Diagnostic for Heart Disease using KNN classification

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Introduction ¶

According to Statistics Canada (2), heart disease is the second leading cause of death in Canada and the leading cause of death in the United States of America, Canada's nearest neighbor. The relatively broad term 'heart disease' can include a number of different health issues within the heart, including, but not limited to: coronary artery disease, congenital heart disease, arrhythmia, myocardial infarction and heart failure (2). This investigation's aim is to figure out which variable in relation to a patient's health can be best used to predict whether or not a patient will have heart disease or is at a high risk from it. The dataset that will be used for the investigation is the Cleveland Heart Disease Dataset. This dataset includes the medical data of 303 individuals from Cleveland Ohio. One of the variable columns in the dataset includes the diagnosis of heart disease in each patient. Whether they suffer from it or not as well as how severe their case may be. Each patient is assigned a number value from 0 to 4, 0 representing no heart disease, then 1 to 4 representing the presence of heart disease. The severity of the disease increases with the number. The aim of this investigation is to evaluate which observations from the Cleveland Heart Disease dataset are most closely related with the diagnosis of heart disease, with 0 representing no risk and any value above that representing risk of heart disease. Our analysis conducts k-nn classification to predict whether someone is at risk for heart disease or not.

Attribute information:

- Age: age of the individual (years)
- Sex: gender of the individual 1 = male 0 = female
- Chest-pain type: type of chest-pain experienced by the individual 1 = typical angina 2 = atypical angina 3 = non anginal pain 4 = asymptotic
- Resting Blood Pressure: resting blood pressure value of an individual (in mmHg)
- Serum Cholestrol: serum cholesterol (mg/dl unit)
- Fasting Blood Sugar: compares the fasting blood sugar value of an individual with 120mg/dl. If fasting blood sugar > 120mg/dl then : 1 (true) else : 0 (false)
- Resting ECG : resting electrocardiographic results 0 = normal 1 = having ST-T wave abnormality 2 = left ventricular hyperthrophy
- Max heart rate achieved : max heart rate achieved by an individual.
- Exercise induced angina : 1 = yes 0 = no
- ST depression induced by exercise relative to rest: displays the value which is an integer or float.
- Peak exercise ST segment : 1 = upsloping 2 = flat 3 = downsloping
- Number of major vessels (0–3) colored by flourosopy : integer or float.
- Thal : thalassemia : 3 = normal 6 = fixed defect 7 = reversible defect

The libraries and coding packages used in this analysis are: tidyverse, caret, ggplot2, forcats, GGally.

In [53]:
```
library(tidyverse)
library(caret)
library(ggplot2)
library(forcats)
library(GGally)
```

1. Load Data

First we load the data set from Cleaveland Heart Disease Database from the web

In [3]:
```
heart_disease_data <- read_csv("http://archive.ics.uci.edu/ml/machine-learning-databases/heart-disease/processed.cleveland.data", col_names = FALSE)
head(heart_disease_data)
```

```
Parsed with column specification:
cols(
  X1 = col_double(),
  X2 = col_double(),
  X3 = col_double(),
  X4 = col_double(),
  X5 = col_double(),
  X6 = col_double(),
  X7 = col_double(),
  X8 = col_double(),
  X9 = col_double(),
  X10 = col_double(),
  X11 = col_double(),
  X12 = col_character(),
  X13 = col_character(),
  X14 = col_double()
)
```

A tibble: 6 × 14

X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X
<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<chr>	<chr>	<d
63	1	1	145	233	1	2	150	0	2.3	3	0.0	6.0	
67	1	4	160	286	0	2	108	1	1.5	2	3.0	3.0	
67	1	4	120	229	0	2	129	1	2.6	2	2.0	7.0	
37	1	3	130	250	0	0	187	0	3.5	3	0.0	3.0	
41	0	2	130	204	0	2	172	0	1.4	1	0.0	3.0	
56	1	2	120	236	0	0	178	0	0.8	1	0.0	3.0	

aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa **Table 1**

2. Clean Data

We add column names

In [4]:
```
colnames(heart_disease_data) <- c('age', 'sex', 'cp', 'trestbps', 'chol', 'fbs', 'restecg', 'thalach', 'exang', 'oldpeak', 'slope', 'ca', 'thal', 'target')
head(heart_disease_data)
```

A tibble: 6 × 14

age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	
<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<chr>	<c
63	1	1	145	233	1	2	150	0	2.3	3	0.0	
67	1	4	160	286	0	2	108	1	1.5	2	3.0	
67	1	4	120	229	0	2	129	1	2.6	2	2.0	
37	1	3	130	250	0	0	187	0	3.5	3	0.0	
41	0	2	130	204	0	2	172	0	1.4	1	0.0	
56	1	2	120	236	0	0	178	0	0.8	1	0.0	

aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa **Table 2**

Then we remove any observations with missing values.

In [5]:
```
heart_disease_data[heart_disease_data == "?"] <- NA
clean_heart <- na.omit(heart_disease_data)
sum(is.na(heart_disease_data))


head(clean_heart)
```

6

A tibble: 6 × 14

age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	
<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<chr>	<c
63	1	1	145	233	1	2	150	0	2.3	3	0.0	
67	1	4	160	286	0	2	108	1	1.5	2	3.0	
67	1	4	120	229	0	2	129	1	2.6	2	2.0	
37	1	3	130	250	0	0	187	0	3.5	3	0.0	
41	0	2	130	204	0	2	172	0	1.4	1	0.0	
56	1	2	120	236	0	0	178	0	0.8	1	0.0	

aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa **Table 3**

Target has five levels of : 0, 1, 2, 3, 4 but we're only interested in predicting a patient has heart disease or not, so our target labels will be:

0 = No Disease

1 = Disease

We will change the integer variables "2", "3", and "4" to "1" in the target column, so only "0" and "1" variables remain.

In [6]:
```
clean_heart$target[clean_heart$target=="4"] <- "1"
clean_heart$target[clean_heart$target=="3"] <- "1"
clean_heart$target[clean_heart$target=="2"] <- "1"



head(clean_heart)
```

A tibble: 6 × 14

age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	
<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<chr>	<
63	1	1	145	233	1	2	150	0	2.3	3	0.0	
67	1	4	160	286	0	2	108	1	1.5	2	3.0	
67	1	4	120	229	0	2	129	1	2.6	2	2.0	
37	1	3	130	250	0	0	187	0	3.5	3	0.0	
41	0	2	130	204	0	2	172	0	1.4	1	0.0	
56	1	2	120	236	0	0	178	0	0.8	1	0.0	

aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa **Table 4**

Since target is the label we want to predict, we must change it to a factor. We also changed "ca" and "thal" to numerical variables because k-nn requires are predictors to be numerical.

In [7]:
```
clean_heart2 <- clean_heart %>%
mutate(target = as.factor(target)) %>%
mutate(thal = as.numeric(thal)) %>%
mutate(ca = as.numeric(ca))

head(clean_heart2)
```

A tibble: 6 × 14

age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	
<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<
63	1	1	145	233	1	2	150	0	2.3	3	0	
67	1	4	160	286	0	2	108	1	1.5	2	3	
67	1	4	120	229	0	2	129	1	2.6	2	2	
37	1	3	130	250	0	0	187	0	3.5	3	0	
41	0	2	130	204	0	2	172	0	1.4	1	0	
56	1	2	120	236	0	0	178	0	0.8	1	0	

Now let's check to see how many levels our labels have. We should expect 2.

In [8]:
```
clean_heart2 %>%
  select(target) %>%
  unlist() %>%
  levels()
```

'0' · '1'

aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa **Table 5**

Now we must check to see the number of observations our data set contains for each of our class labels. This is important because unequal representation can lead to inaccurate predictions.

In [9]:
```
num_obs <- nrow(clean_heart2)

 clean_heart2 %>%
  group_by(target) %>%
  summarize(n = n(),
            percentage = n() / num_obs * 100)
```

A tibble: 2 × 3

target	n	percentage
<fct>	<int>	<dbl>
0	160	53.87205
1	137	46.12795

aaaaaaaaa **Table 6**

Before we go further, we check to see the difference in values of the variables using str function. Significantly different values will influence our classification at varying degrees which will make our predications less accurate.

In [10]:
```
str(clean_heart2)
```

```
Classes ‘tbl_df’, ‘tbl’ and 'data.frame':       297 obs. of  14 variables:
 $ age     : num  63 67 67 37 41 56 62 57 63 53 ...
 $ sex     : num  1 1 1 1 0 1 0 0 1 1 ...
 $ cp      : num  1 4 4 3 2 2 4 4 4 4 ...
 $ trestbps: num  145 160 120 130 130 120 140 120 130 140 ...
 $ chol    : num  233 286 229 250 204 236 268 354 254 203 ...
 $ fbs     : num  1 0 0 0 0 0 0 0 0 1 ...
 $ restecg : num  2 2 2 0 2 0 2 0 2 2 ...
 $ thalach : num  150 108 129 187 172 178 160 163 147 155 ...
 $ exang   : num  0 1 1 0 0 0 0 1 0 1 ...
 $ oldpeak : num  2.3 1.5 2.6 3.5 1.4 0.8 3.6 0.6 1.4 3.1 ...
 $ slope   : num  3 2 2 3 1 1 3 1 2 3 ...
 $ ca      : num  0 3 2 0 0 0 2 0 1 0 ...
 $ thal    : num  6 3 7 3 3 3 3 3 7 7 ...
 $ target  : Factor w/ 2 levels "0","1": 1 2 2 1 1 1 2 1 2 2 ...
```

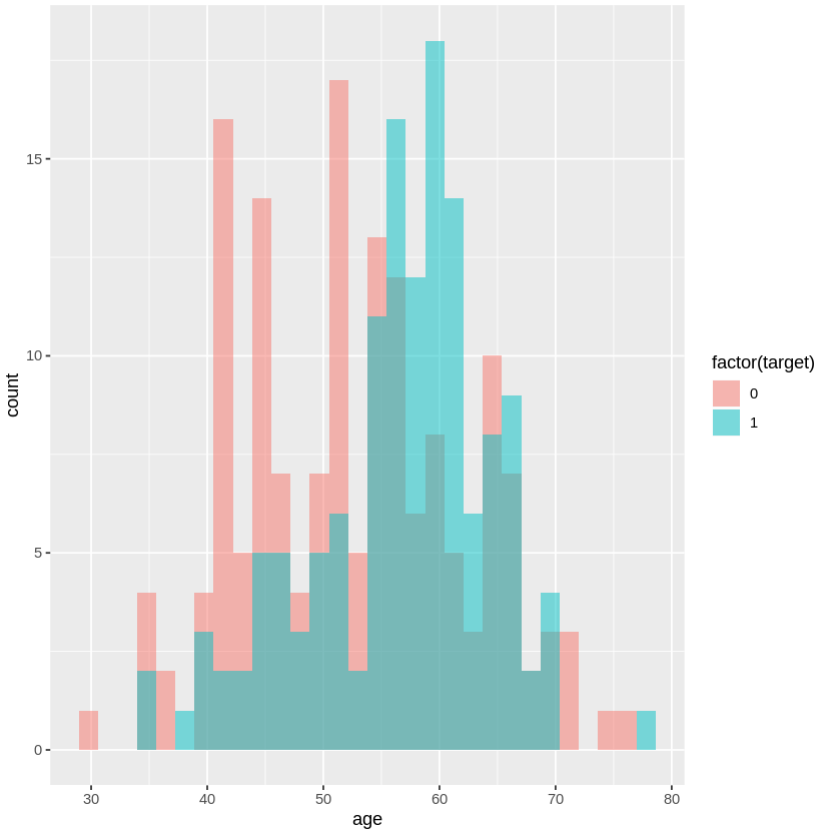
Here we can see that age, trestbps, chol and thalach are greater values and hence the data will need to be standardized (will be done in part 3). Without standardization, predictors will have unequal effect on our classifier and hence lead to inaccurate predictions.

Now that our data is clean, a histogram of each 14 potential predictors from the Cleaveland data set is made (Figure 0). There are obvious relationships between each variable and Heart disease (as seen in the overlap). For example, looking at the first plot of Age, around the age of 60 the number of people with heart disease nearly doubles compared to other ages. To add, looking at the subplot of sex below, we can see that mean (value = 1) are more at risk for heart disease than women (value = 0). There are many more strong relationships present (as seen in the subplots below) and our classification shoul dpick up on these.

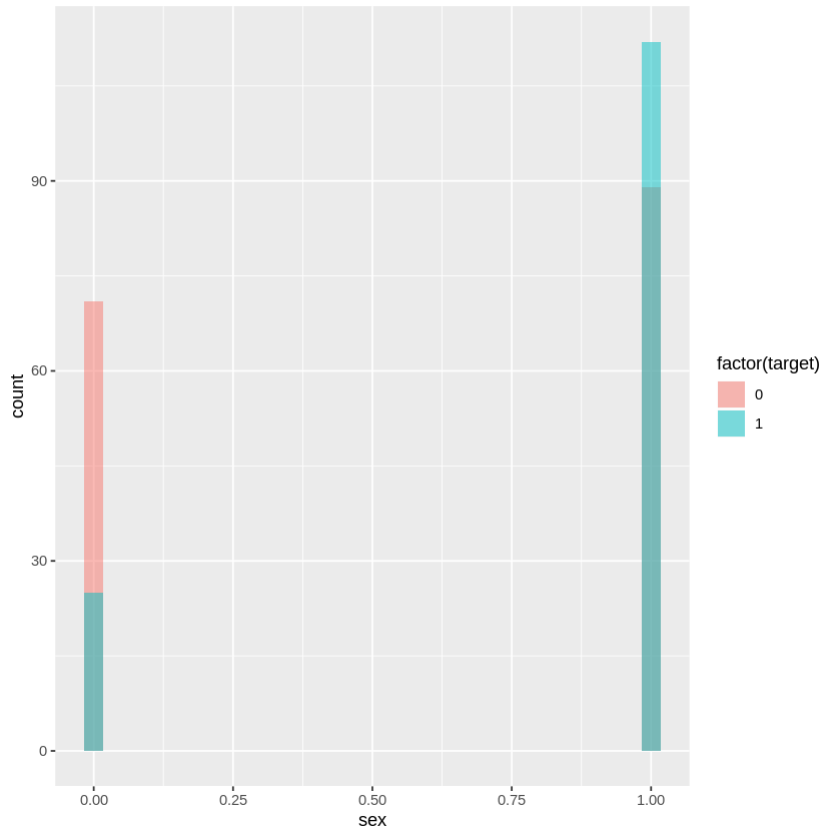
In [52]:
```
heart_age <- ggplot(clean_heart2, aes(x = age, fill = factor(target))) +
                 geom_histogram(position = "identity", alpha = 0.5)
heart_sex <- ggplot(clean_heart2, aes(x = sex, fill = factor(target))) +
                 geom_histogram(position = "identity", alpha = 0.5)
heart_cp <- ggplot(clean_heart2, aes(x = cp, fill = factor(target))) +
                 geom_histogram(position = "identity", alpha = 0.5)
heart_trestbps <- ggplot(clean_heart2, aes(x = trestbps, fill = factor(target
))) +
                 geom_histogram(position = "identity", alpha = 0.5)
heart_chol <- ggplot(clean_heart2, aes(x = chol, fill = factor(target))) +
                 geom_histogram(position = "identity", alpha = 0.5)
heart_fbs <- ggplot(clean_heart2, aes(x = fbs, fill = factor(target))) +
                 geom_histogram(position = "identity", alpha = 0.5)
heart_restecg <- ggplot(clean_heart2, aes(x = restecg, fill = factor(target)))
+
                 geom_histogram(position = "identity", alpha = 0.5)
heart_thalach <- ggplot(clean_heart2, aes(x = thalach, fill = factor(target)))
+
                 geom_histogram(position = "identity", alpha = 0.5)
heart_exang <- ggplot(clean_heart2, aes(x = exang, fill = factor(target))) +
                 geom_histogram(position = "identity", alpha = 0.5)
heart_oldpeak <- ggplot(clean_heart2, aes(x = oldpeak, fill = factor(target)))
+
                 geom_histogram(position = "identity", alpha = 0.5)
heart_slope <- ggplot(clean_heart2, aes(x = slope, fill = factor(target))) +
                 geom_histogram(position = "identity", alpha = 0.5)
heart_ca <- ggplot(clean_heart2, aes(x = ca, fill = factor(target))) +
                 geom_histogram(position = "identity", alpha = 0.5)
heart_thal <- ggplot(clean_heart2, aes(x = thal, fill = factor(target))) +
                 geom_histogram(position = "identity", alpha = 0.5)
heart_age
heart_sex
heart_cp
heart_trestbps
heart_chol
heart_fbs
heart_restecg
heart_thalach
heart_exang
heart_oldpeak
heart_slope
heart_ca
heart_thal
```

```
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

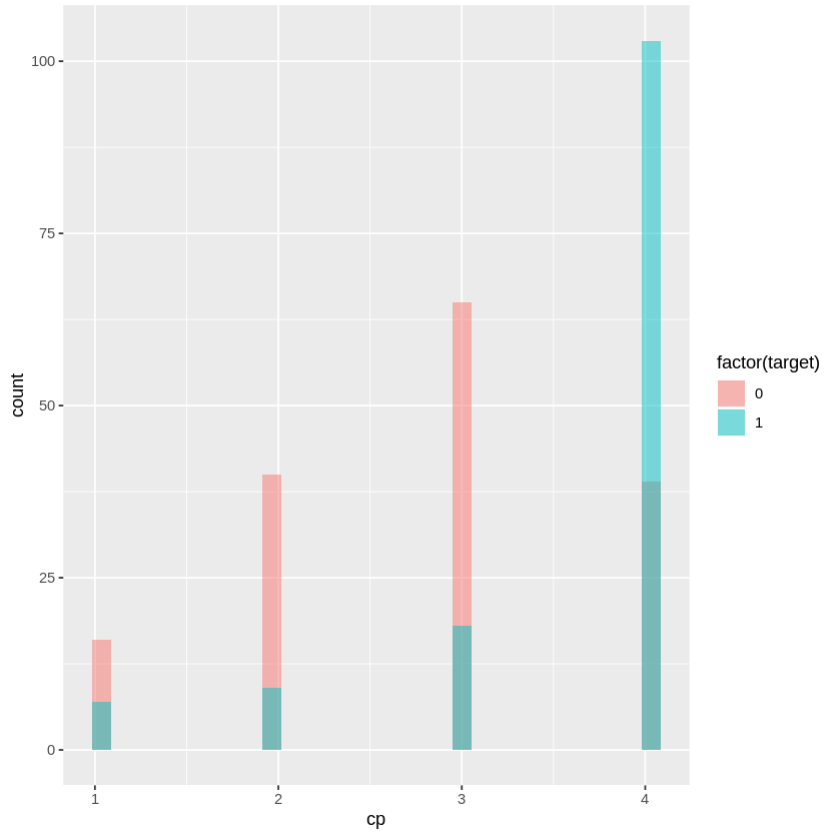

```
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

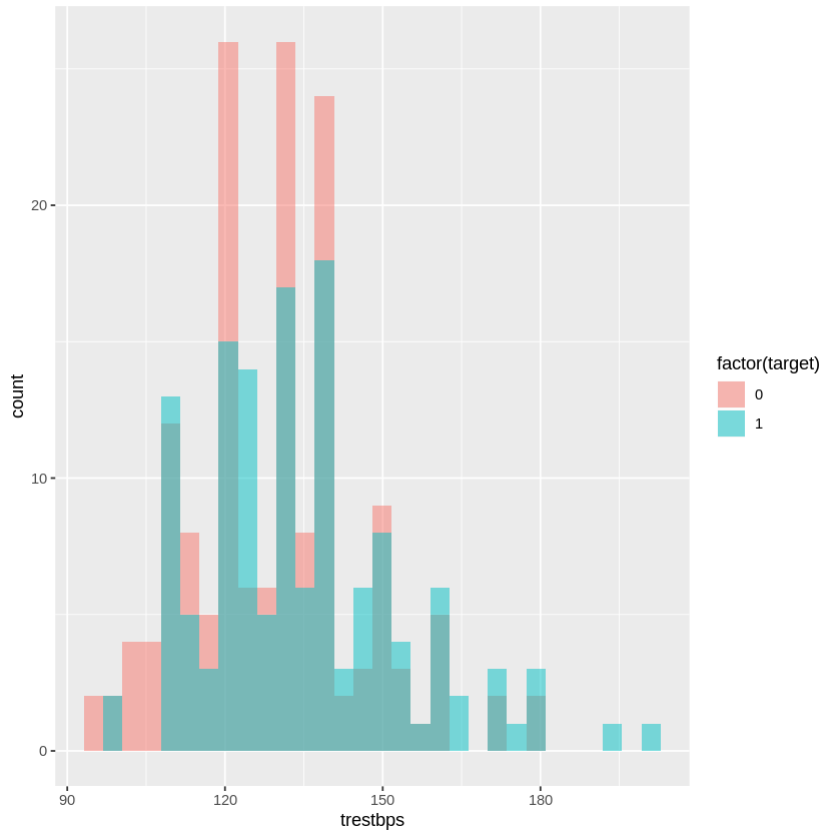

```
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



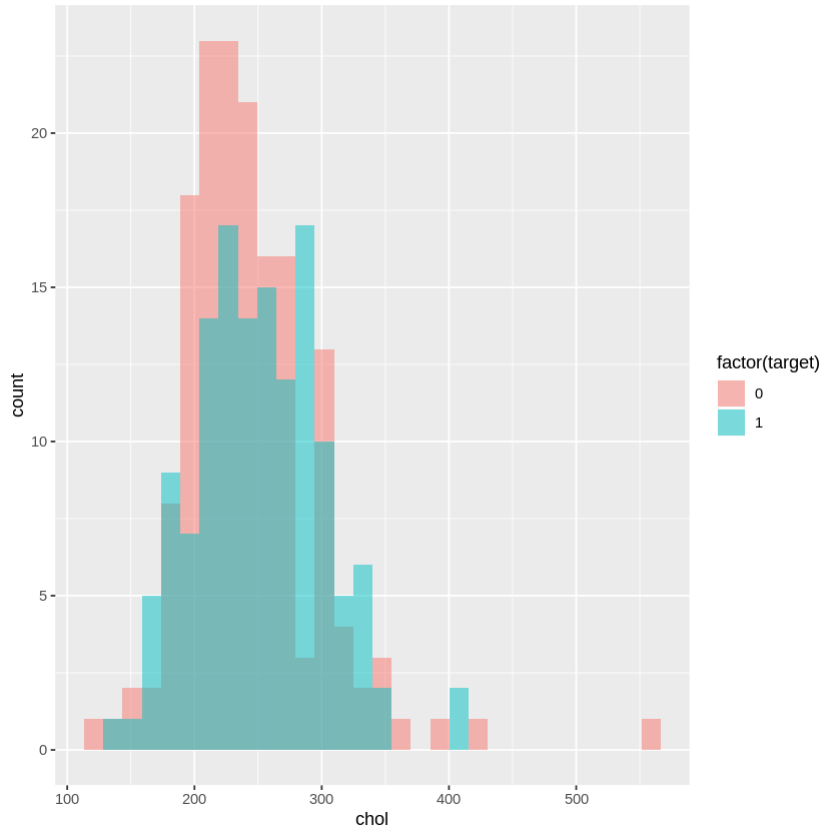
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.



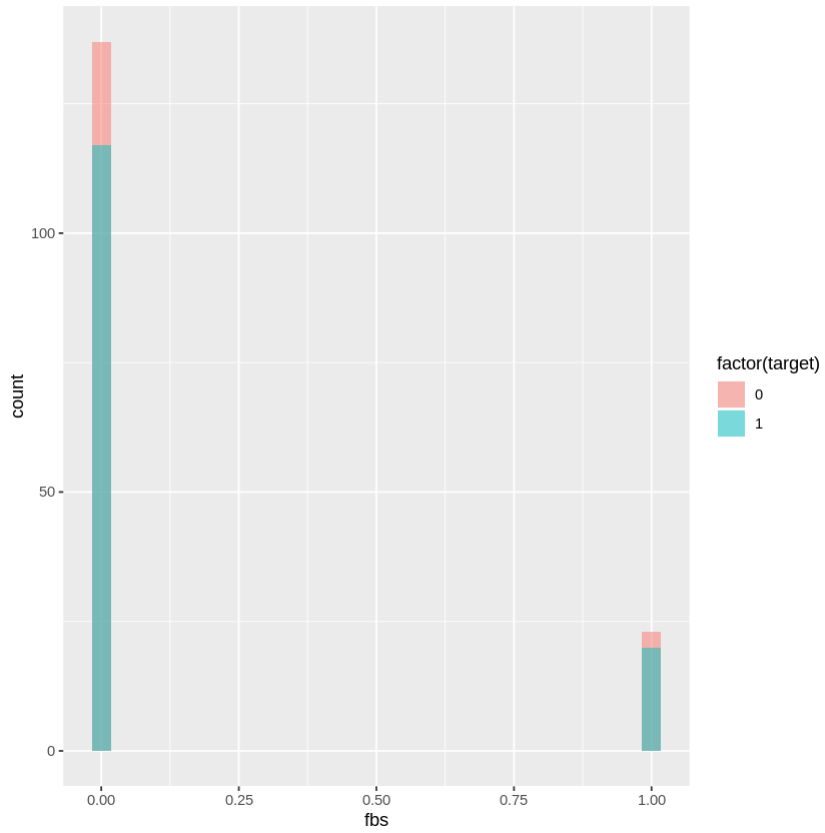
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.



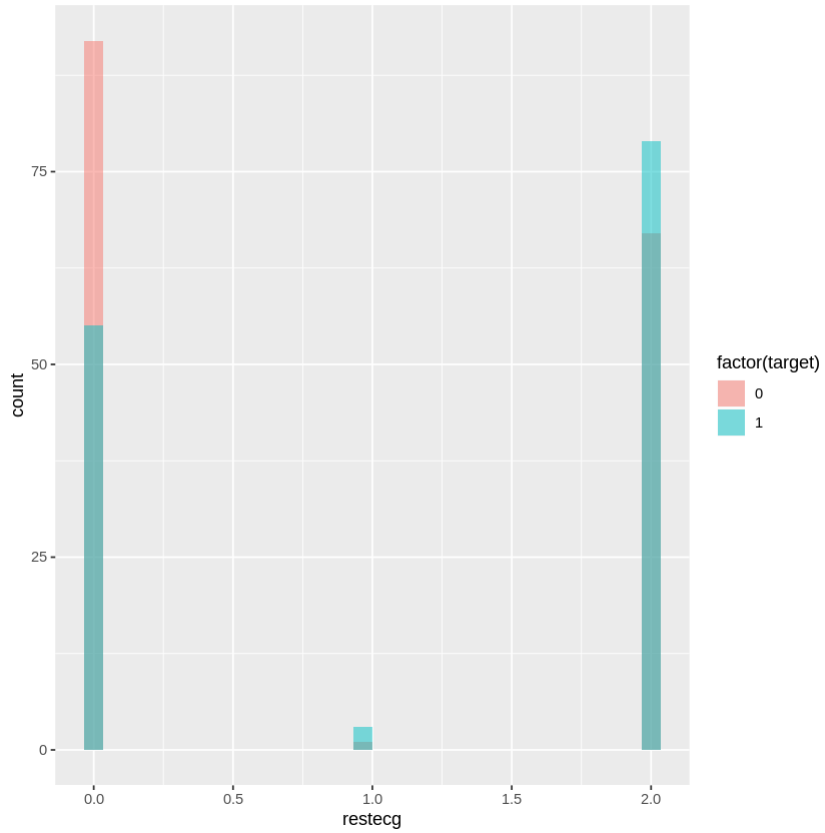
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.



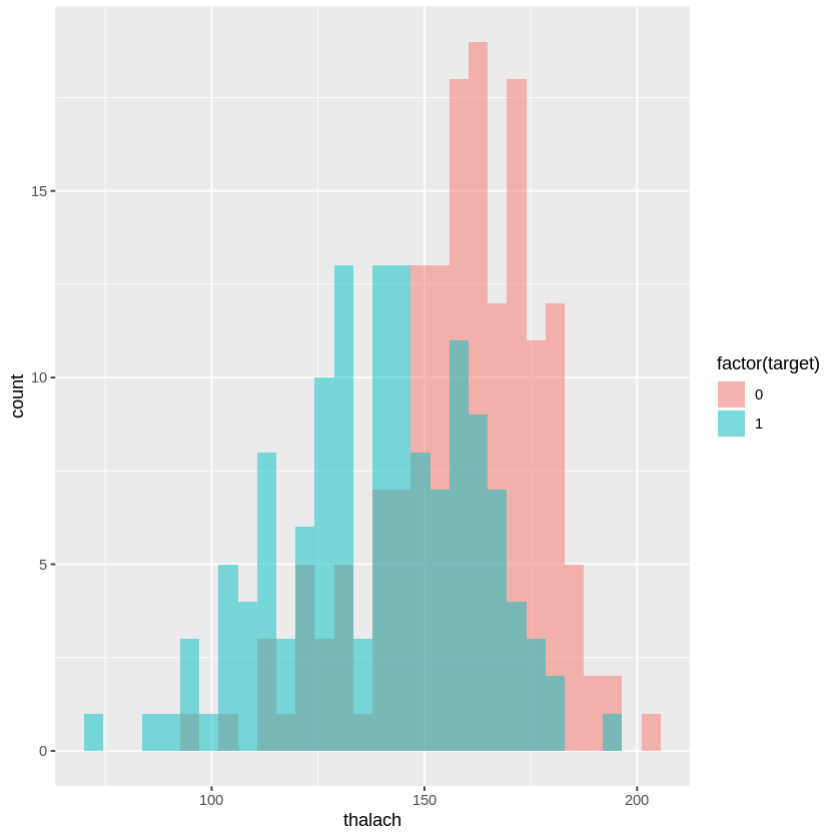
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.



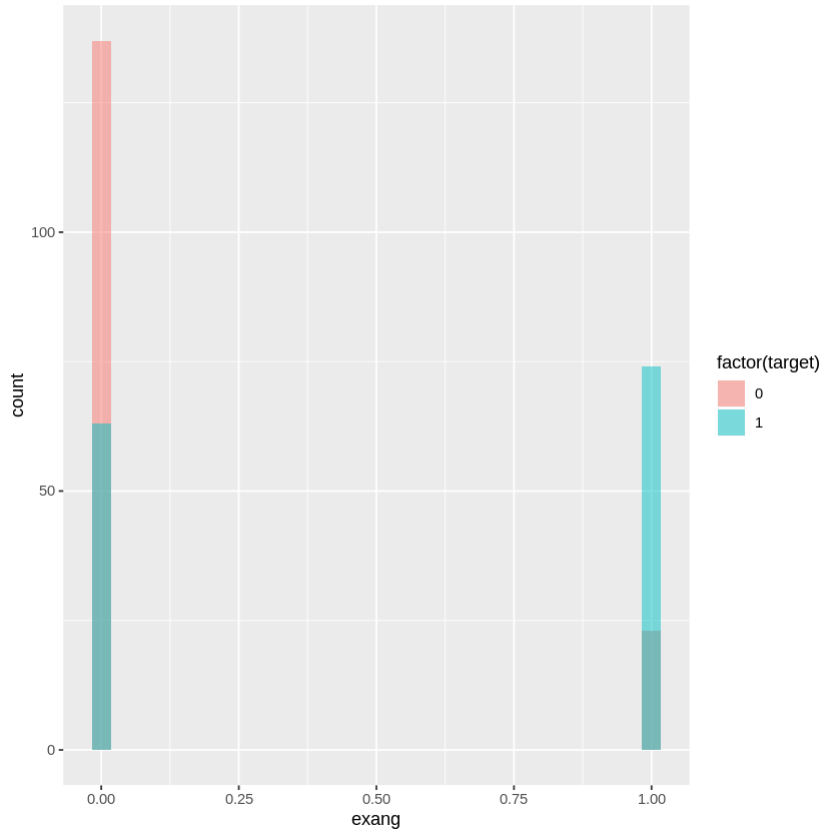
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.



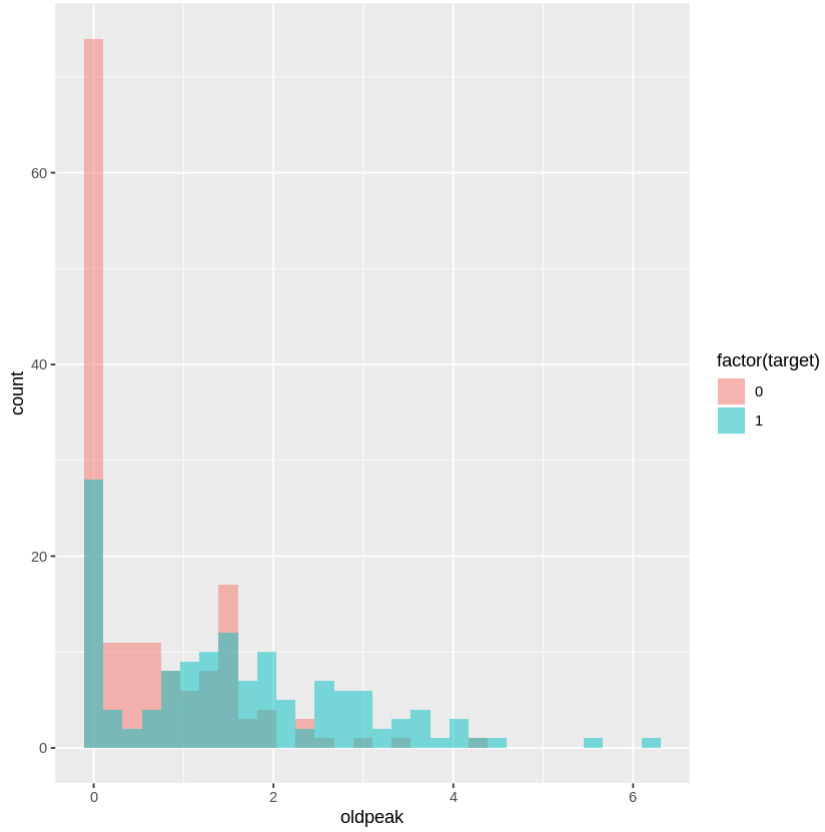
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.



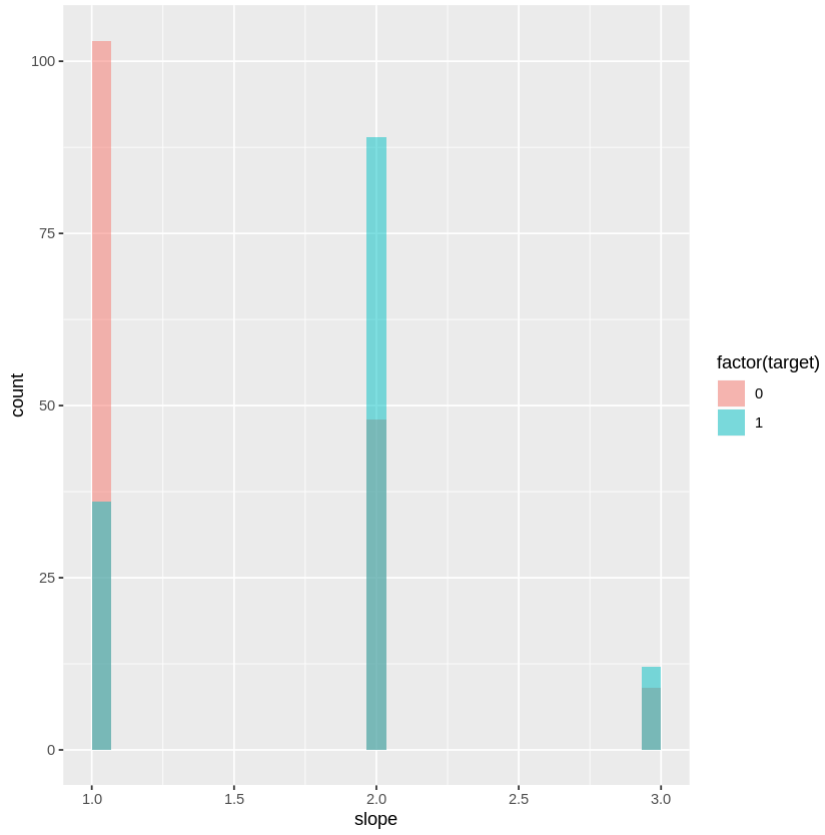
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.



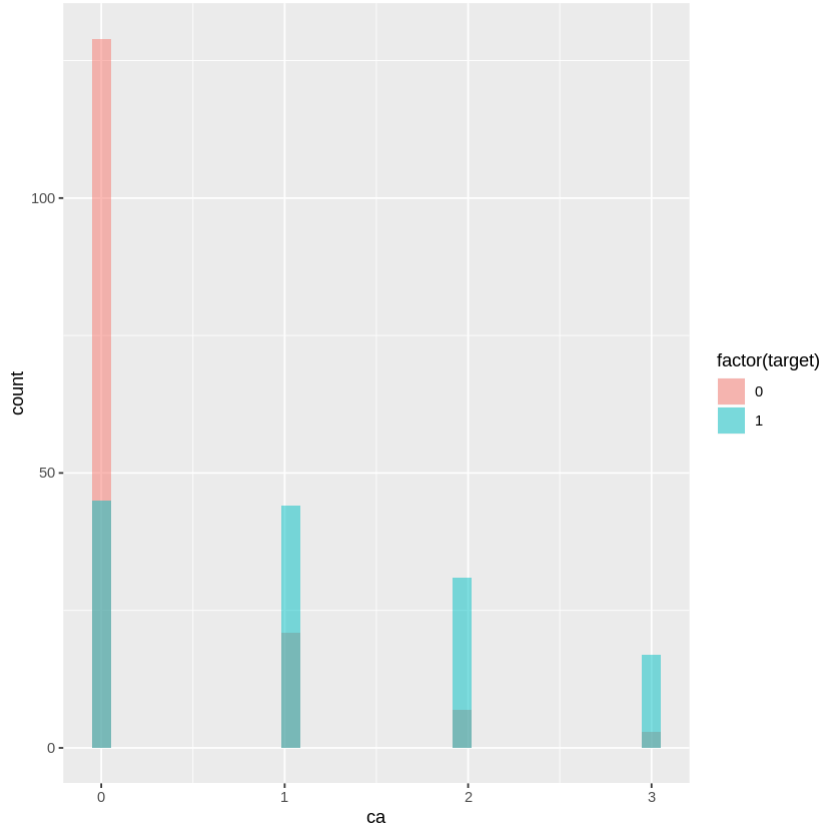
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.

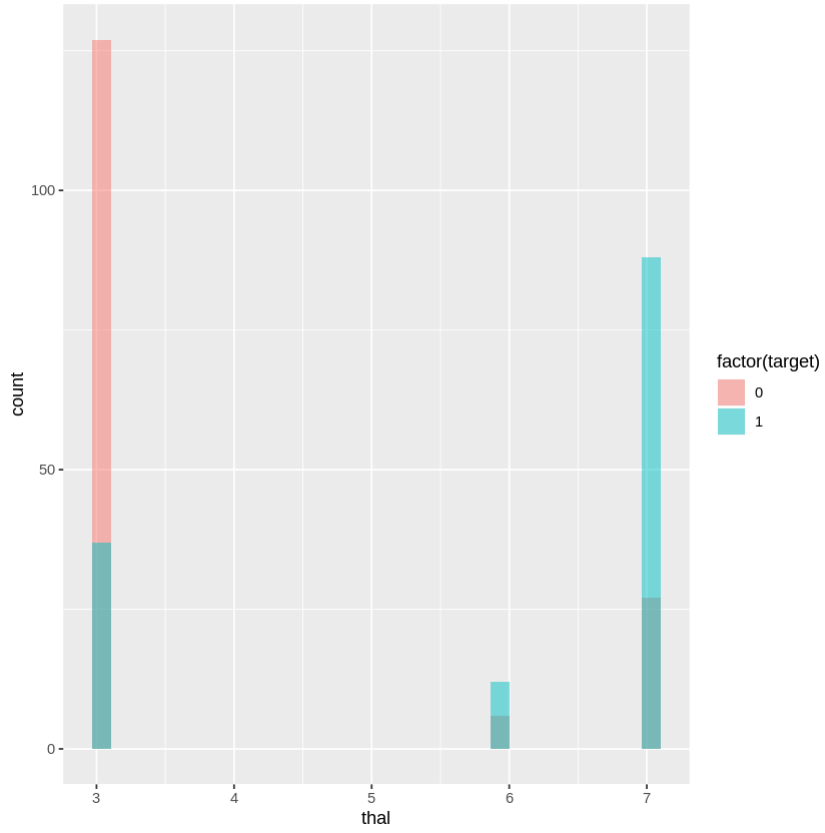


`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.



`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.





3. Splitting the data into training and test set

Next, we be partioning the data into a training (70%) and testing (30%) set using the caret package. As previously mentioned, we will use the variable target as our class label. Using createDataPartition function we get the row numbers of data we should include in our training set.

In [11]:
```
set.seed(1)

training_rows <- clean_heart2 %>%
    select(target) %>%
    unlist() %>%
    createDataPartition(p = 0.70, list = FALSE)
```

Using the rows designated above, we use the slice function to create rows for the training set and testing set

In [12]:
```
training_set <- clean_heart2 %>%
                slice(training_rows)

test_set <- clean_heart2 %>%
                slice(-training_rows)

head(training_set)
```

A tibble: 6 × 14

age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	
<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<
63	1	1	145	233	1	2	150	0	2.3	3	0	
67	1	4	160	286	0	2	108	1	1.5	2	3	
67	1	4	120	229	0	2	129	1	2.6	2	2	
37	1	3	130	250	0	0	187	0	3.5	3	0	
53	1	4	140	203	1	2	155	1	3.1	3	0	
57	1	4	140	192	0	0	148	0	0.4	2	0	

aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa **Table 7**

Now we perform a data transformation to scale and centre our predictors. Scale transformation is only done on the training set to ensure that our test data does not influence any part of our model training, it is then applied to the train and test set seperately.

In [13]:
```
scale_transformer <- preProcess(clean_heart2, method = c("center", "scale"))
training_set <- predict(scale_transformer, clean_heart2)
test_set <- predict(scale_transformer, test_set)
head(training_set)
```

A tibble: 6 × 14

age	sex	cp	trestbps	chol	fbs	restecg	thalach	
<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	
0.9346033	0.6899303	-2.2368535	0.74911571	-0.27597761	2.426332	1.008496	0.01746496	-
1.3766051	0.6899303	0.8724078	1.59357687	0.74330055	-0.410757	1.008496	-1.81327350	
1.3766051	0.6899303	0.8724078	-0.65831955	-0.35290426	-0.410757	1.008496	-0.89790427	
-1.9384088	0.6899303	-0.1640127	-0.09534545	0.05096067	-0.410757	-1.001728	1.63025836	-
-1.4964070	-1.4445416	-1.2004331	-0.09534545	-0.83369584	-0.410757	1.008496	0.97642320	-
0.1611000	0.6899303	-1.2004331	-0.65831955	-0.21828262	-0.410757	-1.001728	1.23795726	-

aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa **Table 8**

We summarize the training data set. The following tables show the number of observations of each case of target(risk), and the percentage as well. We also showed the mean of the predictor variables in another summary table.

In [14]:
```
num_obs <- nrow(training_set)
training_set %>%
  group_by(target) %>%
  summarize(n = n(),
            percentage = n() / num_obs * 100)

training_set_summary <- group_by(training_set, target) %>%
    summarize(mean_trestbps = mean(trestbps),
              mean_chol = mean(chol),
              mean_thalach = mean(thalach),
              mean_age = mean(age),
              mean_oldpeak = mean(oldpeak),
              number_of_observations = length(target))
training_set_summary
```

A tibble: 2 × 3

target	n	percentage
<fct>	<int>	<dbl>
0	160	53.87205
1	137	46.12795

A tibble: 2 × 7

target	mean_trestbps	mean_chol	mean_thalach	mean_age	mean_oldpeak	number_of_observa
<fct>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	
0	-0.1417908	-0.07416534	0.3915132	-0.2097672	-0.3917302	
1	0.1655951	0.08661645	-0.4572416	0.2449836	0.4574952	

aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa **Tables 9 & 10**

4. Choosing K

We will use cross-validation to choose the best K based on all predictors. Target is our class label.

In [15]:
```
X_train <- training_set %>%
  select(age, sex, cp, trestbps, chol, fbs, restecg, thalach, exang, oldpeak,
slope, ca, thal) %>%
  data.frame()

Y_train <- training_set %>%
  select(target) %>%
  unlist()

head(X_train)
head(Y_train)
```

A data.frame: 6 × 13

age	sex	cp	trestbps	chol	fbs	restecg	thalach	
<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	
0.9346033	0.6899303	-2.2368535	0.74911571	-0.27597761	2.426332	1.008496	0.01746496	-
1.3766051	0.6899303	0.8724078	1.59357687	0.74330055	-0.410757	1.008496	-1.81327350	
1.3766051	0.6899303	0.8724078	-0.65831955	-0.35290426	-0.410757	1.008496	-0.89790427	
-1.9384088	0.6899303	-0.1640127	-0.09534545	0.05096067	-0.410757	-1.001728	1.63025836	-
-1.4964070	-1.4445416	-1.2004331	-0.09534545	-0.83369584	-0.410757	1.008496	0.97642320	-
0.1611000	0.6899303	-1.2004331	-0.65831955	-0.21828262	-0.410757	-1.001728	1.23795726	-

target1	0
target2	1
target3	1
target4	0
target5	0
target6	0

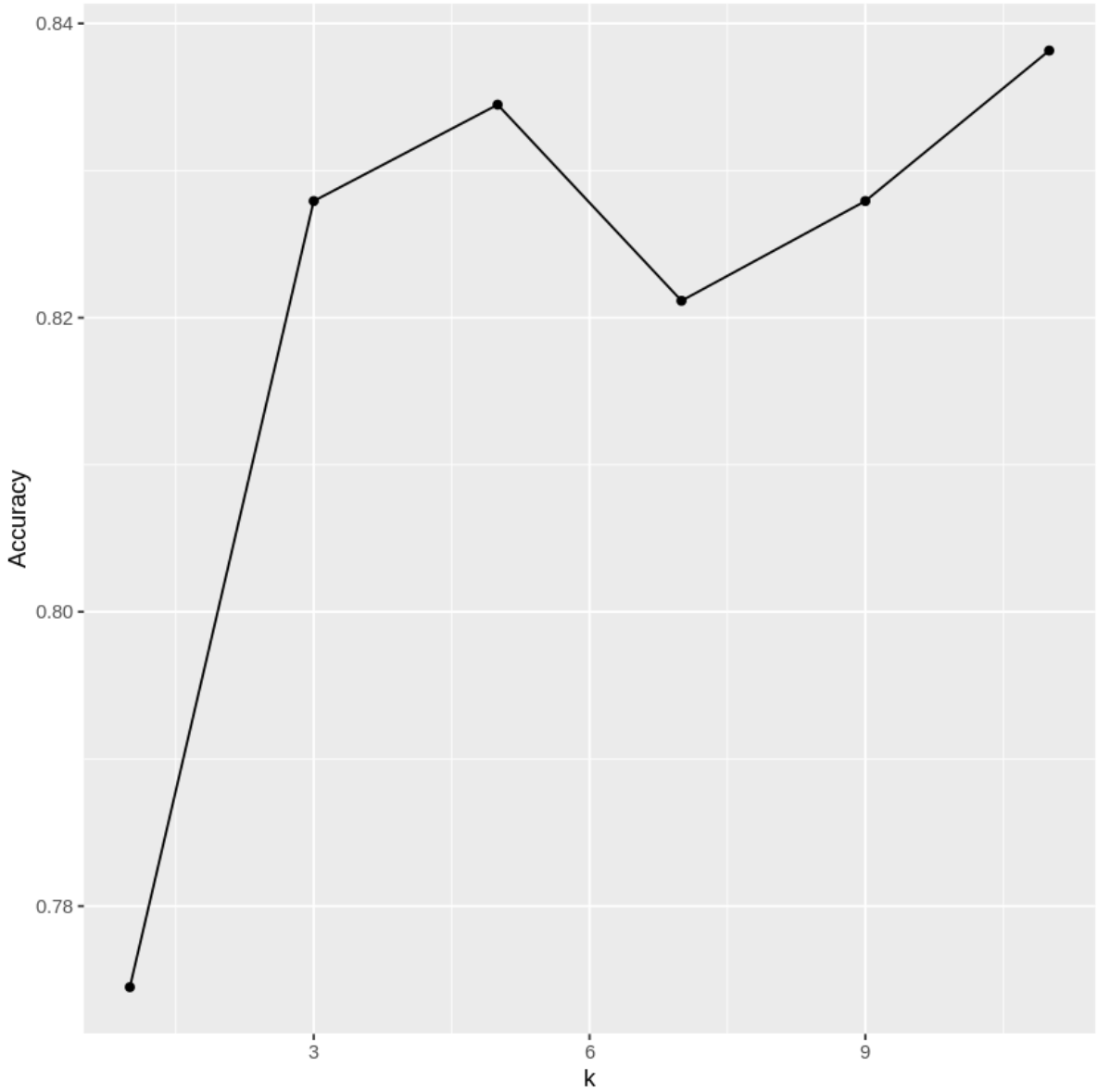
▶ **Levels**:

aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa **Table 11**

We use c function to create a data frame ks with all the Ks we would like to try out and train control function passes on the additional information to the train function we use to train our classifier. Here we set the arguments to method = "cv" which stands for cross-validation and number = 10 for 10-fold cross-validation.

To help assess accuracy of each k we pass train_control to the trControl function and adds this as an argument to the train function. We then visualize the accuracies of each k to help us choose k.

In [16]:
```
set.seed(4321)

ks <- data.frame(k = c(1,3,5,7,9,11))
train_control <- trainControl(method = "cv", number = 10)



choose_k <- train(x = X_train, y = Y_train, method = "knn", tuneGrid = ks ,trC
ontrol = train_control)

k_accuracies <- choose_k$results %>%
select(k, Accuracy)


choose_k_plot <- ggplot(k_accuracies, aes(x = k, y = Accuracy)) +
                         geom_point() +
                        geom_line()
choose_k_plot
```



aaaaaaaaaaaaaaaaaaaaaaaaaassssaaaaaaaaaaaaaaaaaaaaaaaaa **Figure 1**

Based on our visualization above, k = 5 is the optimal k. We create our classifier, model_knn, using our training set .

In [17]:
```
k = data.frame(k = 5)

set.seed(9999)
model_knn <- train(x = X_train, y = Y_train, method = "knn", tuneGrid = k)
model_knn
```

```
k-Nearest Neighbors

297 samples
 13 predictor
  2 classes: '0', '1'

No pre-processing
Resampling: Bootstrapped (25 reps)
Summary of sample sizes: 297, 297, 297, 297, 297, 297, ...
Resampling results:

  Accuracy   Kappa
  0.8000026  0.5965531

Tuning parameter 'k' was held constant at a value of 5
```

Now we predict labels in our training set and evaluate the training accuracy using confusionMatrix function.

In [18]:
```
set.seed(9999)

# your code here
predictions <- predict(model_knn, X_train)
training_results <- confusionMatrix(predictions, Y_train)
training_results
training_results$overall[1]
```

```
Confusion Matrix and Statistics

          Reference
Prediction   0   1
         0 145  19
         1  15 118

               Accuracy : 0.8855
                 95% CI : (0.8437, 0.9194)
    No Information Rate : 0.5387
    P-Value [Acc > NIR] : <2e-16

                  Kappa : 0.7692

 Mcnemar's Test P-Value : 0.6069

            Sensitivity : 0.9062
            Specificity : 0.8613
         Pos Pred Value : 0.8841
         Neg Pred Value : 0.8872
             Prevalence : 0.5387
         Detection Rate : 0.4882
   Detection Prevalence : 0.5522
      Balanced Accuracy : 0.8838

       'Positive' Class : 0
```

Accuracy: 0.885521885521885

5. Assessing our Model

We will test our classifier accuracy by using the test data set that has never been touched up until now.

In [19]:
```
set.seed(4545)

X_test <- test_set %>%
  select(age, sex, cp, trestbps, chol, fbs, restecg, thalach, exang, oldpeak,
slope, ca, thal) %>%
  data.frame()

Y_test <- test_set %>%
    select(target) %>%
    unlist()

test_pred <- predict(model_knn, X_test)
test_results <- confusionMatrix(test_pred, Y_test)
test_results$overall[1]
```

Accuracy: 0.865168539325843

We find that the classifier accuracy after using the model on the test data is 86.5%

Conclusion

Our project goal was to predict whether someone is at risk for heart disease or not using k-nn classification.

First, we load and clean our chosen dataset(Cleveland Heart Disease Dataset) by assigning column names and removing observations with missing values. Our final result variable, Target has 2 labels, namely 0 and 1, indicating risk and no risk respectively. As k-nn requires predictors to be numerical , we change the “ca” and “thal” variable accordingly. Using str functions, we find that age, trestbps, chol and thalach are greater values and hence the data needs to be standardized. Next, we split our data into training and testing sets using caret package and create rows for both using slice function. We then perform a data transformation on our training set, and then applied to both the sets separately. To choose the most accurate k, we perform cross-validation. Finally, we visualize accuracies of each k as shown in choose_k_plot and find k=5 to be the optimal choice. Finally, using the training set, we create our classifier, model_knn. We evaluate the training accuracy using confusionMatrix function, which is found to be Accuracy = 0.885521885521885 . To assess our model, we test classifier accuracy, acting on our test data set.

The impact of our project could be life-saving. Patients can be diagnosed with risk of heart disease in a short time just from the data of the patients’ attributes. Further improvement on the overall functioning can make our predictions for the risk of heart disease even more accurate. This would not only allow the medical authority, but also the people at risk to be more cautious and aware about their health. After all, precaution is better than cure.

Further data collection and analysis could even make it possible to predict the level of risk of heart disease as well the type of heart disease. Besides guiding people to be able to keep better precaution, this can also help the Doctors in Diagnosing a fatal illness at an early stage.

References

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