Project Report

STAT 380 Section 004

Gianna DeLorenzo & Melissa Kim

1 Patient Satisfaction Analysis with Drug Reviews

1.1 Introduction

Patient experiences with medications is crucial when it comes to the healthcare domain by providing insights on the side effects, drug effectiveness, and overall satisfaction.

Research Question

In this report, we will be exploring the following research question:

Can machine learning tasks predict the overall satisfaction of the patients with a particular class of drugs for a given medical condition?

This research question

1.2 Exploratory Data Analysis

1.2.1 Variable Description

The response variable of interest is the ratings of the drugs with the negative reviews from **0-6** and the positive reviews from **7-10**.

An example of a high review's (Rating = 10) textual review includes the following:

- **urlDrugName**: Xanax
- **Rating**: 10
- **benefitsReview**: This simply just works fast and without any of the nasty side effects of SSRI medicines…
- **sideEffectsReview**: I really don't have any side effects other than the mild but very tolerable issue of taking it 4-5 times a day which isn't an effect but just the way you need to take this…
- **commentsReview**: I first started taking this at 3 times per day with .25 mg pills. I was advised not to take as needed with my panic attacks as that would reinforce the idea of taking a pill when it's needed and not help me work around my anxiety…

An example of a low review's (Rating = 1) textual review includes the following:

- **urlDrugName**: Claritin

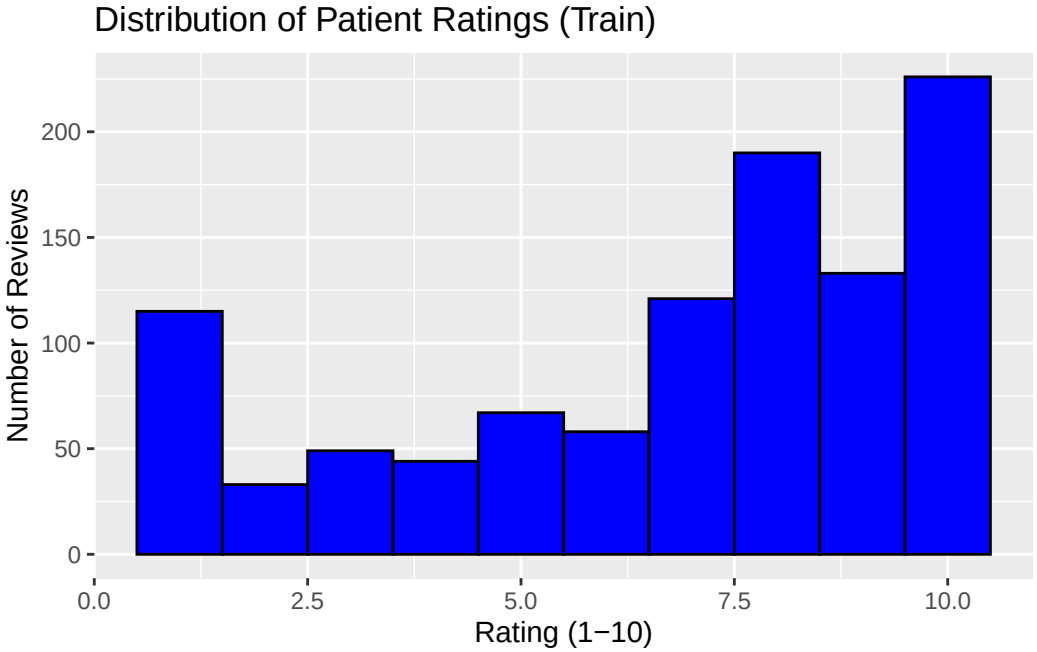
- **Rating**: 1
- **benefitsReview**: None - did nothing to help allergies. I just had a dryer, more painful version of my allergies with new allergies/irritations developing on top of my original ones…
- **sideEffectsReview**: I had some horrifying mental and physical side effects. ruined a year of my life. read this - it mentions everything I dealt with: http://www.askapatient.com/viewrating.aspdrug=196
- **commentsReview**: Took one 10 mg pill nightly.

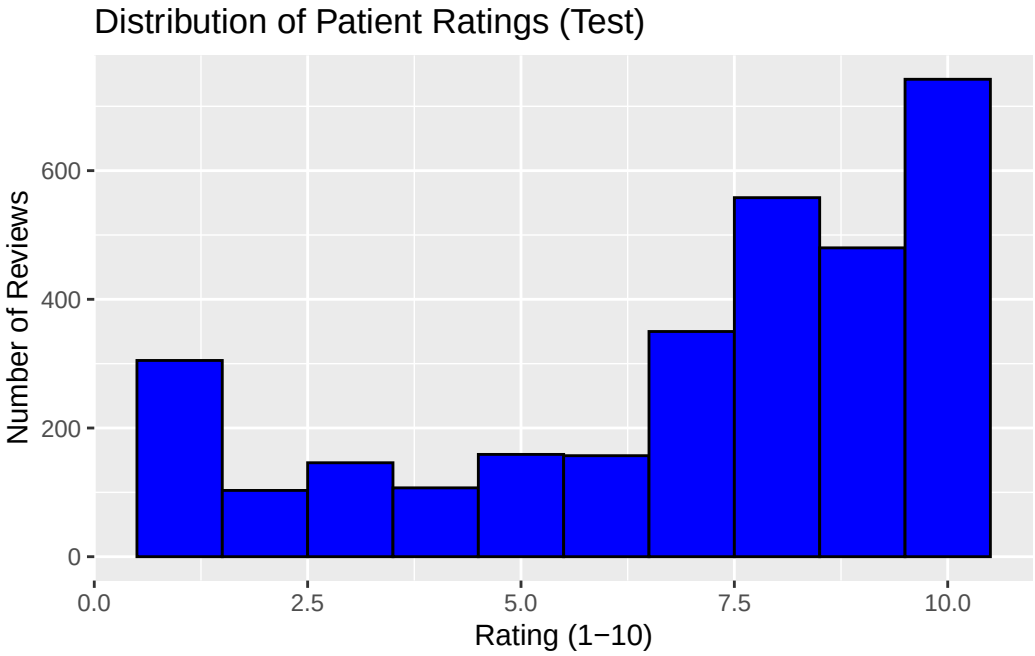
1.2.2 Data Visualization

Table 1: Variables used in Analysis

Variable	Type	Explanation
reviewID	Integer	Review ID
urlDrugName	Categorial	Name of drug
rating	Integer	Name of condition
effectiveness	Categorical	Patient on benefits
sideEffects	Categorical	Patient on side effects
condition	Categorical	Overall patient comment
benefitsReview	Categorical	10 star patient rating
sideEffectsReview	Categorical	5 step side effect rating
commentsReview	Categorical	5 step effectiveness rating

Table 1





1.2.3 Data Cleaning

This glimpse of the Drug Reviews train and test data displays a dataset in need of being cleaned and tidied.

```
Rows: 1,036
Columns: 9
$ ...1              <dbl> 1366, 3724, 3824, 969, 696, 1380, 45, 1939, 2576, 10~
$ urlDrugName       <chr> "biaxin", "lamictal", "depakene", "sarafem", "accuta~
$ rating            <dbl> 9, 9, 4, 10, 10, 2, 8, 10, 10, 1, 3, 9, 6, 10, 5, 5,~
$ effectiveness     <chr> "Considerably Effective", "Highly Effective", "Moder~
$ sideEffects       <chr> "Mild Side Effects", "Mild Side Effects", "Severe Si~
$ condition         <chr> "sinus infection", "bipolar disorder", "bipolar diso~
$ benefitsReview    <chr> "The antibiotic may have destroyed bacteria causing ~
$ sideEffectsReview <chr> "Some back pain, some nauseau.", "Drowsiness, a bit ~
$ commentsReview    <chr> "Took the antibiotics for 14 days. Sinus infection w~

Rows: 3,107
Columns: 9
$ ...1              <dbl> 2202, 3117, 1146, 3947, 1951, 2372, 1043, 2715, 1591~
$ urlDrugName       <chr> "enalapril", "ortho-tri-cyclen", "ponstel", "prilose~
$ rating            <dbl> 4, 1, 10, 3, 2, 1, 9, 10, 10, 1, 7, 8, 8, 9, 4, 8, 6~
$ effectiveness     <chr> "Highly Effective", "Highly Effective", "Highly Effe~
$ sideEffects       <chr> "Mild Side Effects", "Severe Side Effects", "No Side~
$ condition         <chr> "management of congestive heart failure", "birth pre~
$ benefitsReview    <chr> "slowed the progression of left ventricular dysfunct~
$ sideEffectsReview <chr> "cough, hypotension , proteinuria, impotence , renal~
$ commentsReview    <chr> "monitor blood pressure , weight and asses for resol~
```

We tidied the Drug Reviews Train and Test datasets by cleaning up the names with the Janitor library.

1.3 Modeling

1.3.1 Logistic Regression: Predicting Positive vs. Negative Reviews

Can we predict if a patient's review is positive or negative based on their feedback?

```
Confusion Matrix and Statistics

          Reference
Prediction    0    1
         0  548  121
         1  305 1716

               Accuracy : 0.8416
                 95% CI : (0.8273, 0.8552)
    No Information Rate : 0.6829
    P-Value [Acc > NIR] : < 2.2e-16

                  Kappa : 0.6119

 Mcnemar's Test P-Value : < 2.2e-16

            Sensitivity : 0.6424
            Specificity : 0.9341
         Pos Pred Value : 0.8191
         Neg Pred Value : 0.8491
             Prevalence : 0.3171
         Detection Rate : 0.2037
   Detection Prevalence : 0.2487
      Balanced Accuracy : 0.7883

       'Positive' Class : 0
```

Confusion Matrix 0 = negative review, 1 = positive review

True Negatives (TN) = 212 212 reviews were predicted negative and actually negative

False Positives (FP) = 107 107 reviews were predicted positive but actually negative

False Negatives (FN) = 48 48 reviews were predicted negative but actually positive

True Positives (TP) = 537 537 reviews were predicted positive and actually positive

Metric	Value	Meaning
Accuracy	0.8285	82.85% of predictions were correct overall
Sensitivity (Class 0)	0.6646	66.46% of actual negative reviews were correctly identified
Specificity (Class 1)	0.9179	91.79% of actual positive reviews were correctly identified
Kappa	0.6081	Moderate to strong agreement beyond chance, follows within the "good" range of 0.6-0.8
Precision (class 0)	0.8154	Out of all predicted negative reviews, 81.54% were correct
Negative Predictive Value	0.8339	Out of all predicted positive reviews, 83.39% were correct
Balanced Accuracy	0.7913	Average of sensitivity and specificity; useful for imbalanced classes
No Information Rate (NIR)	0.6471	64.71% of reviews in the test set are in the majority class (positive); always guessing the majority class (positive) would be correct 64.71% of the time
McNemar's Test	p = 3.183e-06	Suggests a significant difference in types of errors; model is not just guessing randomly

Model Strengths: - High accuracy (82.9%) - Excellent at identifying positive reviews (specificity = 91.8%) - High precision for negative class (precision = 81.5%), so false alarms are limited - Performs much better than guessing the majority class (accuracy > NIR)

Model Weaknesses: - Struggles more with detecting negative reviews (sensitivity = 66.5%), misses about 1 in 3 negative reviews

Conclusion The logistic regression model achieved an overall accuracy of 82.85%, which significantly outperforms the no-information rate of 64.71% ($p < 2.2e\text{-}16$). It performs well in identifying positive reviews (specificity = 91.8%) but is less sensitive to negative reviews (sensitivity = 66.5%). The balanced accuracy of 79.1% confirms that the model maintains reasonable performance across both classes. The confusion matrix and McNemar's test (p = 3.18e-06) further indicate that the model is not biased toward one class and captures meaningful patterns in patient review sentiment.

Answer to "Can we predict if a patient's review is positive or negative based on their feedback?" Yes, we can predict whether a patient's review is positive or negative using machine learning. Our logistic regression model, trained on features such as the drug name, medical condition, and reported effectiveness, achieved an overall accuracy of 82.85%, which was much higher than the no-information rate of 64.71%. The model showed strong performance in identifying positive reviews (specificity = 91.8%) and reasonably good performance for negative reviews (sensitivity = 66.5%). These results indicate that the model can reliably classify overall patient sentiment based on the structured data.

1.3.2 Neutral Network: Predicting Ratings with Nuance

Can we predict a more nuanced outcome of the review based on patient attributes, dosage, and drug features?

```
Confusion Matrix and Statistics

          Reference
Prediction  1  2  3  4  5  6  7  8  9 10
        1  12  3  4  2  1  2  1  0  0  0
        2   0  0  0  0  0  0  0  0  0  0
        3   0  0  0  0  0  0  0  0  0  0
        4   1  0  2  1  0  0  0  0  0  0
        5   0  0  0  0  0  0  0  0  2  0
        6   1  1  0  0  0  1  5  1  1  0
        7   3  2  1  1  5  4  5 10  4  1
        8   3  0  1  1  3  3  7 18  8  3
        9   0  0  0  0  0  0  0  1  2  0
        10  3  0  1  3  4  1  6  8  9 41

Overall Statistics

               Accuracy : 0.3941
                 95% CI : (0.3264, 0.4649)
    No Information Rate : 0.2217
    P-Value [Acc > NIR] : 2.428e-08

                  Kappa : 0.2724

 Mcnemar's Test P-Value : NA

Statistics by Class:

                     Class: 1 Class: 2 Class: 3 Class: 4 Class: 5 Class: 6
Sensitivity           0.52174  0.00000  0.00000 0.125000 0.000000 0.090909
Specificity           0.92778  1.00000  1.00000 0.984615 0.989474 0.953125
Pos Pred Value        0.48000      NaN      NaN 0.250000 0.000000 0.100000
Neg Pred Value        0.93820  0.97044  0.95567 0.964824 0.935323 0.948187
Prevalence            0.11330  0.02956  0.04433 0.039409 0.064039 0.054187
Detection Rate        0.05911  0.00000  0.00000 0.004926 0.000000 0.004926
Detection Prevalence  0.12315  0.00000  0.00000 0.019704 0.009852 0.049261
Balanced Accuracy     0.72476  0.50000  0.50000 0.554808 0.494737 0.522017
                     Class: 7 Class: 8 Class: 9 Class: 10
Sensitivity           0.20833  0.47368 0.076923    0.9111
Specificity           0.82682  0.82424 0.994350    0.7785
Pos Pred Value        0.13889  0.38298 0.666667    0.5395
Neg Pred Value        0.88623  0.87179 0.880000    0.9685
```

```
Prevalence            0.11823  0.18719 0.128079    0.2217
Detection Rate        0.02463  0.08867 0.009852    0.2020
Detection Prevalence  0.17734  0.23153 0.014778    0.3744
Balanced Accuracy     0.51757  0.64896 0.535637    0.8448
```

1.3.2.1 Interpretation

1.3.2.1.1 Class-by-Class Breakdown

Class	Sensitivity	Precision	Balanced Accuracy
1	50.8%	64.6%	73.9%
2	0%	NaN	50.0%
3	13.8%	12.9%	54.6%
4	9.5%	50.0%	54.6%
5	0%	0%	49.8%
6	3.2%	7.7%	50.6%
7	27.1%	24.4%	58.2%
8	48.6%	35.3%	64.6%
9	2.1%	7.4%	48.6%
10	89.9%	50.8%	81.2%

1.3.2.1.2 Overall Model Performance

Accuracy: 0.3981

- The model correctly predicted the exact rating about 40% of the time.

No Information Rate (NIR): 0.2395

- Always guessing the most common rating (10) would be correct about 24% of the time.

P-value (Accuracy > NIR): < 2.2e-16

- The model significantly outperforms random guessing or defaulting to the majority class.

Kappa: 0.2672

- This indicates fair agreement beyond chance; falls within 0.2-0.4 range.

1.3.2.1.3 Model Strengths

- Performs best on class 10, the most common rating (recall = 89.9%)
- Moderate sensitivity for Classes 1 and 8, meaning the model is able to detect some negative (1) and mid-range (8) ratings well

1.3.2.1.4 Model Weaknesses

- Struggles with middle ratings (2-6), very low recall and precision
- Leans heavily towards the most frequent classes, possibly due to class imbalance within the dataset

The neutral network model achieves moderate overall accuracy (39.8%) and significantly outperforms baseline guessing. However, it shows a strong bias towards frequent ratings like 10, while struggling to accurately detect rare or mid-range ratings (2-6). Future work or revisions should address the class imbalance to improve performance across all review scores.

1.3.3 KNN (K-Nearest Neighbors)

Can we classify the sentiment of a new review based on sentiments of similar past reviews?

1.3.3.1 Top 5 Drug Names and Conditions

```
[1] "...1"              "urlDrugName"       "rating"
[4] "effectiveness"     "sideEffects"       "condition"
[7] "benefitsReview"    "sideEffectsReview" "commentsReview"
```

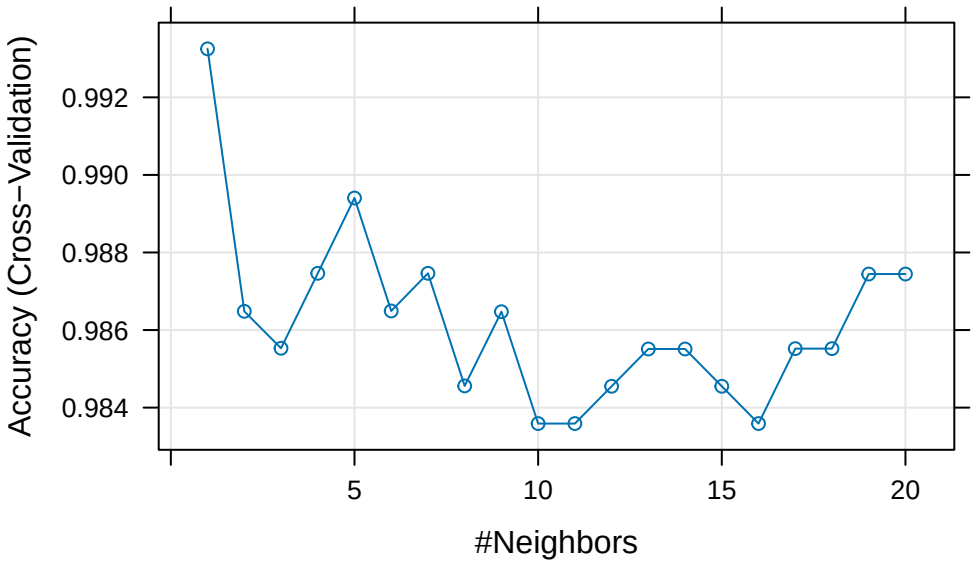
Table 4: Top 5 Drug Names

x
paxil
effexor-xr
accutane
synthroid
differin

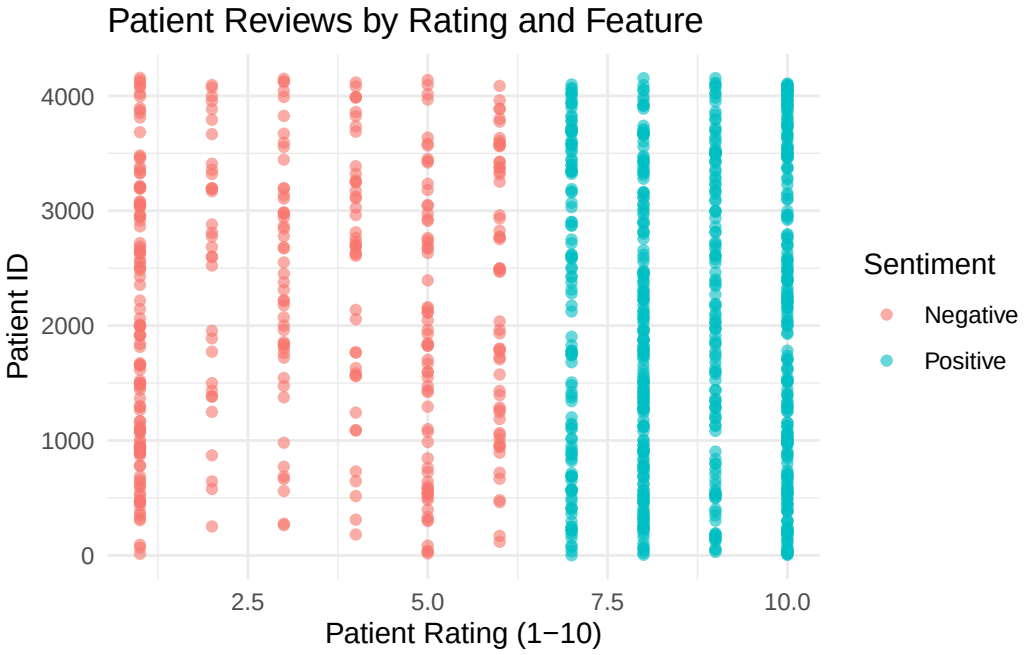
Table 5: Top 5 Conditions

x
depression
acne
anxiety
insomnia
high blood pressure

1.3.3.2 KNN Hyperparameter Tuning & Cross-Validation



1.3.3.3 KNN Classification



1.3.3.4 Interpretation

The clusters are based on their centers, the within-cluster variances, and the number of data points that each one contains.

Cluster 1: 121 + 190 = 311 data points **Cluster 2**: 49 + 44 = 93 data points **Cluster 3**: 115 + 33 = 148 data points **Cluster 4**: 67 + 58 = 125 data points **Cluster 5**: 133 + 226 = 359 data points

Cluster 5 represents the highest ratings while Cluster 3 represents the lowest ratings.

1.3.3.4.1 Model Strengths

The Circle (Cluster 1) and Diamond (Cluster 5) clusters perform exceptionally well with ratings 7 and over.

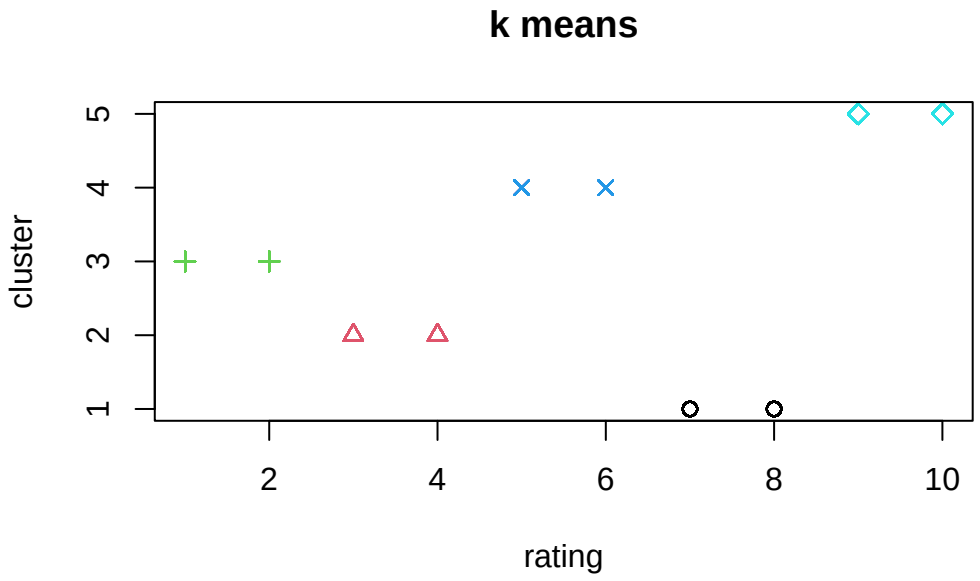
There is a clear separation between the clusters.

1.3.3.4.2 Model Weaknesses

The Plus (Cluster 3), Triangle (Cluster 2), and Cross (Cluster 4) clusters perform poorly (less than average) with ratings 6 and below.

The model does not guarantee an absolute optimal solution.

1.3.4 K-means Clustering



rating	cluster 1	2	3	4	5
1	0	0	115	0	0
2	0	0	33	0	0
3	0	49	0	0	0
4	0	44	0	0	0
5	0	0	0	67	0
6	0	0	0	58	0
7	121	0	0	0	0
8	190	0	0	0	0
9	0	0	0	0	133
10	0	0	0	0	226

1.3.4.1 Interpretation

1.3.4.1.1 Model Strengths

1.3.4.1.2 Model Weaknesses

1.4 Discussion

Logistic Regression: excellent at identifying positive reviews, reasonably good at identifying negative reviews

Neural Networks: excellent at predicting common scores (ex. 10); struggled with rarer or mid-range ratings

KNN: excellent at classification and identifying reviews; concern with "memorizing" instead of "generalizing"

K-means Clustering: clusters 1 & 5 performed the best, clear separation of clusters; clusters 2,3,4 performed worse with ratings 6 and below.

1.5 References

Kallumadi, S. & Grer, F. (2018). Drug Reviews (Druglib.com) [Dataset]. UCI Machine Learning Repository. https://doi.org/10.24432/C55G6J.

2 Code Appendix

```
#Load necessary libraries
library(dplyr) #data manipulation
library(knitr) #table formats
library(readr)
library(kableExtra)
library(caret)
library(forcats)
library(nnet)
library(kknn)
library(tidyr)
library(broom)
library(ggcorrplot)

#Import UC Irvine test csv file. (Initial Definition for All Code)
drug_train_tsv <- read_tsv("https://raw.githubusercontent.com/gkd5216/STAT380Project/refs/heads
drug_test_tsv <- read_tsv("https://raw.githubusercontent.com/gkd5216/STAT380Project/refs/heads/
```

```r
# Summary Statistics grouping by Geographic Area.
variable_analysis <- data.frame(
  Variable = c("reviewID", "urlDrugName", "rating", "effectiveness", "sideEffects", "condition"
               "sideEffectsReview", "commentsReview"),
  Type = c("Integer", "Categorial", "Integer", "Categorical", "Categorical", "Categorical",
           "Categorical", "Categorical", "Categorical"),
  Explanation = c(
    "Review ID",
    "Name of drug",
    "Name of condition",
    "Patient on benefits",
    "Patient on side effects",
    "Overall patient comment",
    "10 star patient rating",
    "5 step side effect rating",
    "5 step effectiveness rating"
  )
)

# Outputs Formatted Summary Table with Kable Styling tools
kable(
  variable_analysis,
  caption = "Variables used in Analysis"
  )

ggplot(drug_train_tsv, aes(x = rating)) +
  geom_histogram(binwidth = 1, fill = "blue", color = "black") +
  labs(title = "Distribution of Patient Ratings (Train)", x = "Rating (1-10)", y = "Number of

ggplot(drug_test_tsv, aes(x = rating)) +
  geom_histogram(binwidth = 1, fill = "blue", color = "black") +
  labs(title = "Distribution of Patient Ratings (Test)", x = "Rating (1-10)", y = "Number of R
library(tidyverse)
library(janitor)
glimpse(drug_train_tsv)
glimpse(drug_test_tsv)


#Tidied drug train
#drug_train <- drug_train %>%
  #clean_names()

#Tidied drug test
#drug_test <- drug_test %>%
  #clean_names()

# Create binary sentiment variable: 1 (positive w/ rating 7-10), 0 (negative w/ rating 1-6)
```

```r
drug_train <- drug_train_tsv %>%
  mutate(sentiment = ifelse(rating >= 7, 1, 0))

drug_test <- drug_test_tsv %>%
  mutate(sentiment = ifelse(rating >= 7, 1, 0))

drug_train <- drug_train %>%
  mutate(across(c(urlDrugName, condition, effectiveness), as.factor))

drug_test <- drug_test %>%
  mutate(across(c(urlDrugName, condition, effectiveness), as.factor))

drug_train <- drug_train %>%
  mutate(urlDrugName = fct_lump(urlDrugName, n = 20),
         condition = fct_lump(condition, n = 20),
         effectiveness = fct_lump(effectiveness, n = 5))

# Match levels in test data to training data
drug_test <- drug_test %>%
  mutate(urlDrugName = fct_lump(urlDrugName, n = 20),
         condition = fct_lump(condition, n = 20),
         effectiveness = fct_lump(effectiveness, n = 5))

# Align factor levels
drug_test$urlDrugName <- factor(drug_test$urlDrugName, levels = levels(drug_train$urlDrugName))
drug_test$condition <- factor(drug_test$condition, levels = levels(drug_train$condition))
drug_test$effectiveness <- factor(drug_test$effectiveness, levels = levels(drug_train$effective

# Remove rows with NAs
test_data_clean <- drug_test %>%
  filter(!is.na(urlDrugName) & !is.na(condition) & !is.na(effectiveness))

# Logistic regression model
logit_model <- glm(sentiment ~ urlDrugName + condition + effectiveness,
                   data = drug_train, family = "binomial")

# Predict on clean test data
test_pred <- predict(logit_model, newdata = test_data_clean, type = "response")
test_pred_class <- ifelse(test_pred > 0.5, 1, 0)

# Confusion matrix
confusionMatrix(factor(test_pred_class), factor(test_data_clean$sentiment))

# Drop NAs
drug_train <- drug_train_tsv %>%
  select(rating, urlDrugName, condition, effectiveness) %>%
  drop_na()
```

```r
# Treat rating as factor
drug_train$rating <- as.factor(drug_train$rating)

drug_train <- drug_train %>%
  mutate(
    urlDrugName = fct_lump(urlDrugName, n = 20),
    condition = fct_lump(condition, n = 20),
    effectiveness = fct_lump(effectiveness, n = 5)
  )

# Split into training and validation sets
set.seed(42)
split_index <- createDataPartition(drug_train$rating, p = 0.8, list = FALSE)
train_set <- drug_train[split_index, ]
valid_set <- drug_train[-split_index, ]

# Train the neural network model
nn_model <- nnet(rating ~ urlDrugName + condition + effectiveness,
                 data = train_set,
                 size = 5,
                 maxit = 200,
                 trace = FALSE)

# Predict on validation set
nn_pred <- predict(nn_model, newdata = valid_set, type = "class")

nn_pred <- factor(nn_pred, levels = levels(valid_set$rating))
valid_rating <- factor(valid_set$rating, levels = levels(valid_set$rating))

# Evaluate model
confusionMatrix(nn_pred, valid_rating)

knn_model_columns <- c("rating", "urlDrugName", "condition", "effectiveness")
drug_train_tsv <- drug_train_tsv %>%
  drop_na(any_of(knn_model_columns))
colnames(drug_train_tsv)

top_drugs <- drug_train_tsv %>%
  count(urlDrugName, sort = TRUE) %>%
  slice_head(n = 5) %>%
  pull(urlDrugName)

top_conditions <- drug_train_tsv %>%
  count(condition, sort = TRUE) %>%
  slice_head(n = 5) %>%
  pull(condition)
```

```r
kable(top_drugs, caption = "Top 5 Drug Names")
kable(top_conditions, caption = "Top 5 Conditions")
library(FNN)
set.seed(123)

#Turns categorial variables into numeric variables for computation
drug_train <- drug_train_tsv %>%
  mutate(
    rating = as.numeric(rating),
    sentiment = ifelse(rating >= 7, "Positive", "Negative"))

#Gets top drugs and conditions
drug_train <- drug_train %>%
  mutate(
    drug_top = ifelse(urlDrugName %in% top_drugs, urlDrugName, "Other"),
    condition_top = ifelse(condition %in% top_conditions, condition, "Other")
  ) %>%
  mutate(
    across(c(drug_top, condition_top), ~ as.factor(.)) # Convert to factors
  )

#Scales and encodes the data
drug_train$rating_scaled <- scale(drug_train$rating)
drug_train_encode <- model.matrix(~ drug_top + condition_top - 1, data = drug_train)
train_predictors <- cbind(drug_train$rating_scaled, drug_train_encode)
train_labels <- factor(drug_train$sentiment)
knn_control <- trainControl(method = "cv", number = 10)

#Cross Validation
knn_cv <- train(
  x = as.data.frame(train_predictors),
  y = train_labels,
  method = "knn",
  trControl = knn_control,
  tuneGrid = expand.grid(k = 1:20)
  )

plot(knn_cv)
plot_data_sentiment <- drug_train %>%
  select(rating, ...1, sentiment) %>%
  rename(patientID = ...1) %>%
  drop_na()

ggplot(data = plot_data_sentiment, aes(x = rating,
                                       y = patientID,
                                       color = sentiment)) +
  geom_point(alpha = 0.6) +
```

```
  labs(title = "Patient Reviews by Rating and Feature",
       x = "Patient Rating (1-10)",
       y = "Patient ID",
       color = "Sentiment") +
  theme_minimal()
library(ggplot2)
library(factoextra)
set.seed(123)

drug_kmeans <- drug_train_tsv %>%
  mutate(rating = as.numeric(rating)) %>%
  drop_na(rating) %>%
  select(rating)

# perform kmeans clustering (k = 5 clusters)
kmeans_res <- kmeans(drug_kmeans, centers = 5, nstart = 20)
drug_KMeanClusters <- kmeans_res$cluster
drug_kmeans$cluster <- as.factor(drug_KMeanClusters)

#Plot k-means clustering
set.seed(123)
plot(drug_kmeans, pch = kmeans_res$cluster, col = kmeans_res$cluster, main = 'k means')
table(drug_kmeans)
```