Appendix

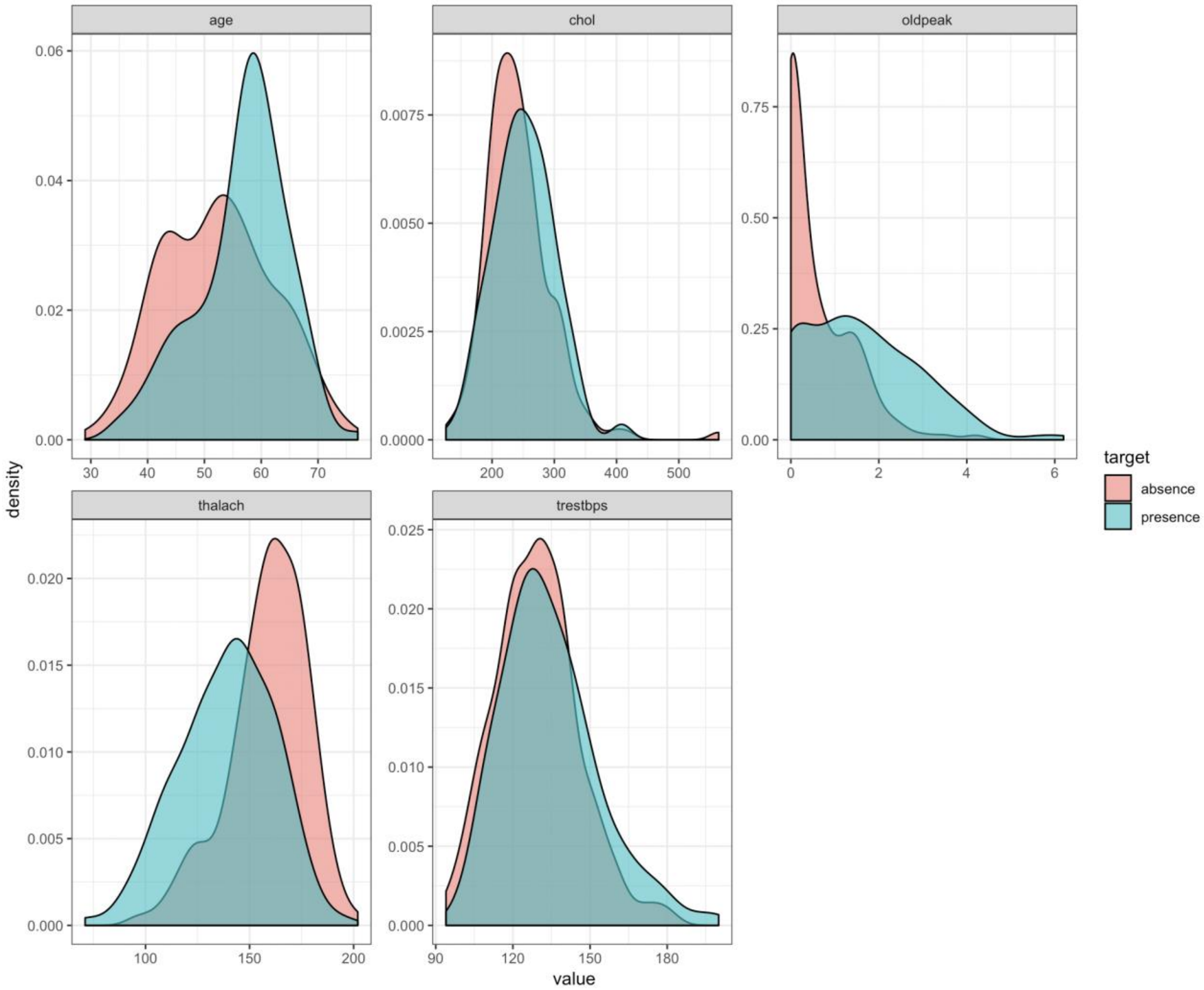


Figure 1. Density Plot of Continuous Variables Stratified by the Response.

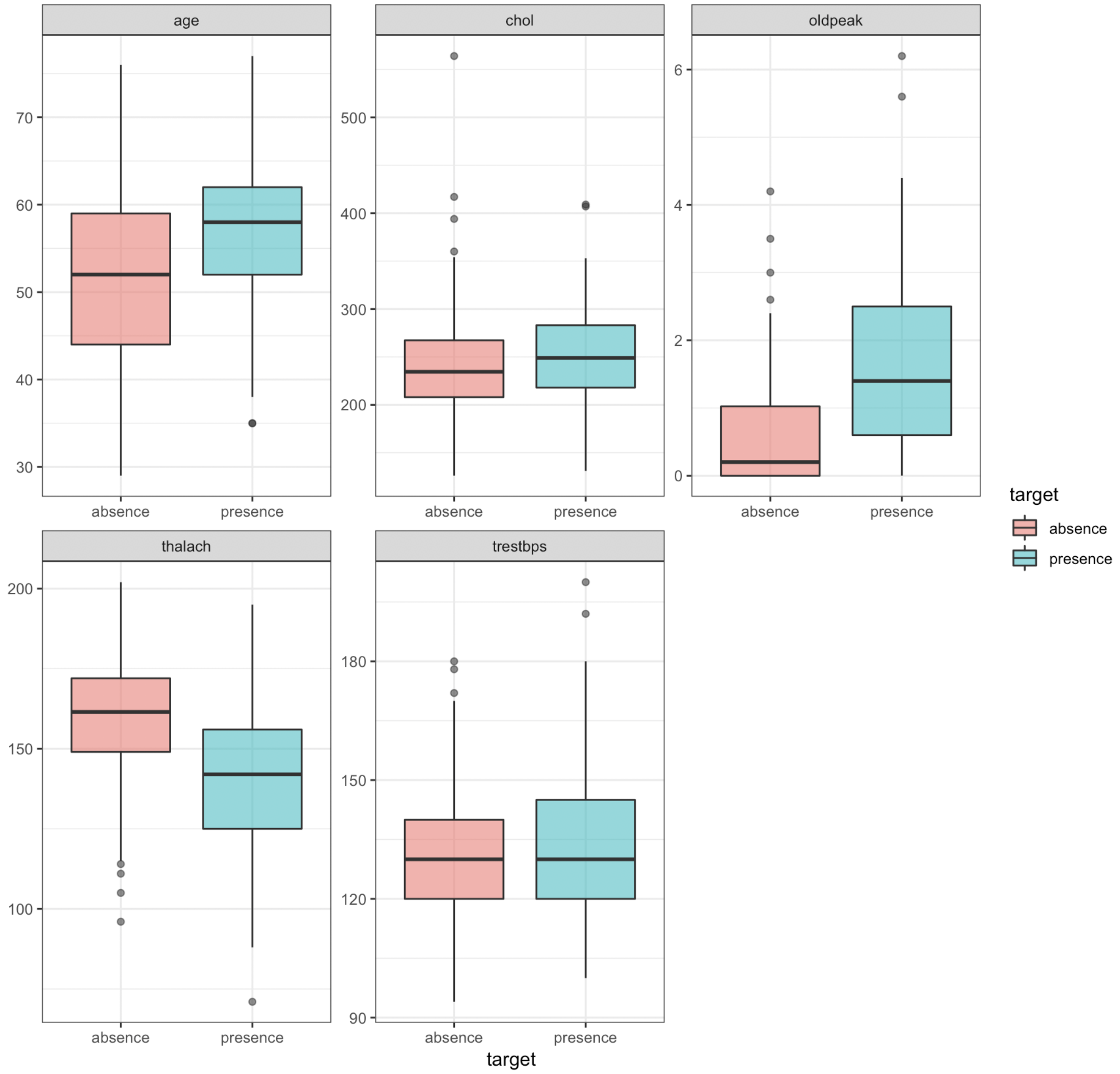


Figure 2. Boxplots of Continuous Variables Stratified by the Response.

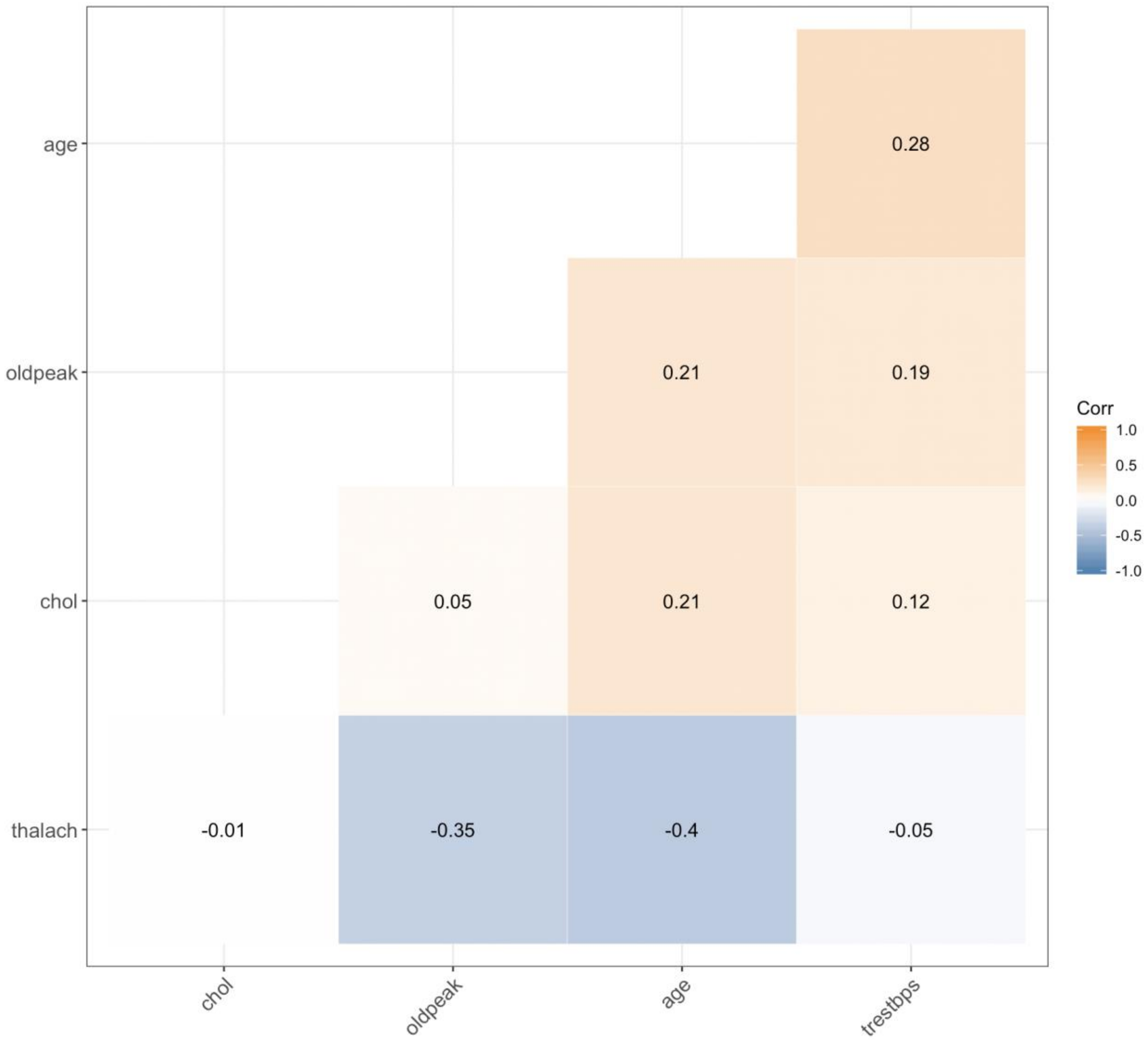
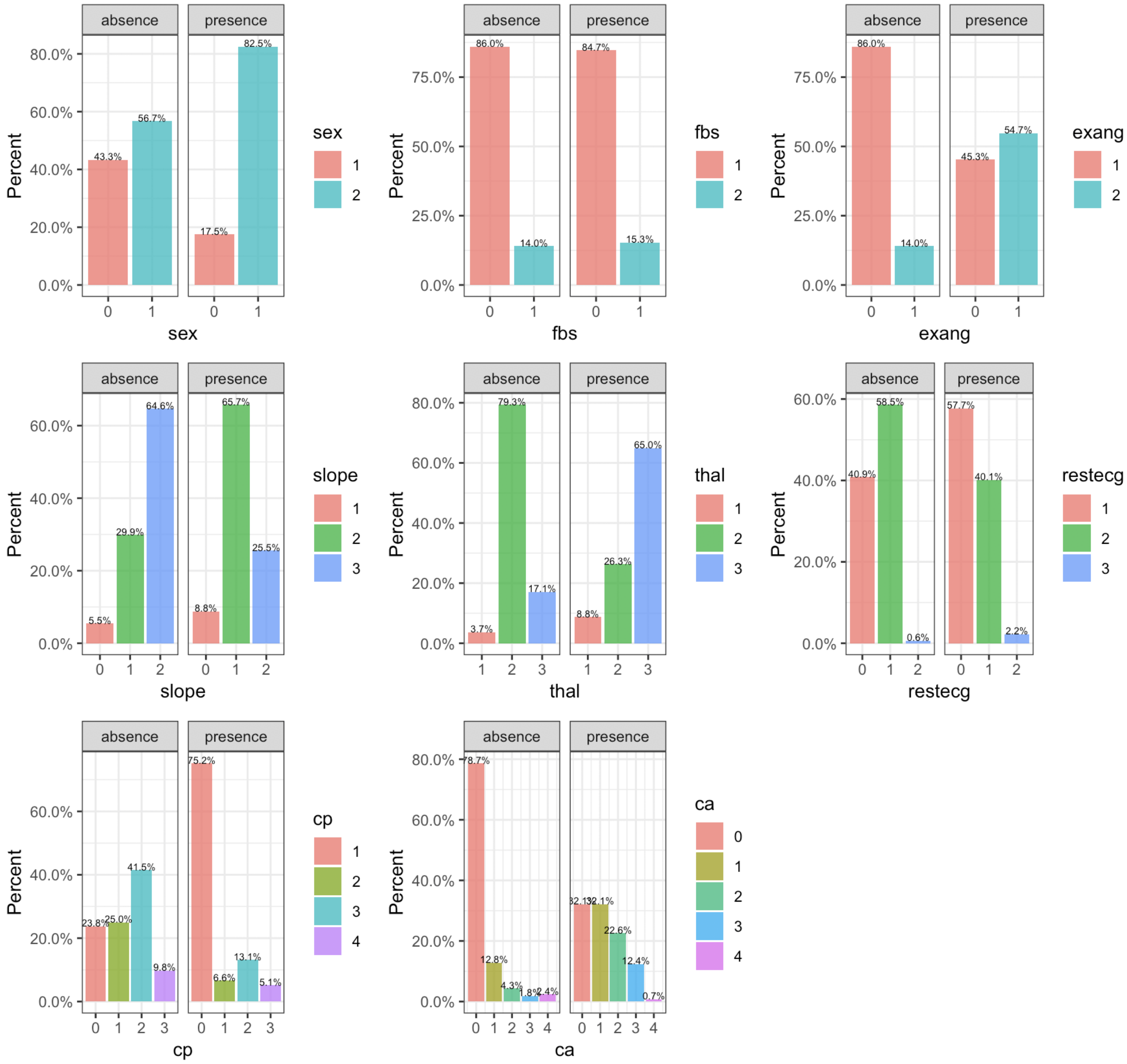


Figure 3. Correlation Plot of Continuous Variables.



Firgure 4. Bar Charts of Categorical Variables.

Table 1: Tuning parameters and selected values. Selection was made based on cross-validated AUC (using the train function in the 'caret' package.

Model	Tuning.Parameter	Selected.Value
Regularized Logistic	alpha	0
	lambda	0.234
LDA	N/A	
Naive Bayes	Kernel	Nonparametric
	Bandwidth	1.474
Classification Tree	Complexity parameter (cp)	0.0038
Bagging	Split rule	Gini impurity
	Minimal node size	40
Random Forest	Num. of Randomly selected predictors at each split	1
	Split rule	Gini impurity
	Minimal node size	25
Boosting	Number of trees	1370
	Shrinkage parameter	0.015
	Number of splits in each tree	1
Neural network	Number of hidden layer nodes	18
	Weight decay	6.448
SVM (linear kernel)	Cost	0.003
SVM (Radial kernel)	Cost	16.38
	Sigma	0.013

Related codes

data cleaning

```
heart_disease = read_csv("./data/heart.csv") %>%
    mutate(target = ifelse(target==1, 0, 1)) %>%
    mutate(target=as.factor(target)) %>%
    mutate(target=as.factor(ifelse(target==0, "absence", "presence")))%>%
    mutate(target = relevel(target, "presence"))

heart_disease = heart_disease %>%
    filter(thal != 0) %>%
    mutate(sex=as.factor(sex),
           cp=as.factor(cp),
           fbs=as.factor(fbs),
           restecg=as.factor(restecg),
           exang=as.factor(exang),
           slope=as.factor(slope),
           thal=factor(thal))

model.x <- model.matrix(target~.,heart_disease)[,-1]
model.y <- heart_disease$target
```

EDA

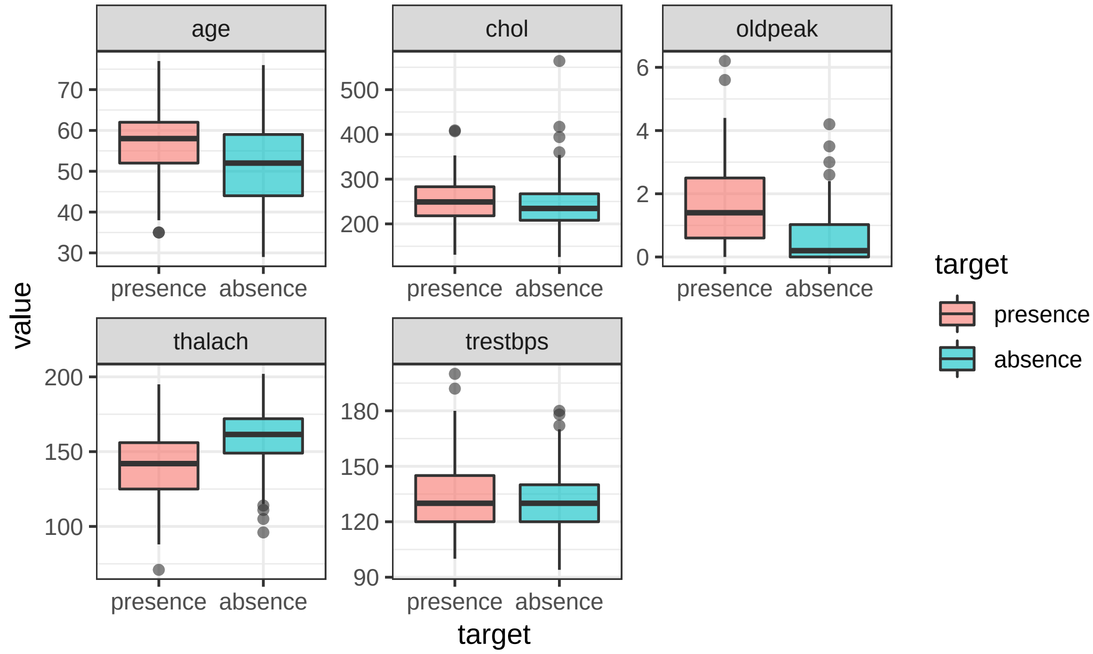
check missing value

```
sapply(X = heart_disease, FUN = function(x) sum(is.na(x)))
```

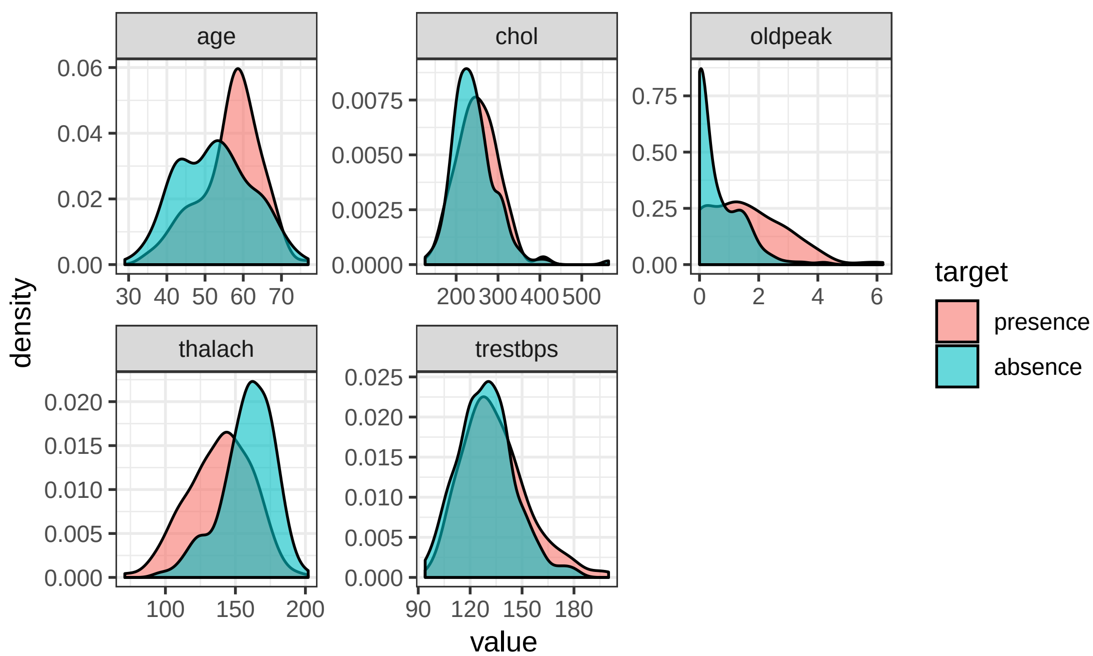
```
##      age      sex       cp trestbps     chol      fbs  restecg  thalach
##        0        0        0        0        0        0        0        0
##    exang  oldpeak    slope       ca     thal   target
##        0        0        0        0        0        0
```

continuous

```
heart_disease %>%
    select(age, trestbps, chol, thalach, oldpeak, target) %>%
    gather(-target, key = "var", value = "value") %>%
    ggplot(aes(x = target, y = value, fill = target)) +
    geom_boxplot(alpha = 0.6) +
    facet_wrap(~ var, scales = "free") +
    theme_bw()
```

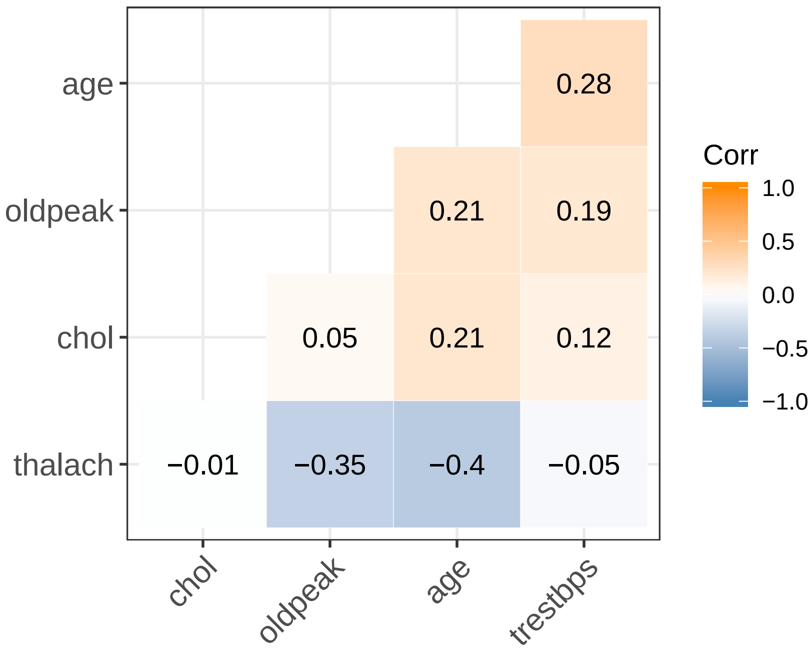



```
heart_disease %>%
    select(age, trestbps, chol, thalach, oldpeak, target) %>%
    gather(-target, key = "var", value = "value") %>%
    ggplot(aes(x = value, fill = target)) +
    geom_density(alpha = 0.6) +
    facet_wrap(~ var, scales = "free") +
    theme_bw()
```



corr matrix

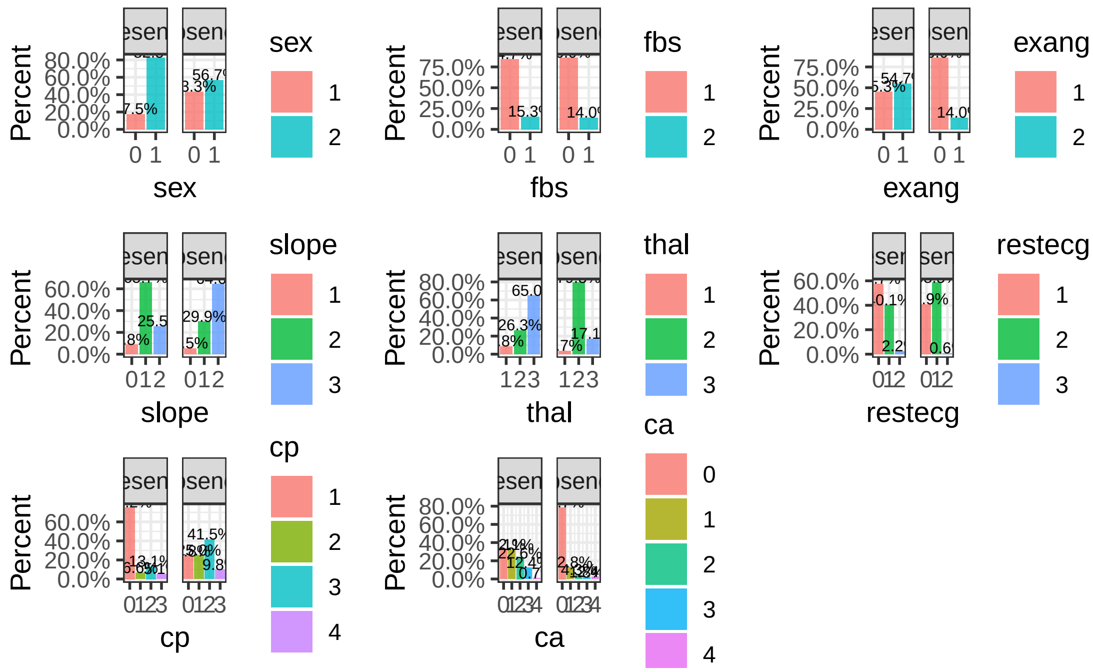
```r
library(ggcorrplot)
heart_continu = heart_disease %>%
    select(age, trestbps, chol, thalach, oldpeak)
corr =  round(cor(heart_continu), 4)

ggcorrplot(corr, hc.order = TRUE, type = "lower",
   outline.col = "white",
   ggtheme = ggplot2::theme_bw,
   lab = T,
   colors =  c("#4682B4", "white", "#FF8C00"))
```



categorical

```r
barplot = function(var){
    ggplot(heart_disease, aes_string(x = var,  group = "target")) +
    geom_bar(aes(y = ..prop.., fill = factor(..x..)),
             stat = "count", alpha = 0.8) +
    geom_text(aes( label = scales::percent(..prop..),
                   y = ..prop.. ),
              stat = "count", vjust = 0, size = 2) +
    labs(y = "Percent", fill = var) +
    facet_grid(~target) +
    scale_y_continuous(labels = scales::percent) +
        theme_bw()
}

a1 = barplot("sex")
a2 = barplot("fbs")
a3 = barplot("exang")
a4 = barplot("slope")
```

```r
a5 = barplot("thal")
a6 = barplot("restecg")
a7 = barplot("cp")
a8 = barplot("ca")

gridExtra::grid.arrange(a1, a2, a3, a4,
                        a5, a6, a7, a8,
                        ncol = 3, nrow = 3)
```



tableone

```r
tableOne = CreateTableOne(vars = c("age", "trestbps", "chol", "thalach",
                                   "oldpeak", "sex", "exang", "fbs",
                                   "slope", "thal", "restecg", "cp","ca"
                                   ),
                          strata = c("target"),
                          data = heart_disease,
                          factorVars = c("sex", "fbs", "exang", "slope",
                                         "thal", "restecg", "cp", "ca"))

table = print(tableOne, cramVars = c("sex", "exang", "fbs"))
```

```
##                          Stratified by target
##                           presence            absence             p      test
##   n                          137                 164
##   age (mean (SD))          56.64 (7.98)        52.49 (9.58)       <0.001
##   trestbps (mean (SD))    134.45 (18.79)      129.31 (16.22)       0.011
##   chol (mean (SD))        251.43 (49.47)      242.39 (53.68)       0.133
##   thalach (mean (SD))     138.98 (22.64)      158.73 (18.93)      <0.001
##   oldpeak (mean (SD))       1.59 (1.30)         0.59 (0.78)       <0.001
##   sex = 0/1 (%)           24/113 (17.5/82.5)   71/93 (43.3/56.7)  <0.001
```

```
##   exang = 0/1 (%)       62/75 (45.3/54.7)  141/23 (86.0/14.0)  <0.001
##   fbs = 0/1 (%)        116/21 (84.7/15.3)  141/23 (86.0/14.0)   0.877
##   slope (%)                                                    <0.001
##      0                    12 ( 8.8)            9 ( 5.5)
##      1                    90 (65.7)           49 (29.9)
##      2                    35 (25.5)          106 (64.6)
##   thal (%)                                                     <0.001
##      1                    12 ( 8.8)            6 ( 3.7)
##      2                    36 (26.3)          130 (79.3)
##      3                    89 (65.0)           28 (17.1)
##   restecg (%)                                                   0.005
##      0                    79 (57.7)           67 (40.9)
##      1                    55 (40.1)           96 (58.5)
##      2                     3 ( 2.2)            1 ( 0.6)
##   cp (%)                                                       <0.001
##      0                   103 (75.2)           39 (23.8)
##      1                     9 ( 6.6)           41 (25.0)
##      2                    18 (13.1)           68 (41.5)
##      3                     7 ( 5.1)           16 ( 9.8)
##   ca (%)                                                       <0.001
##      0                    44 (32.1)          129 (78.7)
##      1                    44 (32.1)           21 (12.8)
##      2                    31 (22.6)            7 ( 4.3)
##      3                    17 (12.4)            3 ( 1.8)
##      4                     1 ( 0.7)            4 ( 2.4)
```

```r
table = as.data.frame(table)

table = table %>%
    mutate(name = rownames(table)) %>%
    select(name, everything())



mydoc <- read_docx()
mydoc = mydoc %>%
    body_add_flextable(flextable(table))

print(mydoc, target = "./table.docx")
```

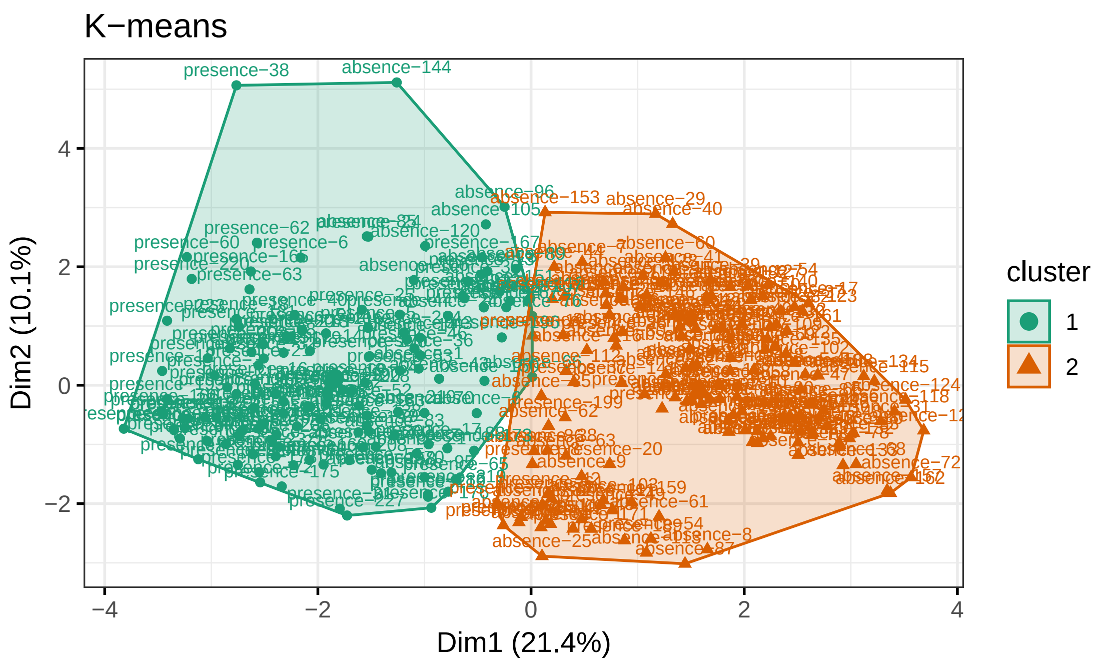
```
## [1] "C:/Users/Holly/Desktop/dsII/final/P8106-FinalProject/table.docx"
```

Unsupervised learning

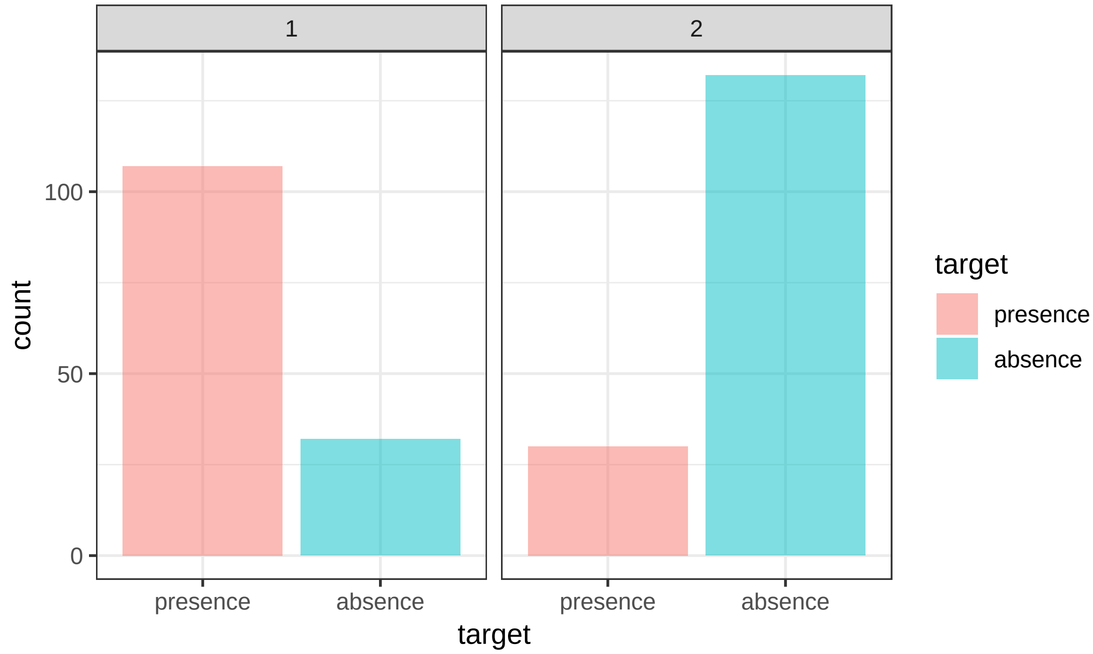
K-means

```r
set.seed(1)

model.x_scale = scale(model.x)

rownames(model.x_scale) = paste(heart_disease$target, 1:228, sep = "-")


km = kmeans(model.x_scale, centers = 2, nstart = 20)
km_vis = fviz_cluster(list(data = model.x_scale,
```

```
                              cluster = km$cluster),
                         ellipse.type = "convex",
                         geom = c("point","text"),
                         ggtheme = theme_bw(),
                         labelsize = 7, palette = "Dark2") +
    labs(title = "K-means")

km_vis
```




```
heart_kmeans = heart_disease
heart_kmeans$kmean = km$cluster
heart_kmeans %>% ggplot(aes(x = target, fill = target)) +
    geom_bar(alpha = 0.5) +
    facet_grid(.~kmean) +
    theme_bw()
```

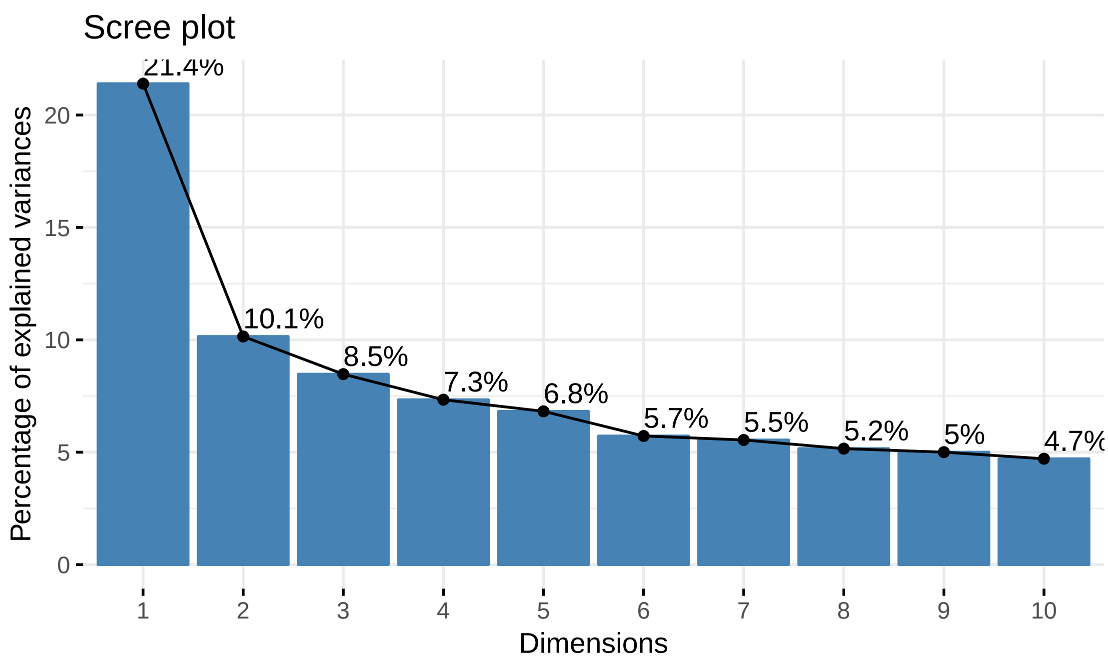



```
center = t(apply(km$centers, 1, function(r)r*attr(model.x_scale,'scaled:scale') + attr(model.x_scale, '

center
```

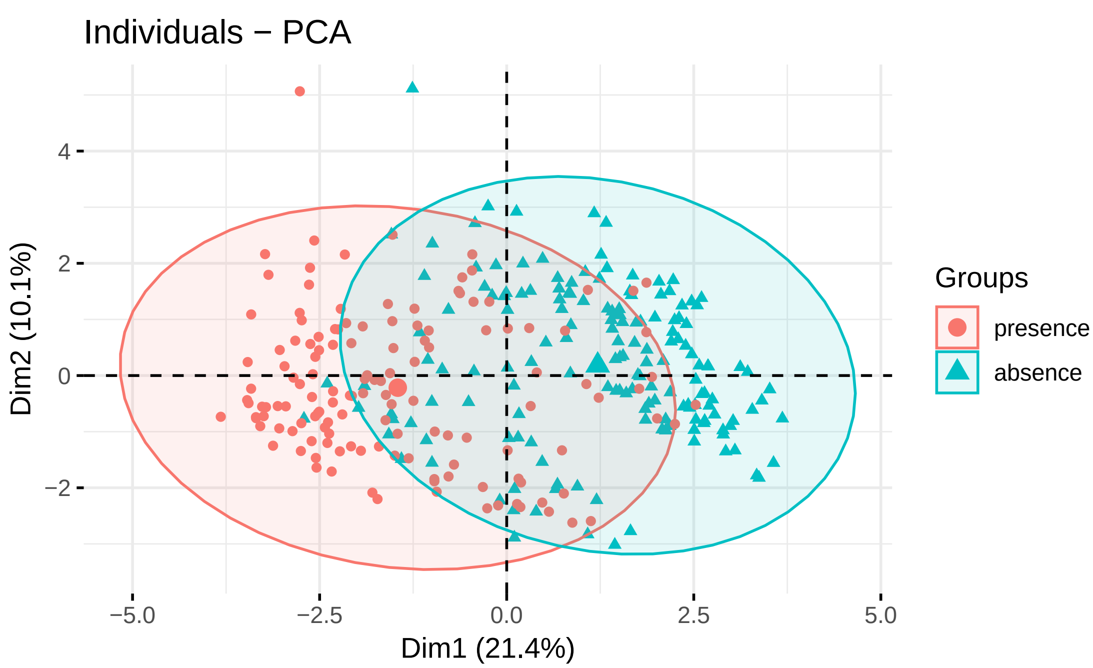
```
##        age      sex1        cp1       cp2        cp3 trestbps     chol
## 1 57.85612 0.7769784 0.02158273 0.1726619 0.09352518 135.1079 251.3022
## 2 51.39506 0.6049383 0.29012346 0.3827160 0.06172840 128.6790 242.3889
##        fbs1  restecg1     restecg2  thalach    exang1  oldpeak    slope1
## 1 0.1798561 0.3884892 2.877698e-02 135.1511 0.5683453 1.797842 0.8273381
## 2 0.1172840 0.5987654 2.949030e-17 162.2593 0.1172840 0.395679 0.1481481
##       slope2        ca     thal2     thal3
## 1 0.07194245 1.0431655 0.2661871 0.6258993
## 2 0.80864198 0.4691358 0.7962963 0.1851852
```

PCA

```
pca <- prcomp(model.x_scale)
fviz_eig(pca, addlabels = TRUE)
```




```
fviz_pca_ind(pca,
             habillage = model.y,
             label = "none",
             addEllipses = TRUE)
```

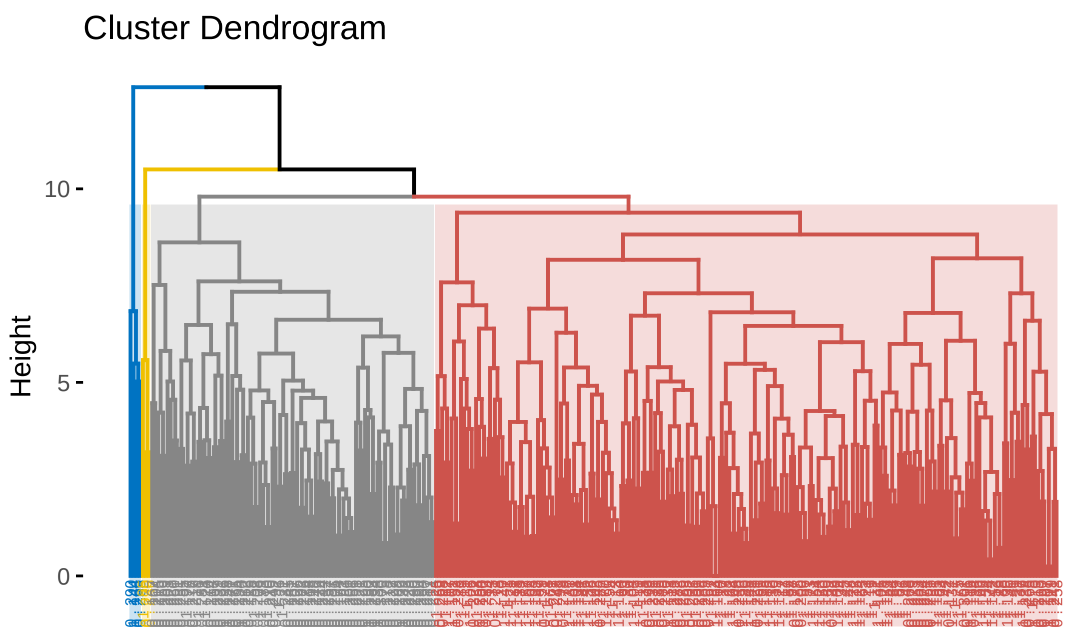


Hierarchical clustering

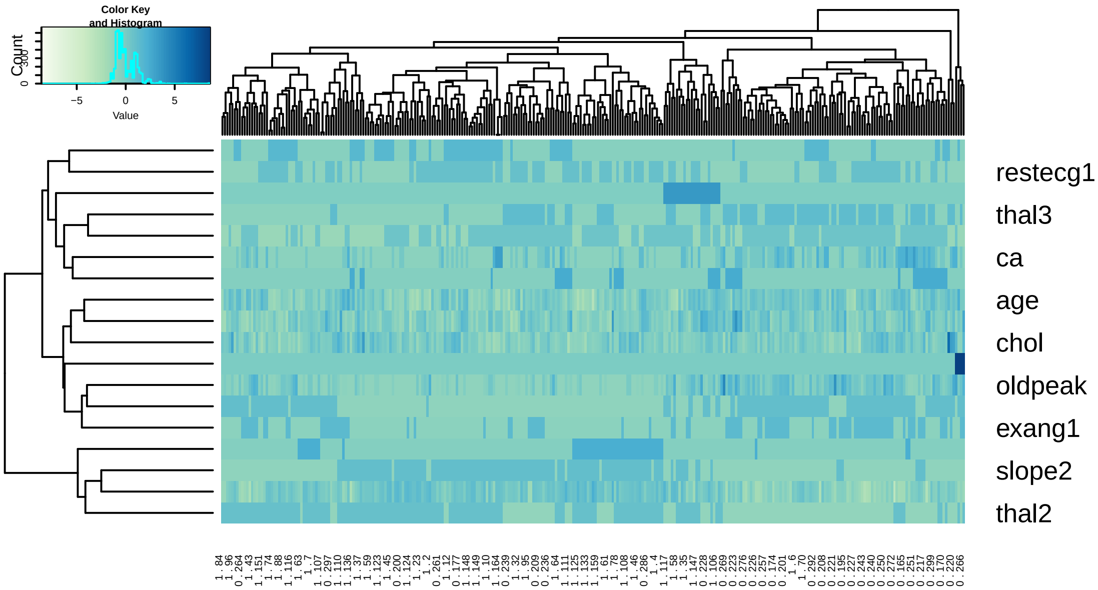
```
hd_1 = heart_disease %>%
    mutate(target = ifelse(target == "absence",1,0))
train.hc = model.x_scale %>% as.data.frame() %>%
```

```r
    mutate(target = as.character(hd_1$target),
           num = as.character(1:301)) %>%
    mutate(name = paste(target,".", num)) %>%
    select(-num, -target) %>%
    column_to_rownames(var = "name") %>% scale()
```

```r
hc.heart = hclust(dist(train.hc), method = "complete")


fviz_dend(hc.heart, k = 4,
          cex = 0.4,
          palette = "jco",
          color_labels_by_k = TRUE,
          rect = TRUE, rect_fill = TRUE, rect_border = "jco",
          labels_track_height = 0.8)
```




```r
col1 <- colorRampPalette(brewer.pal(9, "GnBu"))(100)

heatmap.2(t(train.hc),
        col = col1, keysize = 1, key.par = list(cex = .3),
        cexRow = 1,
        #dendrogram = "col",
        trace = "none", key = TRUE, cexCol = 0.4,
        margins = c(5, 5))
```

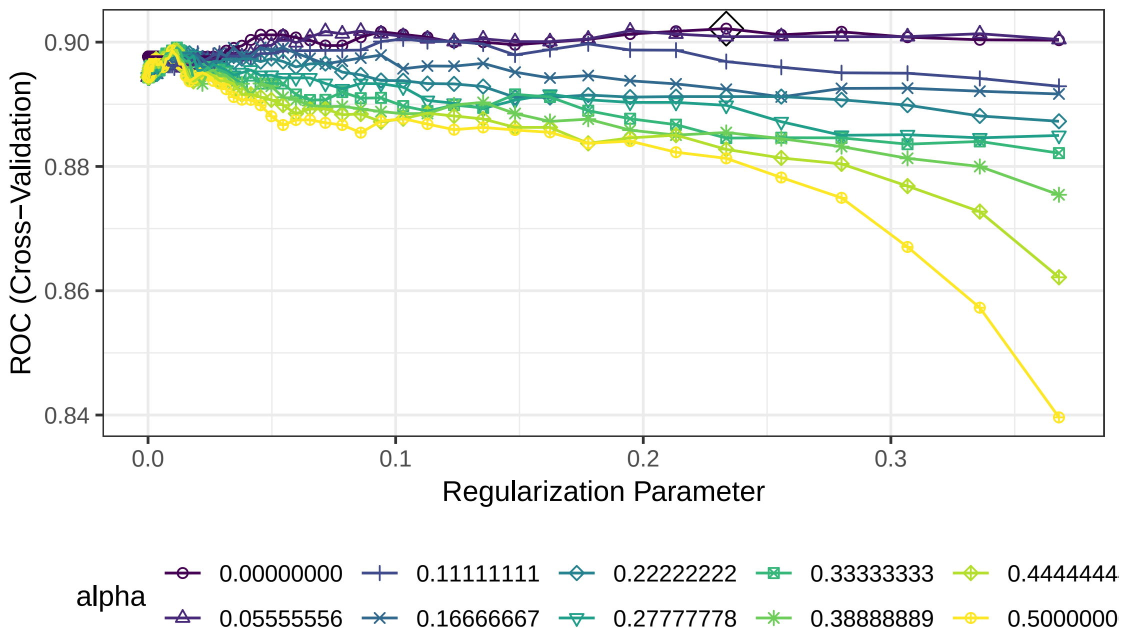

Color Key
and Histogram
Count
Value
restecg1
thal3
ca
age
chol
oldpeak
exang1
slope2
thal2

```r
heart_disease = read_csv("./heart.csv") %>%
    mutate(target = ifelse(target==1, 0, 1)) %>%
    mutate(target=as.factor(target)) %>%
    mutate(target=as.factor(ifelse(target==0, "absence", "presence")))%>%
    mutate(target = relevel(target, "presence"))

heart_disease = heart_disease %>%
    filter(thal != 0) %>%
    mutate(sex=as.factor(sex),
           cp=as.factor(cp),
           fbs=as.factor(fbs),
           restecg=as.factor(restecg),
           exang=as.factor(exang),
           slope=as.factor(slope),
           thal=factor(thal))

model.x <- model.matrix(target~.,heart_disease)[,-1]
model.y <- heart_disease$target
```

Regularized logistic

```r
ctrl = trainControl(method = "cv",
                    classProbs = TRUE,
                    summaryFunction = twoClassSummary)


glmnGrid <- expand.grid(.alpha = seq(0, 0.5, length = 10),
                        .lambda = exp(seq(-10,-1, length = 100)))
set.seed(1)
model.glm <- train(x = model.x,
                   y = model.y,
                   method = "glmnet",
                   tuneGrid = glmnGrid,
                   metric = "ROC",
                   trControl = ctrl)

ggplot(model.glm, highlight = T)  +
    viridis::scale_color_viridis(discrete = TRUE) +
    scale_shape_manual(values = seq(1,10))
```

```
## Scale for 'colour' is already present. Adding another scale for
## 'colour', which will replace the existing scale.

## Scale for 'shape' is already present. Adding another scale for 'shape',
## which will replace the existing scale.
```




```
model.glm$bestTune
```

```
##    alpha    lambda
## 95     0 0.2335065
```

```
glmnet = glmnet(x = model.x, y = model.y,
       family = "binomial",
       alpha = 0,
       lambda = 0.1946867)
broom::tidy(glmnet)
```

```
## # A tibble: 19 x 5
##    term         step estimate lambda dev.ratio
##    <chr>       <dbl>    <dbl>  <dbl>     <dbl>
##  1 (Intercept)     1  0.624    0.195     0.431
##  2 age             1 -0.00885  0.195     0.431
##  3 sex1            1 -0.462    0.195     0.431
##  4 cp1             1  0.385    0.195     0.431
##  5 cp2             1  0.586    0.195     0.431
##  6 cp3             1  0.524    0.195     0.431
##  7 trestbps        1 -0.00476  0.195     0.431
##  8 chol            1 -0.00120  0.195     0.431
##  9 fbs1            1  0.0693   0.195     0.431
## 10 restecg1        1  0.246    0.195     0.431
## 11 restecg2        1 -0.198    0.195     0.431
## 12 thalach         1  0.00952  0.195     0.431
## 13 exang1          1 -0.522    0.195     0.431
## 14 oldpeak         1 -0.199    0.195     0.431
## 15 slope1          1 -0.293    0.195     0.431
## 16 slope2          1  0.290    0.195     0.431
## 17 ca              1 -0.306    0.195     0.431
## 18 thal2           1  0.527    0.195     0.431
## 19 thal3           1 -0.526    0.195     0.431
```

LDA

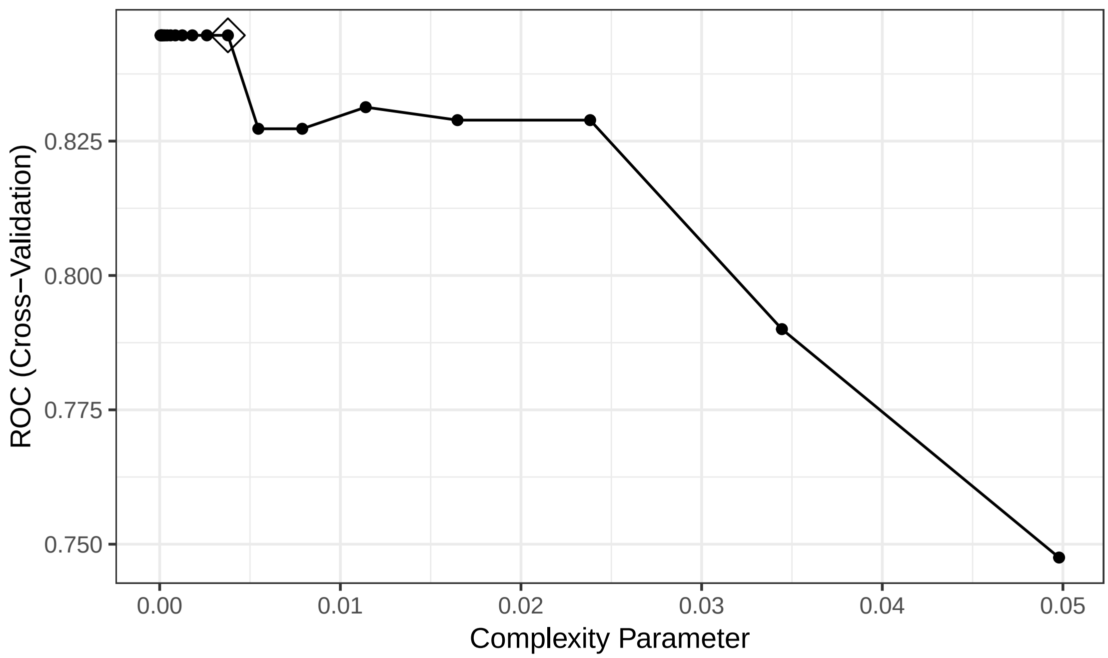
```r
set.seed(1)
model.lda = train(x = model.x,
                   y = model.y,
                  method = "lda",
                  metric = "ROC",
                  trControl = ctrl)
```

Naive bayes

```r
set.seed(1)
nbGrid = expand.grid(usekernel = c(FALSE,TRUE),
                     fL = 1, adjust = seq(0, 4, length = 20))
model.bayes = train(x = model.x,
                    y = model.y,
                    method = "nb",
                    tuneGrid = nbGrid,
                    metric = "ROC",
                    trControl = ctrl)

ggplot(model.bayes, highlight = T)

model.bayes$bestTune
```

##Tree

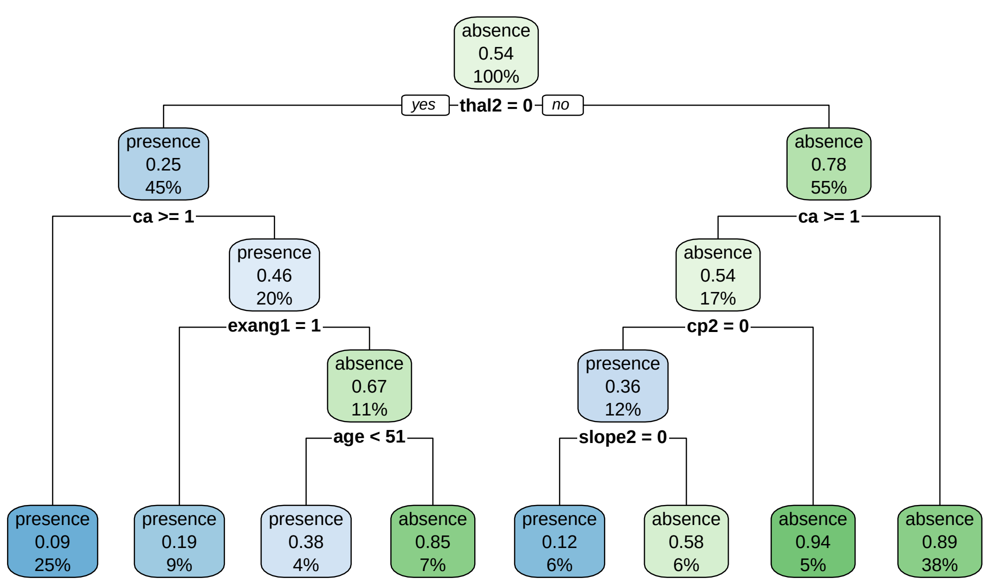
```r
set.seed(1)
tree.class <- train(model.x, model.y,
                    method = "rpart",
                    tuneGrid = data.frame(cp = exp(seq(-10,-3, len = 20))),
                    trControl = ctrl,
                    metric = "ROC")
ggplot(tree.class, highlight = TRUE)
```




```
tree.class$bestTune
```

```
##             cp
## 13 0.003776539
```

```
rpart.plot(tree.class$finalModel)
```



##Bagging

```
bagging.grid <- expand.grid(mtry = 18,
                            splitrule = "gini",
                            min.node.size = 10:50)
```

```r
set.seed(1)
bagging.class <- train(model.x, model.y,
                method = "ranger",
                tuneGrid = bagging.grid,
                metric = "ROC",
                trControl = ctrl,
                importance = "impurity")

ggplot(bagging.class, highlight = TRUE)
bagging.class$bestTune

barplot(sort(ranger::importance(bagging.class$finalModel),
             decreasing = FALSE),
las = 2, horiz = TRUE, cex.names = 0.7,
col = colorRampPalette(colors = c("darkred","white","darkblue"))(18))
```

##Random Forest

```r
rf.grid <- expand.grid(mtry = 1:6,
                       splitrule = "gini",
                       min.node.size = seq(1,191, by = 2))

set.seed(1)
rf.class <- train(model.x, model.y,
                  method = "ranger",
                  tuneGrid = rf.grid,
                  metric = "ROC",
                  trControl = ctrl,
                  importance = "impurity")

rf.class$bestTune

ggplot(rf.class, highlight = TRUE) +
    viridis::scale_color_viridis(discrete = TRUE) +
    scale_shape_manual(values = seq(1,7))

barplot(sort(ranger::importance(rf.class$finalModel), decreasing = FALSE),
las = 2, horiz = TRUE, cex.names = 0.7,
col = colorRampPalette(colors = c("darkred","white","darkblue"))(18))
```

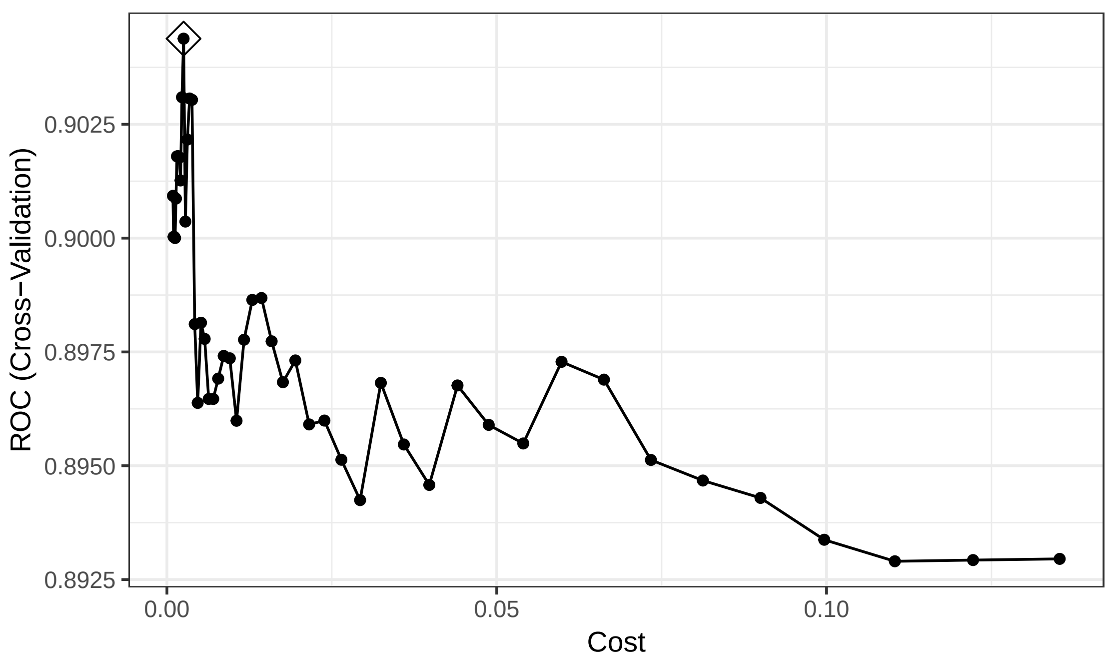
##Boosting

```r
boost.grid <- expand.grid(n.trees = seq(20, 1700, by = 25),
                          interaction.depth = 1:6,
                          shrinkage =  seq(0.005, 0.06, by = 0.005),
                          n.minobsinnode = 1)

set.seed(1)
# Adaboost loss function
boost.class = train(model.x, model.y,
                    tuneGrid = boost.grid,
                    trControl = ctrl,
                    method = "gbm",
                    distribution = "adaboost",
```

```
                     metric = "ROC",
                     verbose = FALSE)

boost.class$bestTune

ggplot(boost.class, highlight = TRUE) +
    viridis::scale_color_viridis(discrete = TRUE) +
    scale_shape_manual(values = seq(0,11))

summary(boost.class$finalModel, las = 2, cBars = 19, cex.names = 0.6)
```

SVM ROC

```
## linear boundary
set.seed(1)
svml.fit <- train(target~.,
                  data = heart_disease,
                  method = "svmLinear2",
                  preProcess = c("center", "scale"),
                  tuneGrid = data.frame(cost = exp(seq(-7,-2,len=50))),
                  trControl = ctrl,
                  metric = "ROC")

ggplot(svml.fit, highlight = TRUE)
```




```
svml.fit$bestTune
```

```
##           cost
## 11 0.002529859
```

```
## radial kernel
svmr.grid <- expand.grid(C = exp(seq(-4,5,len=50)),
```

```
                          sigma = exp(seq(-5,-2,len=10)))
set.seed(1)
svmr.fit <- train(target~.,
                  data = heart_disease,
                  method = "svmRadial",
                  preProcess = c("center", "scale"),
                  tuneGrid = svmr.grid,
                  trControl = ctrl,
                  metric = "ROC")

ggplot(svmr.fit, highlight = TRUE) +
    viridis::scale_color_viridis(discrete = TRUE) +
    scale_shape_manual(values = seq(1,10))
svmr.fit$bestTune
```

Neural network

```
nnetGrid <- expand.grid(size = seq(from = 16, to = 30, by = 2),
                        decay = seq(from = 5, to = 8, length = 30))

set.seed(1)
cnnet.fit <- train(target~.,
                   heart_disease,
                   method = "nnet",
                   tuneGrid = nnetGrid,
                   preProcess = c("center","scale"),
                   trControl = ctrl,
                   metric = "ROC",
                   trace = FALSE)

ggplot(cnnet.fit, highlight = TRUE) +
    viridis::scale_color_viridis(discrete = TRUE) +
    scale_shape_manual(values = seq(1,13))

cnnet.fit$bestTune
```

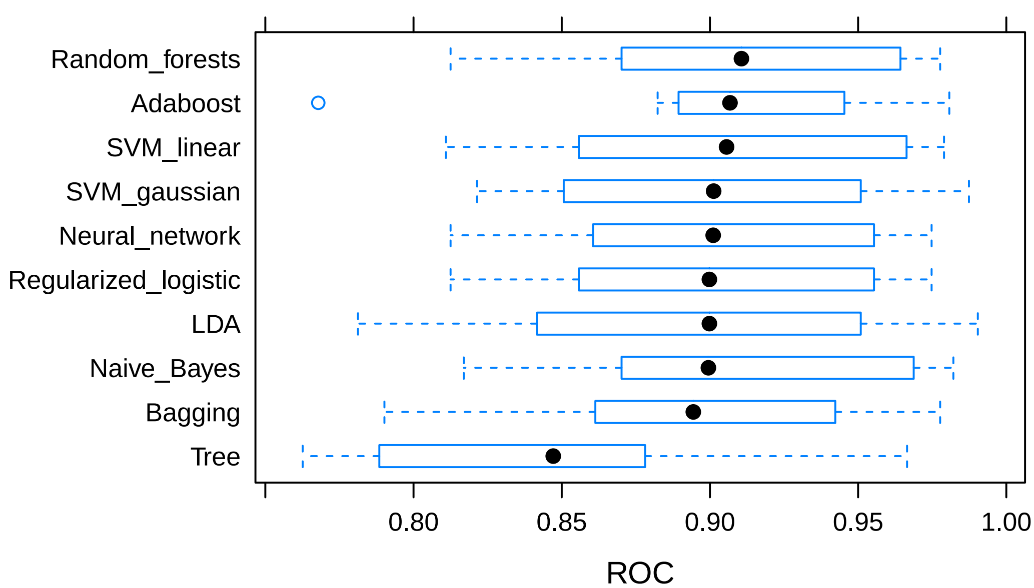
```
load(file = "./saved_results/cnnet.rda")
load(file = "./saved_results/boost.rda")
load(file = "./saved_results/rf.rda")
load(file = "./saved_results/bagging.rda")
load(file = "./saved_results/bayes.rda")
load(file = "./saved_results/svmr.rda")

resamp = resamples(list(
                        Regularized_logistic = model.glm,
                        LDA = model.lda,
                        Naive_Bayes = model.bayes,
                        Adaboost = boost.class,
                        Random_forests = rf.class,
                        Bagging = bagging.class,
                        Tree = tree.class,
                        Neural_network = cnnet.fit,
                        SVM_linear = svml.fit,
```

```
                          SVM_gaussian = svmr.fit
                          ))
summary(resamp)
```

```
##
## Call:
## summary.resamples(object = resamp)
##
## Models: Regularized_logistic, LDA, Naive_Bayes, Adaboost, Random_forests, Bagging, Tree, Neural_netw
## Number of resamples: 10
##
## ROC
##                           Min.   1st Qu.    Median      Mean   3rd Qu.
## Regularized_logistic 0.8125000 0.8612839 0.8998162 0.9021715 0.9553571
## LDA                  0.7812500 0.8463660 0.8998162 0.8981719 0.9497768
## Naive_Bayes          0.8169643 0.8725103 0.8994829 0.9097952 0.9681490
## Adaboost             0.7678571 0.8918572 0.9067752 0.9062419 0.9434086
## Random_forests       0.8125000 0.8747424 0.9106335 0.9091185 0.9637605
## Bagging              0.7901786 0.8613445 0.8943924 0.8934995 0.9357224
## Tree                 0.7626050 0.7968750 0.8471386 0.8446792 0.8771008
## Neural_network       0.8125000 0.8641827 0.9010989 0.9026261 0.9553571
## SVM_linear           0.8109244 0.8605769 0.9056238 0.9043815 0.9658310
## SVM_gaussian         0.8214286 0.8567590 0.9012605 0.9027614 0.9497768
##                           Max. NA's
## Regularized_logistic 0.9747899    0
## LDA                  0.9903846    0
## Naive_Bayes          0.9821429    0
## Adaboost             0.9807692    0
## Random_forests       0.9776786    0
## Bagging              0.9776786    0
## Tree                 0.9665179    0
## Neural_network       0.9747899    0
## SVM_linear           0.9789916    0
## SVM_gaussian         0.9873950    0
##
## Sens
##                           Min.   1st Qu.    Median      Mean   3rd Qu.
## Regularized_logistic 0.5714286 0.6923077 0.7857143 0.7950549 0.9065934
## LDA                  0.5714286 0.6978022 0.7857143 0.7725275 0.8310440
## Naive_Bayes          0.6428571 0.7857143 0.8159341 0.8258242 0.9038462
## Adaboost             0.6153846 0.6978022 0.7857143 0.7879121 0.8571429
## Random_forests       0.6428571 0.6923077 0.7142857 0.7659341 0.8310440
## Bagging              0.6428571 0.6978022 0.7500000 0.7659341 0.8310440
## Tree                 0.6153846 0.7280220 0.7774725 0.7725275 0.8392857
## Neural_network       0.5714286 0.6923077 0.7857143 0.7950549 0.9065934
## SVM_linear           0.5714286 0.6552198 0.7500000 0.7653846 0.8543956
## SVM_gaussian         0.5384615 0.6401099 0.7857143 0.7653846 0.8571429
##                           Max. NA's
## Regularized_logistic 1.0000000    0
## LDA                  1.0000000    0
## Naive_Bayes          1.0000000    0
## Adaboost             1.0000000    0
## Random_forests       1.0000000    0
## Bagging              0.9285714    0
```

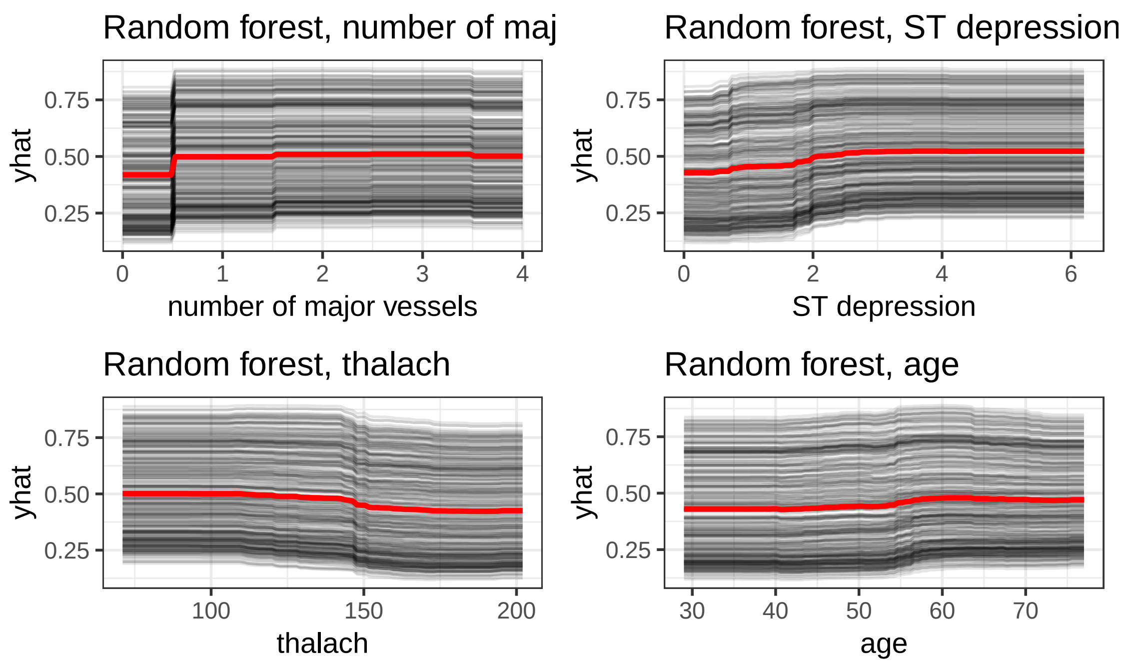
```
## Tree                   0.9285714    0
## Neural_network         1.0000000    0
## SVM_linear             1.0000000    0
## SVM_gaussian           1.0000000    0
##
## Spec
##                             Min.   1st Qu.    Median      Mean   3rd Qu.
## Regularized_logistic 0.7500000 0.8152574 0.8786765 0.8838235 0.9411765
## LDA                  0.7500000 0.8152574 0.9099265 0.8838235 0.9411765
## Naive_Bayes          0.7500000 0.7500000 0.8235294 0.8470588 0.9264706
## Adaboost             0.6875000 0.8281250 0.9375000 0.8775735 0.9402574
## Random_forests       0.7058824 0.7812500 0.8786765 0.8658088 0.9402574
## Bagging              0.6875000 0.7766544 0.8235294 0.8297794 0.8621324
## Tree                 0.5625000 0.8152574 0.8492647 0.8349265 0.8823529
## Neural_network       0.7500000 0.8152574 0.8786765 0.8838235 0.9411765
## SVM_linear           0.7500000 0.7766544 0.8786765 0.8658088 0.9264706
## SVM_gaussian         0.7500000 0.8125000 0.8492647 0.8536765 0.9237132
##                           Max. NA's
## Regularized_logistic 1.0000000    0
## LDA                  1.0000000    0
## Naive_Bayes          1.0000000    0
## Adaboost             0.9411765    0
## Random_forests       1.0000000    0
## Bagging              1.0000000    0
## Tree                 0.9375000    0
## Neural_network       1.0000000    0
## SVM_linear           1.0000000    0
## SVM_gaussian         0.9411765    0
```

```
bwplot(resamp, metric = "ROC")
```



###centered ICE

```r
ice_thalach.rf = rf.class %>%
    pdp::partial(pred.var = "thalach",
            grid.resolution = 100,
            ice = TRUE,
            prob = TRUE) %>%
    autoplot(train = heart_disease, alpha = .1) +
    ggtitle("Random forest, thalach")

ice_ca.rf = rf.class %>%
    pdp::partial(pred.var = "ca",
            grid.resolution = 100,
            ice = TRUE,
            prob = TRUE) %>%
    autoplot(train = heart_disease, alpha = .1,
             xlab = "number of major vessels") +
    ggtitle("Random forest, number of major vessels")

ice_oldpeak.rf =  rf.class %>%
    partial(pred.var = "oldpeak",
            grid.resolution = 100,
            ice = TRUE,
            prob = TRUE) %>%
    autoplot(train = heart_disease, alpha = .1,
             xlab = "ST depression") +
    ggtitle("Random forest, ST depression")

ice_age.rf = rf.class %>%
    pdp::partial(pred.var = "age",
            grid.resolution = 100,
            ice = TRUE,
            prob = TRUE) %>%
    autoplot(train = heart_disease, alpha = .1) +
    ggtitle("Random forest, age")

grid.arrange(ice_ca.rf, ice_oldpeak.rf,
             ice_thalach.rf, ice_age.rf, nrow = 2)
```



Variable importance

```r
library(gbm)
```

```
## Loaded gbm 2.1.5
```

```r
varImp(model.glm)
```

```
## glmnet variable importance
##
##             Overall
## cp2        100.0000
## thal2       94.8188
## thal3       93.4880
## exang1      92.3686
## cp3         87.3424
## sex1        79.4864
## cp1         66.9913
## slope2      52.7207
## slope1      52.7011
## ca          52.4277
## restecg1    42.4609
## restecg2    36.5417
## oldpeak     34.8283
## fbs1        10.6763
## thalach      1.4898
## age          1.4370
## trestbps     0.6164
## chol         0.0000
```

```r
varImp(model.lda)
```

```
## ROC curve variable importance
```

```
##
##          Importance
## thal2      100.0000
## thalach     95.2812
## thal3       90.1317
## oldpeak     89.9165
## ca          89.7356
## exang1      76.2594
## slope2      73.0991
## slope1      66.7700
## cp2         52.2776
## age         51.1237
## sex1        47.3435
## cp1         33.1353
## restecg1    33.0578
## chol        25.1356
## trestbps    24.9634
## cp3          6.4669
## restecg2     0.5339
## fbs1         0.0000
```

```r
varImp(model.bayes)
```

```
## ROC curve variable importance
##
##          Importance
## thal2      100.0000
## thalach     95.2812
## thal3       90.1317
## oldpeak     89.9165
## ca          89.7356
## exang1      76.2594
## slope2      73.0991
## slope1      66.7700
## cp2         52.2776
## age         51.1237
## sex1        47.3435
## cp1         33.1353
## restecg1    33.0578
## chol        25.1356
## trestbps    24.9634
## cp3          6.4669
## restecg2     0.5339
## fbs1         0.0000
```

```r
varImp(boost.class)
```

```
## gbm variable importance
##
##           Overall
## ca       100.0000
## oldpeak   79.6457
## thal2     77.0270
## thalach   61.2231
## chol      52.8994
```

```
## trestbps  50.8206
## age       42.3494
## exang1    40.8228
## cp2       28.2991
## thal3     28.0742
## sex1      19.9508
## cp3       19.4944
## slope2    17.4076
## slope1     9.4854
## restecg1   8.0607
## cp1        7.8021
## fbs1       0.9966
## restecg2   0.0000
```

```r
varImp(rf.class)
```

```
## ranger variable importance
##
##          Overall
## thal2    100.000
## ca        94.184
## thal3     78.793
## oldpeak   77.081
## thalach   71.046
## exang1    59.586
## slope2    49.347
## age       48.026
## cp2       34.566
## chol      33.949
## sex1      32.134
## slope1    31.905
## trestbps  30.498
## cp1       15.616
## restecg1  10.725
## cp3        8.663
## fbs1       2.118
## restecg2   0.000
```

```r
varImp(bagging.class)
```

```
## ranger variable importance
##
##            Overall
## thal2    100.00000
## ca        47.18886
## oldpeak   32.70738
## thalach   27.53944
## age       14.77607
## exang1    13.43368
## trestbps  10.65010
## cp2       10.41997
## thal3      9.60369
## chol       8.71625
## cp3        5.61067
## slope2     3.96182
```

```
## sex1       3.24090
## restecg1   1.96555
## slope1     1.74960
## cp1        0.74229
## fbs1       0.04796
## restecg2   0.00000
```

```r
varImp(tree.class)
```

```
## rpart variable importance
##
##           Overall
## thalach  100.000
## ca        96.684
## exang1    87.087
## thal2     80.067
## thal3     68.075
## oldpeak   37.514
## age       25.951
## slope2    17.578
## cp2       15.249
## sex1      14.902
## slope1    13.928
## cp3        8.264
## chol       7.543
## cp1        4.269
## fbs1       0.000
## restecg1   0.000
## restecg2   0.000
## trestbps   0.000
```

```r
varImp(cnnet.fit)
```

```
## nnet variable importance
##
##           Overall
## ca       100.000
## thal2     85.381
## thal3     82.923
## cp2       82.012
## exang1    77.280
## oldpeak   71.835
## thalach   68.244
## sex1      65.485
## slope2    44.568
## slope1    44.370
## cp1       40.316
## cp3       38.814
## restecg1  32.957
## trestbps  21.097
## age       21.068
## chol      12.338
## fbs1       1.239
## restecg2   0.000
```

#Comparing accuracy

##Regularized logistic

```
ctrl2 <- trainControl(method = "cv")

glmnGrid <- expand.grid(.alpha = 0,
                        .lambda = 0.2335065)

set.seed(1)
model.glm.2 <- train(x = model.x,
                   y = model.y,
                   tuneGrid = glmnGrid,
                   method = "glmnet",
                   metric = "Accuracy",
                   trControl = ctrl2)
```

##LDA

```
set.seed(1)
model.lda.2 = train(x = model.x,
                  y = model.y,
                  method = "lda",
                  metric = "Accuracy",
                  trControl = ctrl2)
```

##Naive bayes

```
set.seed(1)
nbGrid = expand.grid(usekernel = TRUE,
                     fL = 1, adjust = 1.473684)
model.bayes.2 = train(x = model.x,
                    y = model.y,
                    method = "nb",
                    tuneGrid = nbGrid,
                    metric = "Accuracy",
                    trControl = ctrl2)
```

##Tree

```
set.seed(1)
tree.class.2 <- train(model.x, model.y,
                    method = "rpart",
                    tuneGrid = data.frame(cp = 0.003776539),
                    trControl = ctrl2,
                    metric = "Accuracy")
```

##Bagging

```
bagging.grid <- expand.grid(mtry = 18,
                            splitrule = "gini",
                            min.node.size = 40)

set.seed(1)
bagging.class.2 <- train(model.x, model.y,
                method = "ranger",
                tuneGrid = bagging.grid,
                metric = "Accuracy",
                trControl = ctrl2,
                importance = "impurity")
```

##Random Forest

```
rf.grid <- expand.grid(mtry = 1,
                       splitrule = "gini",
                       min.node.size = 25)

set.seed(1)
rf.class.2 <- train(model.x, model.y,
                  method = "ranger",
                  tuneGrid = rf.grid,
                  metric = "Accuracy",
                  trControl = ctrl2,
                  importance = "impurity")
```

##Boosting

```
boost.grid <- expand.grid(n.trees = 1370,
                          interaction.depth = 1,
                          shrinkage = 0.015,
                          n.minobsinnode = 1)

set.seed(1)
# Adaboost loss function
boost.class.2 = train(model.x, model.y,
                    tuneGrid = boost.grid,
                    trControl = ctrl2,
                    method = "gbm",
                    distribution = "adaboost",
                    metric = "Accuracy",
                    verbose = FALSE)
```

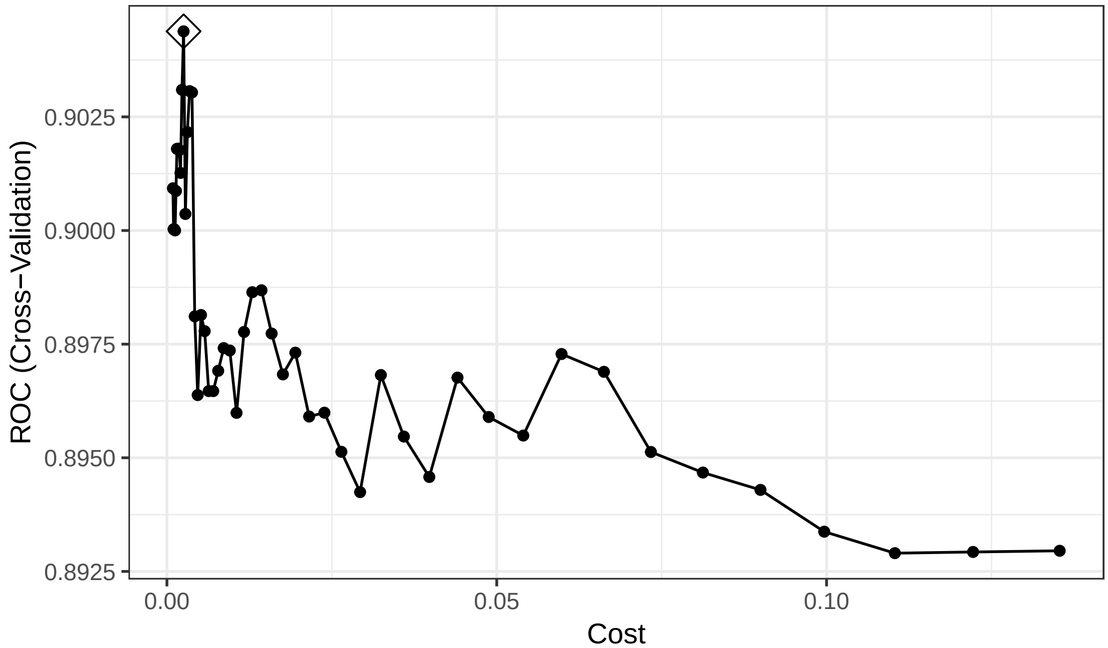
Neural network

```
nnetGrid <- expand.grid(size = 18,
                        decay = 6.448276)

set.seed(1)
cnnet.fit.2 <- train(target~.,
                   heart_disease,
                   method = "nnet",
                   tuneGrid = nnetGrid,
                   preProcess = c("center","scale"),
                   trControl = ctrl2,
                   metric = "Accuracy",
                   trace = FALSE)
```

SVM

```
## linear boundary
set.seed(1)
svml.fit.2 <- train(target~.,
                  data = heart_disease,
                  method = "svmLinear2",
```

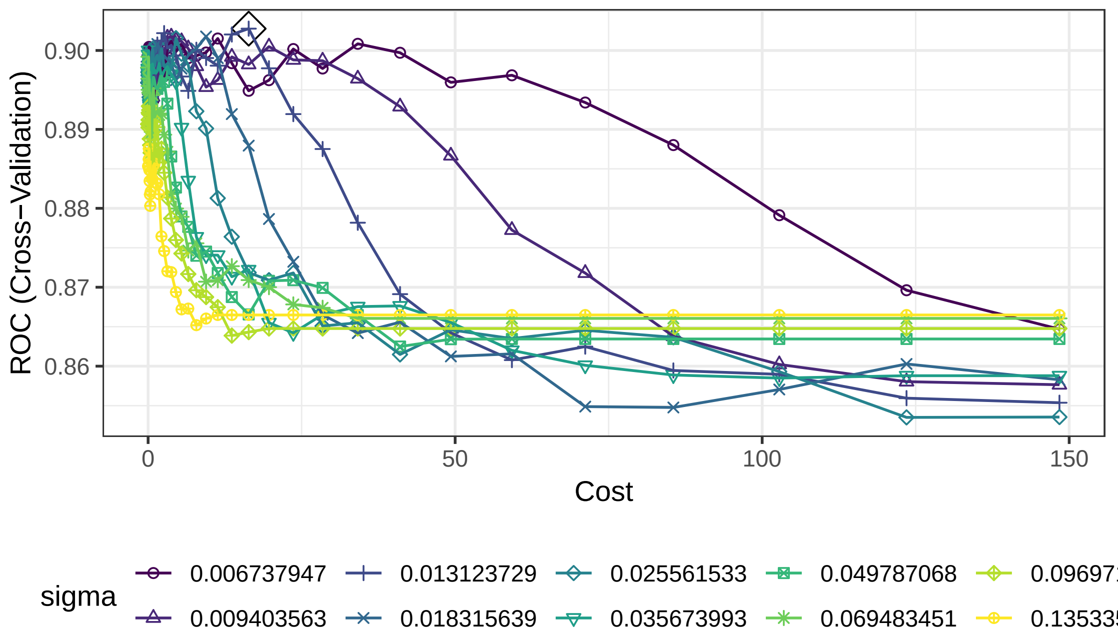
```r
                   preProcess = c("center", "scale"),
                   tuneGrid = data.frame(cost = exp(seq(-7,-2,len=50))),
                   trControl = ctrl2)

ggplot(svml.fit, highlight = TRUE)
```




```r
svml.fit$bestTune
```

```
##           cost
## 11 0.002529859
```

```r
## radial kernel
svmr.grid <- expand.grid(C = exp(seq(-4,5,len=50)),
                         sigma = exp(seq(-5,-2,len=10)))
set.seed(1)
svmr.fit.2 <- train(target~.,
                   data = heart_disease,
                   method = "svmRadial",
                   preProcess = c("center", "scale"),
                   tuneGrid = svmr.grid,
                   trControl = ctrl2)

ggplot(svmr.fit, highlight = TRUE) +
    viridis::scale_color_viridis(discrete = TRUE) +
    scale_shape_manual(values = seq(1,10))
```




```
svmr.fit$bestTune
```

```
##           sigma        C
## 373 0.01312373 16.37766
```

```
resamp = resamples(list(
                        glm.fit = model.glm.2,
                        lda.fit = model.lda.2,
                        bayes.fit = model.bayes.2,
                        boost = boost.class.2,
                        rf = rf.class.2,
                        bagging = bagging.class.2,
                        tree = tree.class.2,
                        cnnet.fit = cnnet.fit.2,
                        svml.fit = svml.fit.2,
                        svmr.fit = svmr.fit.2
                        ))
summary(resamp)
```

```
##
## Call:
## summary.resamples(object = resamp)
##
## Models: glm.fit, lda.fit, bayes.fit, boost, rf, bagging, tree, cnnet.fit, svml.fit, svmr.fit
## Number of resamples: 10
##
## Accuracy
##                Min.   1st Qu.    Median      Mean   3rd Qu.      Max. NA's
## glm.fit   0.7000000 0.8031609 0.8360215 0.8441416 0.9000000 0.9677419    0
## lda.fit   0.7096774 0.7732759 0.8333333 0.8340267 0.8846774 0.9677419    0
## bayes.fit 0.7000000 0.7732759 0.8526882 0.8374750 0.8916667 0.9677419    0
## boost     0.7096774 0.7482759 0.8500000 0.8341416 0.8927419 0.9655172    0
## rf        0.6774194 0.7606322 0.8032258 0.8175677 0.9066092 0.9354839    0
```

```
## bagging   0.6666667 0.7806452 0.8331479 0.8141268 0.8562291 0.9000000    0
## tree      0.6666667 0.7789210 0.8166667 0.8066704 0.8666667 0.8709677    0
## cnnet.fit 0.7000000 0.8031609 0.8360215 0.8441416 0.9000000 0.9677419    0
## svml.fit  0.6774194 0.8000000 0.8360215 0.8378124 0.9155172 0.9677419    0
## svmr.fit  0.7419355 0.8068966 0.8500000 0.8473674 0.8927419 0.9354839    0
##
## Kappa
##                Min.   1st Qu.    Median      Mean   3rd Qu.      Max. NA's
## glm.fit   0.3946188 0.5944980 0.6694856 0.6826138 0.8004166 0.9352818    0
## lda.fit   0.4025696 0.5423267 0.6603832 0.6617627 0.7653612 0.9352818    0
## bayes.fit 0.3946188 0.5469194 0.7004056 0.6724875 0.7814956 0.9352818    0
## boost     0.4101480 0.4940966 0.6916528 0.6626159 0.7826973 0.9307876    0
## rf        0.3404255 0.5082084 0.6012348 0.6283910 0.8082234 0.8697479    0
## bagging   0.3303571 0.5478123 0.6580195 0.6220325 0.7099677 0.7963801    0
## tree      0.3421053 0.5469316 0.6266968 0.6090815 0.7315396 0.7427386    0
## cnnet.fit 0.3946188 0.5944980 0.6694856 0.6826138 0.8004166 0.9352818    0
## svml.fit  0.3404255 0.5893826 0.6709540 0.6710978 0.8279169 0.9352818    0
## svmr.fit  0.4655172 0.6095944 0.6904463 0.6889089 0.7861955 0.8697479    0
```

```r
bwplot(resamp)
```