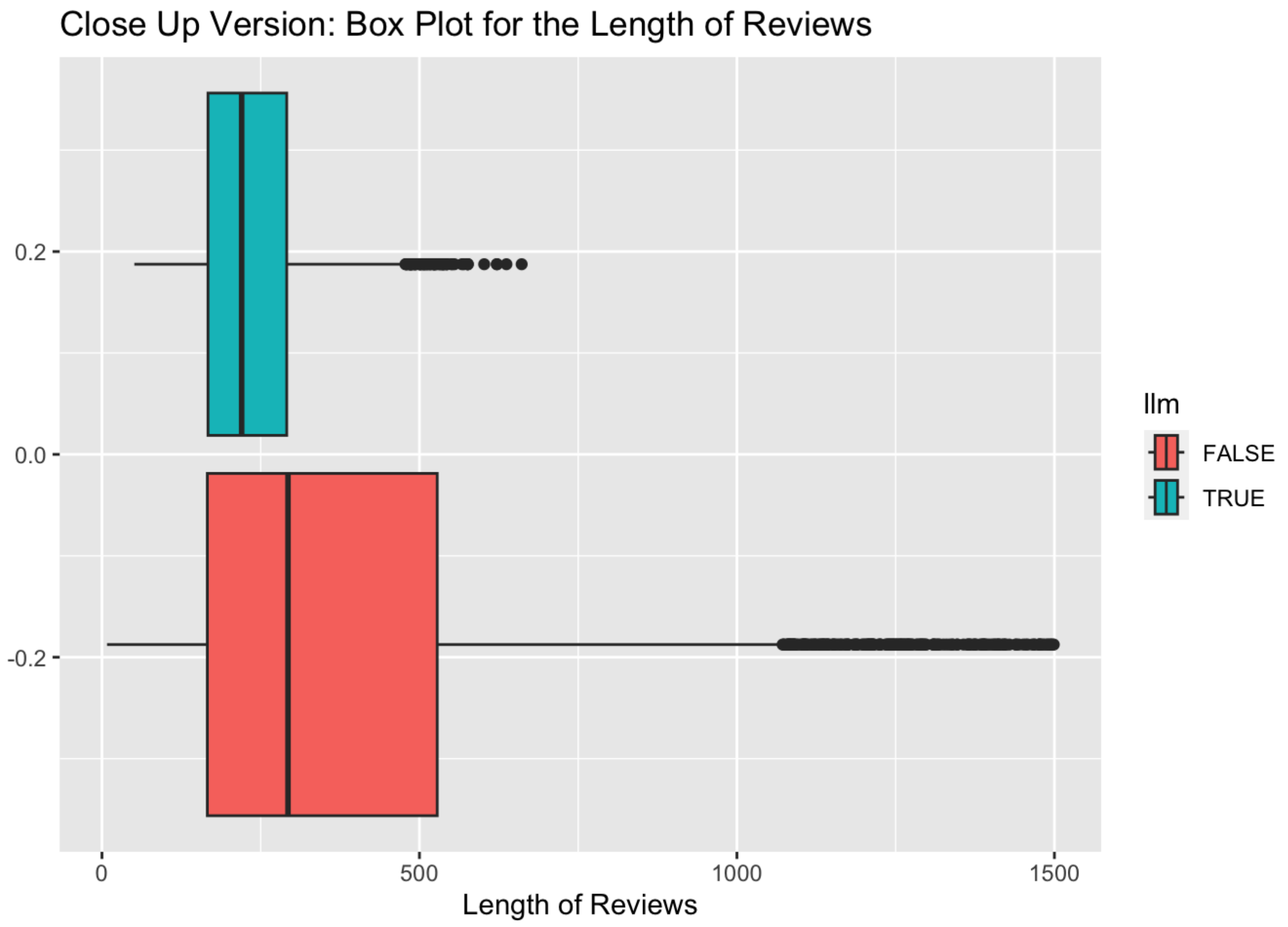


In this box plot we can see that the AI tends to have a higher number of reviews posted, and more outliers than the Humans. In the close up version we can see that the upper quartile for the humans is the mean and lower quartile for the AI. This means that this is a good predictor and the higher the number of posts made by a review the higher the chance the review is AI generated. Also it seem that on average the human makes only 1 post, which makes sense since as humans we don’t regularly post a review instead we tend to tell our friends and family. Also we can see that the range of number of reviews posted is higher for the AI model compared to Humans. Overall, we should use this as a predictor in our model when predicting.

```
# Makes a box_plot for the Length of the Review
reviews %>%
  ggplot(aes(length, group = llm)) +
  geom_boxplot(aes(fill = llm)) +
  labs(x = "Length of Reviews", title = "Box Plot for the Length of Reviews", color
= "LLM")
```



```
# Makes a box_plot for the Length of the Review - Close Up Version
reviews %>%
  filter(length < 1500) %>% # Takes away the upper values to make a close up
  ggplot(aes(length, group = llm)) +
  geom_boxplot(aes(fill = llm)) +
  labs(x = "Length of Reviews", title = "Close Up Version: Box Plot for the Length
of Reviews", color = "LLM")
```



In this box plot we can see that Humans tend to post longer reviews than AI models. In fact we can see that the upper quartile of the length of review for the AI model is the mean of the Humans. Also Humans tend to have a high number of outliers, and a much higher range of values compared to the AI model. This matches the expectation I mentioned before, and furthermore validates the idea that humans have longer responses since they tend to express emotion through an personal experience and the AI is often incapable of this. Overall, this is a great predictor and we can use this when making a prediction model.

Prediction and Cross-Validation:

I will use the three predictors mentioned (as good predictors) above: grammar_score, overall, review_freq, and length.

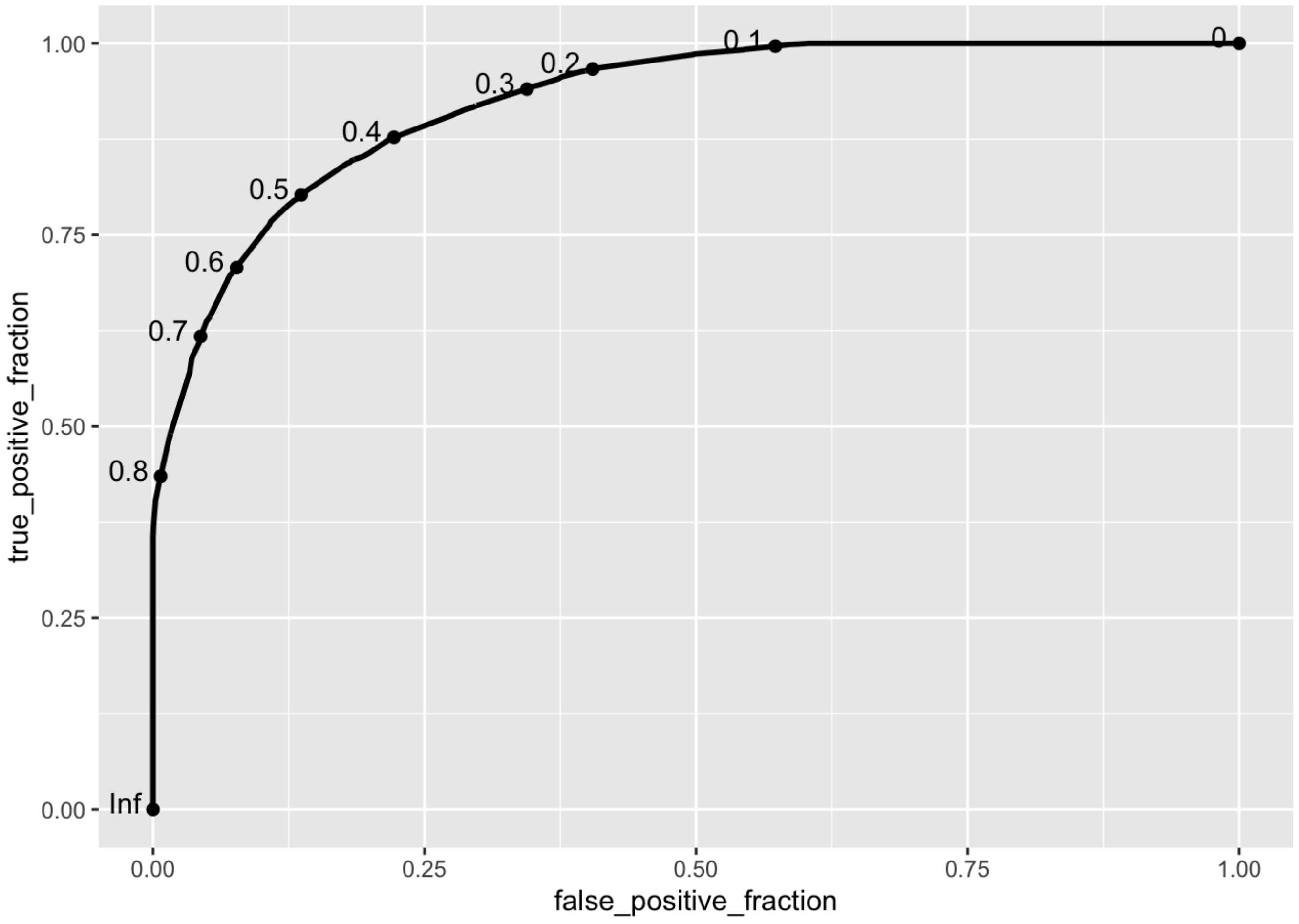
Makes the prediction model:

```
# Prediction Model to detect AI using k-Nearest Neighbor (looks at closest 5)
reviews_knn <- knn3(llm ~ grammar_score + overall + review_freq + length,
                data = reviews,
                k = 5)

# Makes a prediction on the whole data set
predict(reviews_knn, reviews) %>% as.data.frame %>% head
```

```
##       FALSE      TRUE
## 1 0.5000000 0.5000000
## 2 0.1428571 0.8571429
## 3 1.0000000 0.0000000
## 4 0.6000000 0.4000000
## 5 1.0000000 0.0000000
## 6 1.0000000 0.0000000
```

Makes the ROC curve:

```
# Build new ROC curve using the knn model
ROC <- ggplot(reviews) +
  geom_roc(aes(d = llm_result, m = predict(reviews_knn, reviews)[,2]), n.cuts = 10)

# Displays the curve
ROC
```



```
# Calculates the value of AUC and displays it
calc_auc(ROC)
```

```
##   PANEL group       AUC
## 1     1    -1 0.9229676
```

The AUC value is seen to be .923 which is a very good AUC value showing that this model preforms well for this dataset.

10 Fold Cross Validation:

```
# 10 fold - Cross validation for the kNN model
kNN_cv <- train(as.factor(llm) ~ grammar_score + overall + review_freq + length,
      data = reviews,
      method = "knn",
      trControl = trainControl(method = "cv", number = 10)) # 10-fold cv

# Displays the summary/results
kNN_cv
```

```
## k-Nearest Neighbors
##
## 10000 samples
##     4 predictor
##     2 classes: 'FALSE', 'TRUE'
##
## No pre-processing
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 9000, 9000, 9000, 9000, 9000, 9000, ...
## Resampling results across tuning parameters:
##
##   k  Accuracy  Kappa
##   5  0.7754    0.5508
##   7  0.7742    0.5484
##   9  0.7736    0.5472
##
## Accuracy was used to select the optimal model using the largest value.
## The final value used for the model was k = 5.
```

We can see that for the knn with 5 neighbors we get an average accuracy of .7711 which mean that on average we can get 77% accuracy when bringing in new data.

Our model with new data tends to do more than 50% accuracy making it a better than random model for predicting AI versus Human reviews. We can see that the AUC value was .9229 which means this model is excellent when its predicting values given the whole dataset, but not as good when new data is introduced. This indicates that there is some over fitting occurring and this could be fixed by giving it more data as the dataset would be more diluted. The data set has 204k rows, however to balance the dataset I chose 5k AI and 5k human, but if we wanted to give it more data it is possible. Also this means we can also use more neighbors, perhaps 7 might be a better choice. However, overall the model is works well even when new data is introduced.

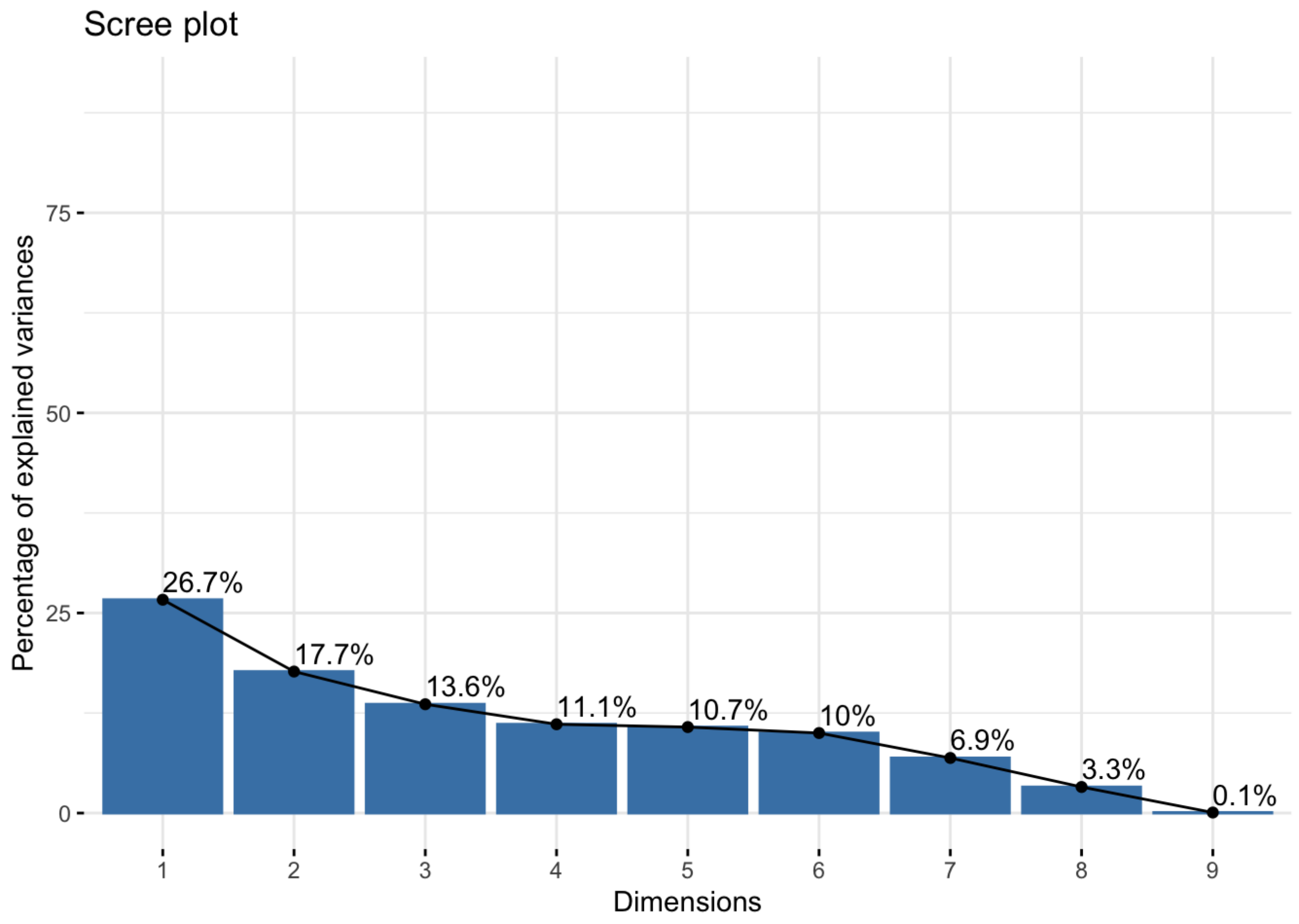
Dimensionality Reduction:

PCA analysis:

```
# Making the data only numeric and scaling it
reviews_num <- reviews %>%
   select_if(is.numeric) %>%
   scale

# performing PCA
reviews_pca <- reviews_num %>% prcomp

# New perspective on our data
reviews_pca$x %>% as.data.frame
```

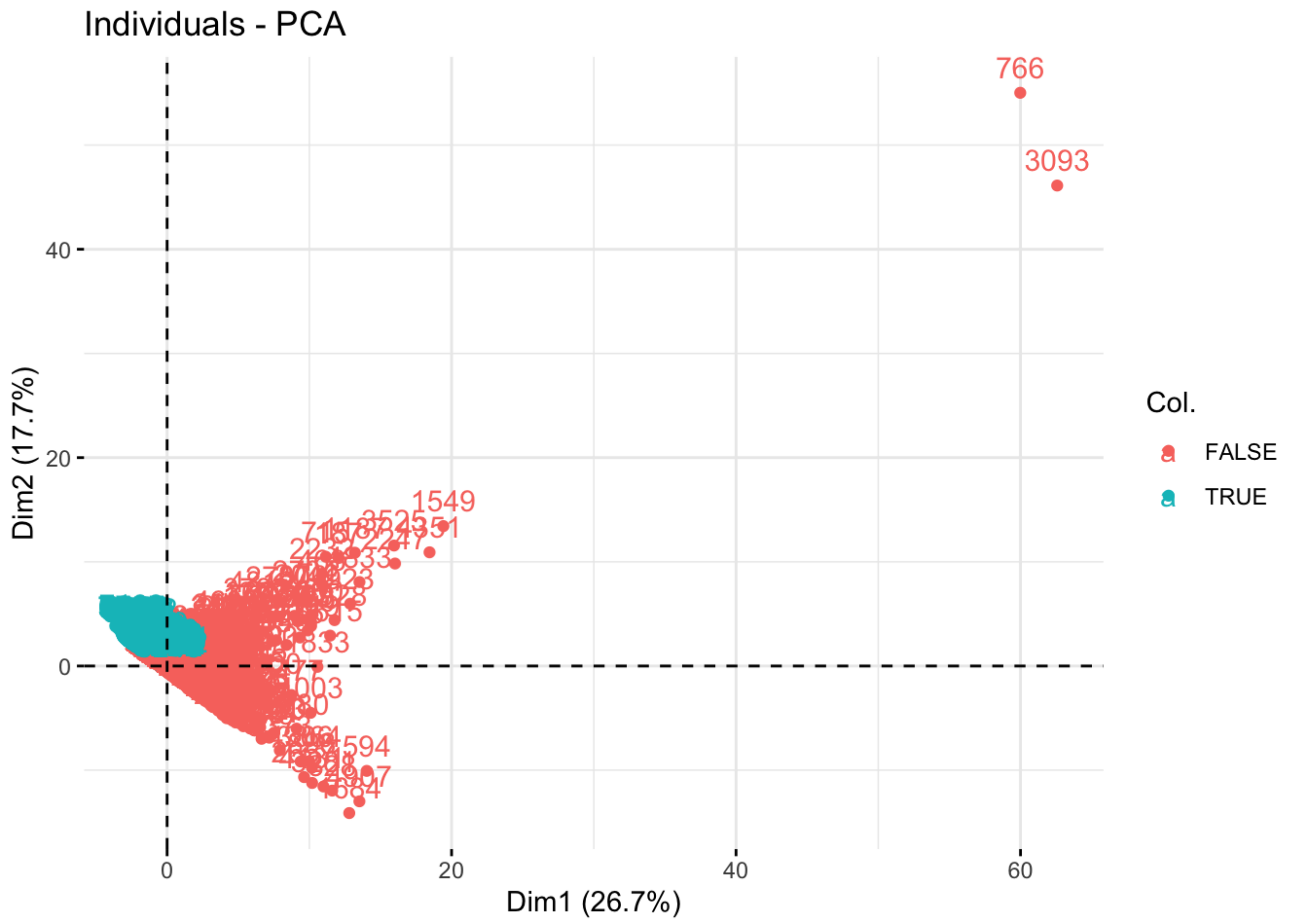
```
##            PC1          PC2         PC3        PC4        PC5        PC6
## 1  -0.16617624 -0.207061019 -0.69590416 -0.5043719  0.4652618 -0.8033418
## 2  -0.44094285  0.026771361 -0.76533359  0.5602442  0.8874655 -0.3269072
## 3   2.93467465 -3.371126849  1.28204568  0.8713164  0.5944425  1.9961992
## 4  -0.04109365 -0.003809805 -0.55396487  3.1425538 -0.5335116 -0.1487055
## 5   0.83426317 -1.301389750  0.04633326  0.3459635  0.9761151  0.5917479
## 6   1.57700379 -1.561258029  0.20041805 -0.7700240  0.7150499  0.3636462
## 7   0.45475879  0.039449466 -0.67948997 -0.5276132  0.6447950 -0.6312864
## 8  -0.20073692 -0.223761147 -0.72926903 -0.4757361  0.6475168 -0.6966271
## 9   1.41835090 -1.527139140  0.23112364  1.1869107  0.6565203  0.9030498
## 10 -0.06553966 -0.338445106 -0.73276171  0.4809497  0.6817991 -0.3338821
## 11 -0.29188875  0.054119920 -0.65554670  1.3771807  0.1744212 -0.4072224
##            PC7         PC8          PC9
## 1  -0.61594066 -0.01768498 -0.012201281
## 2  -0.76918986  0.10858998 -0.016072445
## 3   0.09020669  1.36051719 -0.056812842
## 4  -0.77684154  0.16324911 -0.056554524
## 5  -0.46430315  0.74340858 -0.027187674
## 6  -0.14902407 -0.61814537 -0.036542945
## 7  -0.54047566  0.28635625  0.049180843
## 8  -0.58056559 -0.41100549 -0.009215338
## 9  -0.37514175  1.75824257 -0.053491657
## 10 -0.53252430  0.21366642 -0.020575408
## 11 -0.80033181  0.06047160 -0.031399612
##  [ reached 'max' / getOption("max.print") -- omitted 9989 rows ]
```

```
# Visualize percentage of variance explained for each PC in a scree plot
fviz_eig(reviews_pca, addlabels = TRUE, ylim = c(0, 90))
```

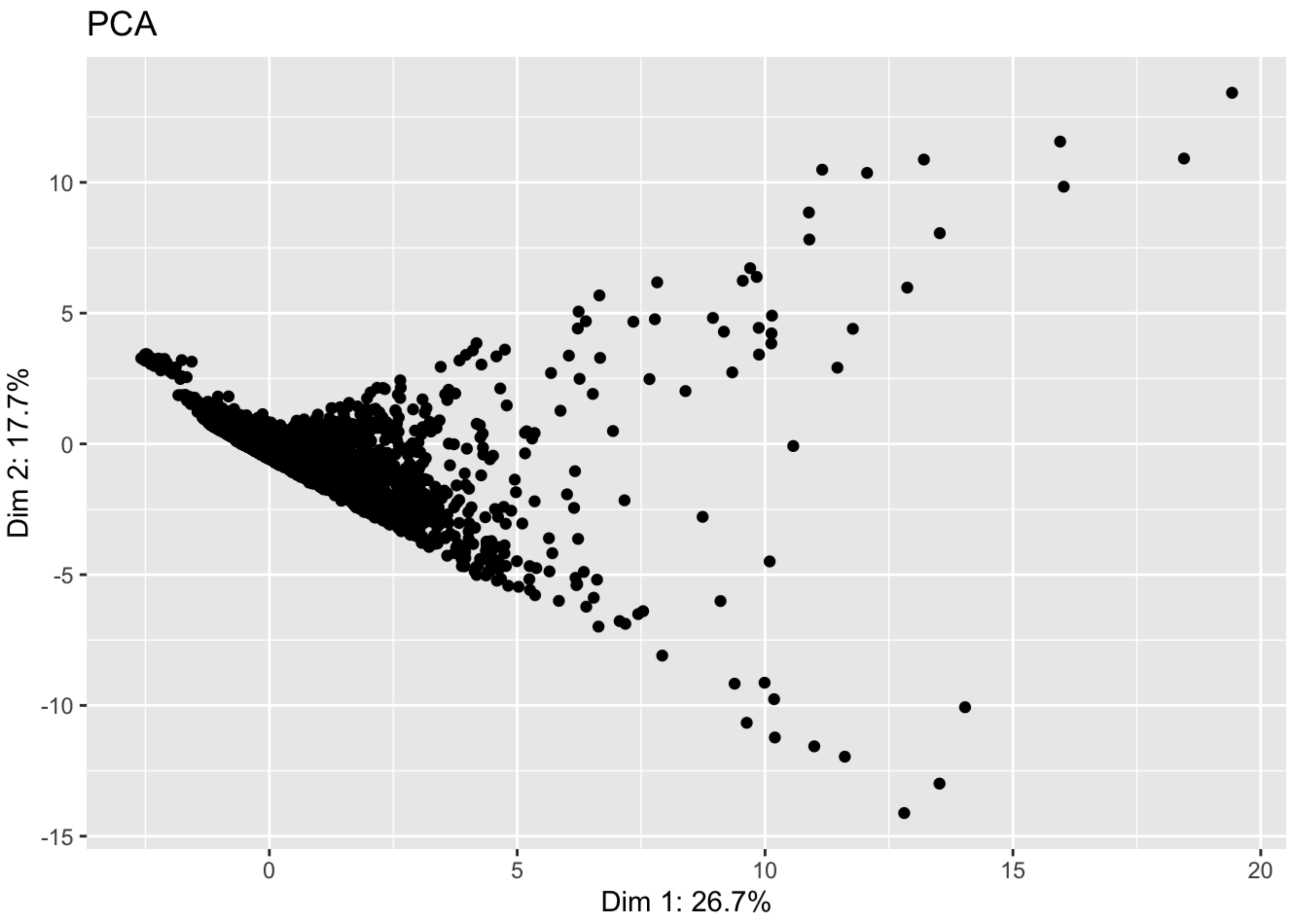


We can see in the scree plot that to Dim 1 explain 26.7% variance and Dim 2 explains 17.7% variance. Overall the first 2 Dimensions explain 44.4% of the variance. In order to explain ~80% it would make sense to keep the first five Dimensions.

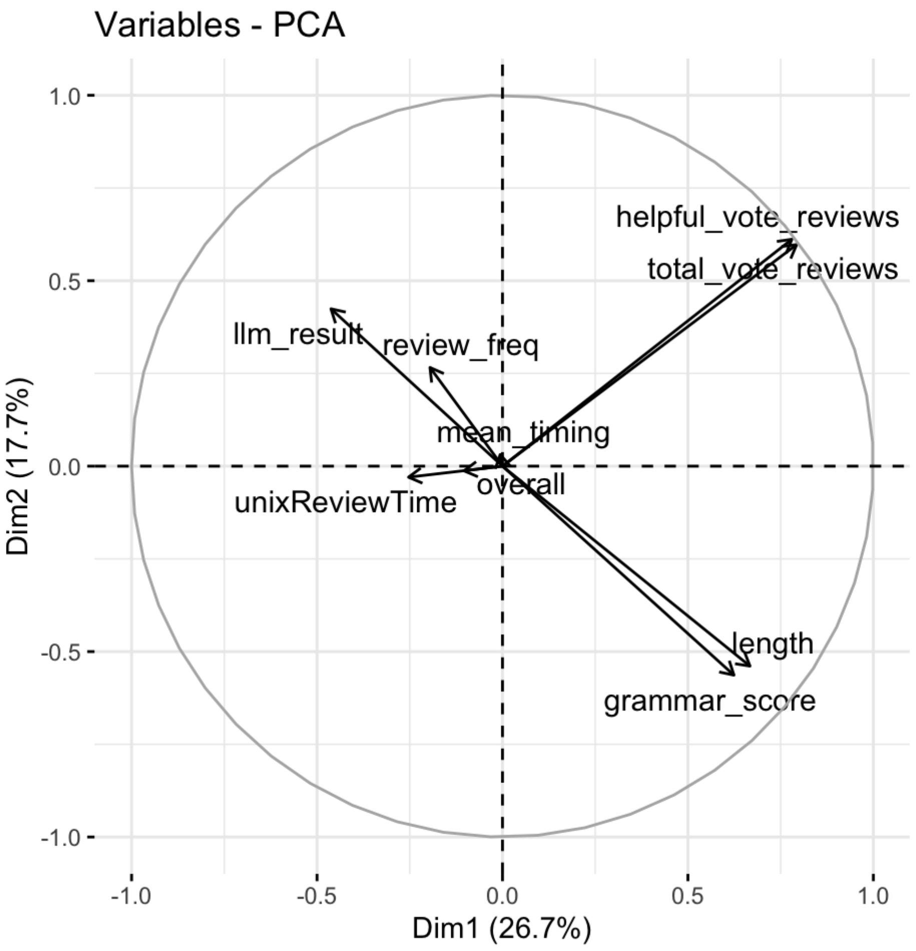
```
# Write code here
fviz_pca_ind(reviews_pca,
             col.ind = reviews$llm,
             repel = FALSE)
```



```
# Plot the first two principal components (filtering outliers for a close up)
pc_scores <- as.data.frame(reviews_pca$x)
pc_scores %>%
  filter(PC1 < 40) %>%
  ggplot(aes(x = PC1, y = PC2)) +
  geom_point() +
  labs(title = "PCA", x = "Dim 1: 26.7%", y = "Dim 2: 17.7%")
```



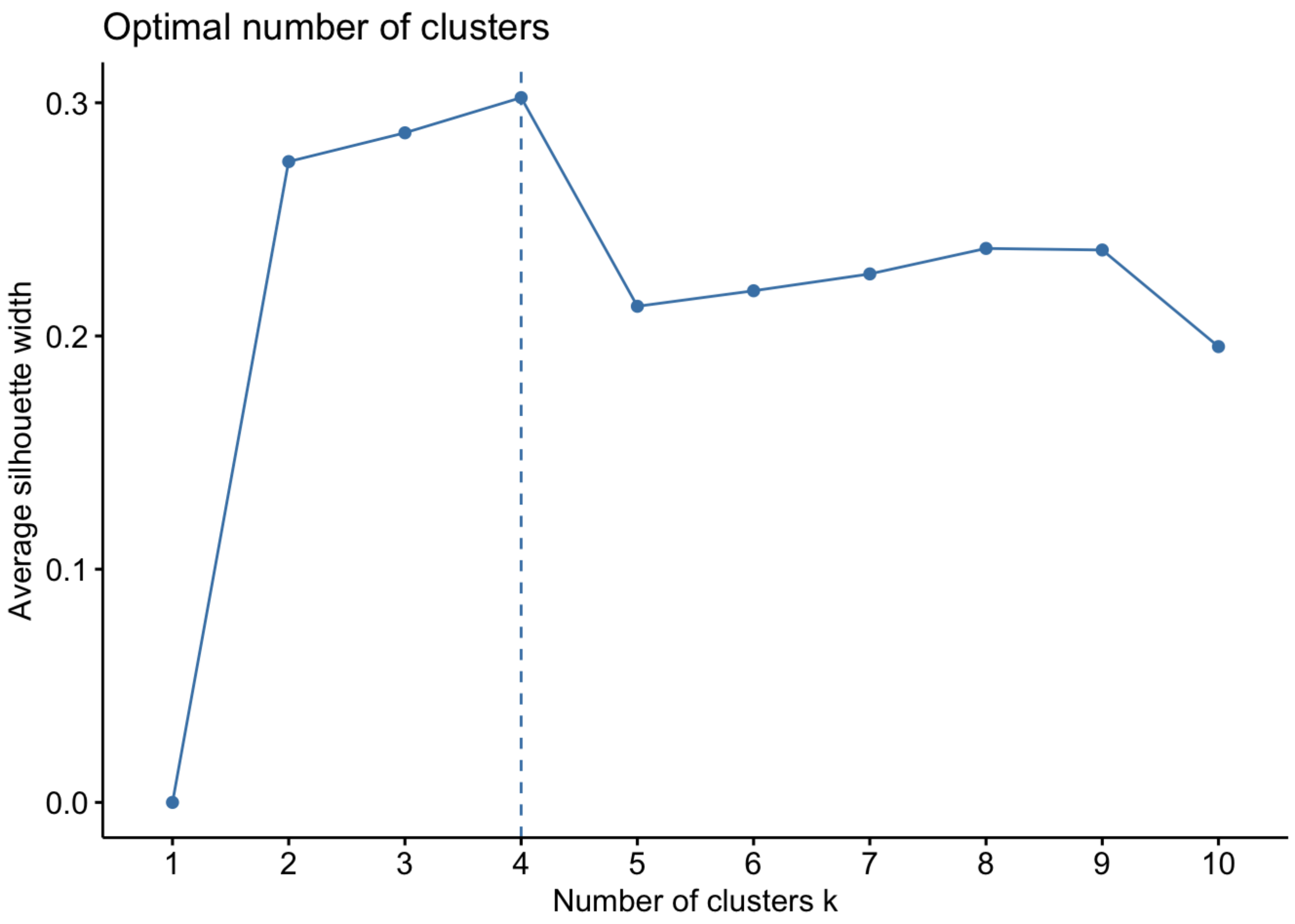
```
# Makes a correlation circle
fviz_pca_var(reviews_pca, col.var = "black",
             repel = TRUE)
```



We can see that these PCs explain 44.4% of the variance in our dataset. We can see in out correlation circle that helpful_vote_reviews and total_vote_reviews are highly correlation as well as length and grammar_score. Mean timing and unixReviewTime are at ~90 degrees making them have no correlation. Based on the PCA graph we can see that a high/positive value on dimension 1 tends to mean you are a human review, and a negative/low value on Dimension 1 means that the review is AI generated. On Dimension 2 we can see that a positive value indicates both AI and Human (but positive Dim 1 and Dim 2 indicates mostly Human and negative Dim 1 and positive Dim 2 indicates AI). We also see a negative Dim 2 value indicates human generated.

Clustering:

```
# Inorder to save time takes a random sample of 2000 from the 10k dataset
sampled_data <- reviews_num[sample(1:nrow(reviews_num), 2000), ]

# Gets the number of clusters it should make based on silhouette width
fviz_nbclust(sampled_data, pam, method = "silhouette")
```



We see that the it should make 6 clusters based on silhouette width, however since we only have two groups of either AI generated or Human generated reviews, we should use 2 as the number of groups. We can also see that 2 groups is similar to 6 groups from the graph above making it reasonable to use 2 groups.

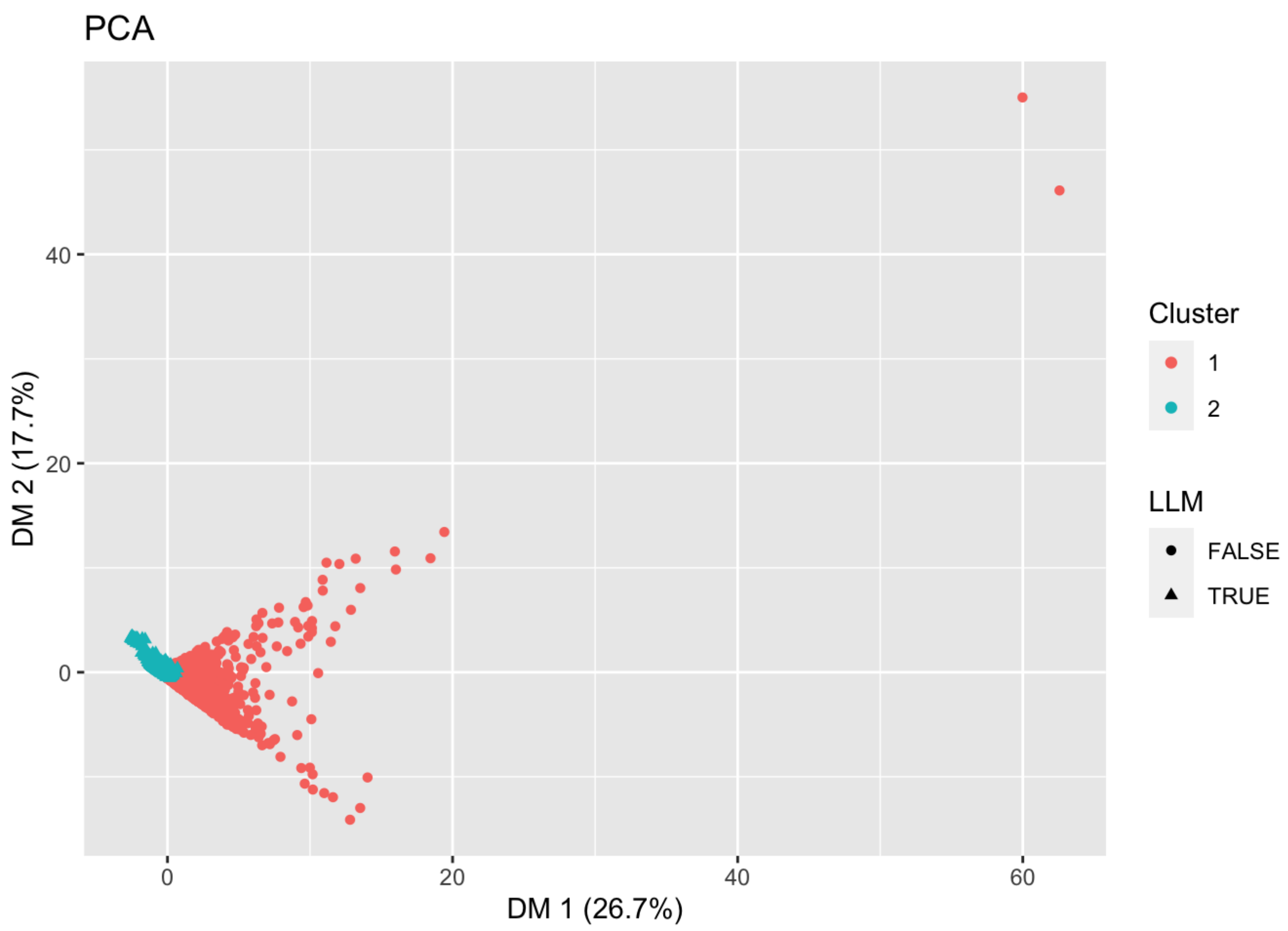
PAM Clustering:

```
# for reproduction
set.seed(123)

# Use the function pam() to find clusters
pam_results <- reviews_num %>%
  pam(k = 2) # k is the number of clusters

# Take a look at the resulting object
pam_results
```

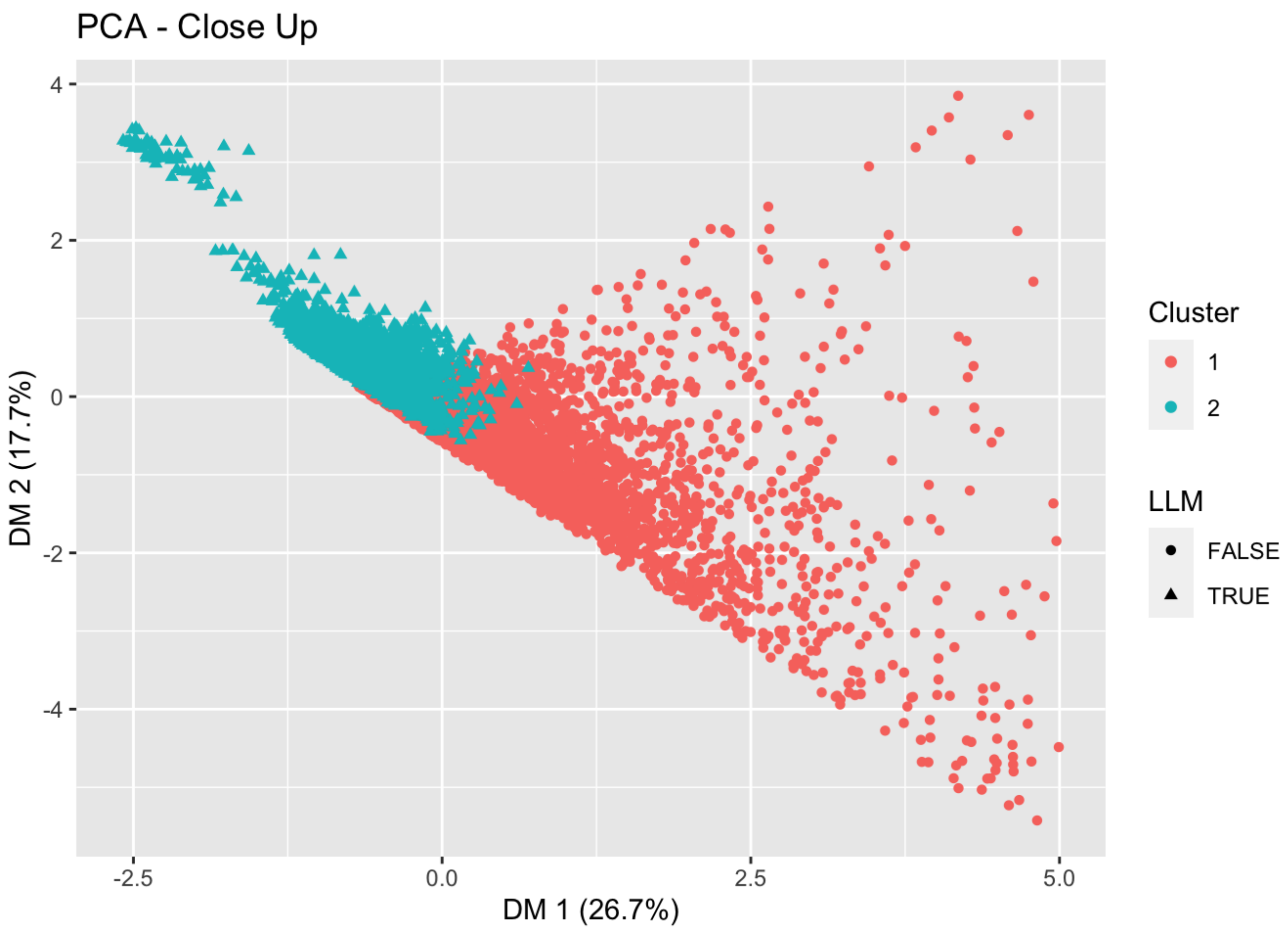
```
## Medoids:
##        ID helpful_vote_reviews total_vote_reviews    overall unixReviewTime
## [1,] 2377           0.02057527       -0.009913866 -0.2014448      0.2077173
## [2,] 8586          -0.11550455       -0.133528160  0.2780486      0.2481917
##      grammar_score review_freq mean_timing llm_result     length
## [1,]    -0.1062132  -0.3680560 -0.07849342   -0.99995 -0.1013502
## [2,]    -0.3997821   0.1273087 -0.07848519    0.99995 -0.2066190
## Clustering vector:
##   [1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
##  [38] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
##  [75] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
##  [ reached getOption("max.print") -- omitted 9900 entries ]
## Objective function:
##    build     swap
## 1.803218 1.797666
##
## Available components:
##  [1] "medoids"    "id.med"     "clustering" "objective"  "isolation"
##  [6] "clusinfo"   "silinfo"    "diss"       "call"       "data"
```

2-Dimension Plot:

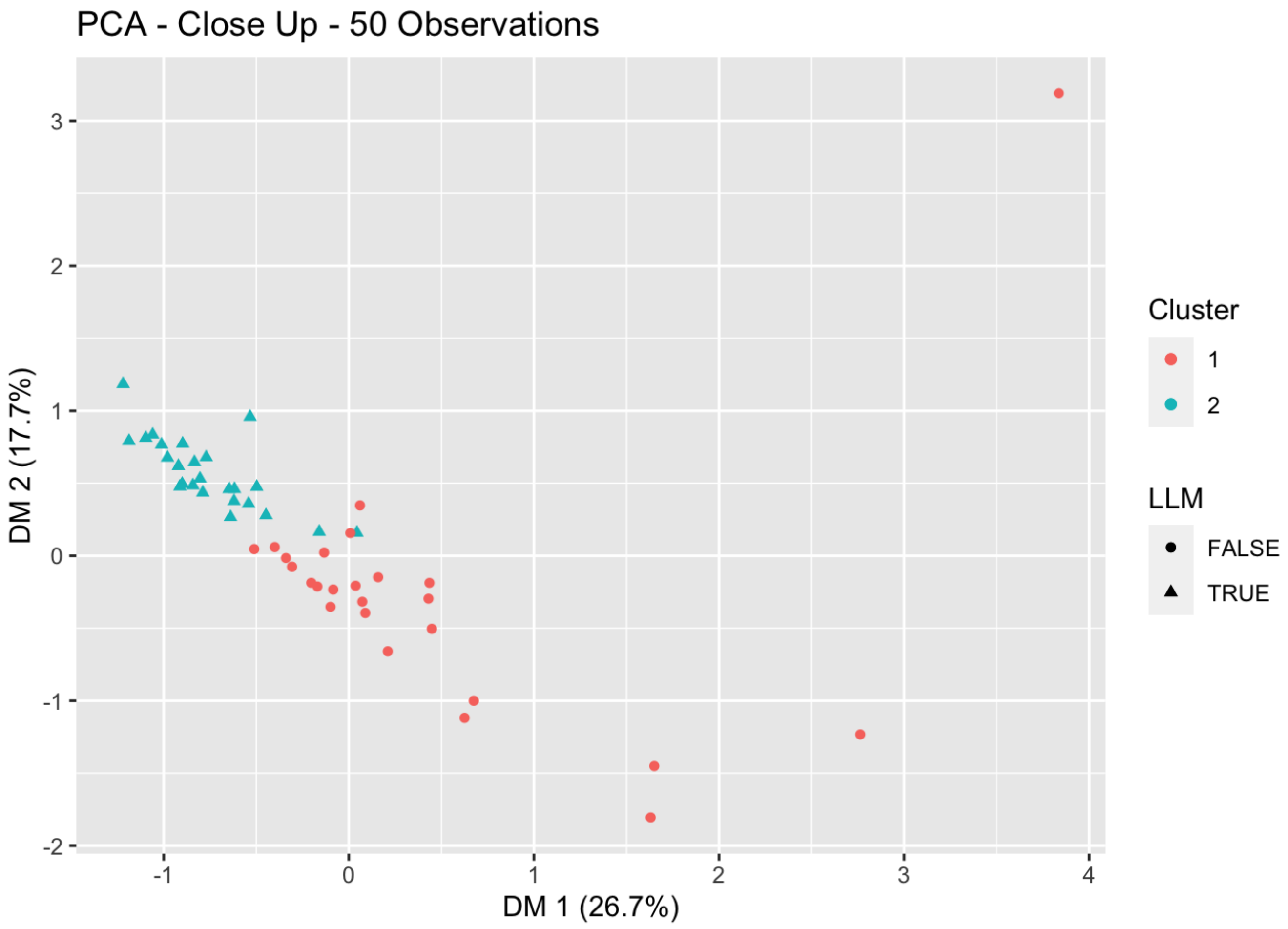
```r
# Converts clustring results into a factor
cluster_labels <- as.factor(pam_results$clustering)

# Makes the PCA scores into a dataframe
x <- as.data.frame(reviews_pca$x)

# Adds the clustring results into the dataframe
x$cluster <- cluster_labels

# Add llm information to the principal component scores
x$llm <- as.factor(reviews$llm)

x$reviewerID <- reviews$reviewerID


# Plot the results
x %>%
  ggplot(aes(x = PC1, y = PC2, color = cluster, shape = llm)) +
  geom_point() +
  labs(title = "PCA",
       x = "DM 1 (26.7%)",
       y = "DM 2 (17.7%)",
       color = "Cluster",
       shape = "LLM")
```



```
# Plot the results (Close Up)
x %>%
  filter(PC1 < 5) %>% # Helps filter outliers to get a closer look
  ggplot(aes(x = PC1, y = PC2, color = cluster, shape = llm)) +
  geom_point() +
  labs(title = "PCA - Close Up",
       x = "DM 1 (26.7%)",
       y = "DM 2 (17.7%)",
       color = "Cluster" ,
       shape = "LLM")
```



```
# Same Grpahs as above
# Much smaller dataset
# Done to see if the red points are mostly Human or not

set.seed(123)  # set seed to 123

# Random Sampling
x_true <- x %>%
  filter(llm == TRUE) %>%
  sample_n(25)

x_false <- x %>%
  filter(llm == FALSE) %>%
  sample_n(25)

# PCA graph like above
ggplot() +
  geom_point(data = x_true, aes(x = PC1, y = PC2, color = cluster, shape = llm)) +
  geom_point(data = x_false, aes(x = PC1, y = PC2, color = cluster, shape = llm)) +
  labs(title = "PCA - Close Up - 50 Observations",
       x = "DM 1 (26.7%)",
       y = "DM 2 (17.7%)",
       color = "Cluster",
       shape = "LLM")
```



```
# Displays the PAM Results:
pam_results
```

```
## Medoids:
##        ID helpful_vote_reviews total_vote_reviews    overall unixReviewTime
## [1,] 2377           0.02057527       -0.009913866 -0.2014448      0.2077173
## [2,] 8586          -0.11550455       -0.133528160  0.2780486      0.2481917
##      grammar_score review_freq mean_timing llm_result     length
## [1,]    -0.1062132  -0.3680560 -0.07849342   -0.99995 -0.1013502
## [2,]    -0.3997821   0.1273087 -0.07848519    0.99995 -0.2066190
## Clustering vector:
##    [1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
##   [38] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
##   [75] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
##   [ reached getOption("max.print") -- omitted 9900 entries ]
## Objective function:
##    build     swap
## 1.803218 1.797666
##
## Available components:
##  [1] "medoids"    "id.med"     "clustering" "objective"  "isolation"
##  [6] "clusinfo"   "silinfo"    "diss"       "call"       "data"
```

```
# Number of cluster
length(unique(pam_results$clustering))
```

```
## [1] 2
```

```
# Sizes of the clusters
table(pam_results$clustering)
```

```
##
##    1    2
## 5000 5000
```

```
# the medoids - centers
pam_results$medoids
```

```
##      helpful_vote_reviews total_vote_reviews    overall unixReviewTime
## [1,]           0.02057527       -0.009913866 -0.2014448      0.2077173
## [2,]          -0.11550455       -0.133528160  0.2780486      0.2481917
##      grammar_score review_freq mean_timing llm_result     length
## [1,]    -0.1062132  -0.3680560 -0.07849342   -0.99995 -0.1013502
## [2,]    -0.3997821   0.1273087 -0.07848519    0.99995 -0.2066190
```

```
# calculate the silhouette width only for the medoids
sil_width <- silhouette(pam_results$clustering, dist(reviews_num))
sil_width[2377, ] # -> Cluster 1 center sil width
```

```
##   cluster  neighbor sil_width
## 1.0000000 2.0000000 0.1784092
```

```
sil_width[8586, ] # -> Cluster 2 center sil width
```

```
##   cluster  neighbor sil_width
## 2.0000000 1.0000000 0.5567528
```

```
x[2377, ] # -> Cluster 1 center sil reviewerID
```

```
##            PC1       PC2        PC3       PC4       PC5        PC6        PC7
## 2377 0.2436375 -0.322643 -0.6059858 0.3795575 0.3422994 -0.4413677 -0.5083408
##              PC8         PC9 cluster   llm                           reviewerID
## 2377 -0.03403069 -0.03231816       1 FALSE f051b6c4-4987-43e9-bded-aca25ac040f3
```

```
x[8586, ] # -> Cluster 2 center sil reviewerID
```

```
##              PC1       PC2      PC3        PC4         PC5       PC6       PC7
## 8586 -0.7500939 0.5001294 0.100331 -0.3275966 -0.01806072 0.4213529 0.5011048
##            PC8         PC9 cluster  llm                           reviewerID
## 8586 0.189005 0.004047758       2 TRUE 82acf5e5-260a-48c6-877a-9ca80ef6428e
```

Here we can see the two clusters, where cluster 1 represents mostly humans, and cluster 2 represents mostly AI reviewers. We can see this more closely in the 50 Observations graph where we have a much smaller data set but all of the red points are humans and all the blue points are AI. This makes sense as we know there are two groups, and using the PMA we are able to see the two clusters form naturally where it distinguished them based on AI or Human. The centers are at ID 2377 for cluster 1 and ID 8586 for cluster 2, and we can further see the reviewerID for these: center of cluster 1 is f051b6c4-4987-43e9-bded-aca25ac040f3 (human) and center of cluster 2 is 82acf5e5-260a-48c6-877a-9ca80ef6428e (AI). The silhouette width for each respectively is 0.1784092 and 0.5567528.

Discussion:

So can we detect AI generated reviews?

Yes we can, although the acuracy of the knn model we created is not perfect, the PAM clustering, knn model, and graphs created before show that we can detect AI generated models to an extent. As we saw grammar score is a good indicator of an AI, the lower the score the higher the chance of a AI model generating a review. We can also see this with the length of the review, the lower the length the higher the chance that an AI generated the review. One other good indicator is number of reviews made by a reviews, the more posts the higher the chance of it being an AI. The accuracy of our model was 77% with a 10-fold cross validation. Along with this the PAM clustering also clustered such that one cluster is AI and the other is Humans.

Some ways Amazon could make this accuracy better is by investigating the ASIN values, these are ids that Amazon assigns to products and this information is not of public use. If they can see which product types tend to have more human reviews and more AI reviews that could be a good predictor, as it would make sense that the AI would not post a review for something which already has many reviews. As we saw in our Overall Review Box Plot humans tend to give a 5 on average meaning the AI would not be needed for those products for which humans already review to a great extent.

What was challenging?

This project was particularly fun, and gave me a chance to get out of comfort zone. Throughout the project I have learned that planning is very important, when I first started the project I was coding randomly, but got lost quickly. After some time I made a planning document from which I decided that I needed to quantify my data, and that I need to get a grammar score from python. Also I learned that Google is a great resource, and that Stack-Overflow has questions to random errors that might arise. Overall I learned that its important to exhaust the resources at hand as most likely it will get you the answer you are looking for.

Credits:

- https://builtin.com/data-science/step-step-explanation-principal-component-analysis (https://builtin.com/data-science/step-step-explanation-principal-component-analysis)
- https://stackoverflow.com/questions/35252833/how-to-import-data-set-in-r (https://stackoverflow.com/questions/35252833/how-to-import-data-set-in-r)

- https://stats.stackexchange.com/questions/22569/pca-and-proportion-of-variance-explained (https://stats.stackexchange.com/questions/22569/pca-and-proportion-of-variance-explained)