CS 221 Project Final R Code

library and helpers

This R-markdown file contains the R-code for the project report of my CS 221 project.

```
library(caTools)
library(caret)
```

```
## Loading required package: lattice
```

```
## Loading required package: ggplot2
```

```
library(e1071)
library(MASS)
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
```

```
## The following object is masked from 'package:MASS':
##
##     select
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
library(ggplot2)
library(naniar)
#library(randomForest)
```

This "convert" helper function is due to Brigitte Mueller, Predicting Heart Disease UCI. I'm borrowing this helper here to change the data type of the Cleveland data read from the website.

```
convert = function(obj,types){
    for (i in 1:length(obj)){
        FUN = switch(types[i],character = as.character,
                                   numeric = as.numeric,
                                   factor = as.factor)
        obj[,i] = FUN(obj[,i])
    }
    obj
}
```

Data Processing and Visualization

Data Preprocessing

The heart disease data are directly read from the UCI website.

```
cleveland.data = read.csv("https://archive.ics.uci.edu/ml/machine-learning-databases/heart-disease/proc
va.data = read.csv("http://archive.ics.uci.edu/ml/machine-learning-databases/heart-disease/processed.va
switzerland.data = read.csv("http://archive.ics.uci.edu/ml/machine-learning-databases/heart-disease/pro
hungarian.data = read.csv("http://archive.ics.uci.edu/ml/machine-learning-databases/heart-disease/proce
df_list <- list(cleveland.data, va.data, switzerland.data, hungarian.data)
combined.data = Reduce(function(x, y) merge(x, y, all=TRUE), df_list, accumulate=FALSE)
names(combined.data) = c( "age", "sex", "cp", "trestbps", "chol","fbs", "restecg",
                   "thalach","exang", "oldpeak","slope", "ca", "thal", "status")
combined.data$status[combined.data$status > 0] = 1
chclass = c("numeric","factor","factor","numeric","numeric","factor","factor","numeric","factor","numer
combined.data = convert(combined.data,chclass)
levels(combined.data$status) = c("healthy", "disease")
levels(combined.data$sex) = c("female", "male")
summary(combined.data)
```

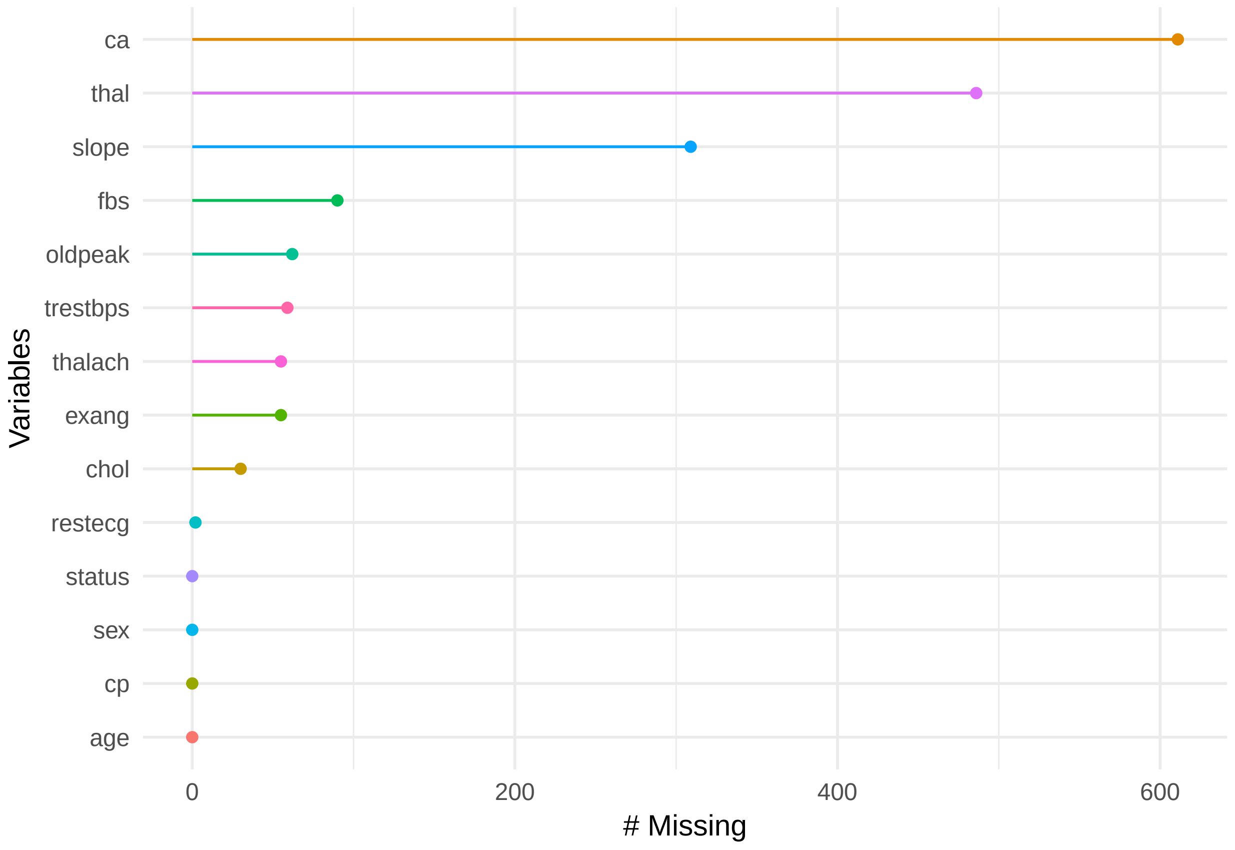
```
##       age             sex        cp         trestbps           chol      
##  Min.   :28.00   female:194   1: 46   Min.   :  0.0   Min.   :  0.0  
##  1st Qu.:47.00   male  :726   2:174   1st Qu.:120.0   1st Qu.:175.0  
##  Median :54.00                3:204   Median :130.0   Median :223.0  
##  Mean   :53.51                4:496   Mean   :132.1   Mean   :199.1  
##  3rd Qu.:60.00                        3rd Qu.:140.0   3rd Qu.:268.0  
##  Max.   :77.00                        Max.   :200.0   Max.   :603.0  
##                                       NA's   :59      NA's   :30     
##    fbs       restecg       thalach       exang        oldpeak       
##  0   :692   0   :551   Min.   : 60.0   0   :528   Min.   :-2.6000  
##  1   :138   1   :179   1st Qu.:120.0   1   :337   1st Qu.: 0.0000  
##  NA's: 90   2   :188   Median :140.0   NA's: 55   Median : 0.5000  
##             NA's:  2   Mean   :137.5              Mean   : 0.8788  
##                        3rd Qu.:157.0              3rd Qu.: 1.5000  
##                        Max.   :202.0              Max.   : 6.2000  
##                        NA's   :55                 NA's   :62      
##   slope        ca         thal         status   
##  1   :203   0   :181   3   :196   healthy:411  
##  2   :345   1   : 67   6   : 46   disease:509  
##  3   : 63   2   : 41   7   :192                
##  NA's:309   3   : 20   NA's:486                
##             NA's:611                           
##                                                
## 
```

```
str(combined.data)
```

```
## 'data.frame':    920 obs. of  14 variables:
##  $ age     : num  28 29 29 29 30 31 31 32 32 32 ...
##  $ sex     : Factor w/ 2 levels "female","male": 2 2 2 2 1 1 2 1 2 2 ...
##  $ cp      : Factor w/ 4 levels "1","2","3","4": 2 2 2 2 1 2 4 2 1 2 ...
##  $ trestbps: num  130 120 130 140 170 100 120 105 95 110 ...
##  $ chol    : num  132 243 204 NA 237 219 270 198 0 225 ...
##  $ fbs     : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 NA 1 ...
##  $ restecg : Factor w/ 3 levels "0","1","2": 3 1 3 1 2 2 1 1 1 1 ...
##  $ thalach : num  185 160 202 170 170 150 153 165 127 184 ...
##  $ exang   : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 2 1 1 1 ...
##  $ oldpeak : num  0 0 0 0 0 0 1.5 0 0.7 0 ...
##  $ slope   : Factor w/ 3 levels "1","2","3": NA NA 1 NA NA NA 2 NA 1 NA ...
##  $ ca      : Factor w/ 4 levels "0","1","2","3": NA NA 1 NA NA NA NA NA NA NA ...
##  $ thal    : Factor w/ 3 levels "3","6","7": NA NA 1 NA 2 NA NA NA NA NA ...
##  $ status  : Factor w/ 2 levels "healthy","disease": 1 1 1 1 1 1 2 1 2 1 ...
```

Graphing missing data

```
gg_miss_var(combined.data)
```

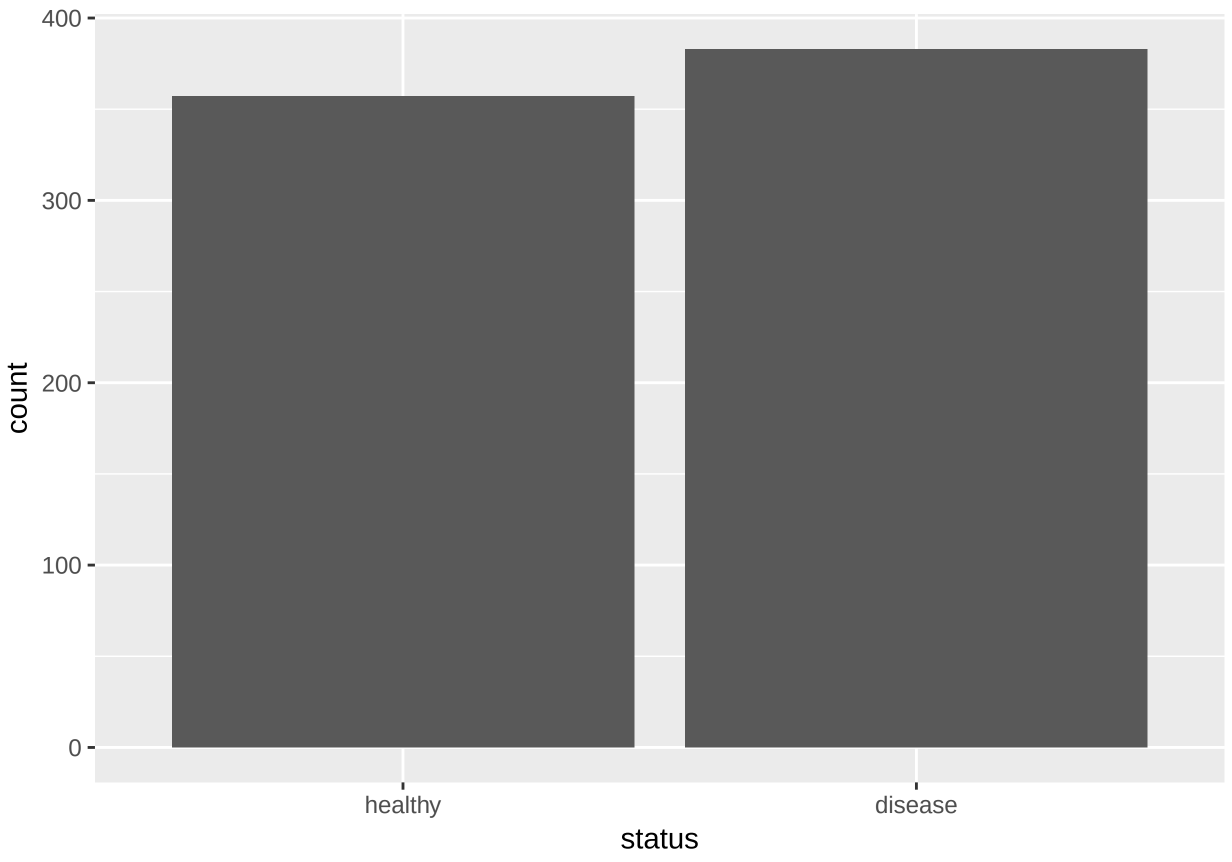


Processing missing data

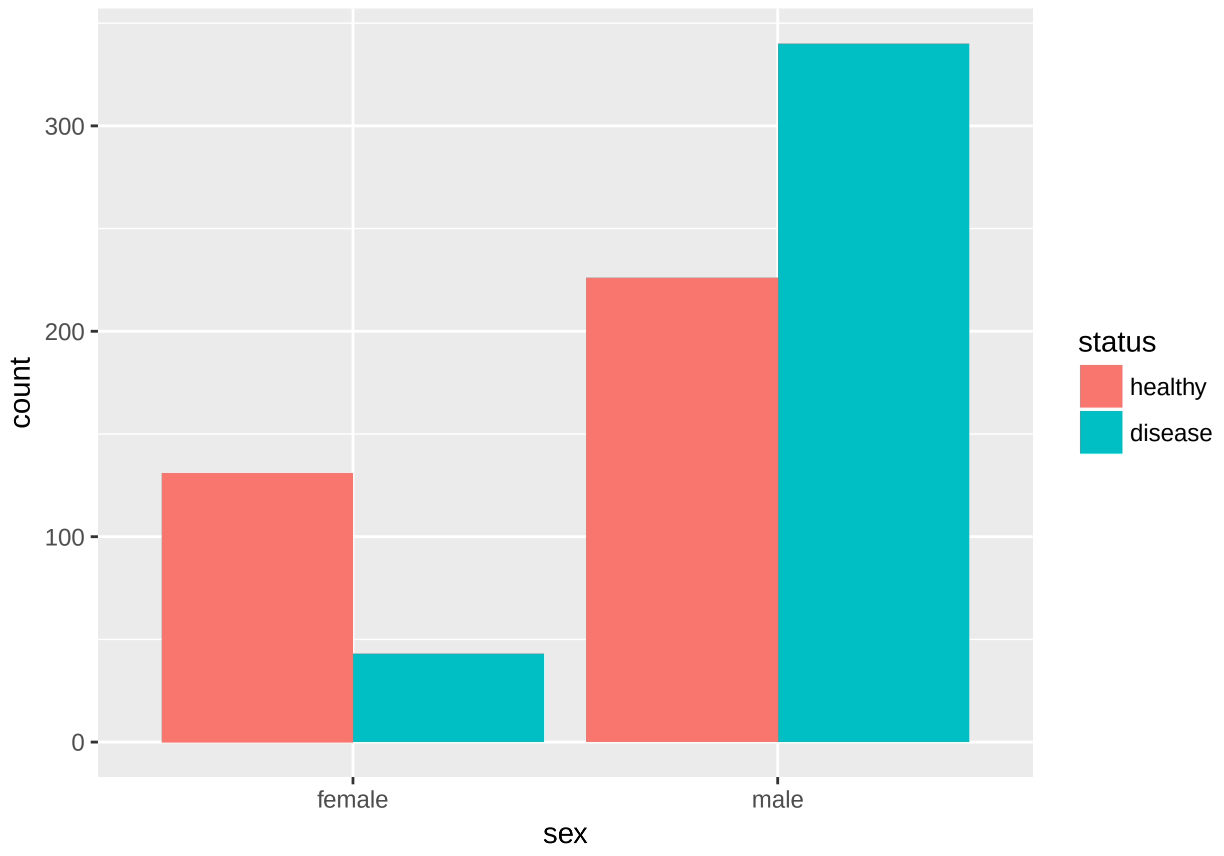
```
combined.data = subset(combined.data, select = -c(11, 12, 13))
combined.data = na.omit(combined.data)
```

Graphics for data exploration

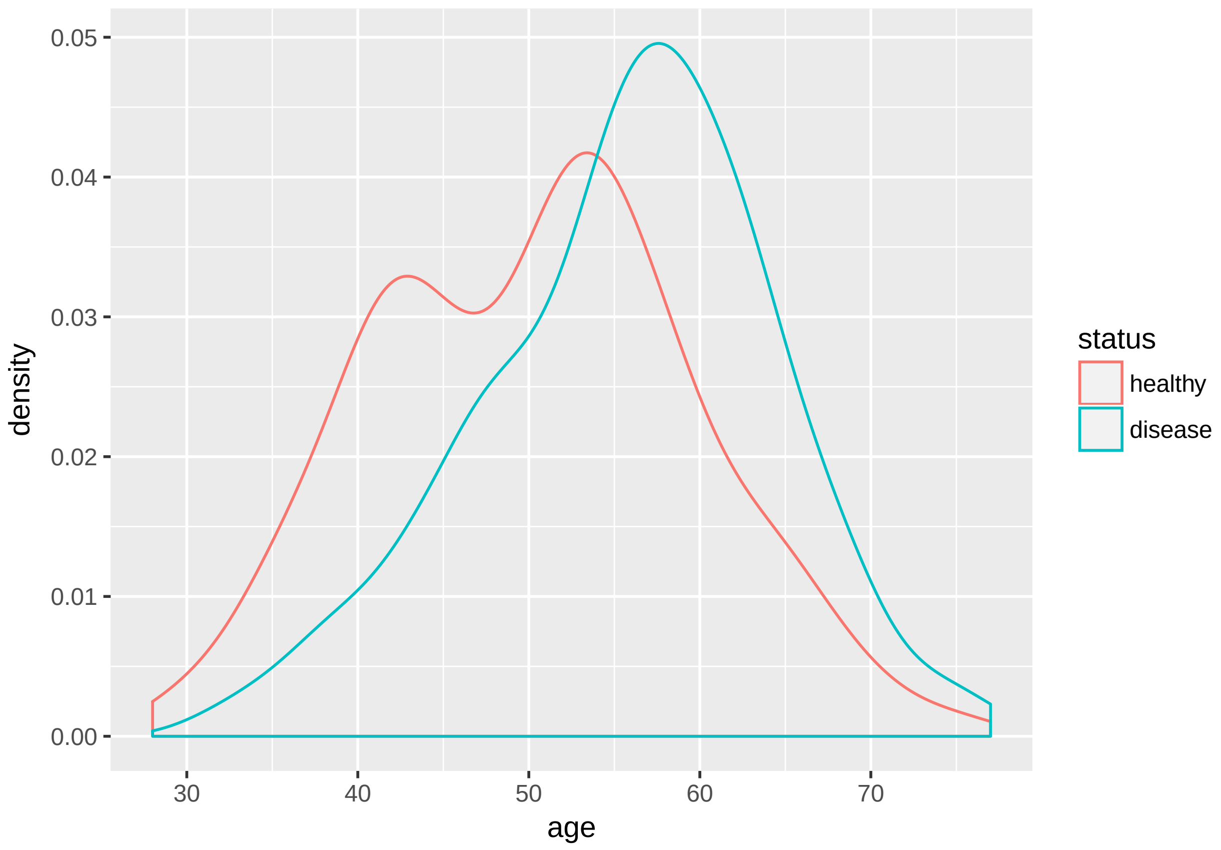
```
ggplot(combined.data, aes(x = status)) + geom_bar()
```



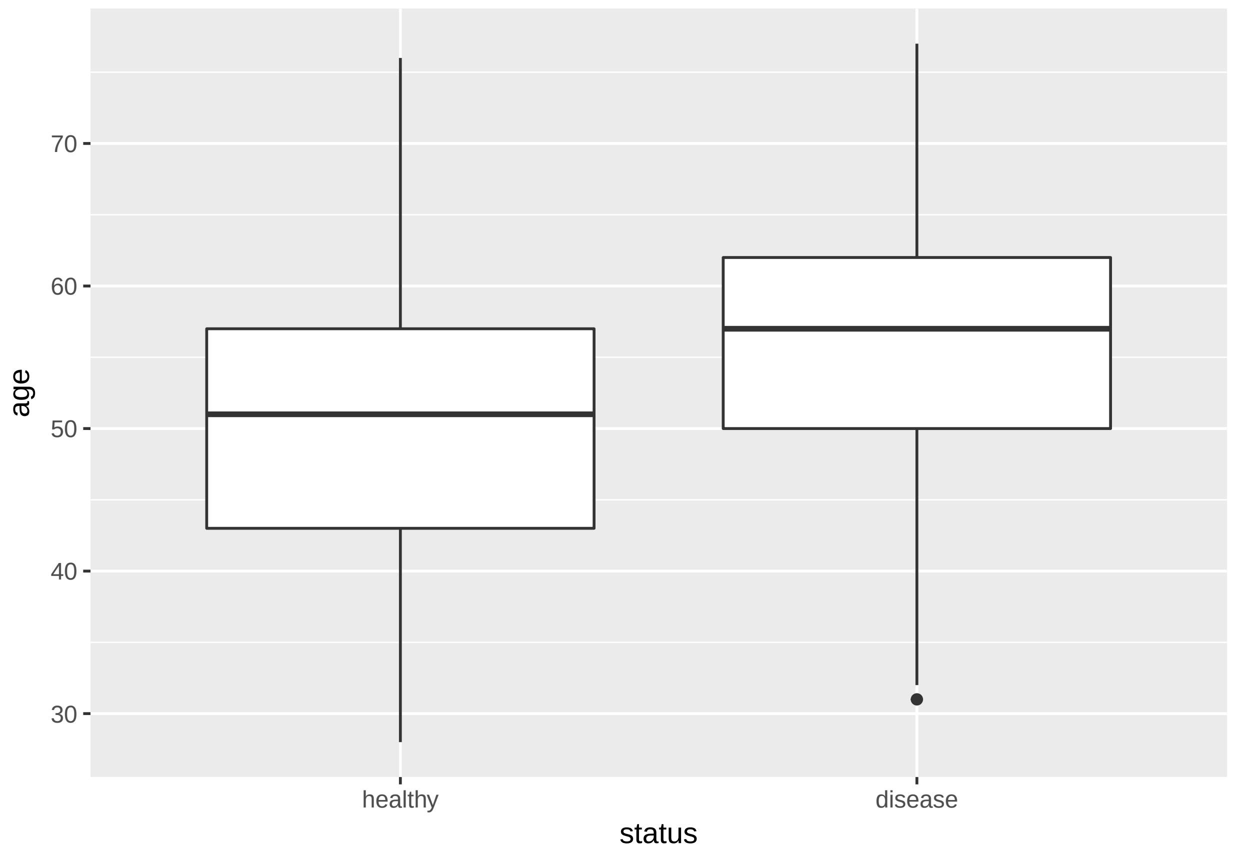
```r
ggplot(combined.data, aes(x = sex, fill=status)) + geom_bar(position="dodge")
```



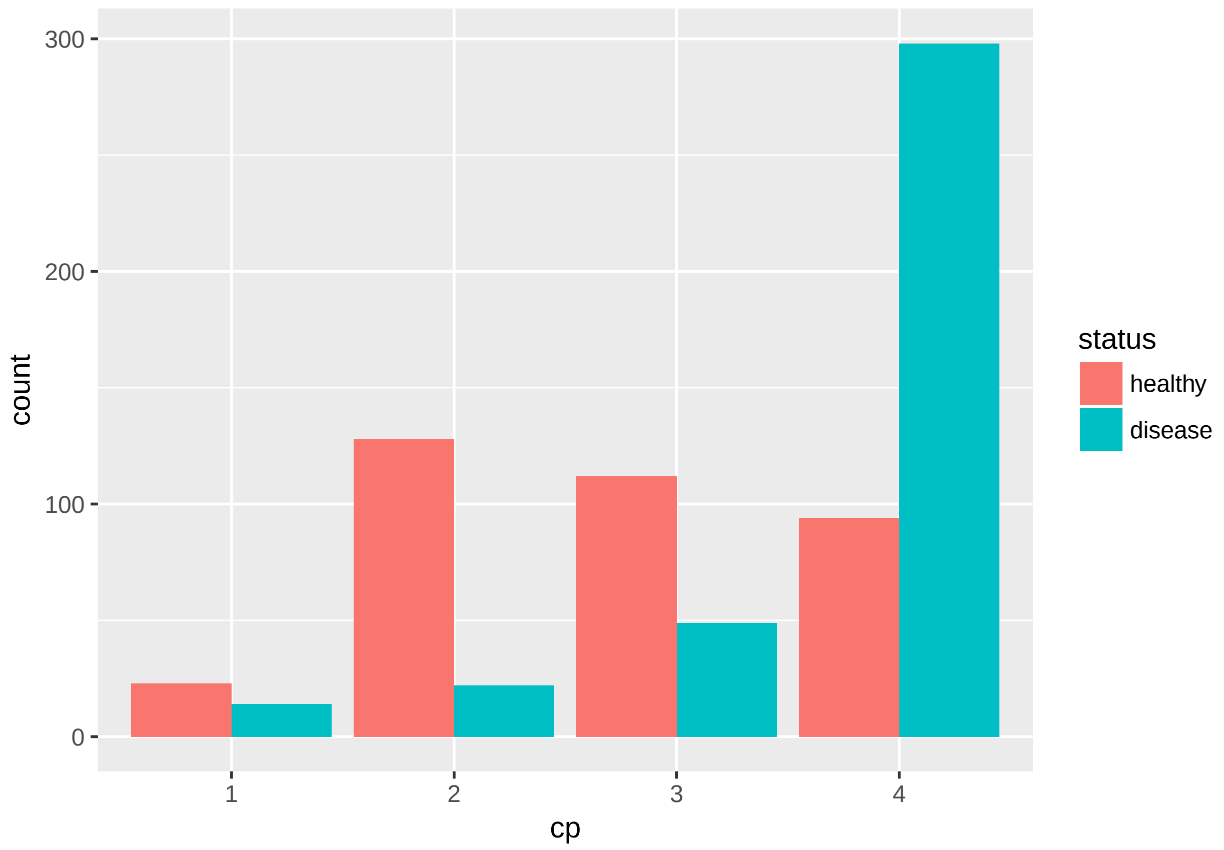
```r
ggplot(combined.data, aes(x=age, color = status)) + geom_density()
```



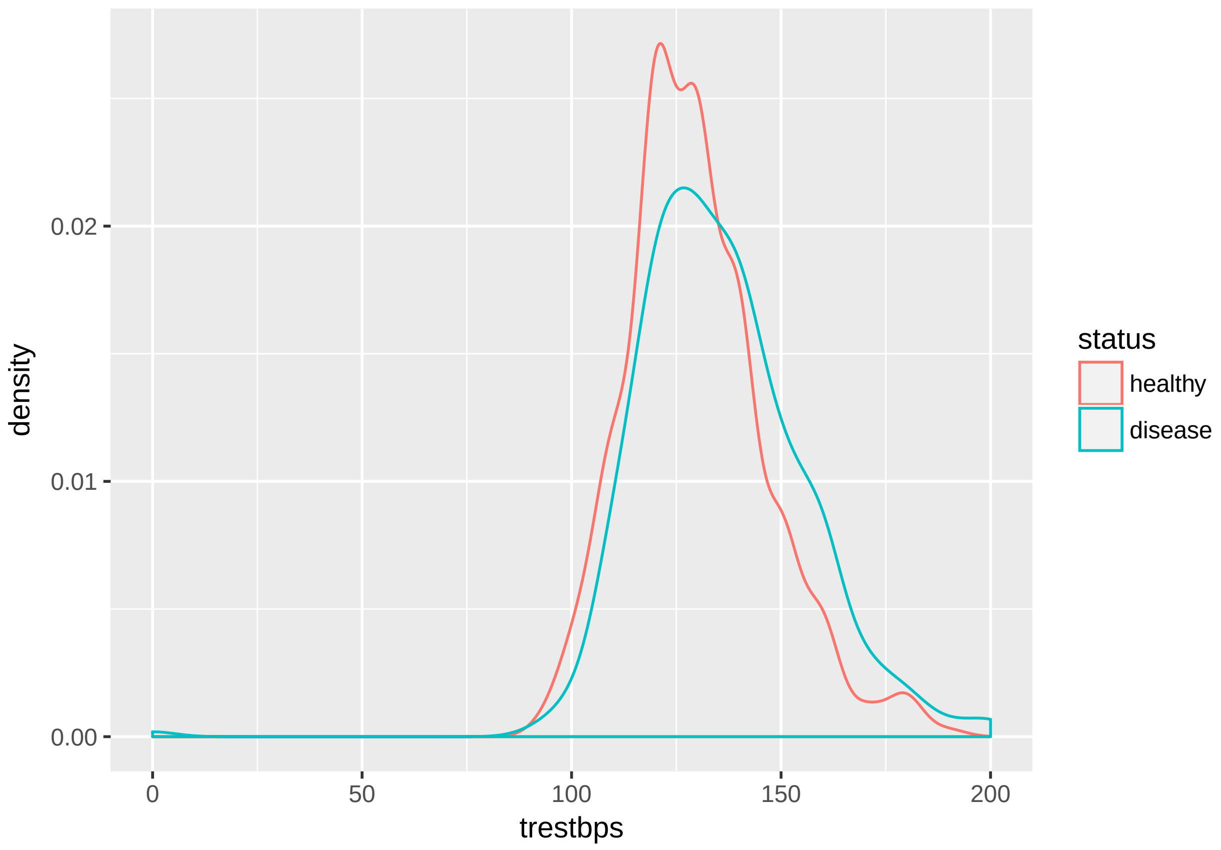
```r
ggplot(combined.data, aes(x=status, y = age)) + geom_boxplot()
```



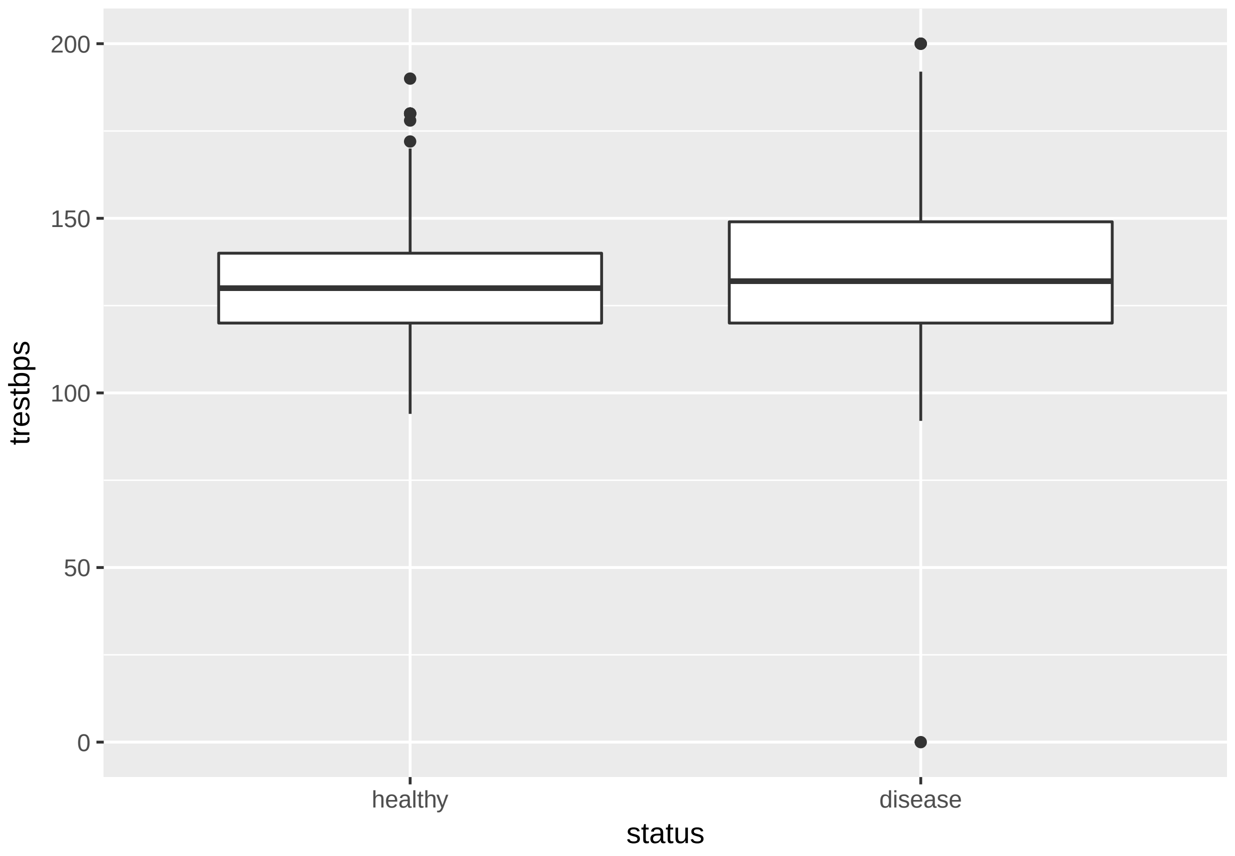
```r
ggplot(combined.data, aes(x = cp, fill=status)) + geom_bar(position="dodge")
```



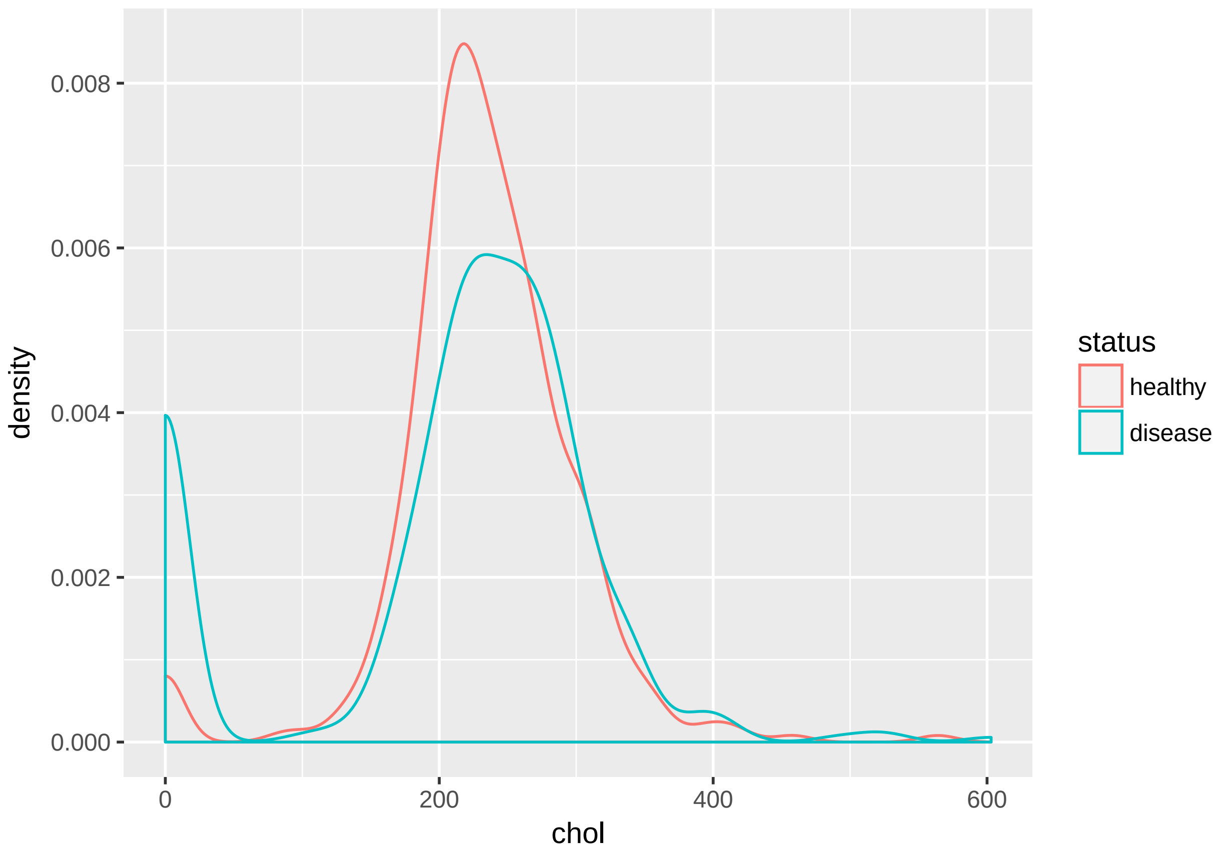
```r
ggplot(combined.data, aes(x=trestbps, color = status)) + geom_density()
```



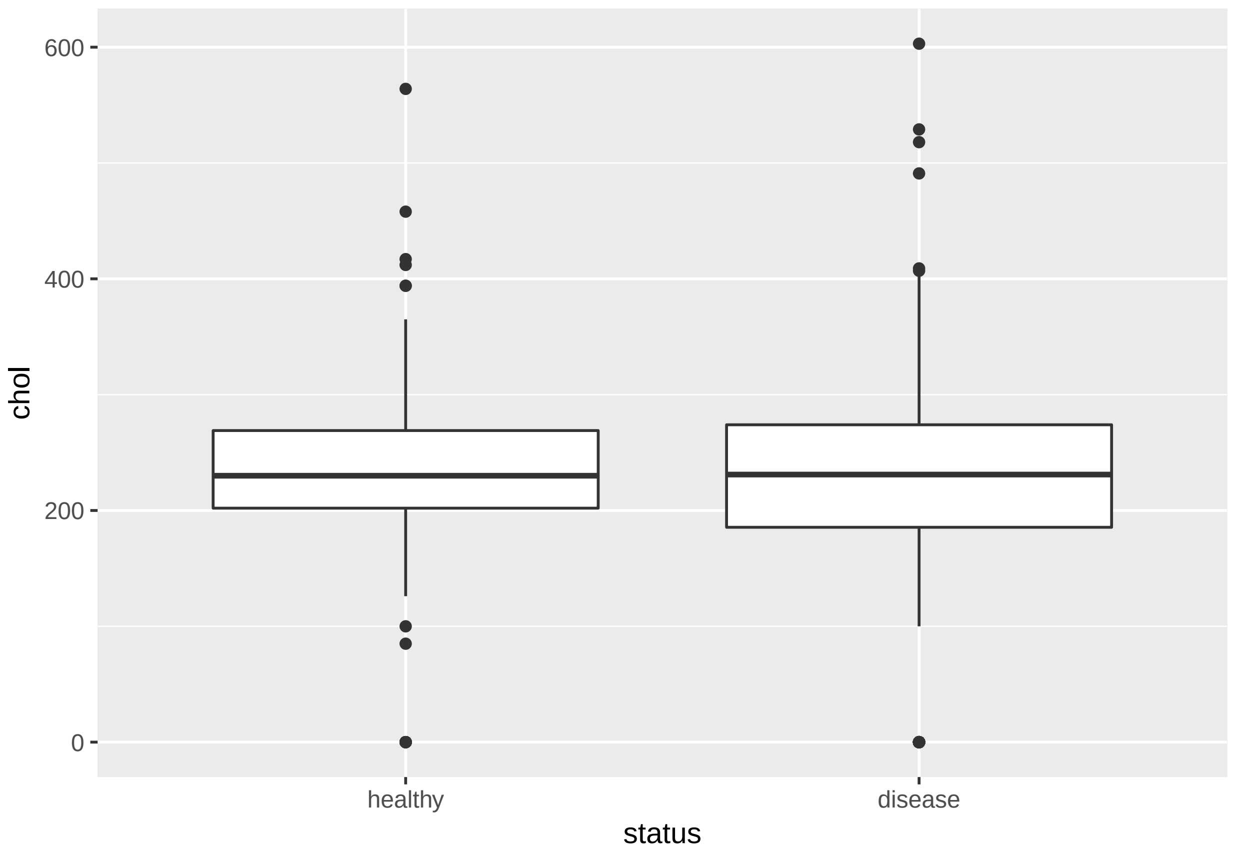
```
ggplot(combined.data, aes(x=status, y = trestbps)) + geom_boxplot()
```



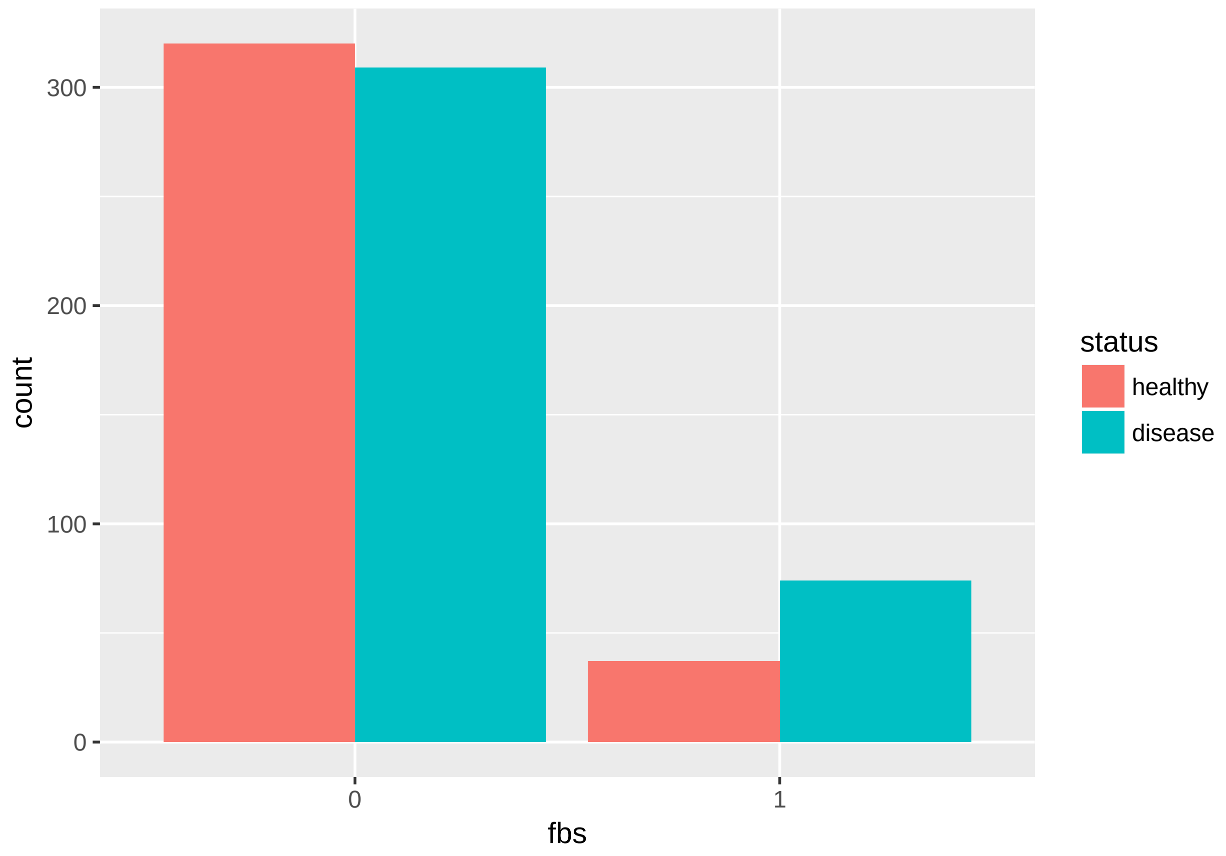
```r
ggplot(combined.data, aes(x=chol, color = status)) + geom_density()
```



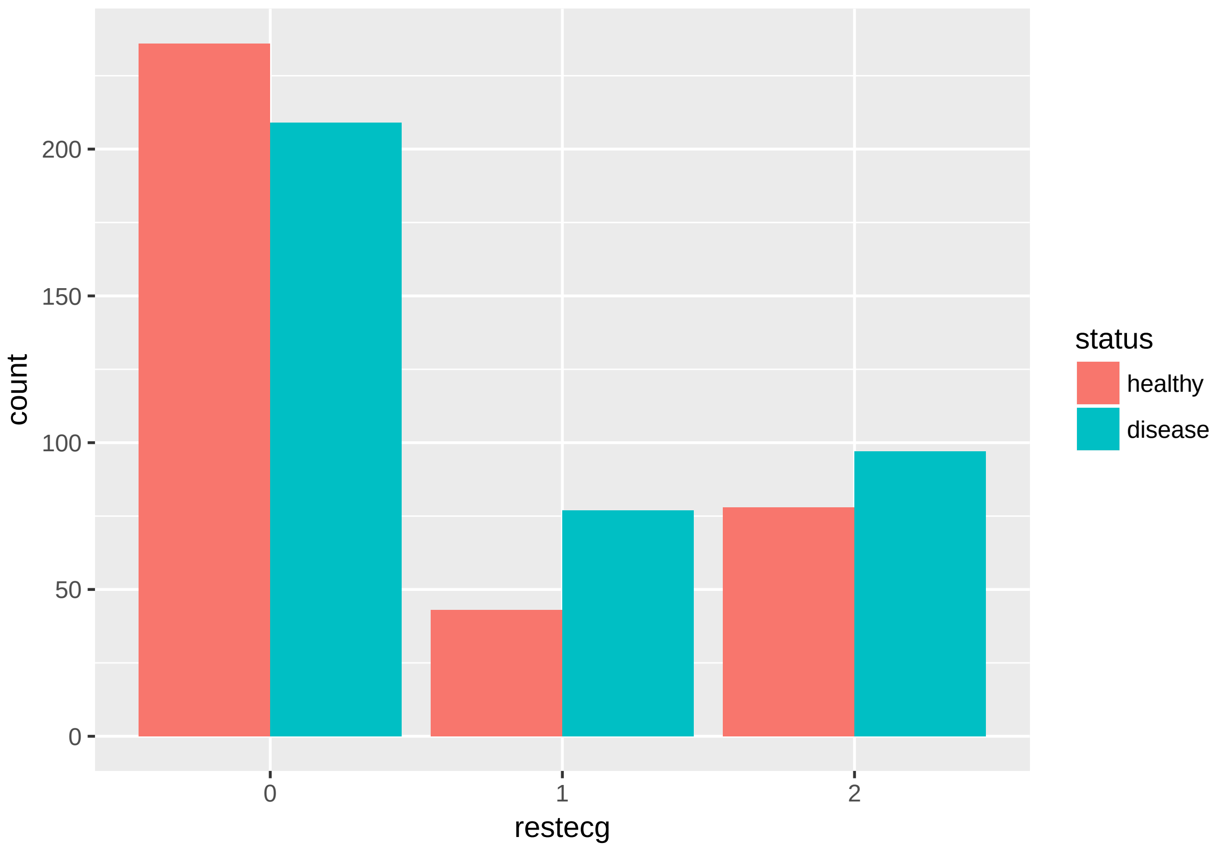
```r
ggplot(combined.data, aes(x=status, y = chol)) + geom_boxplot()
```



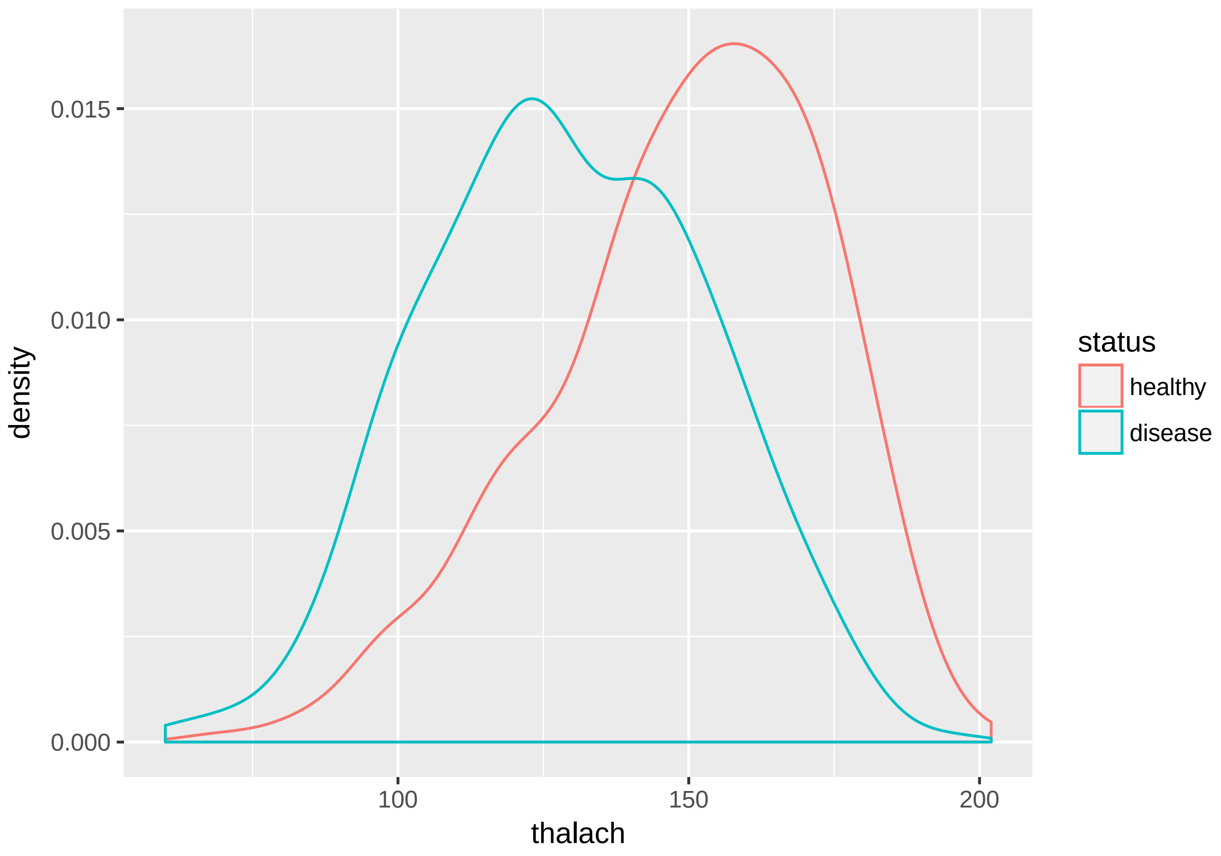
```
ggplot(combined.data, aes(x = fbs, fill=status)) + geom_bar(position="dodge")
```



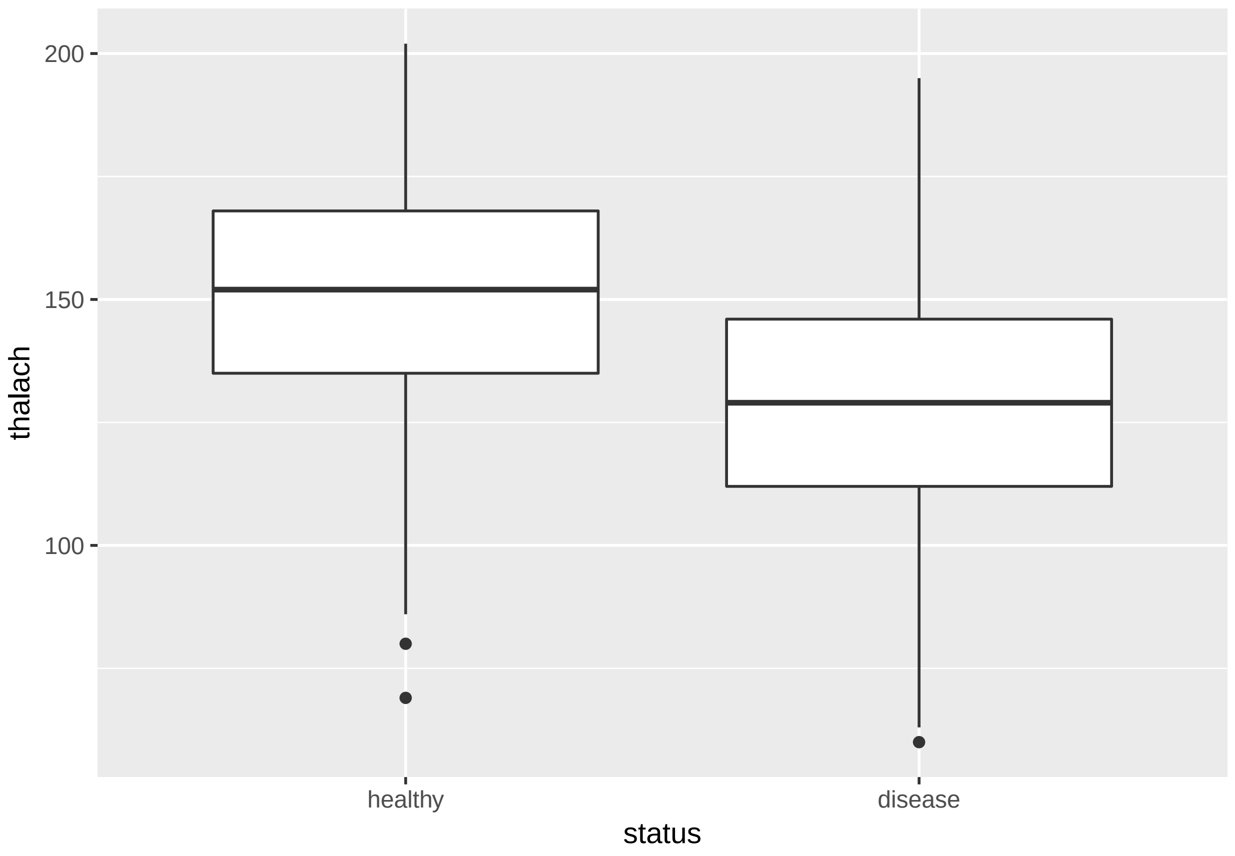
```r
ggplot(combined.data, aes(x = restecg, fill=status)) + geom_bar(position="dodge")
```



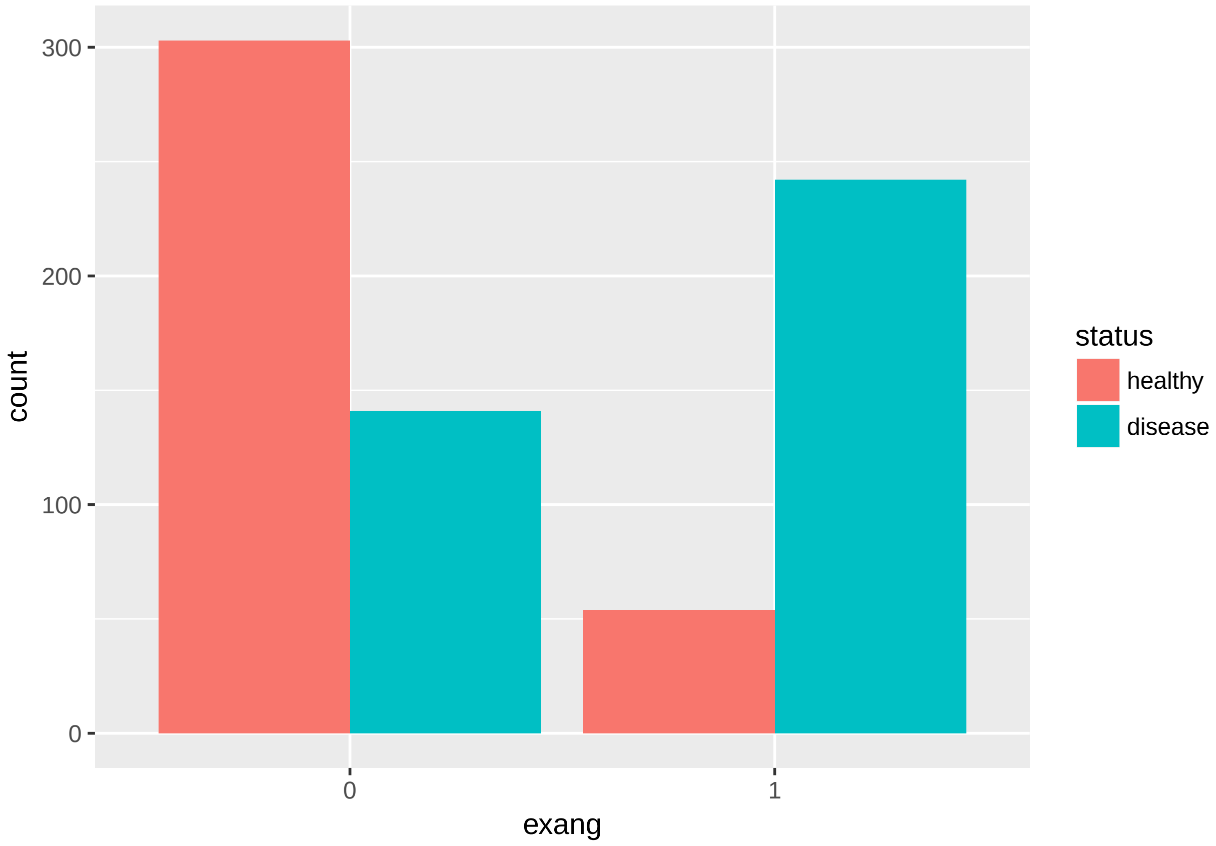
```r
ggplot(combined.data, aes(x=thalach, color = status)) + geom_density()
```



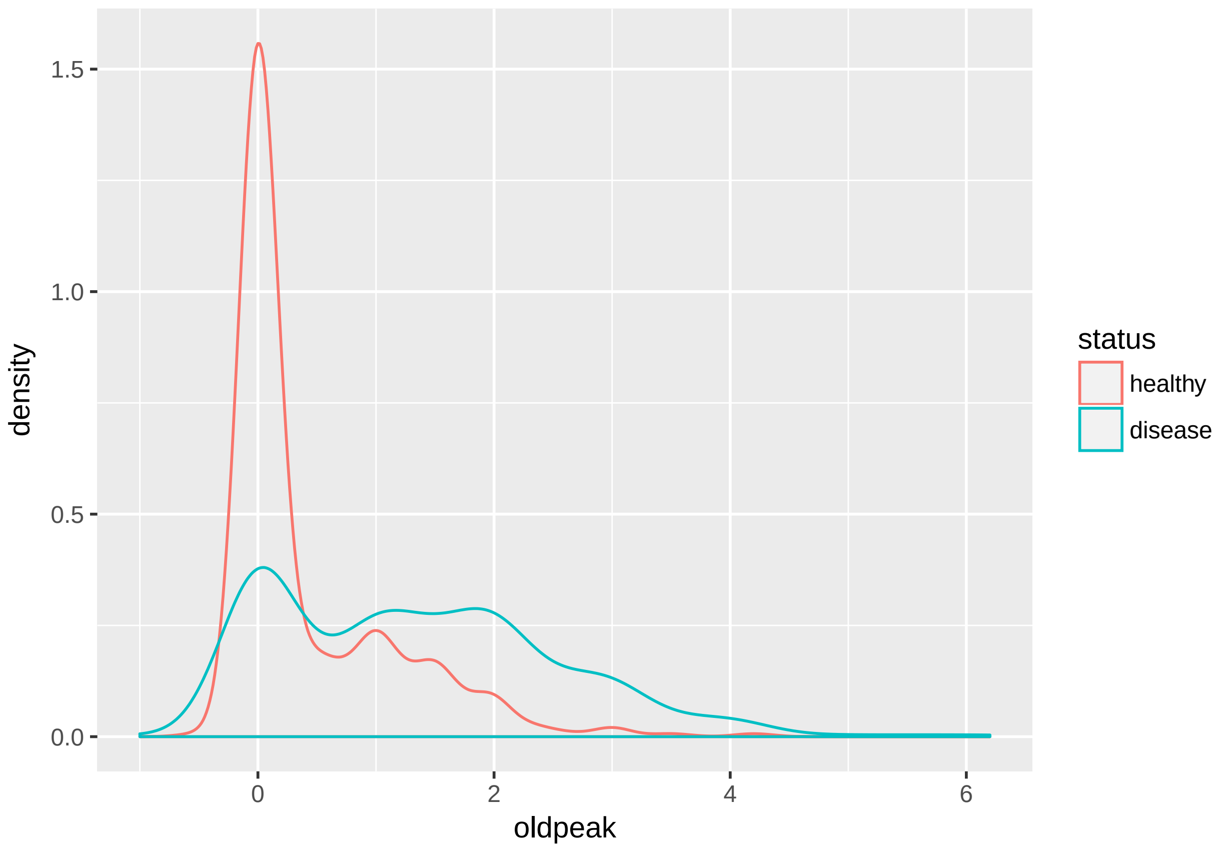
```
ggplot(combined.data, aes(x=status, y = thalach)) + geom_boxplot()
```



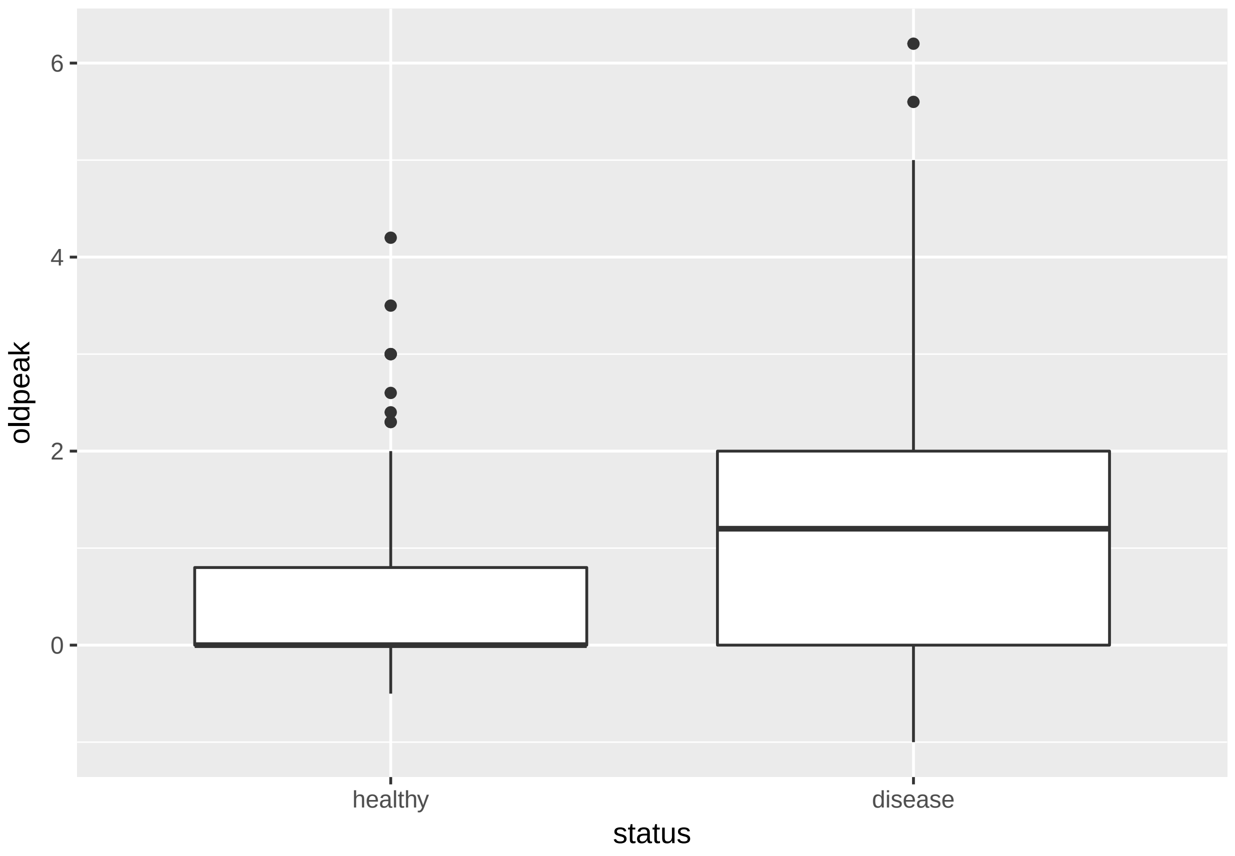
```r
ggplot(combined.data, aes(x = exang, fill=status)) + geom_bar(position="dodge")
```



```r
ggplot(combined.data, aes(x=oldpeak, color = status)) + geom_density()
```



```
ggplot(combined.data, aes(x=status, y = oldpeak)) + geom_boxplot()
```

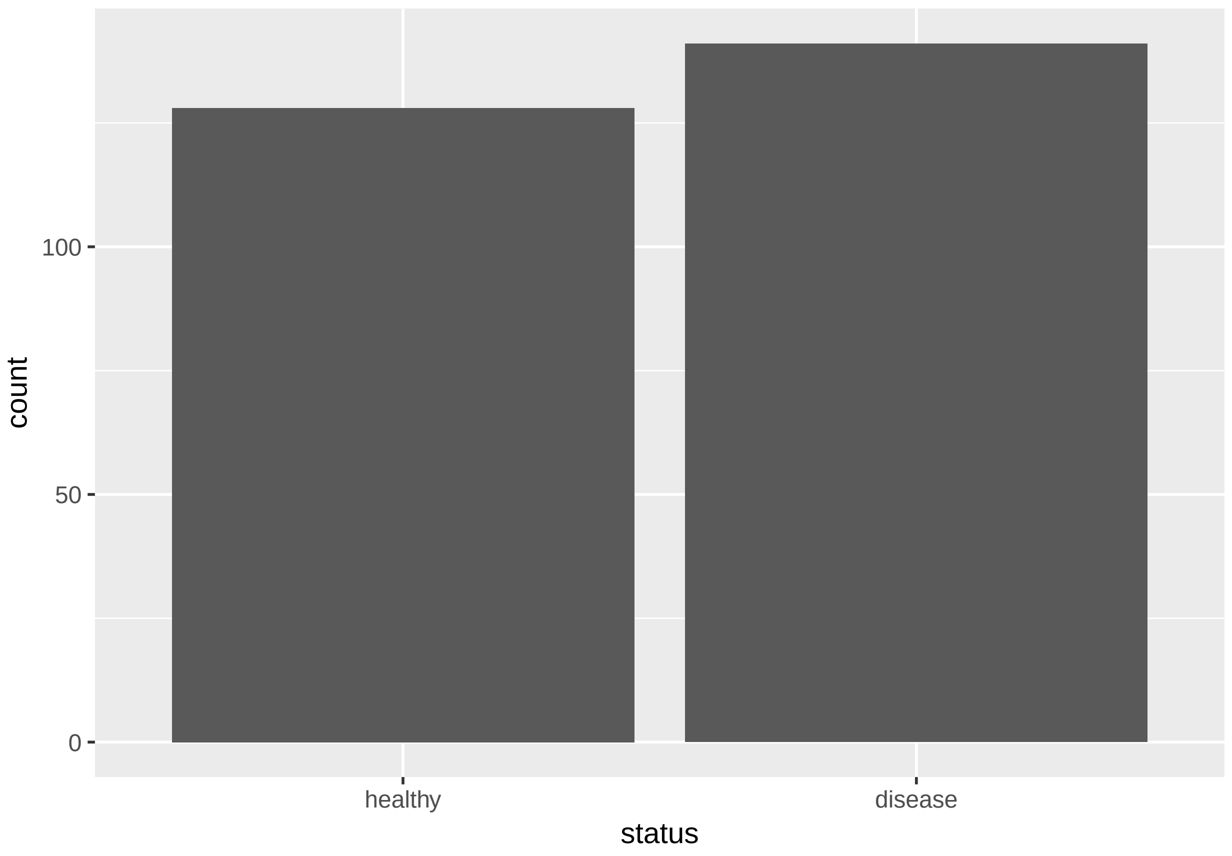


Splitting training and testing data

```r
set.seed(100)
sample = sample.split(combined.data, SplitRatio = 0.70)
train = subset(combined.data, sample == T)
test = subset(combined.data, sample == F)
summary(test)
```

```
##       age             sex        cp         trestbps          chol      
##  Min.   :29.0   female: 67   1: 14   Min.   :  0.0   Min.   :  0.0  
##  1st Qu.:46.0   male  :202   2: 53   1st Qu.:120.0   1st Qu.:203.0  
##  Median :54.0                3: 59   Median :130.0   Median :234.0  
##  Mean   :53.2                4:143   Mean   :132.3   Mean   :220.9  
##  3rd Qu.:60.0                        3rd Qu.:140.0   3rd Qu.:268.0  
##  Max.   :77.0                        Max.   :200.0   Max.   :564.0  
##  fbs     restecg    thalach      exang      oldpeak          status   
##  0:228   0:166   Min.   : 69.0   0:164   Min.   :0.0000   healthy:128  
##  1: 41   1: 44   1st Qu.:120.0   1:105   1st Qu.:0.0000   disease:141  
##          2: 59   Median :140.0           Median :0.4000                
##                  Mean   :139.4           Mean   :0.8643                
##                  3rd Qu.:160.0           3rd Qu.:1.5000                
##                  Max.   :202.0           Max.   :5.0000                
```

```r
ggplot(test, aes(x = status)) + geom_bar()
```



Methods and Results

Baseline approach: Logistic regression.

Training the full model, the model using the five selected features (sex, cp, thalach, exang, oldpeak), and the model using all predictors except trestbps.

```
logit.model = train(status ~ ., data=train, method = 'glm', family = 'binomial')
summary(logit.model)
```

```
##
## Call:
## NULL
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.8479  -0.6053   0.1551   0.5699   2.6069
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept) -2.9049653  1.7734166  -1.638 0.101409
## age          0.0162828  0.0161423   1.009 0.313119
## sexmale      1.3139698  0.3380953   3.886 0.000102 ***
## cp2         -0.0368386  0.6284873  -0.059 0.953259
## cp3          0.2472175  0.5918941   0.418 0.676187
## cp4          1.5137979  0.5736822   2.639 0.008321 **
## trestbps     0.0138848  0.0075800   1.832 0.066986 .
## chol        -0.0009002  0.0015325  -0.587 0.556919
## fbs1         0.5491646  0.3725546   1.474 0.140468
## restecg1     0.0207829  0.3743793   0.056 0.955730
## restecg2     0.3275127  0.3183371   1.029 0.303562
## thalach     -0.0187948  0.0058359  -3.221 0.001279 **
## exang1       0.9493386  0.2832175   3.352 0.000802 ***
## oldpeak      0.7788933  0.1484223   5.248 1.54e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 652.59  on 470  degrees of freedom
## Residual deviance: 390.26  on 457  degrees of freedom
## AIC: 418.26
##
## Number of Fisher Scoring iterations: 5
```

```
logit.result = predict(logit.model, test)
confusionMatrix(test$status, logit.result)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction healthy disease
##    healthy     109      19
##    disease      35     106
##
##                Accuracy : 0.7993
##                  95% CI : (0.7463, 0.8454)
##     No Information Rate : 0.5353
##     P-Value [Acc > NIR] : < 2e-16
##
##                   Kappa : 0.5999
##  Mcnemar's Test P-Value : 0.04123
##
##             Sensitivity : 0.7569
##             Specificity : 0.8480
##          Pos Pred Value : 0.8516
##          Neg Pred Value : 0.7518
##              Prevalence : 0.5353
##          Detection Rate : 0.4052
##    Detection Prevalence : 0.4758
##       Balanced Accuracy : 0.8025
##
##        'Positive' Class : healthy
##
```

```
smalllogit.model = train(status ~ sex +cp + thalach +exang +oldpeak, data=train, method = 'glm', family
smalllogit.result = predict(smalllogit.model, test)
confusionMatrix(test$status, smalllogit.result)
```

```
## Confusion Matrix and Statistics
```

```
##
##           Reference
## Prediction healthy disease
##    healthy     108      20
##    disease      32     109
##
##                Accuracy : 0.8067
##                  95% CI : (0.7544, 0.8521)
##     No Information Rate : 0.5204
##     P-Value [Acc > NIR] : <2e-16
##
##                   Kappa : 0.6141
##  Mcnemar's Test P-Value : 0.1272
##
##             Sensitivity : 0.7714
##             Specificity : 0.8450
##          Pos Pred Value : 0.8438
##          Neg Pred Value : 0.7730
##              Prevalence : 0.5204
##          Detection Rate : 0.4015
##    Detection Prevalence : 0.4758
##       Balanced Accuracy : 0.8082
##
##        'Positive' Class : healthy
##
```

```
allbutonelogit.model = train(status ~ sex +cp + thalach +exang +oldpeak+restecg+fbs+chol+age, data=trai
allbutonelogit.result = predict(allbutonelogit.model, test)
confusionMatrix(test$status, allbutonelogit.result)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction healthy disease
##    healthy     111      17
##    disease      34     107
##
##                Accuracy : 0.8104
##                  95% CI : (0.7584, 0.8555)
##     No Information Rate : 0.539
##     P-Value [Acc > NIR] : < 2e-16
##
##                   Kappa : 0.6222
##  Mcnemar's Test P-Value : 0.02506
##
##             Sensitivity : 0.7655
##             Specificity : 0.8629
##          Pos Pred Value : 0.8672
##          Neg Pred Value : 0.7589
##              Prevalence : 0.5390
##          Detection Rate : 0.4126
##    Detection Prevalence : 0.4758
##       Balanced Accuracy : 0.8142
##
##        'Positive' Class : healthy
```

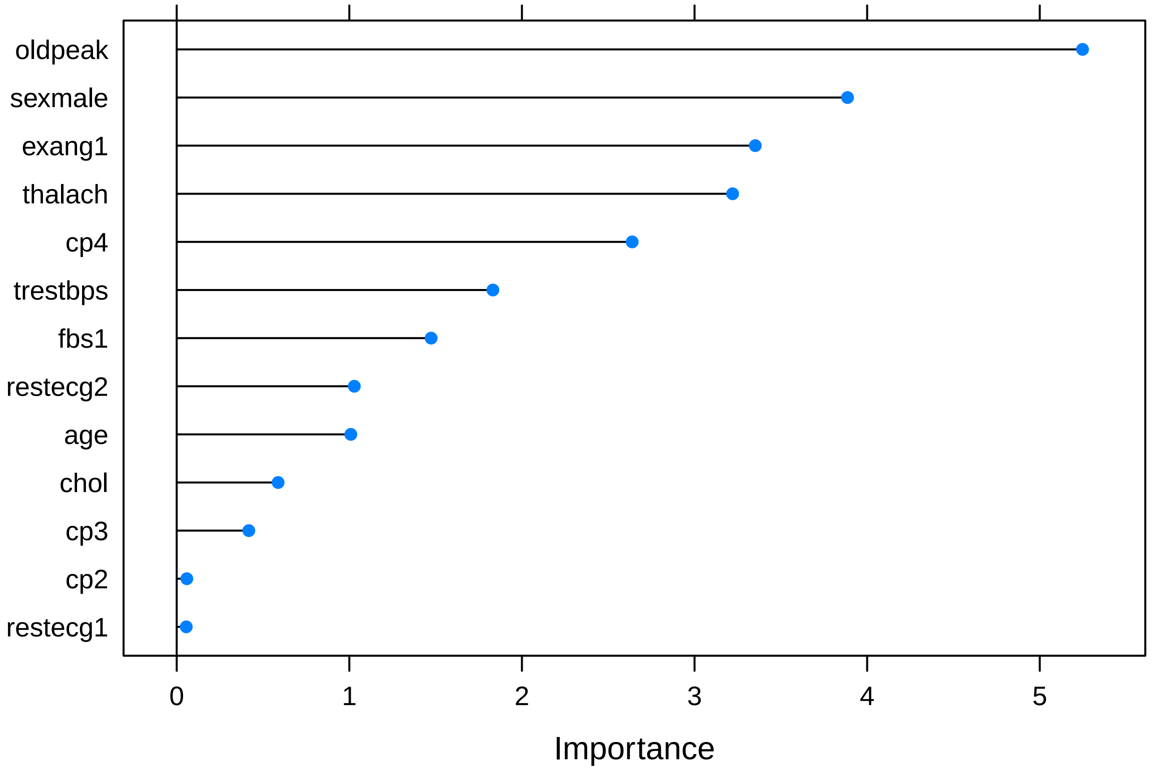
```
##
```

variable importance for logistic model: t statistic/statistical significance

```
importance = varImp(logit.model, scale=FALSE)
importance
```

```
## glm variable importance
##
##           Overall
## oldpeak  5.24782
## sexmale  3.88639
## exang1   3.35198
## thalach  3.22054
## cp4      2.63874
## trestbps 1.83177
## fbs1     1.47405
## restecg2 1.02882
## age      1.00870
## chol     0.58742
## cp3      0.41767
## cp2      0.05861
## restecg1 0.05551
```

```
plot(importance)
```



Approach 2: Naive Bayes classification

Training the full model, the model using the five selected features (sex, cp, thalach, exang, oldpeak), and the model using all predictors except trestbps (best model).

```r
naiveBayes.model = naiveBayes(status ~., data = train)
naiveBayes.model
```

```
##
## Naive Bayes Classifier for Discrete Predictors
##
## Call:
## naiveBayes.default(x = X, y = Y, laplace = laplace)
##
## A-priori probabilities:
## Y
##   healthy   disease
## 0.4861996 0.5138004
##
## Conditional probabilities:
##          age
## Y             [,1]     [,2]
##   healthy 50.30131 9.527479
##   disease 55.63223 8.548681
##
##          sex
## Y            female      male
##   healthy 0.3580786 0.6419214
##   disease 0.1033058 0.8966942
##
##          cp
## Y                  1          2          3          4
##   healthy 0.06550218 0.34934498 0.31441048 0.27074236
##   disease 0.03305785 0.07024793 0.12396694 0.77272727
##
##          trestbps
## Y             [,1]     [,2]
##   healthy 129.7380 16.77721
##   disease 136.0744 18.21457
##
##          chol
## Y             [,1]     [,2]
##   healthy 230.5939  65.9265
##   disease 209.3430 109.4753
##
##          fbs
## Y                 0         1
##   healthy 0.8908297 0.1091703
##   disease 0.8140496 0.1859504
##
##          restecg
## Y                 0         1         2
##   healthy 0.6593886 0.1179039 0.2227074
##   disease 0.5289256 0.2024793 0.2685950
##
##          thalach
## Y             [,1]     [,2]
##   healthy 149.2314 22.97049
##   disease 128.0372 23.89766
```

```
##
##          exang
## Y                 0         1
##   healthy 0.8384279 0.1615721
##   disease 0.3636364 0.6363636
##
##          oldpeak
## Y              [,1]      [,2]
##   healthy 0.4039301 0.6572352
##   disease 1.3917355 1.2229538
```

```r
naiveBayes.result = predict(naiveBayes.model, train)
confusionMatrix(train$status, naiveBayes.result)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction healthy disease
##    healthy     188      41
##    disease      47     195
##
##                Accuracy : 0.8132
##                  95% CI : (0.775, 0.8474)
##     No Information Rate : 0.5011
##     P-Value [Acc > NIR] : <2e-16
##
##                   Kappa : 0.6263
##  Mcnemar's Test P-Value : 0.594
##
##             Sensitivity : 0.8000
##             Specificity : 0.8263
##          Pos Pred Value : 0.8210
##          Neg Pred Value : 0.8058
##              Prevalence : 0.4989
##          Detection Rate : 0.3992
##    Detection Prevalence : 0.4862
##       Balanced Accuracy : 0.8131
##
##        'Positive' Class : healthy
##
```

```r
smallnaiveBayes.model = naiveBayes(status ~sex +cp + thalach +exang +oldpeak, data = train)
smallnaiveBayes.result = predict(smallnaiveBayes.model, test)
confusionMatrix(test$status, smallnaiveBayes.result)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction healthy disease
##    healthy     108      20
##    disease      35     106
##
##                Accuracy : 0.7955
##                  95% CI : (0.7423, 0.8421)
##     No Information Rate : 0.5316
##     P-Value [Acc > NIR] : < 2e-16
##
##                   Kappa : 0.5923
##  Mcnemar's Test P-Value : 0.05906
##
##             Sensitivity : 0.7552
##             Specificity : 0.8413
##          Pos Pred Value : 0.8438
##          Neg Pred Value : 0.7518
##              Prevalence : 0.5316
##          Detection Rate : 0.4015
##    Detection Prevalence : 0.4758
##       Balanced Accuracy : 0.7983
##
##        'Positive' Class : healthy
##
```

```
bestnaiveBayes.model = naiveBayes(status ~sex +cp + thalach +exang +oldpeak+restecg+fbs+chol+age, data
bestnaiveBayes.result = predict(bestnaiveBayes.model, test)
confusionMatrix(test$status, bestnaiveBayes.result)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction healthy disease
##    healthy     109      19
##    disease      24     117
##
##                Accuracy : 0.8401
##                  95% CI : (0.7908, 0.8818)
##     No Information Rate : 0.5056
##     P-Value [Acc > NIR] : <2e-16
##
##                   Kappa : 0.6801
##  Mcnemar's Test P-Value : 0.5419
##
##             Sensitivity : 0.8195
##             Specificity : 0.8603
##          Pos Pred Value : 0.8516
##          Neg Pred Value : 0.8298
##              Prevalence : 0.4944
##          Detection Rate : 0.4052
##    Detection Prevalence : 0.4758
##       Balanced Accuracy : 0.8399
##
##        'Positive' Class : healthy
##
```

Approach 3: Support vector machines

Using 10-fold, 3-repeat to tune parameter C. Training the full model, the model using the five selected features (sex, cp, thalach, exang, oldpeak), and the model using all predictors except trestbps.

```r
fitControl = trainControl(method = "repeatedcv", number = 10, repeats = 3)
set.seed(100)
svm.model = train(status ~., data = train, method = "svmRadial", trControl = fitControl)
svm.model
```

```
## Support Vector Machines with Radial Basis Function Kernel
##
## 471 samples
##  10 predictor
##   2 classes: 'healthy', 'disease'
##
## No pre-processing
## Resampling: Cross-Validated (10 fold, repeated 3 times)
## Summary of sample sizes: 424, 424, 424, 424, 424, 424, ...
## Resampling results across tuning parameters:
##
##   C     Accuracy   Kappa
##   0.25  0.7890052  0.5774449
##   0.50  0.7911630  0.5825566
##   1.00  0.7926425  0.5856137
##
## Tuning parameter 'sigma' was held constant at a value of 0.05299966
## Accuracy was used to select the optimal model using the largest value.
## The final values used for the model were sigma = 0.05299966 and C = 1.
```

```r
svm.result = predict(svm.model, newdata = test)
confusionMatrix(test$status, svm.result)
```

```
## Confusion Matrix and Statistics
##
##              Reference
## Prediction healthy disease
##    healthy     111      17
##    disease      33     108
##
##                Accuracy : 0.8141
##                  95% CI : (0.7624, 0.8588)
##     No Information Rate : 0.5353
##     P-Value [Acc > NIR] : < 2e-16
##
##                   Kappa : 0.6295
##  Mcnemar's Test P-Value : 0.03389
##
##             Sensitivity : 0.7708
##             Specificity : 0.8640
##          Pos Pred Value : 0.8672
##          Neg Pred Value : 0.7660
##              Prevalence : 0.5353
##          Detection Rate : 0.4126
##    Detection Prevalence : 0.4758
##       Balanced Accuracy : 0.8174
##
##        'Positive' Class : healthy
##
```

```r
set.seed(100)
smallsvm.model = train(status ~sex +cp + thalach +exang +oldpeak, data = train,
                 method = "svmRadial",
                 trControl = fitControl)
smallsvm.result = predict(smallsvm.model, newdata = test)
confusionMatrix(test$status, smallsvm.result)
```

```
## Confusion Matrix and Statistics
##
##              Reference
## Prediction healthy disease
##    healthy     112      16
##    disease      41     100
##
##                Accuracy : 0.7881
##                  95% CI : (0.7344, 0.8354)
##     No Information Rate : 0.5688
##     P-Value [Acc > NIR] : 3.319e-14
##
##                   Kappa : 0.579
##  Mcnemar's Test P-Value : 0.001478
##
##             Sensitivity : 0.7320
##             Specificity : 0.8621
##          Pos Pred Value : 0.8750
##          Neg Pred Value : 0.7092
##              Prevalence : 0.5688
##          Detection Rate : 0.4164
##    Detection Prevalence : 0.4758
##       Balanced Accuracy : 0.7970
##
##        'Positive' Class : healthy
##
```

```r
set.seed(100)
allbutonesvm.model = train(status ~sex +cp + thalach +exang +oldpeak+restecg+fbs+chol+age, data = train
                 method = "svmRadial",
                 trControl = fitControl)
allbutonesvm.result = predict(allbutonesvm.model, newdata = test)
confusionMatrix(test$status, allbutonesvm.result)
```

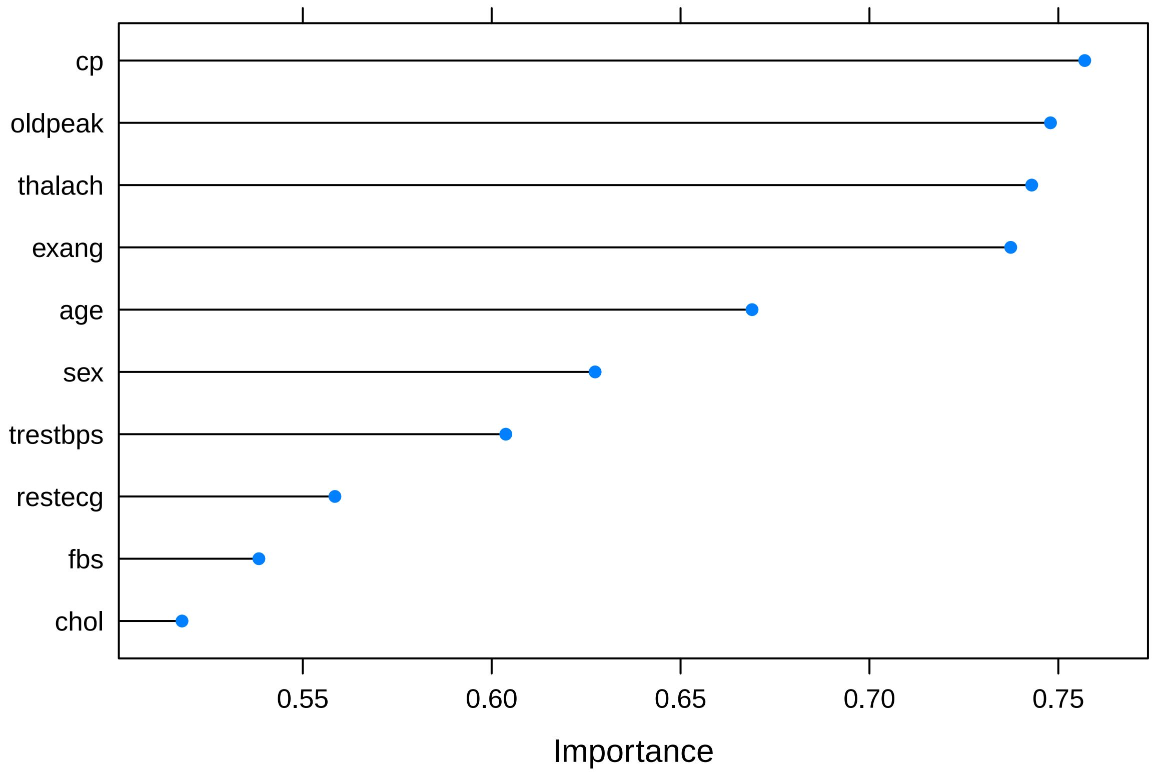
```
## Confusion Matrix and Statistics
##
##              Reference
## Prediction healthy disease
##    healthy     111      17
##    disease      31     110
##
##                Accuracy : 0.8216
##                  95% CI : (0.7705, 0.8654)
##     No Information Rate : 0.5279
##     P-Value [Acc > NIR] : <2e-16
##
##                   Kappa : 0.6441
##  Mcnemar's Test P-Value : 0.0606
##
##             Sensitivity : 0.7817
##             Specificity : 0.8661
##          Pos Pred Value : 0.8672
##          Neg Pred Value : 0.7801
##              Prevalence : 0.5279
##          Detection Rate : 0.4126
##    Detection Prevalence : 0.4758
##       Balanced Accuracy : 0.8239
##
##        'Positive' Class : healthy
##
```

Variable importance for the full svm model, using ROC value as variable importance.

```
importance = varImp(svm.model, scale=FALSE)
importance
```

```
## ROC curve variable importance
##
##          Importance
## cp           0.7570
## oldpeak      0.7479
## thalach      0.7430
## exang        0.7374
## age          0.6689
## sex          0.6274
## trestbps     0.6037
## restecg      0.5585
## fbs          0.5384
## chol         0.5180
```

```
plot(importance)
```



Approach 4: Random forests

with 10 fold, 3 repeat cross validation to tune the parameter mtry. Training the full model, the model using the five selected features (sex, cp, thalach, exang, oldpeak), and the model using all predictors except trestbps.

```r
fitControl = trainControl(method = "repeatedcv", number = 10, repeats = 3)
set.seed(100)
rf.model = train(status~., data=train, method="rf", trControl = fitControl)
rf.model
```

```
## Random Forest
##
## 471 samples
##  10 predictor
##   2 classes: 'healthy', 'disease'
##
## No pre-processing
## Resampling: Cross-Validated (10 fold, repeated 3 times)
## Summary of sample sizes: 424, 424, 424, 424, 424, 424, ...
## Resampling results across tuning parameters:
##
##   mtry  Accuracy   Kappa
##    2    0.7855053  0.5706418
##    7    0.7685130  0.5366725
##   13    0.7550667  0.5098978
##
## Accuracy was used to select the optimal model using the largest value.
## The final value used for the model was mtry = 2.
```

```r
rf.result = predict(rf.model, test)
confusionMatrix(test$status, rf.result)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction healthy disease
##    healthy     109      19
##    disease      30     111
##
##                Accuracy : 0.8178
##                  95% CI : (0.7664, 0.8621)
##     No Information Rate : 0.5167
##     P-Value [Acc > NIR] : <2e-16
##
##                   Kappa : 0.6363
##  Mcnemar's Test P-Value : 0.1531
##
##             Sensitivity : 0.7842
##             Specificity : 0.8538
##          Pos Pred Value : 0.8516
##          Neg Pred Value : 0.7872
##              Prevalence : 0.5167
##          Detection Rate : 0.4052
##    Detection Prevalence : 0.4758
##       Balanced Accuracy : 0.8190
##
##        'Positive' Class : healthy
##
```

```r
predictors(rf.model)
```

```
##  [1] "age"      "sexmale"  "cp2"      "cp3"      "cp4"      "trestbps"
##  [7] "chol"     "fbs1"     "restecg1" "restecg2" "thalach"  "exang1"
## [13] "oldpeak"
```

Small random forests model using only the 5 selected predictors.

```r
set.seed(100)
fitControl = trainControl(method = "repeatedcv", number = 10, repeats = 3)
smallrf.model = train(status~sex +cp + thalach +exang +oldpeak, data=train, method="rf")
smallrf.model
```

```
## Random Forest
##
## 471 samples
##   5 predictor
##   2 classes: 'healthy', 'disease'
##
## No pre-processing
## Resampling: Bootstrapped (25 reps)
## Summary of sample sizes: 471, 471, 471, 471, 471, 471, ...
## Resampling results across tuning parameters:
##
##   mtry  Accuracy   Kappa
##   2     0.7731039  0.5455893
##   4     0.7484221  0.4966682
##   7     0.7363129  0.4727022
##
## Accuracy was used to select the optimal model using the largest value.
## The final value used for the model was mtry = 2.
```

```r
smallrf.result = predict(smallrf.model, test)
confusionMatrix(test$status, smallrf.result)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction healthy disease
##    healthy     107      21
##    disease      36     105
##
##                Accuracy : 0.7881
##                  95% CI : (0.7344, 0.8354)
##     No Information Rate : 0.5316
##     P-Value [Acc > NIR] : < 2e-16
##
##                   Kappa : 0.5775
##  Mcnemar's Test P-Value : 0.06369
##
##             Sensitivity : 0.7483
##             Specificity : 0.8333
##          Pos Pred Value : 0.8359
##          Neg Pred Value : 0.7447
##              Prevalence : 0.5316
##          Detection Rate : 0.3978
##    Detection Prevalence : 0.4758
##       Balanced Accuracy : 0.7908
##
##        'Positive' Class : healthy
##
```

```r
set.seed(100)
fitControl = trainControl(method = "repeatedcv", number = 10, repeats = 3)
allbutonerf.model = train(status~sex +cp + thalach +exang +oldpeak+restecg+fbs+chol+age, data=train, me
allbutonerf.model
```

```
## Random Forest
##
## 471 samples
##   9 predictor
##   2 classes: 'healthy', 'disease'
##
## No pre-processing
## Resampling: Bootstrapped (25 reps)
## Summary of sample sizes: 471, 471, 471, 471, 471, 471, ...
## Resampling results across tuning parameters:
##
##   mtry  Accuracy   Kappa
##    2    0.7667562  0.5331466
##    7    0.7478859  0.4954635
##   12    0.7393062  0.4781812
```

```
##
## Accuracy was used to select the optimal model using the largest value.
## The final value used for the model was mtry = 2.
```

```
allbutonerf.result = predict(allbutonerf.model, test)
confusionMatrix(test$status, allbutonerf.result)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction healthy disease
##    healthy     108      20
##    disease      31     110
##
##                Accuracy : 0.8104
##                  95% CI : (0.7584, 0.8555)
##     No Information Rate : 0.5167
##     P-Value [Acc > NIR] : <2e-16
##
##                   Kappa : 0.6214
##  Mcnemar's Test P-Value : 0.1614
##
##             Sensitivity : 0.7770
##             Specificity : 0.8462
##          Pos Pred Value : 0.8438
##          Neg Pred Value : 0.7801
##              Prevalence : 0.5167
##          Detection Rate : 0.4015
##    Detection Prevalence : 0.4758
##       Balanced Accuracy : 0.8116
##
##        'Positive' Class : healthy
##
```

Variable selection via recursive variable elimination using random forests

```
set.seed(100)
control = rfeControl(functions=rfFuncs, method="cv", number=10, repeats = 3, returnResamp = "all")
results = rfe(train[, 1:10], train[, 11],  rfeControl=control)
results
```

```
##
## Recursive feature selection
##
## Outer resampling method: Cross-Validated (10 fold)
##
## Resampling performance over subset size:
##
##  Variables Accuracy  Kappa AccuracySD KappaSD Selected
##          4   0.7284 0.4564    0.06860  0.1375
##          8   0.7538 0.5078    0.05571  0.1113
##         10   0.7580 0.5162    0.06024  0.1197        *
##
## The top 5 variables (out of 10):
##    cp, oldpeak, exang, sex, thalach
```

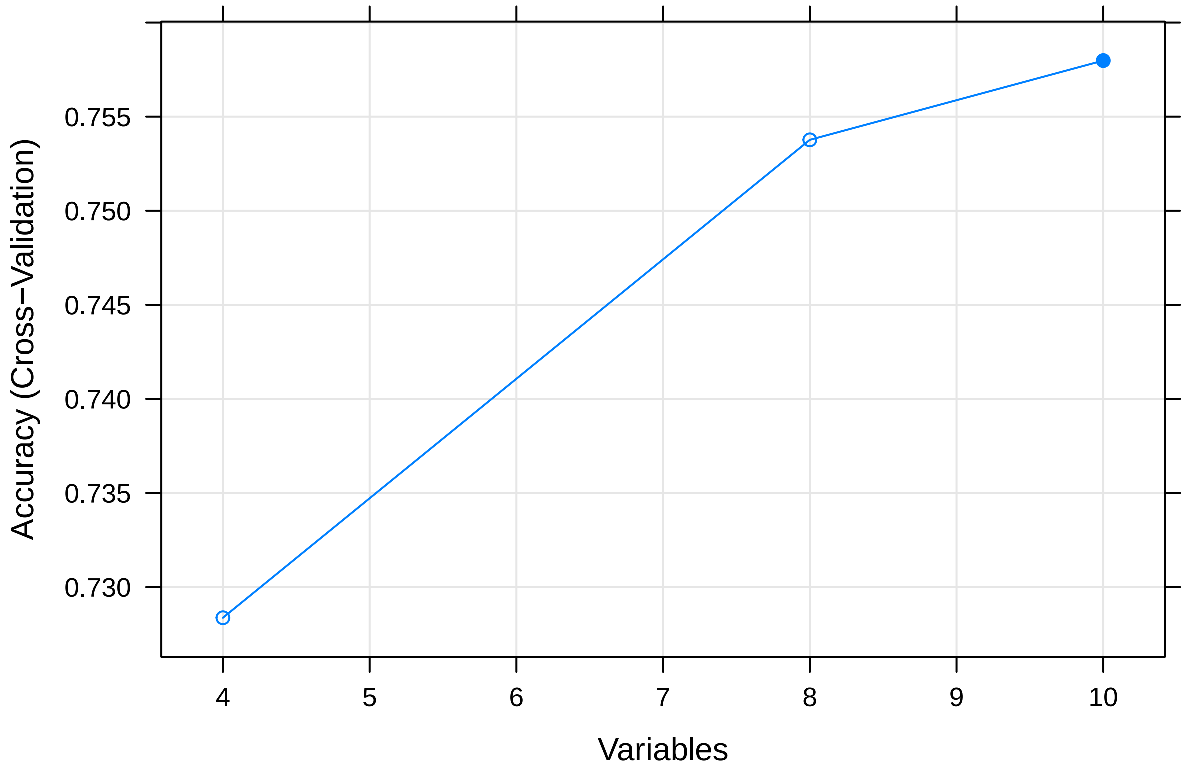
```r
print(results)
```

```
##
## Recursive feature selection
##
## Outer resampling method: Cross-Validated (10 fold)
##
## Resampling performance over subset size:
##
##  Variables Accuracy  Kappa AccuracySD KappaSD Selected
##          4   0.7284 0.4564    0.06860  0.1375
##          8   0.7538 0.5078    0.05571  0.1113
##         10   0.7580 0.5162    0.06024  0.1197        *
##
## The top 5 variables (out of 10):
##    cp, oldpeak, exang, sex, thalach
```

```r
predictors(results)
```

```
##  [1] "cp"       "oldpeak"  "exang"    "sex"      "thalach"  "age"
##  [7] "fbs"      "chol"     "restecg"  "trestbps"
```

```r
plot(results, type = c("g", "o"))
```



Approach 5: Single layer neural network

Using 10 fold, 3 repeat cross validation to tune the parameters size and decay. Training the full model, the model using the five selected features (sex, cp, thalach, exang, oldpeak), and the model using all predictors except trestbps.

```r
fitControl = trainControl(method = "repeatedcv", number = 10, repeats = 3)
set.seed(100)
nnet.model = train(status ~ ., data = train, method = "nnet",  trControl = fitControl, verbose = FALSE,
nnet.model
```

```
## Neural Network
##
## 471 samples
##  10 predictor
##   2 classes: 'healthy', 'disease'
##
## No pre-processing
## Resampling: Cross-Validated (10 fold, repeated 3 times)
## Summary of sample sizes: 424, 424, 424, 424, 424, 424, ...
## Resampling results across tuning parameters:
##
##   size  decay  Accuracy   Kappa
##   1     0e+00  0.5762129  0.1388614
##   1     1e-04  0.5661360  0.1161913
##   1     1e-01  0.7755011  0.5522494
##   3     0e+00  0.6563483  0.3152133
##   3     1e-04  0.6554091  0.3066531
##   3     1e-01  0.7962181  0.5927021
##   5     0e+00  0.7206413  0.4429703
##   5     1e-04  0.7256090  0.4526095
##   5     1e-01  0.7826678  0.5655450
##
## Accuracy was used to select the optimal model using the largest value.
## The final values used for the model were size = 3 and decay = 0.1.
```

```r
nnet.result = predict(nnet.model, test)
confusionMatrix(test$status, nnet.result)
```

```
## Confusion Matrix and Statistics
##
##             Reference
## Prediction healthy disease
##    healthy     113      15
##    disease      37     104
##
##                Accuracy : 0.8067
##                  95% CI : (0.7544, 0.8521)
##     No Information Rate : 0.5576
##     P-Value [Acc > NIR] : < 2.2e-16
##
##                   Kappa : 0.6155
##  Mcnemar's Test P-Value : 0.003589
##
##             Sensitivity : 0.7533
##             Specificity : 0.8739
##          Pos Pred Value : 0.8828
##          Neg Pred Value : 0.7376
##              Prevalence : 0.5576
##          Detection Rate : 0.4201
##    Detection Prevalence : 0.4758
##       Balanced Accuracy : 0.8136
##
##        'Positive' Class : healthy
##
```

```
set.seed(100)
smallnnet.model = train(status ~ sex +cp + thalach +exang +oldpeak, data = train, method = "nnet",  trC
smallnnet.model
```

```
## Neural Network
##
## 471 samples
##   5 predictor
##   2 classes: 'healthy', 'disease'
##
## No pre-processing
## Resampling: Cross-Validated (10 fold, repeated 3 times)
## Summary of sample sizes: 424, 424, 424, 424, 424, 424, ...
## Resampling results across tuning parameters:
##
##   size  decay  Accuracy   Kappa
##   1     0e+00  0.5329357  0.04123052
##   1     1e-04  0.5230066  0.01914251
##   1     1e-01  0.7770981  0.55263622
##   3     0e+00  0.5857308  0.15125408
##   3     1e-04  0.6149688  0.21190317
##   3     1e-01  0.7875591  0.57553217
##   5     0e+00  0.5984794  0.17879022
##   5     1e-04  0.6477696  0.28080780
##   5     1e-01  0.7854925  0.57149119
##
## Accuracy was used to select the optimal model using the largest value.
## The final values used for the model were size = 3 and decay = 0.1.
```

```
smallnnet.result = predict(smallnnet.model, test)
confusionMatrix(test$status, smallnnet.result)
```

```
## Confusion Matrix and Statistics
##
##            Reference
## Prediction healthy disease
##    healthy     111      17
##    disease      46      95
##
##                Accuracy : 0.7658
##                  95% CI : (0.7106, 0.8151)
##     No Information Rate : 0.5836
##     P-Value [Acc > NIR] : 2.732e-10
##
##                   Kappa : 0.5354
##  Mcnemar's Test P-Value : 0.0004192
##
##             Sensitivity : 0.7070
##             Specificity : 0.8482
##          Pos Pred Value : 0.8672
##          Neg Pred Value : 0.6738
##               Prevalence : 0.5836
##           Detection Rate : 0.4126
##     Detection Prevalence : 0.4758
##        Balanced Accuracy : 0.7776
##
##         'Positive' Class : healthy
##
```

```
set.seed(100)
allbutonennet.model = train(status ~ sex +cp + thalach +exang +oldpeak+restecg+fbs+chol+age, data = tra
allbutonennet.model
```

```
## Neural Network
##
## 471 samples
##   9 predictor
##   2 classes: 'healthy', 'disease'
##
## No pre-processing
## Resampling: Cross-Validated (10 fold, repeated 3 times)
## Summary of sample sizes: 424, 424, 424, 424, 424, 424, ...
## Resampling results across tuning parameters:
##
##   size  decay  Accuracy   Kappa
##   1     0e+00  0.5583076  0.11128240
##   1     1e-04  0.5492034  0.08640709
##   1     1e-01  0.7465695  0.49623483
##   3     0e+00  0.6270512  0.25256294
##   3     1e-04  0.6169506  0.23775842
##   3     1e-01  0.7912080  0.58247455
##   5     0e+00  0.6840850  0.37639982
##   5     1e-04  0.6555164  0.32074816
##   5     1e-01  0.7962503  0.59262688
##
## Accuracy was used to select the optimal model using the largest value.
## The final values used for the model were size = 5 and decay = 0.1.
```

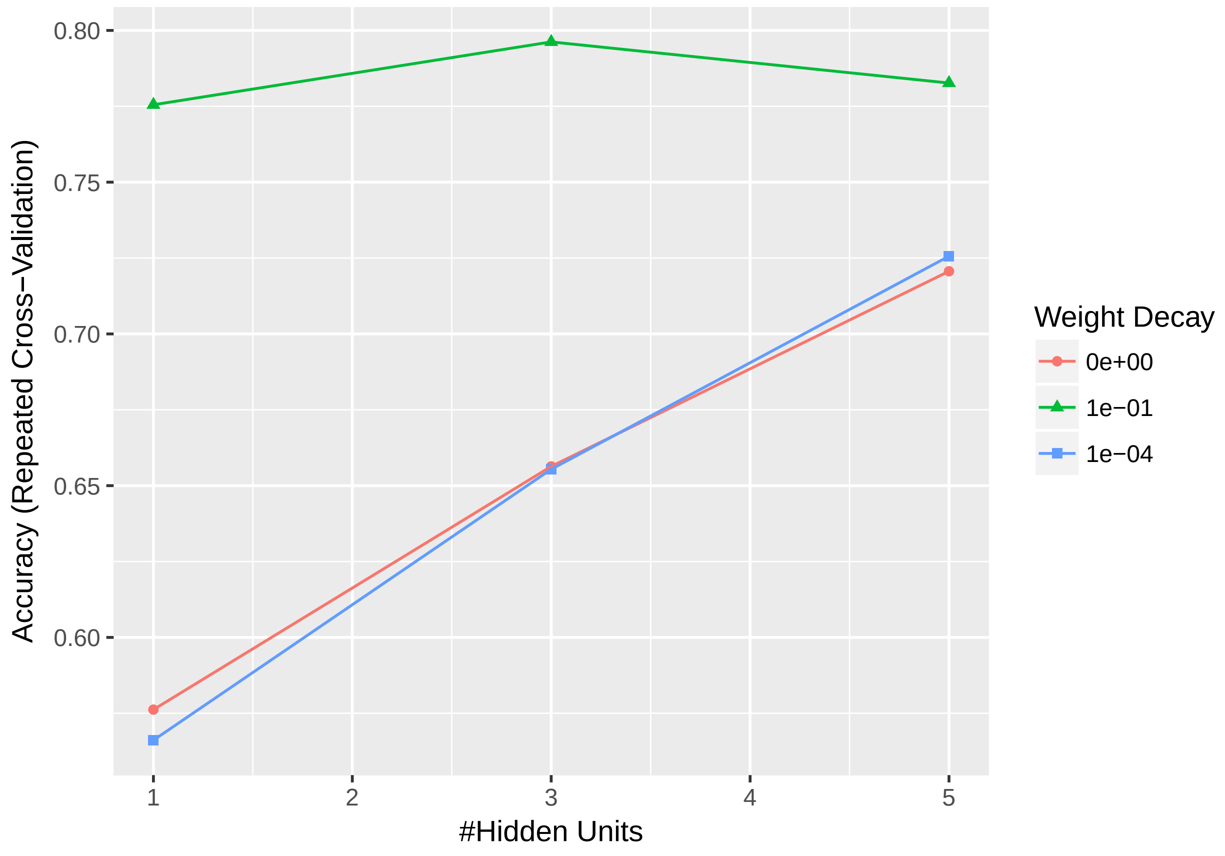
```
allbutonennet.result = predict(allbutonennet.model, test)
confusionMatrix(test$status, allbutonennet.result)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction healthy disease
##    healthy     112      16
##    disease      37     104
##
##                Accuracy : 0.803
##                  95% CI : (0.7503, 0.8488)
##     No Information Rate : 0.5539
##     P-Value [Acc > NIR] : < 2e-16
##
##                   Kappa : 0.608
##  Mcnemar's Test P-Value : 0.00601
##
##             Sensitivity : 0.7517
##             Specificity : 0.8667
##          Pos Pred Value : 0.8750
##          Neg Pred Value : 0.7376
##              Prevalence : 0.5539
##          Detection Rate : 0.4164
##    Detection Prevalence : 0.4758
##       Balanced Accuracy : 0.8092
##
##        'Positive' Class : healthy
##
```

variable importance based on neural network model, using ROC value as variable importance.

```
ggplot(nnet.model)
```

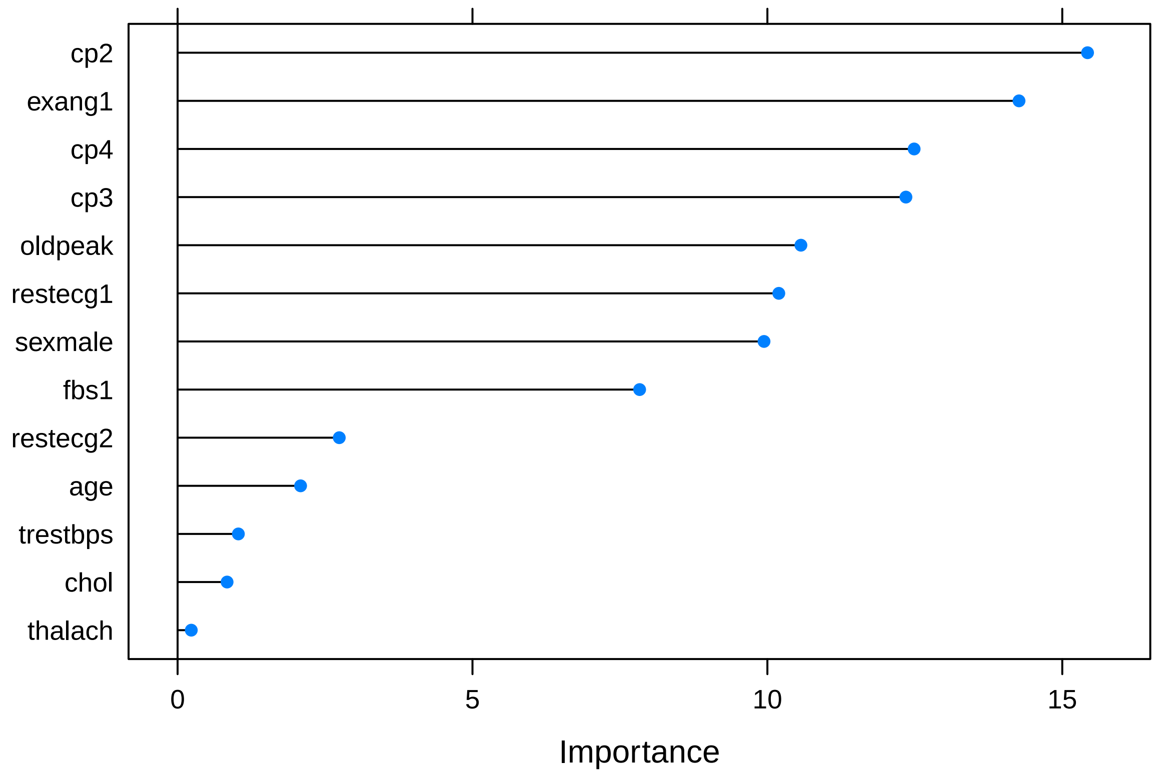
```
## Warning: Ignoring unknown aesthetics: shape
```



```
importance = varImp(nnet.model, scale=FALSE)
importance
```

```
## nnet variable importance
##
##          Overall
## cp2      15.4286
## exang1   14.2669
## cp4      12.4885
## cp3      12.3490
## oldpeak  10.5689
## restecg1 10.1935
## sexmale   9.9430
## fbs1      7.8338
## restecg2  2.7411
## age       2.0853
## trestbps  1.0302
## chol      0.8389
## thalach   0.2322
```

```
plot(importance)
```


cp2
exang1
cp4
cp3
oldpeak
restecg1
sexmale
fbs1
restecg2
age
trestbps
chol
thalach
Importance