Heart Data Set Analysis

Code ▾

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```
# Exploratory Analysis of the Data Set:

library(ggplot2)
library(dplyr)
```

```
Attaching package: 'dplyr'

The following objects are masked from 'package:stats':

    filter, lag

The following objects are masked from 'package:base':

    intersect, setdiff, setequal, union
```

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```
library(tidyr)

setwd("/Users/fizalshaikh/Downloads/archive")
```

```
Warning: The working directory was changed to /Users/fizalshaikh/Downloads/archive inside a notebook chunk. The working directory will be reset when the chunk is finished running. Use the knitr root.dir option in the setup chunk to change the working directory for notebook chunks.
```

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```
heart_data <- read.csv("heart.csv")

# Viewing the structure of the data set:
str(heart_data)
```

```
'data.frame':   303 obs. of  14 variables:
 $ age     : int  63 37 41 56 57 57 56 44 52 57 ...
 $ sex     : int  1 1 0 1 0 1 0 1 1 1 ...
 $ cp      : int  3 2 1 1 0 0 1 1 2 2 ...
 $ trtbps  : int  145 130 130 120 120 140 140 120 172 150 ...
 $ chol    : int  233 250 204 236 354 192 294 263 199 168 ...
 $ fbs     : int  1 0 0 0 0 0 0 0 1 0 ...
 $ restecg : int  0 1 0 1 1 1 0 1 1 1 ...
 $ thalachh: int  150 187 172 178 163 148 153 173 162 174 ...
 $ exng    : int  0 0 0 0 1 0 0 0 0 0 ...
 $ oldpeak : num  2.3 3.5 1.4 0.8 0.6 0.4 1.3 0 0.5 1.6 ...
 $ slp     : int  0 0 2 2 2 1 1 2 2 2 ...
 $ caa     : int  0 0 0 0 0 0 0 0 0 0 ...
 $ thall   : int  1 2 2 2 2 1 2 3 3 2 ...
 $ output  : int  1 1 1 1 1 1 1 1 1 1 ...
```

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```
# Summary statistics of the numeric variables:
summary(heart_data[c("age", "trtbps", "chol", "thalachh")])
```

```
      age            trtbps           chol         thalachh    
 Min.   :29.00   Min.   : 94.0   Min.   :126.0   Min.   : 71.0  
 1st Qu.:47.50   1st Qu.:120.0   1st Qu.:211.0   1st Qu.:133.5  
 Median :55.00   Median :130.0   Median :240.0   Median :153.0  
 Mean   :54.37   Mean   :131.6   Mean   :246.3   Mean   :149.6  
 3rd Qu.:61.00   3rd Qu.:140.0   3rd Qu.:274.5   3rd Qu.:166.0  
 Max.   :77.00   Max.   :200.0   Max.   :564.0   Max.   :202.0  
```

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```
# Creating frequency table for the categorical variables:
table(heart_data$sex)
```

```

  0   1 
 96 207 
```

Hide

```
table(heart_data$exng)
```

```

  0   1 
204  99 
```

Hide

```
table(heart_data$fbs)
```

```

  0   1 
258  45 
```

Hide

```
table(heart_data$cp)
```

```

  0   1   2   3 
143  50  87  23 
```

Hide

```
table(heart_data$restecg)
```

```

  0   1 
 79 224 
```

Hide

```
table(heart_data$slp)
```

```

  0   1   2 
 21 140 142 
```

Hide

```
table(heart_data$caa)
```

```

  0   1   2   3   4 
175  65  38  20   5 
```

Hide

```
table(heart_data$thall)
```

```

  0   1   2   3 
  2  18 166 117 
```

Hide

```
table(heart_data$output)
```

```

  0   1 
138 165 
```

Hide

```
# Creating frequency table for the categorical variables:
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  0   1 
 96 207 
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```
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  0   1 
204  99 
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table(heart_data$fbs)
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  0   1 
258  45 
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table(heart_data$cp)
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  0   1   2   3 
143  50  87  23 
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  0   1 
 79 224 
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Hide

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table(heart_data$slp)
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  0   1   2 
 21 140 142 
```

Hide

```
table(heart_data$caa)
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  0   1   2   3   4 
175  65  38  20   5 
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Hide

```
table(heart_data$thall)
```

```

  0   1   2   3 
  2  18 166 117 
```

Hide

```
table(heart_data$output)
```

```

  0   1 
138 165 
```

Hide

```
# Plotting distribution of the numeric variables:
numeric_plots <- lapply(numeric_vars, function(var) {
  ggplot(heart_data, aes_string(x = var)) +
    geom_histogram(fill = "blue", color = "black") +
    labs(title = paste("Distribution of", var), x = var, y = "Frequency")
})
```

```
Warning: `aes_string()` was deprecated in ggplot2 3.0.0.
ℹ Please use tidy evaluation idioms with `aes()`.
See also `vignette("ggplot2-in-packages")` for more information.
```

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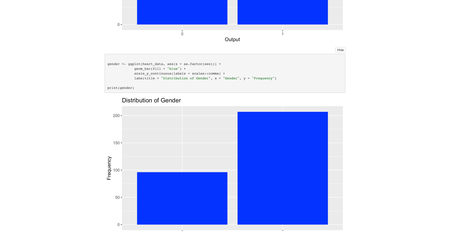
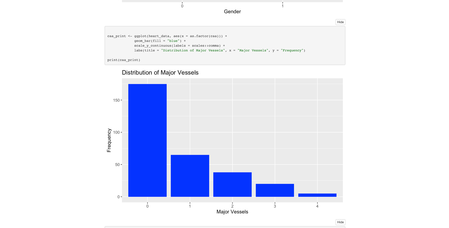
```
output_plot <- ggplot(heart_data, aes(x = as.factor(output))) +
               geom_bar(fill = "blue") +
               scale_y_continuous(labels = scales::comma) +
               labs(title = "Distribution of Output", x = "Output", y = "Frequency")

print(output_plot)
```



Hide

```
gender <- ggplot(heart_data, aes(x = as.factor(sex))) +
          geom_bar(fill = "blue") +
          scale_y_continuous(labels = scales::comma) +
          labs(title = "Distribution of Gender", x = "Gender", y = "Frequency")

print(gender)
```



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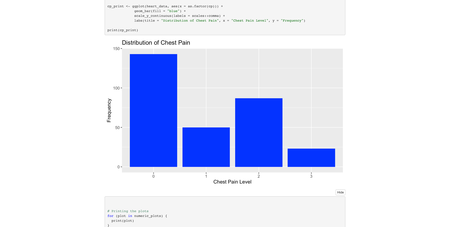
```
caa_plot <- ggplot(heart_data, aes(x = as.factor(caa))) +
            geom_bar(fill = "blue") +
            scale_y_continuous(labels = scales::comma) +
            labs(title = "Distribution of Major Vessels", x = "Major Vessels", y = "Frequency")

print(caa_plot)
```



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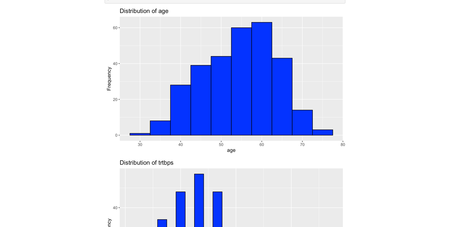
```
cp_plot <- ggplot(heart_data, aes(x = as.factor(cp))) +
           geom_bar(fill = "blue") +
           scale_y_continuous(labels = scales::comma) +
           labs(title = "Distribution of Chest Pain", x = "Chest Pain Level", y = "Frequency")

print(cp_plot)
```



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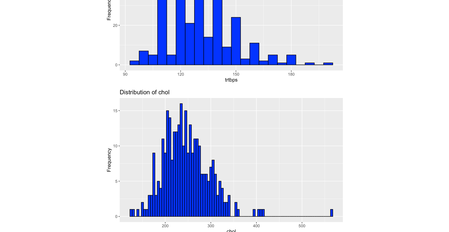
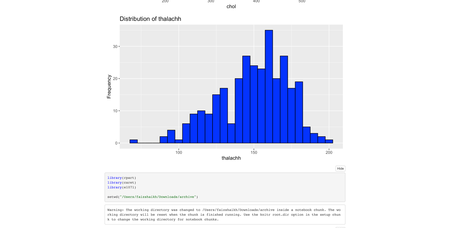
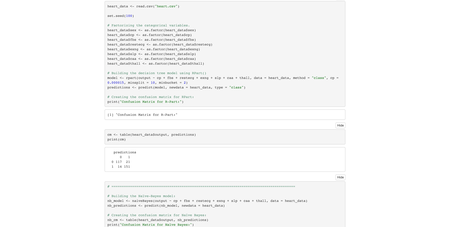
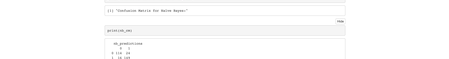
```
# Printing the plots
for (plot in numeric_plots) {
  print(plot)
}
```









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```
library(rpart)
library(caret)
library(e1071)

setwd("/Users/fizalshaikh/Downloads/archive")
```

```
Warning: The working directory was changed to /Users/fizalshaikh/Downloads/archive inside a notebook chunk. The working directory will be reset when the chunk is finished running. Use the knitr root.dir option in the setup chunk to change the working directory for notebook chunks.
```

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```
heart_data <- read.csv("heart.csv")

set.seed(1101)

# Partitioning the categorical variables:
heart_data$sex <- as.factor(heart_data$sex)
heart_data$exng <- as.factor(heart_data$exng)
heart_data$cp <- as.factor(heart_data$cp)
heart_data$fbs <- as.factor(heart_data$fbs)
heart_data$restecg <- as.factor(heart_data$restecg)
heart_data$slp <- as.factor(heart_data$slp)
heart_data$caa <- as.factor(heart_data$caa)
heart_data$thall <- as.factor(heart_data$thall)

# Building the decision tree model using CART:
model <- rpart(output ~ cp + fbs + restecg + exng + slp + caa + thall, data = heart_data, method = "class", cp = 0.000833, minsplit = 10, minbucket = 2)
predictions <- predict(model, newdata = heart_data, type = "class")

# Creating the confusion matrix for #Part:
print("Confusion Matrix for R-Part:")
```

```
[1] "Confusion Matrix for R-Part:"
```

Hide

```
cm <- table(heart_data$output, predictions)
print(cm)
```

```
   predictions
     0   1
  0 127  11
  1  16 151
```

Hide

```
# ----------------------------------------------------------------------

# Building the Naive-Bayes model:
nb_model <- naiveBayes(output ~ cp + fbs + restecg + exng + slp + caa + thall, data = heart_data)
nb_predictions <- predict(nb_model, newdata = heart_data)

# Creating the confusion matrix for Naive Bayes:
nb_cm <- table(heart_data$output, nb_predictions)
print("Confusion Matrix for Naive Bayes:")
```

```
[1] "Confusion Matrix for Naive Bayes:"
```

Hide

```
print(nb_cm)
```

```
   nb_predictions
     0   1
  0 118  20
  1  16 149
```

Hide

```
# ----------------------------------------------------------------------

# Calculating accuracy for Naive-Bayes (based upon confusion matrix results):
nb_accuracy <- sum(diag(nb_cm)) / sum(nb_cm)
print(paste("Accuracy for Naive-Bayes:", nb_accuracy))
```

```
[1] "Accuracy for Naive-Bayes: 0.867986798679868"
```

Hide

```
# Calculating accuracy for Rpart (based upon confusion matrix results):
rpart_accuracy <- sum(diag(cm)) / sum(cm)
print(paste("Accuracy for rpart:", rpart_accuracy))
```

```
[1] "Accuracy for rpart: 0.904455445544555"
```