Cardiovascular Disease Prediction with Machine Learning

Andrew Choi

2022-10-16

Contents

- `AGE`: integer (years of age)
- `HEIGHT`: integer (cm)
- `WEIGHT`: integer (kg)
- `GENDER`: categorical (1: female, 2: male)
- `AP_HIGH`: systolic blood pressure, integer
- `AP_LOW`: diastolic blood pressure, integer
- `CHOLESTEROL`: categorical (1: normal, 2: above normal, 3: well above normal)
- `GLUCOSE`: categorical (1: normal, 2: above normal, 3: well above normal)
- `SMOKE`: categorical (0: no, 1: yes)
- `ALCOHOL`: categorical (0: no, 1: yes)
- `PHYSICAL_ACTIVITY`: categorical (0: no, 1: yes)
- `CARDIO_DISEASE`: categorical (0: no, 1: yes)

Loading and Cleaning Raw Data

Although the data set has already been cleaned, we can take several steps to ensure that the data and column names are as tidy as possible.

```
# Loading in the data set
cardio <- read.csv('cardiovascular_diseases_dv3 2.csv', sep = ';')
```

- Cleaning variable names

```
cardio <- cardio %>%
  clean_names()
```

- Converting height to feet, weight to pounds, and pounds to integer values
- Converting categorical variables to factors
- One-hot-encoding our factor variables
- Removing one dummy variable from each category to avoid the dummy variable trap

```
# Preparing cardio data set for use in correlation heat map
cardio_cor <- cardio

# Converting categorical variables to factors
cardio$gender <- as.factor(cardio$gender)
cardio$cholesterol <- as.factor(cardio$cholesterol)
cardio$glucose <- as.factor(cardio$glucose)
cardio$smoke <- as.factor(cardio$smoke)
cardio$alcohol <- as.factor(cardio$alcohol)
cardio$physical_activity <- as.factor(cardio$physical_activity)
cardio$cardio_disease <- as.factor(cardio$cardio_disease)

# One-hot-encoding all factors
cardio_one_hot <- one_hot(as.data.table(cardio))

cardio_one_hot <- cardio_one_hot %>%
  mutate(
    # Converting height from centimeters to feet
    height = height * 0.0328084,
    # Converting weight from kilograms to pounds
    weight = round(weight * 2.20462),
```

```
    # Converting new one-hot-encoded variables to factors
    cardio_disease_1 = factor(cardio_disease_1),
    gender_2 = factor(gender_2),
    cholesterol_2 = factor(cholesterol_2),
    cholesterol_3 = factor(cholesterol_3),
    glucose_2 = factor(glucose_2),
    glucose_3 = factor(glucose_3)
  )

# Removing one dummy variable from each category
cardio_one_hot[ , c('gender_1', 'cholesterol_1', 'glucose_1', 'smoke_0', 'alcohol_0', 'physical_activity
```

Exploratory Data Analysis

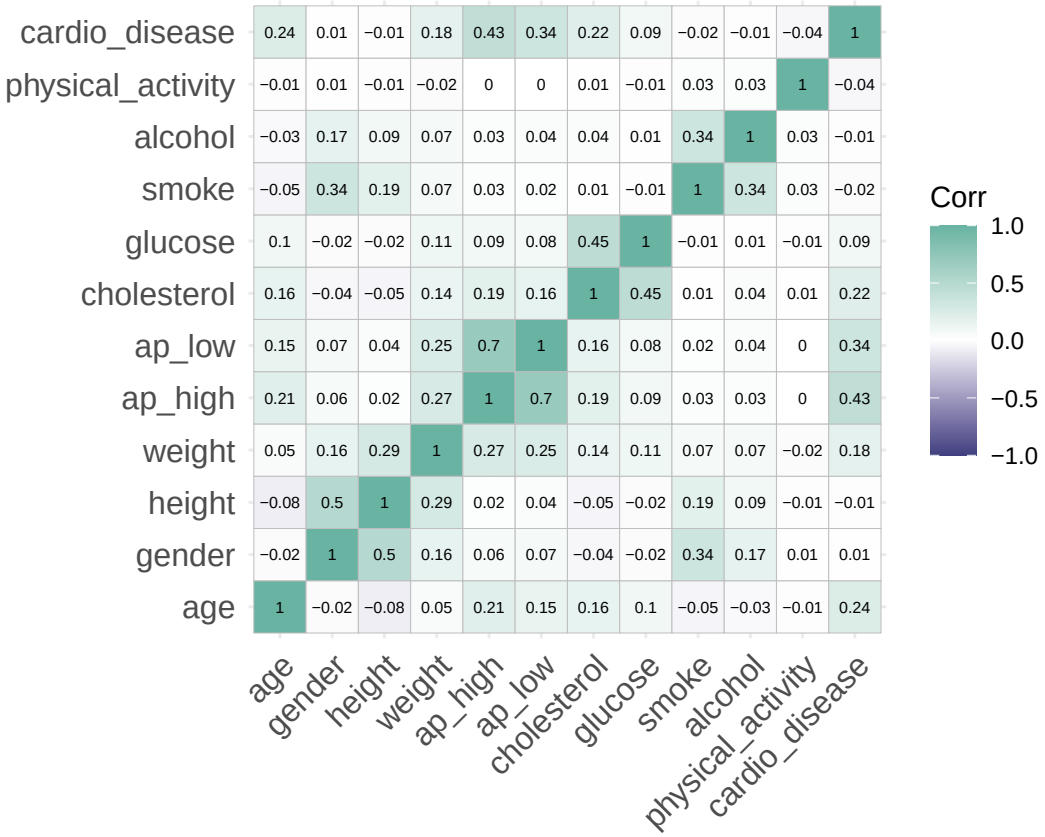
Although it's not likely that any single variable in our data set directly causes or prevents cardiovascular disease, there may be a link between certain variables and coronary disease. We will visualize these links through a correlation plot, as well as individual barplots of our predictor variables against `cardio_disease`

Correlation Plot

change ***

Although it's not likely that any single variable in our data set directly causes or prevents cardiovascular disease, there may be a link between certain variables and coronary health. We can create the equivalent of a correlation plot between our numeric and categorical variables since we've one-hot-encoded our categorical variables. This heat map can help visualize the connection between each variable.

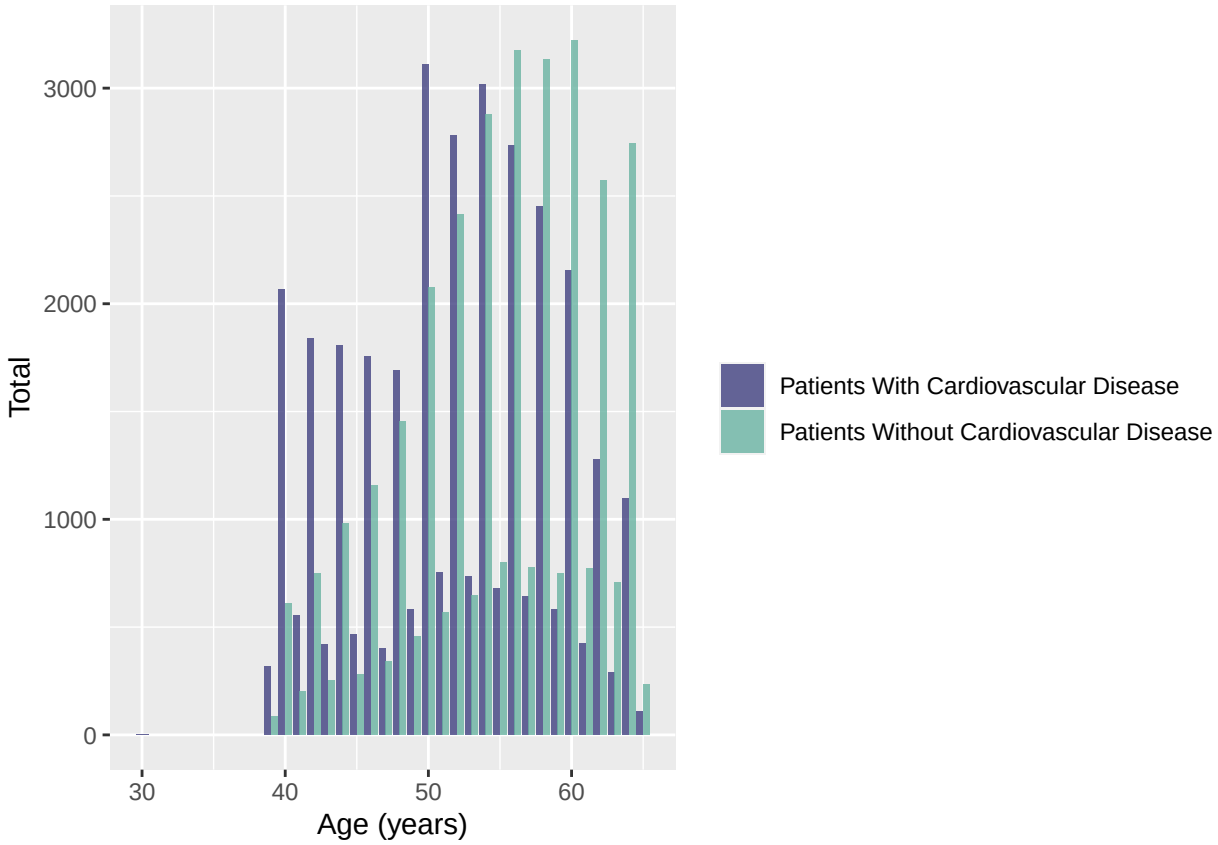
```
cor(cardio_cor, use = 'all.obs') %>%
  ggcorrplot(colors = c('#404080', 'white',  '#69b3a2'), lab = TRUE, lab_size = 2)
```



Many of the results of this heat map show connections that were expected. For example, the fact that age, weight, diastolic and systolic blood pressure, and high cholesterol levels are all positively correlated with cardiovascular disease is unsurprising. However, there are also a few results that are a bit more interesting. Smoking, drinking alcohol, and exercise all have close to no correlation with cardiovascular disease. This can be attributed to a variety of factors, one of which is the fact that `smoke`, `alcohol`, and `physical_activity` are all binary variables. This implies that someone who smokes a pack of Marlboro reds a day, drinks enough alcohol to score an integer value BAC percentage, and lives an extremely sedentary lifestyle is given the same score as someone who smokes as rarely as they drink, and chooses not to exercise. Another possible factor is that every person in this data set drinks, smokes, and exercises so moderately that their cardiovascular health is not affected. We can continue to explore the relationships between our predictors and cardiovascular disease by generating histograms and barplots between these variables.

```
# Creating data frame that contains 'age' and 'cardio_disease' if 'cardio_disease' is 0
cardio_disease_age_0 <- select(
  cardio[cardio$cardio_disease == 0, ],
  c('age', 'cardio_disease')
  )

cardio_disease_age_0$disease <- 'Patients With Cardiovascular Disease'


# Creating data frame that contains 'age' and 'cardio_disease' if 'cardio_disease' is 1
cardio_disease_age_1 <- select(
  cardio[cardio$cardio_disease == 1, ],
```

```
  c('age', 'cardio_disease')
  )

cardio_disease_age_1$disease <- 'Patients Without Cardiovascular Disease'


# Combining the new data frames
cardio_age <- rbind(
  cardio_disease_age_0,
  cardio_disease_age_1
  )


# Plotting the data side by side
ggplot(cardio_age, aes(x = age)) +
  geom_bar(stat = 'count', aes(fill = disease), position = 'dodge', alpha = .8) +
  scale_fill_manual(values = c('#404080', '#69b3a2'), name = '') +
  labs(x = 'Age (years)', y = 'Total')
```

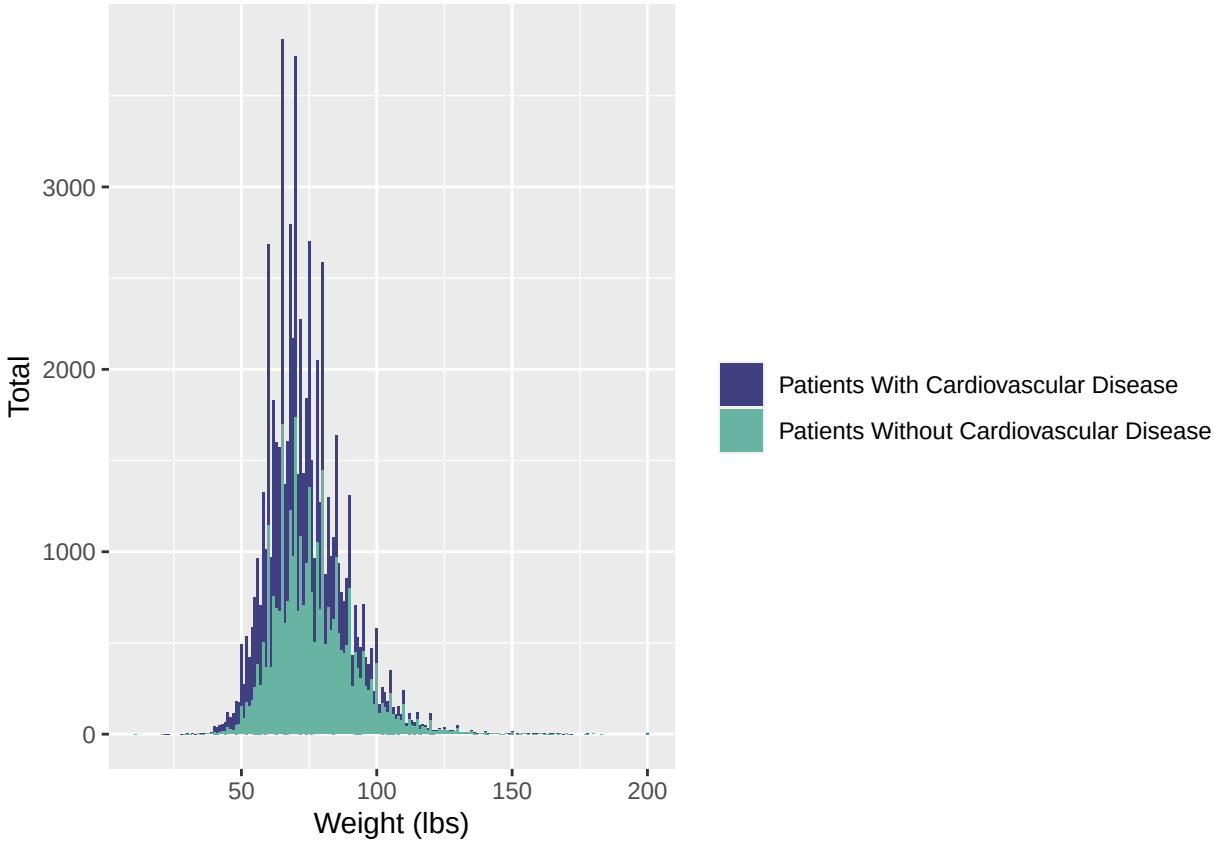


Age

Weight Extreme values of weight don't appear to have higher or lower rates of cardiovascular disease when compared to the average values of weight. In fact, we can see that

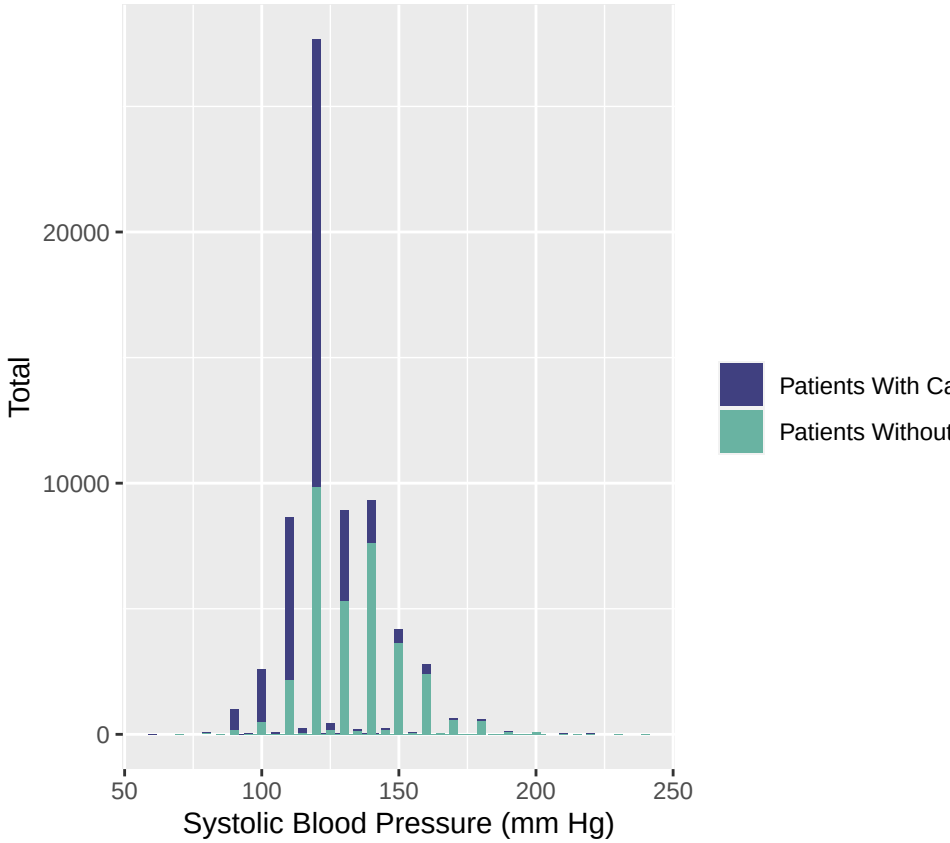
```
# Creating data frame that contains 'weight' and 'cardio_disease' if 'cardio_disease' is 0
cardio_disease_weight_0 <- select(
```

```
  cardio[cardio$cardio_disease == 0,],
  c('weight' ,'cardio_disease')
)

cardio_disease_weight_0$disease <- 'Patients With Cardiovascular Disease'


# Creating data frame that contains 'weight' and 'cardio_disease' if 'cardio_disease' is 1
cardio_disease_weight_1 <- select(
  cardio[cardio$cardio_disease == 1,],
  c('weight', 'cardio_disease')
)

cardio_disease_weight_1$disease <- 'Patients Without Cardiovascular Disease'


# Combining the new data frames
cardio_weight <- rbind(
  cardio_disease_weight_0,
  cardio_disease_weight_1
)


# Plotting the data
ggplot(cardio_weight, aes(x = weight, fill = disease), alpha = .8) +
  geom_bar() +
  labs(x = 'Weight (lbs)', y = 'Total') +
  scale_fill_manual(values = c('#404080', '#69b3a2'), name = '')
```




```
# Creating data frame that contains 'ap_high' and 'cardio_disease' if 'cardio_disease' is 0
cardio_disease_ap_high_0 <- select(
  cardio[cardio$cardio_disease == 0,],
  c('ap_high' ,'cardio_disease')
)

cardio_disease_ap_high_0$disease <- 'Patients With Cardiovascular Disease'


# Creating data frame that contains 'ap_high' and 'cardio_disease' if 'cardio_disease' is 1
cardio_disease_ap_high_1 <- select(
  cardio[cardio$cardio_disease == 1,],
  c('ap_high', 'cardio_disease')
)

cardio_disease_ap_high_1$disease <- 'Patients Without Cardiovascular Disease'


# Combining the new data frames
cardio_ap_high <- rbind(
  cardio_disease_ap_high_0,
  cardio_disease_ap_high_1
)
```

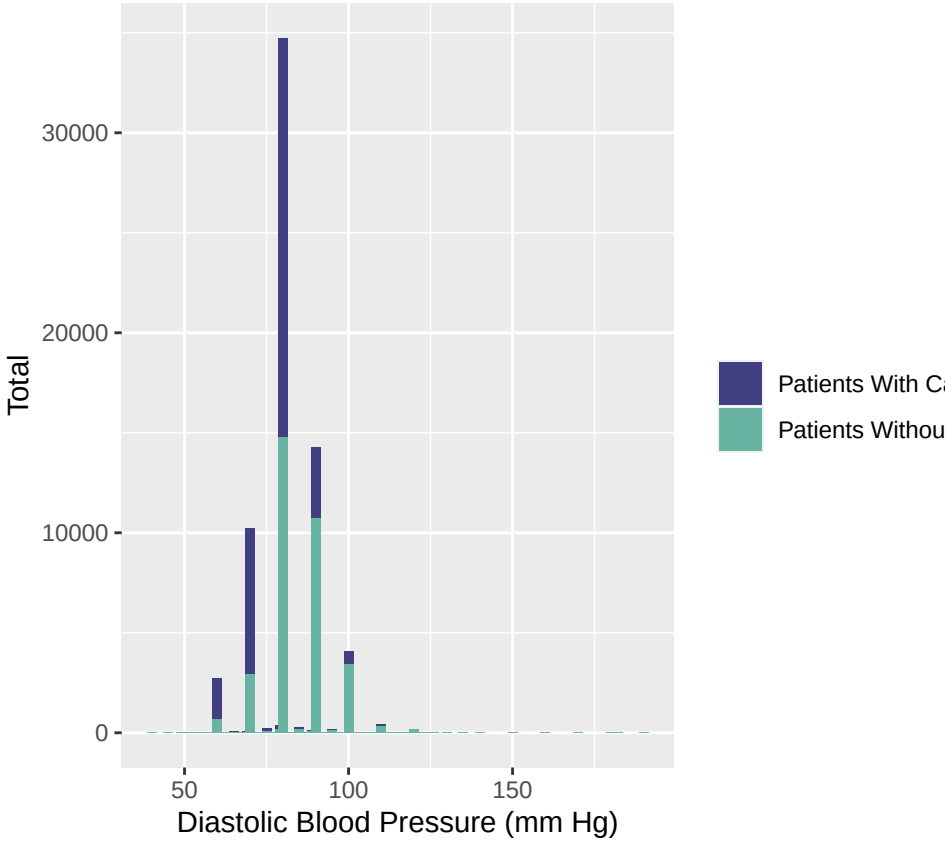
```r
# Plotting the data
ggplot(cardio_ap_high, aes(x = ap_high, fill = disease), alpha = .7) +
  geom_bar(width = 3) +
  labs(x = 'Systolic Blood Pressure (mm Hg)', y = 'Total') +
  scale_fill_manual(values = c('#404080', '#69b3a2'), name = '')
```



AP High (Systolic Blood Pressure)

```r
# Creating data frame that contains 'ap_low' and 'cardio_disease' if 'cardio_disease' is 0
cardio_disease_ap_low_0 <- select(
  cardio[cardio$cardio_disease == 0,],
  c('ap_low' ,'cardio_disease')
)

cardio_disease_ap_low_0$disease <- 'Patients With Cardiovascular Disease'


# Creating data frame that contains 'ap_low' and 'cardio_disease' if 'cardio_disease' is 1
cardio_disease_ap_low_1 <- select(
  cardio[cardio$cardio_disease == 1,],
  c('ap_low', 'cardio_disease')
)
```

```r
cardio_disease_ap_low_1$disease <- 'Patients Without Cardiovascular Disease'


# Combining the new data frames
cardio_ap_low <- rbind(
  cardio_disease_ap_low_0,
  cardio_disease_ap_low_1
)


# Plotting the data
ggplot(cardio_ap_low, aes(x = ap_low, fill = disease), alpha = .7) +
  geom_bar(width = 3) +
  labs(x = 'Diastolic Blood Pressure (mm Hg)', y = 'Total') +
  scale_fill_manual(values = c('#404080', '#69b3a2'), name = '')
```

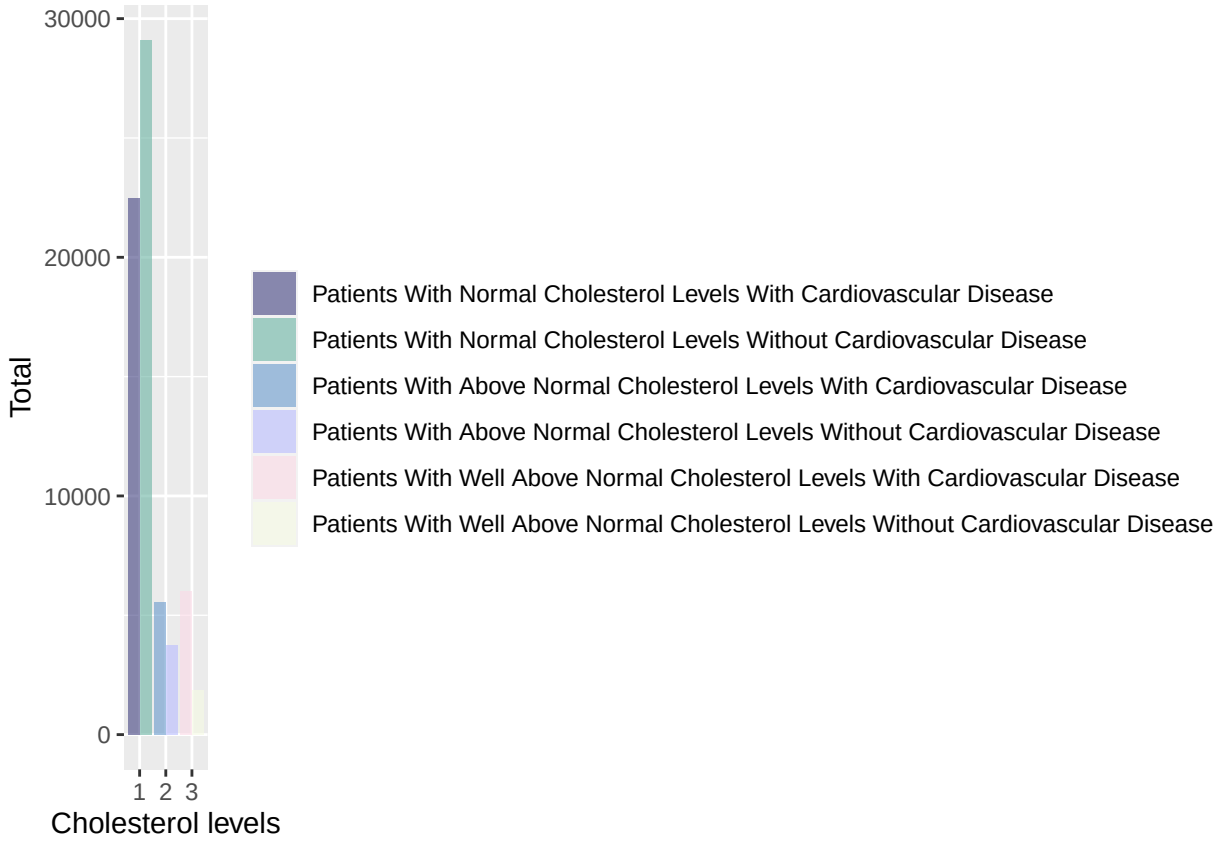


AP Low (Diastolic Blood Pressure)

```r
# Creating data frame that contains 'cholesterol' and 'cardio_disease' if 'cardio_disease' is 0 and 'ch
cardio_disease_cholesterol_0_1 <- select(
  cardio[cardio$cardio_disease == 0 & cardio$cholesterol == 1, ],
  c('cholesterol', 'cardio_disease')
)
```

```
cardio_disease_cholesterol_0_1$disease <- 'Patients With Normal Cholesterol Levels Without Cardiovascula


# Creating data frame that contains 'cholesterol' and 'cardio_disease' if 'cardio_disease' is 0 and 'ch
cardio_disease_cholesterol_0_2 <- select(
  cardio[cardio$cardio_disease == 0 & cardio$cholesterol == 2, ],
  c('cholesterol', 'cardio_disease')
)

cardio_disease_cholesterol_0_2$disease <- 'Patients With Above Normal Cholesterol Levels Without Cardiov


# Creating data frame that contains 'cholesterol' and 'cardio_disease' if 'cardio_disease' is 0 and 'ch
cardio_disease_cholesterol_0_3 <- select(
  cardio[cardio$cardio_disease == 0 & cardio$cholesterol == 3, ],
  c('cholesterol', 'cardio_disease')
)

cardio_disease_cholesterol_0_3$disease <- 'Patients With Well Above Normal Cholesterol Levels Without Ca


# Creating data frame that contains 'cholesterol' and 'cardio_disease' if 'cardio_disease' is 1 and 'ch
cardio_disease_cholesterol_1_1 <- select(
  cardio[cardio$cardio_disease == 1 & cardio$cholesterol == 1, ],
  c('cholesterol', 'cardio_disease')
)

cardio_disease_cholesterol_1_1$disease <- 'Patients With Normal Cholesterol Levels With Cardiovascular


# Creating data frame that contains 'cholesterol' and 'cardio_disease' if 'cardio_disease' is 1 and 'ch
cardio_disease_cholesterol_1_2 <- select(
  cardio[cardio$cardio_disease == 1 & cardio$cholesterol == 2, ],
  c('cholesterol', 'cardio_disease')
)

cardio_disease_cholesterol_1_2$disease <- 'Patients With Above Normal Cholesterol Levels With Cardiovas


# Creating data frame that contains 'cholesterol' and 'cardio_disease' if 'cardio_disease' is 1 and 'ch
cardio_disease_cholesterol_1_3 <- select(
  cardio[cardio$cardio_disease == 1 & cardio$cholesterol == 3, ],
  c('cholesterol', 'cardio_disease')
)

cardio_disease_cholesterol_1_3$disease <- 'Patients With Well Above Normal Cholesterol Levels With Cardi


# Combining the new data frames
cardio_cholesterol <- rbind(
  cardio_disease_cholesterol_0_1,
  cardio_disease_cholesterol_0_2,
  cardio_disease_cholesterol_0_3,
```

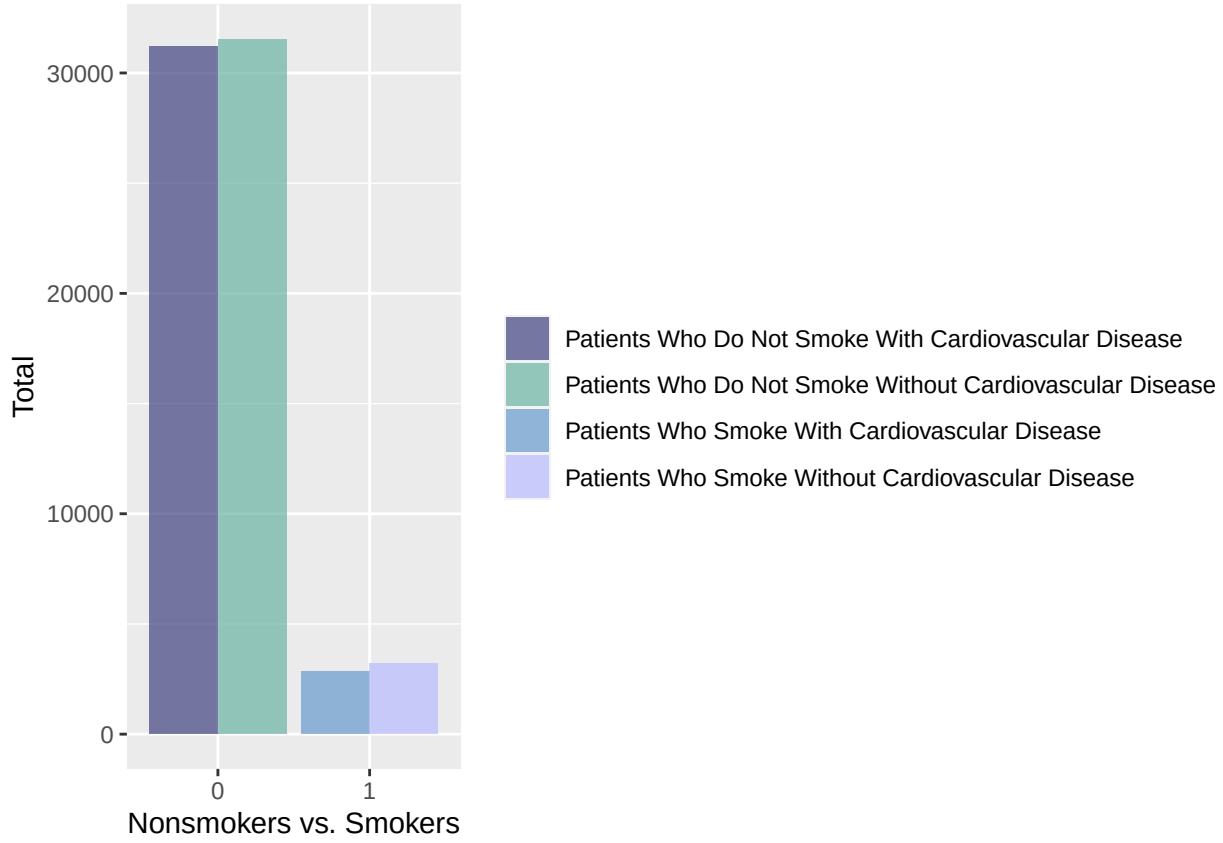
```
  cardio_disease_cholesterol_1_1,
  cardio_disease_cholesterol_1_2,
  cardio_disease_cholesterol_1_3)

cardio_cholesterol$disease <- factor(cardio_cholesterol$disease, levels = c('Patients With Normal Choles

# Plotting the data
ggplot(cardio_cholesterol, aes(x = cholesterol)) +
  geom_bar(stat = 'count', aes(fill = disease), position = 'dodge', alpha = .6) +
  labs(x = 'Cholesterol levels', y = 'Total') +
  scale_fill_manual(values = c('#404080', '#69B3A2', '#6699CC', '#B8BCFF', '#FBD9E6', '#F6FBE4'), name =
```



Cholesterol

```
# Creating data frame that contains 'smoke' and 'cardio_disease' if 'smoke' is 0 and 'cardio_disease' i
cardio_disease_smoke_0_0 <- select(
  cardio[cardio$smoke == 0 & cardio$cardio_disease == 0,],
  c('smoke' ,'cardio_disease')
)

cardio_disease_smoke_0_0$disease <- 'Patients Who Do Not Smoke Without Cardiovascular Disease'
```

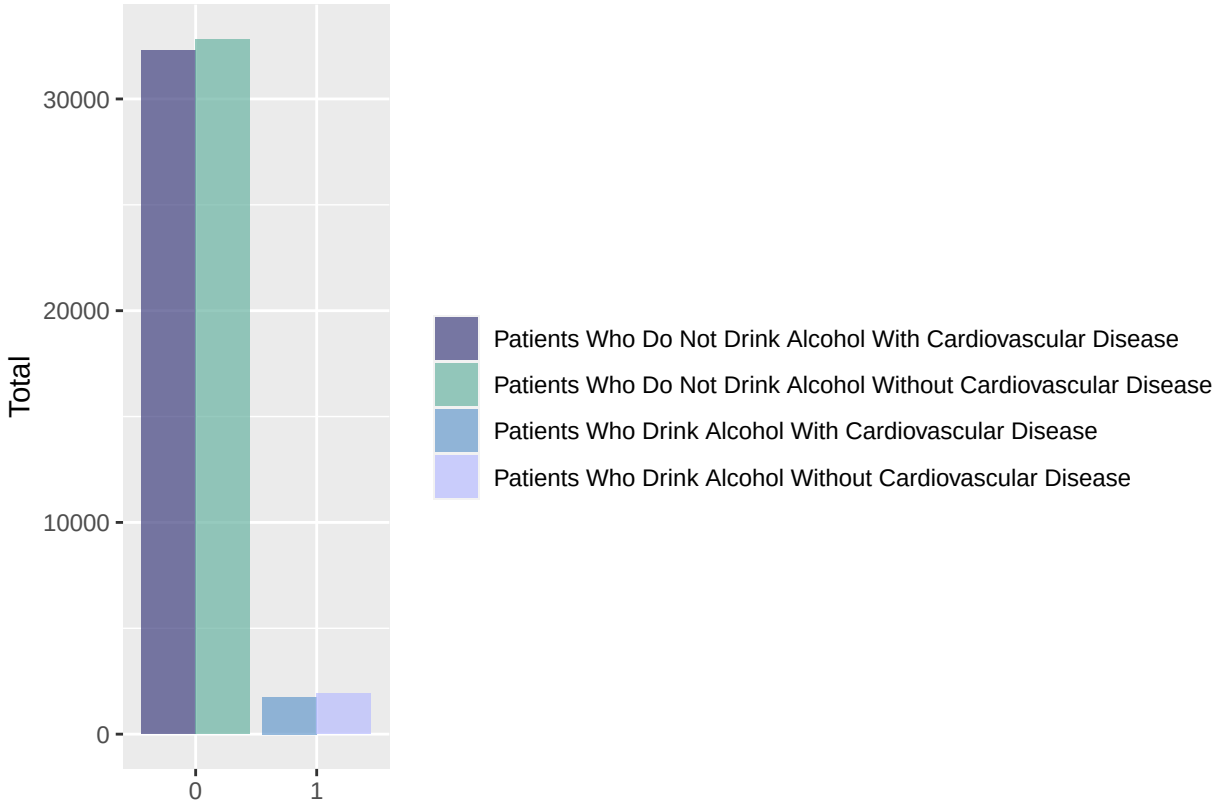
```r
# Creating data frame that contains 'smoke' and 'cardio_disease' if 'smoke' is 0 'cardio_disease' is 1
cardio_disease_smoke_0_1 <- select(
  cardio[cardio$smoke == 0 & cardio$cardio_disease == 1,],
  c('smoke' ,'cardio_disease')
)

cardio_disease_smoke_0_1$disease <- 'Patients Who Do Not Smoke With Cardiovascular Disease'


# Creating data frame that contains 'smoke' and 'cardio_disease' if 'smoke' is 1 'cardio_disease' is 0
cardio_disease_smoke_1_0 <- select(
  cardio[cardio$smoke == 1 & cardio$cardio_disease == 0,],
  c('smoke' ,'cardio_disease')
)

cardio_disease_smoke_1_0$disease <- 'Patients Who Smoke Without Cardiovascular Disease'


# Creating data frame that contains 'smoke' and 'cardio_disease' if 'smoke' is 1 'cardio_disease' is 1
cardio_disease_smoke_1_1 <- select(
  cardio[cardio$smoke == 1 & cardio$cardio_disease == 1,],
  c('smoke' ,'cardio_disease')
)

cardio_disease_smoke_1_1$disease <- 'Patients Who Smoke With Cardiovascular Disease'


# Combining the new data frames
cardio_smoke <- rbind(
  cardio_disease_smoke_0_0,
  cardio_disease_smoke_0_1,
  cardio_disease_smoke_1_0,
  cardio_disease_smoke_1_1
)


# Plotting the data
ggplot(cardio_smoke, aes(x = smoke)) +
  geom_bar(stat = 'count', aes(fill = disease), position = 'dodge', alpha = .7) +
  labs(x = 'Nonsmokers vs. Smokers', y = 'Total') +
  scale_fill_manual(values = c('#404080', '#69B3A2', '#6699CC', '#B8BCFF'), name = '')
```



Smoke

```
# Creating data frame that contains 'alcohol' and 'cardio_disease' if 'alcohol' is 0 and 'cardio_diseas
cardio_disease_alcohol_0_0 <- select(
  cardio[cardio$alcohol == 0 & cardio$cardio_disease == 0,],
  c('alcohol' ,'cardio_disease')
)

cardio_disease_alcohol_0_0$disease <- 'Patients Who Do Not Drink Alcohol Without Cardiovascular Disease


# Creating data frame that contains 'alcohol' and 'cardio_disease' if 'alcohol' is 0 'cardio_disease' i
cardio_disease_alcohol_0_1 <- select(
  cardio[cardio$alcohol == 0 & cardio$cardio_disease == 1,],
  c('alcohol' ,'cardio_disease')
)

cardio_disease_alcohol_0_1$disease <- 'Patients Who Do Not Drink Alcohol With Cardiovascular Disease'


# Creating data frame that contains 'alcohol' and 'cardio_disease' if 'alcohol' is 1 'cardio_disease' i
cardio_disease_alcohol_1_0 <- select(
  cardio[cardio$alcohol == 1 & cardio$cardio_disease == 0,],
  c('alcohol' ,'cardio_disease')
)
```

```r
cardio_disease_alcohol_1_0$disease <- 'Patients Who Drink Alcohol Without Cardiovascular Disease'


# Creating data frame that contains 'alcohol' and 'cardio_disease' if 'alcohol' is 1 'cardio_disease' i
cardio_disease_alcohol_1_1 <- select(
  cardio[cardio$alcohol == 1 & cardio$cardio_disease == 1,],
  c('alcohol' ,'cardio_disease')
)

cardio_disease_alcohol_1_1$disease <- 'Patients Who Drink Alcohol With Cardiovascular Disease'


# Combining the new data frames
cardio_alcohol <- rbind(
  cardio_disease_alcohol_0_0,
  cardio_disease_alcohol_0_1,
  cardio_disease_alcohol_1_0,
  cardio_disease_alcohol_1_1
)


# Plotting the data
ggplot(cardio_alcohol, aes(x = alcohol)) +
  geom_bar(stat = 'count', aes(fill = disease), position = 'dodge', alpha = .7) +
  labs(x = 'Patients Who Drink vs. Patients Who Abstain', y = 'Total') +
  scale_fill_manual(values = c('#404080', '#69B3A2', '#6699CC', '#B8BCFF'), name = '')
```

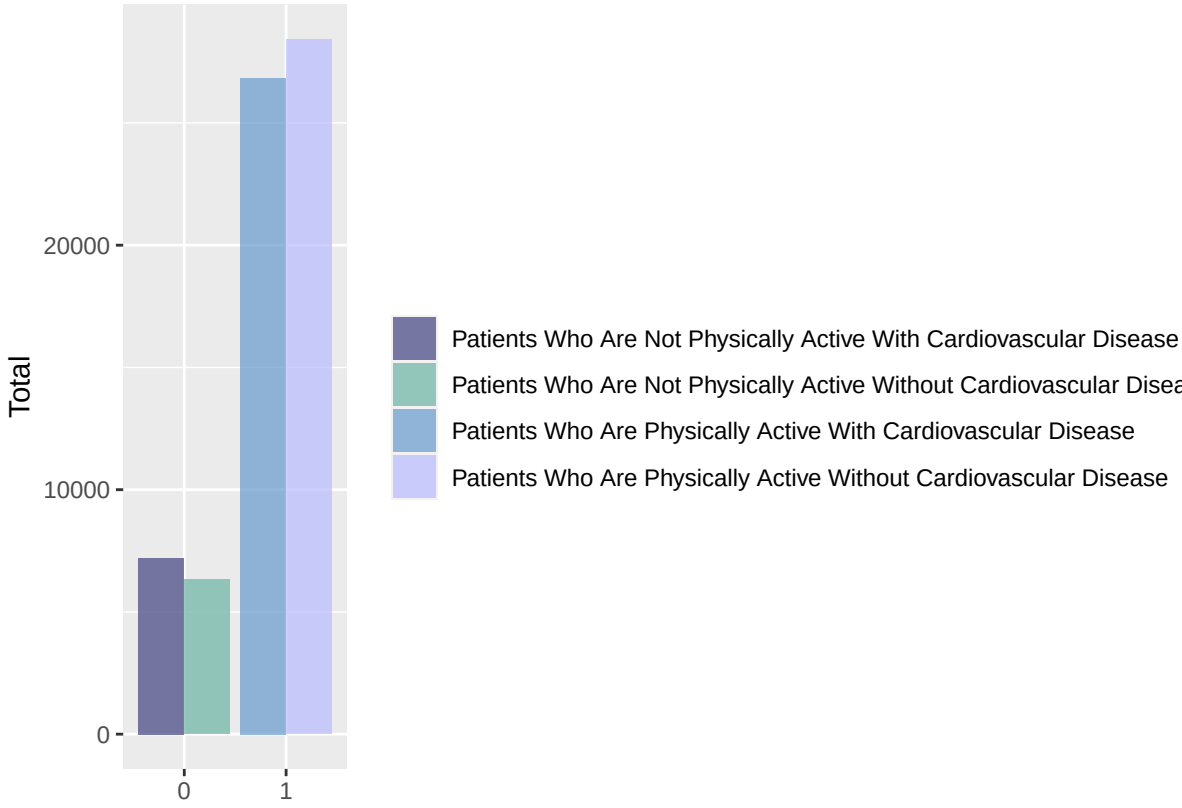


atients Who Drink vs. Patients Who Abstain

Alcohol

```
# Creating data frame that contains 'physical_activity' and 'cardio_disease' if 'physical_activity' is
cardio_disease_p_a_0_0 <- select(
  cardio[cardio$physical_activity == 0 & cardio$cardio_disease == 0,],
  c('physical_activity' ,'cardio_disease')
)

cardio_disease_p_a_0_0$disease <- 'Patients Who Are Not Physically Active Without Cardiovascular Disease


# Creating data frame that contains 'physical_activity' and 'cardio_disease' if 'physical_activity' is
cardio_disease_p_a_0_1 <- select(
  cardio[cardio$physical_activity == 0 & cardio$cardio_disease == 1,],
  c('physical_activity' ,'cardio_disease')
)

cardio_disease_p_a_0_1$disease <- 'Patients Who Are Not Physically Active With Cardiovascular Disease'


# Creating data frame that contains 'physical_activity' and 'cardio_disease' if 'physical_activity' is
cardio_disease_p_a_1_0 <- select(
  cardio[cardio$physical_activity == 1 & cardio$cardio_disease == 0,],
  c('physical_activity' ,'cardio_disease')
)
```

```r
cardio_disease_p_a_1_0$disease <- 'Patients Who Are Physically Active Without Cardiovascular Disease'


# Creating data frame that contains 'physical_activity' and 'cardio_disease' if 'physical_activity' is
cardio_disease_p_a_1_1 <- select(
  cardio[cardio$physical_activity == 1 & cardio$cardio_disease == 1,],
  c('physical_activity' ,'cardio_disease')
)

cardio_disease_p_a_1_1$disease <- 'Patients Who Are Physically Active With Cardiovascular Disease'


# Combining the new data frames
cardio_p_a <- rbind(
  cardio_disease_p_a_0_0,
  cardio_disease_p_a_0_1,
  cardio_disease_p_a_1_0,
  cardio_disease_p_a_1_1
)


# Plotting the data
ggplot(cardio_p_a, aes(x = physical_activity)) +
  geom_bar(stat = 'count', aes(fill = disease), position = 'dodge', alpha = .7) +
  labs(x = '', y = 'Total') +
  scale_fill_manual(values = c('#404080', '#69B3A2', '#6699CC', '#B8BCFF'), name = '')
```



Physical Activity

Summary Based on the fact that the histograms of `smoke`, drinking and physical activity as well as the correlation = 0, we remoce these variables from our analysis

Creating the Model

The process of creating a model begins by first splitting the data into training and testing sets. Because the data set we're working with has a large number of observations, we can afford to split it into 90% training and 10% testing without worrying that there won't be enough observations in the testing set. We will also stratify the split on our response variable, `cardio_disease`

```
cardio_split <- cardio_one_hot %>%
  initial_split(strata = cardio_disease_1, prop = .90)

cardio_train <- training(cardio_split) %>% as_tibble()
cardio_train[ ,c('smoke_1', 'alcohol_1', 'physical_activity_1')] <- list(NULL)

cardio_test <- testing(cardio_split)
```

Creating the Recipe

```
#lda, qda, naive bayes, logistic reg, boosted, svm
# good
```

```
cardio_recipe <- recipe(cardio_disease_1 ~ age + gender_2 + height + weight + ap_high + ap_low + choles
  step_dummy(gender_2) %>%
  step_dummy(cholesterol_2) %>%
  step_dummy(cholesterol_3) %>%
  step_dummy(glucose_2) %>%
  step_dummy(glucose_3) %>%
  step_normalize(all_predictors())


cardio_folds <- vfold_cv(cardio_train, v = 10, strata = cardio_disease_1)
```

```
cardio_lda <- discrim_linear() %>%
  set_mode('classification') %>%
  set_engine('MASS')

cardio_lda_workflow <- workflow() %>%
  add_model(cardio_lda) %>%
  add_recipe(cardio_recipe)

cardio_lda_fit <- fit(cardio_lda_workflow, cardio_train)


predict(cardio_lda_fit, new_data = cardio_train, type = 'prob')
```

```
## # A tibble: 61,903 x 2
##    .pred_0 .pred_1
##      <dbl>   <dbl>
##  1   0.798  0.202
##  2   0.905  0.0948
##  3   0.435  0.565
##  4   0.159  0.841
##  5   0.810  0.190
##  6   0.794  0.206
##  7   0.496  0.504
##  8   0.695  0.305
##  9   0.801  0.199
## 10   0.617  0.383
## # ... with 61,893 more rows
```

```
augment(cardio_lda_fit, new_data = cardio_train) %>%
  conf_mat(truth = cardio_disease_1, estimate = .pred_class)
```

```
##           Truth
## Prediction     0     1
##          0 24898 10739
##          1  6369 19897
```

```
augment(cardio_lda_fit, new_data = cardio_train) %>%
  roc_auc(truth = cardio_disease_1, estimate = .pred_0)
```

```
## # A tibble: 1 x 3
```

```
##   .metric .estimator .estimate
##   <chr>   <chr>          <dbl>
## 1 roc_auc binary         0.789
```

```
#naive bayes
cardio_nb <- naive_Bayes() %>%
  set_mode('classification') %>%
  set_engine('klaR')

cardio_nb_workflow <- workflow() %>%
  add_model(cardio_nb) %>%
  add_recipe(cardio_recipe)

cardio_nb_fit <- fit(cardio_nb_workflow, cardio_train)

augment(cardio_nb_fit, new_data = cardio_train) %>%
  roc_auc(truth = cardio_disease_1, estimate = .pred_0)
```

```
## # A tibble: 1 x 3
##   .metric .estimator .estimate
##   <chr>   <chr>          <dbl>
## 1 roc_auc binary         0.785
```

```
#qda
cardio_qda <- discrim_quad() %>%
  set_mode('classification') %>%
  set_engine('MASS')

cardio_qda_workflow <- workflow() %>%
  add_model(cardio_qda) %>%
  add_recipe(cardio_recipe)

cardio_qda_fit <- fit(cardio_qda_workflow, cardio_train)

augment(cardio_qda_fit, new_data = cardio_train) %>%
  roc_auc(truth = cardio_disease_1, estimate = .pred_0)
```

```
## # A tibble: 1 x 3
##   .metric .estimator .estimate
##   <chr>   <chr>          <dbl>
## 1 roc_auc binary         0.756
```

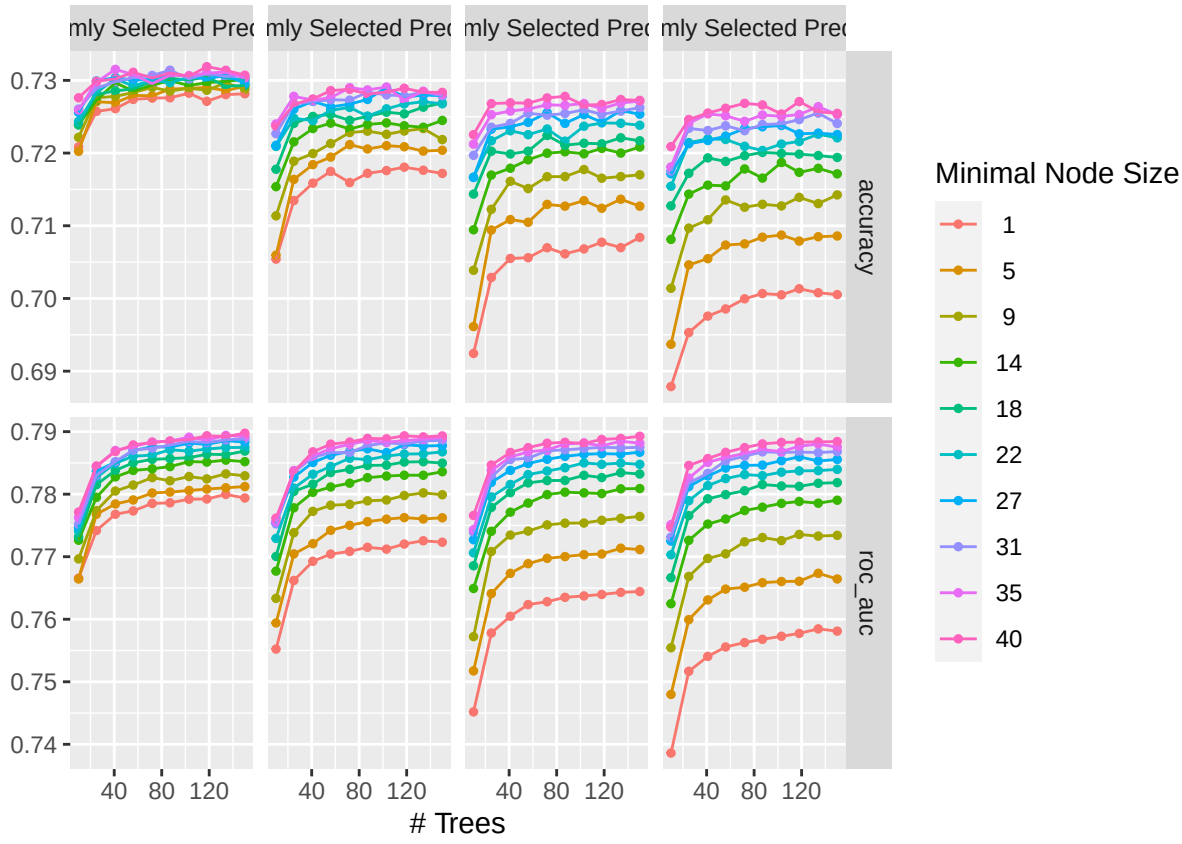
```
# logistic regression
cardio_log <- logistic_reg() %>%
  set_engine('glm') %>%
  set_mode('classification')

cardio_log_workflow <- workflow() %>%
  add_model(cardio_log) %>%
  add_recipe(cardio_recipe)

cardio_log_fit <- fit(cardio_log_workflow, cardio_train)
```

```
augment(cardio_log_fit, new_data = cardio_train) %>%
  roc_auc(cardio_disease_1, estimate = .pred_0)
```

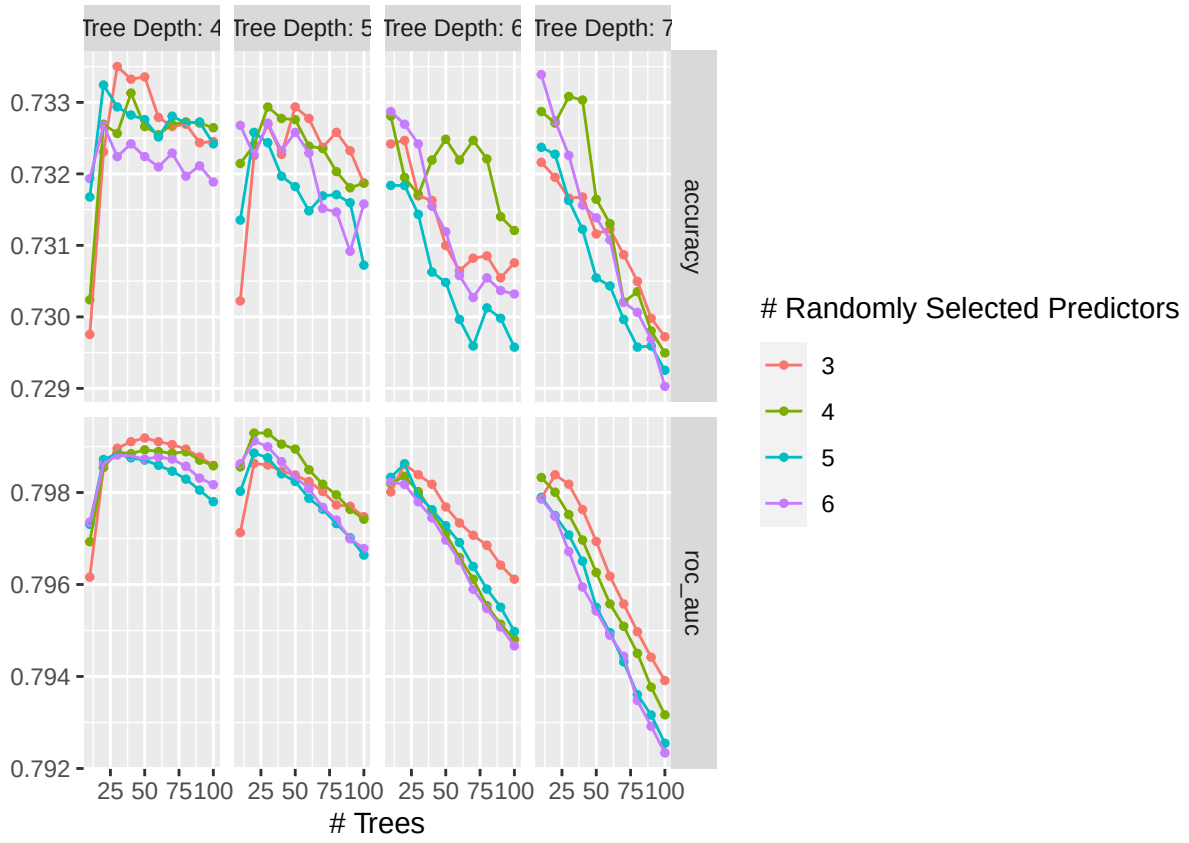
```
## # A tibble: 1 x 3
##   .metric .estimator .estimate
##   <chr>   <chr>          <dbl>
## 1 roc_auc binary         0.789
```

```
load('/Users/andrewchoi/Downloads/PSTAT131_FINAL_PROJECT/PSTAT131_FINAL_PROJECT/Random_Forest_Model.rda
load('/Users/andrewchoi/Downloads/PSTAT131_FINAL_PROJECT/PSTAT131_FINAL_PROJECT/Boosted_Model.rda')
load('/Users/andrewchoi/Downloads/PSTAT131_FINAL_PROJECT/PSTAT131_FINAL_PROJECT/Support_Vector_Machine_
```

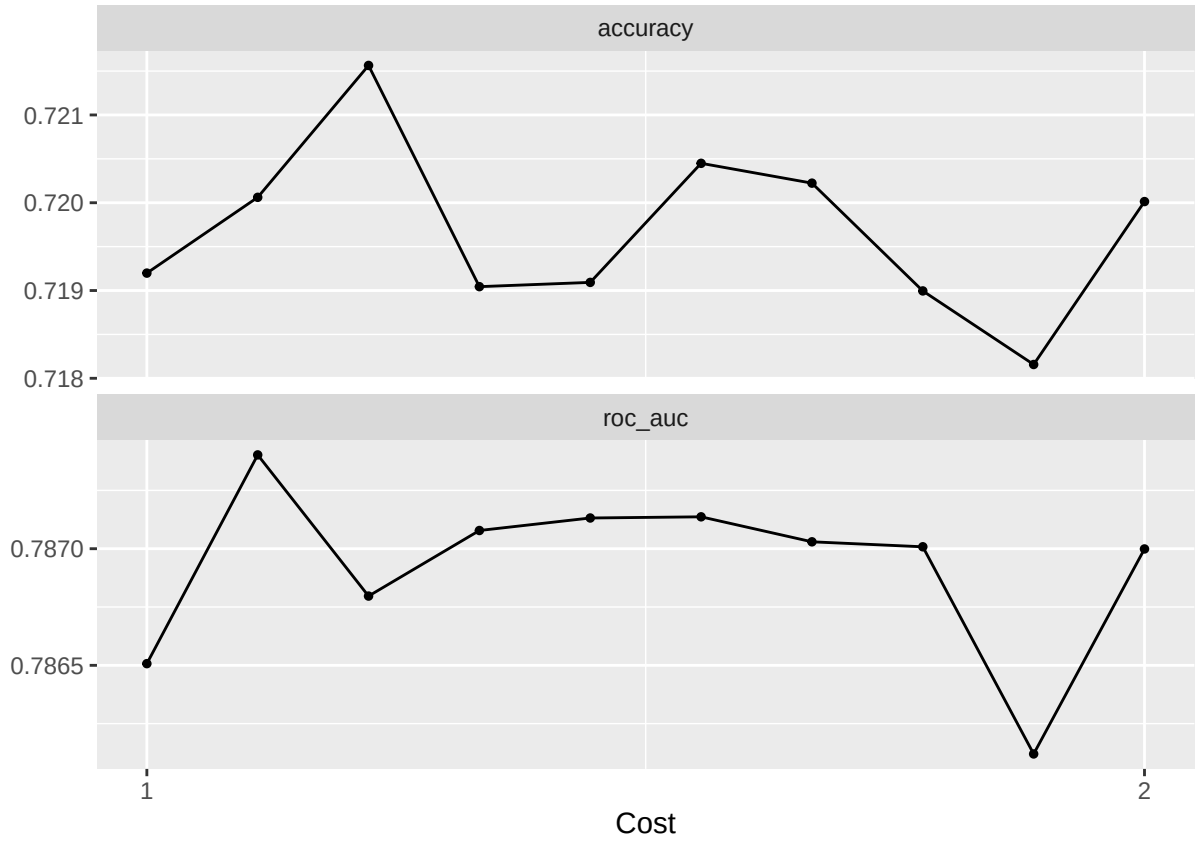
```
autoplot(cardio_forest_tune_res)
```




```
autoplot(cardio_boost_tune_res)
```




```
autoplot(cardio_svm_tune_res)
```


accuracy
0.721
0.720
0.719
0.718
roc_auc
0.7870
0.7865
1
2
Cost