P8106_final_sd3731

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```r
library(tidyverse)
library(ggplot2)
library(lattice)
library(GGally)
library(summarytools)
library(corrplot)
library(caret)
library(vip)
library(rpart.plot)
library(ranger)
library(gridExtra)
library(e1071)
library(pROC)

# import data
load("./severity_training.RData")
load("./severity_test.RData")

# train data
trainData = training_data |>
  select(-id) |>
  janitor::clean_names() |>
  mutate(
    gender = factor(gender,levels = c("0","1"), labels = c("Female", "M
ale")),
    race = factor(race,levels = c("1","2","3","4"), labels = c("White",
 "Asian","Black","Hispanic")),
    smoking = factor(smoking,levels = c("0","1","2"), labels = c("Never
_smoked", "Former_smoker", "Current_smoker")),
    hypertension = factor(hypertension,levels = c("0", "1"), labels = c
("No", "Yes")),
    diabetes = factor(diabetes,levels = c("0", "1"), labels = c("No", "
Yes")),
    vaccine = factor(vaccine,levels = c("0", "1"), labels = c("Not_vacc
inated", "Vaccinated")),
    severity = factor(severity,levels = c("0", "1"), labels = c("not_se
vere", "severe"))
    )


# test data
testData = test_data |>
  select(-id) |>
  janitor::clean_names() |>
```

```r
  mutate(
    gender = factor(gender,levels = c("0","1"), labels = c("Female", "M
ale")),
    race = factor(race,levels = c("1","2","3","4"), labels = c("White",
 "Asian","Black","Hispanic")),
    smoking = factor(smoking,levels = c("0","1","2"), labels = c("Never
_smoked", "Former_smoker", "Current_smoker")),
    hypertension = factor(hypertension,levels = c("0", "1"), labels = c
("No", "Yes")),
    diabetes = factor(diabetes,levels = c("0", "1"), labels = c("No", "
Yes")),
    vaccine = factor(vaccine,levels = c("0", "1"), labels = c("Not_vacc
inated", "Vaccinated")),
    severity = factor(severity,levels = c("0", "1"), labels = c("not_se
vere", "severe"))
    )

# summary
skimr::skim(trainData)
```

Data summary

Name	trainData
Number of rows	800
Number of columns	14

Column type frequency:	
factor	7
numeric	7

Group variables	None

Variable type: factor

skim_variable	n_missing	complete_rate	ordered	n_unique	top_counts
gender	0	1	FALSE	2	Fem: 410, Mal: 390
race	0	1	FALSE	4	Whi: 521, Bla: 149, His: 80, Asi: 50
smoking	0	1	FALSE	3	Nev: 467, For: 248, Cur: 85
diabetes	0	1	FALSE	2	No: 679, Yes: 121
hypertension	0	1	FALSE	2	No: 432, Yes: 368
vaccine	0	1	FALSE	2	Vac: 464, Not: 336

skim_variable	n_missing	complete_rate	ordered	n_unique	top_counts
severity	0	1	FALSE	2	not: 514, sev: 286

Variable type: numeric

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	p75	p100	hist
age	0	1	60.03	4.30	46.0	57.00	60.0	63.0	72.0	▁▂▅▇▆▁
height	0	1	170.00	6.09	150.2	165.70	170.0	174.1	190.3	▁▃▅▇▃▁
weight	0	1	79.42	7.26	56.6	74.38	79.3	84.4	104.8	▁▃▅▇▃▁
bmi	0	1	27.54	2.74	19.6	25.78	27.6	29.1	37.4	▁▃▅▇▃▁
sbp	0	1	129.85	7.97	109.0	124.00	130.0	135.0	154.0	▁▃▅▇▃▁
ldl	0	1	110.25	20.05	41.0	98.00	111.0	123.0	174.0	▁▂▅▇▆▁
depression	0	1	6.91	2.12	0.0	5.00	7.0	8.0	13.0	▁▃▅▇▆▁

```
skimr::skim(testData)
```

Data summary

Name	testData
Number of rows	200
Number of columns	14

Column type frequency:	
factor	7
numeric	7

Group variables	None

Variable type: factor

skim_variable	n_missing	complete_rate	ordered	n_unique	top_counts
gender	0	1	FALSE	2	Fem: 112, Mal: 88
race	0	1	FALSE	4	Whi: 135, Bla: 35, His: 16, Asi: 14

skim_variable	n_missing	complete_rate	ordered	n_unique	top_counts
smoking	0	1	FALSE	3	Nev: 117, For: 65, Cur: 18
diabetes	0	1	FALSE	2	No: 176, Yes: 24
hypertension	0	1	FALSE	2	No: 104, Yes: 96
vaccine	0	1	FALSE	2	Vac: 127, Not: 73
severity	0	1	FALSE	2	not: 135, sev: 65

Variable type: numeric

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	p75	p100	hist
age	0	1	60.24	4.18	49.0	58.00	60.00	63.00	71.0	▁▂▅▇▂▁
height	0	1	169.63	6.15	152.0	166.00	169.65	174.12	188.1	▁▂▅▇▂▁
weight	0	1	79.51	6.51	61.5	74.80	79.20	84.15	96.3	▁▂▅▇▂▂
bmi	0	1	27.72	2.72	20.4	26.05	27.50	29.70	35.3	▁▂▅▇▂▁
sbp	0	1	130.01	7.49	108.0	125.00	130.00	135.00	148.0	▁▂▅▇▂▂
ldl	0	1	111.30	18.45	70.0	98.75	111.50	124.00	165.0	▂▅▇▂▁
depression	0	1	6.72	2.21	2.0	5.00	7.00	8.00	12.0	▂▅▇▅▁

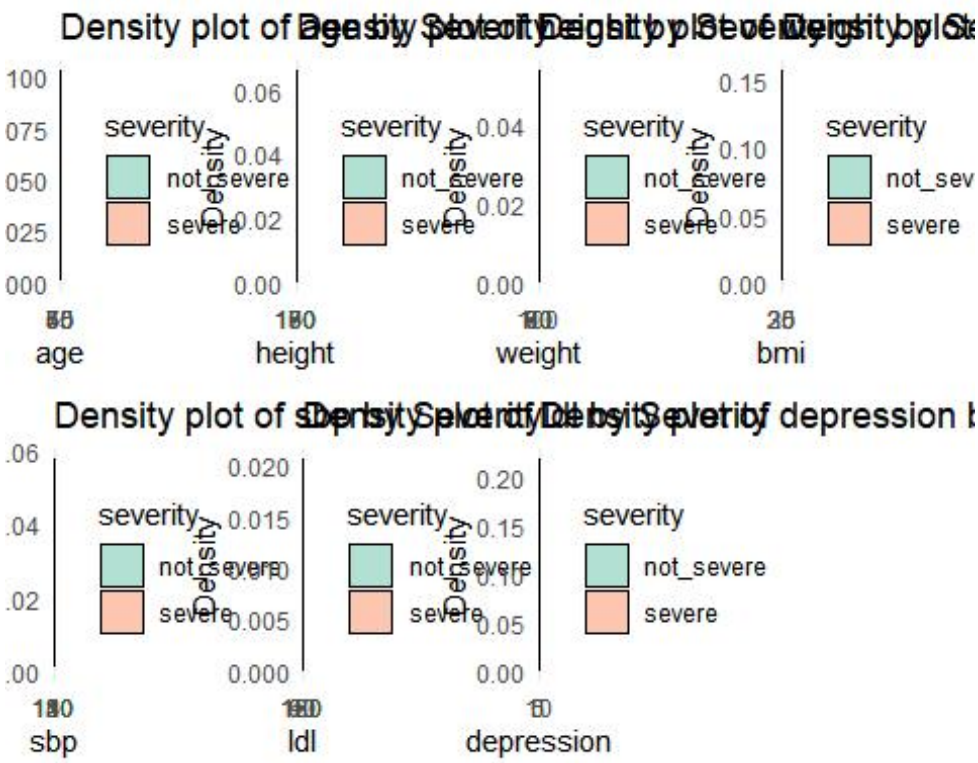
Exploratory analysis and data visualization

```
con_var = c("age", "height", "weight", "bmi", "sbp", "ldl", "depression
")
fac_var = c("gender", "race", "smoking", "diabetes", "hypertension", "v
accine", "severity")
```

continuous variable

```
plot_con_severity = lapply(con_var, function(var) {
  ggplot(trainData, aes_string(x = var, fill = "severity")) +
    geom_density(alpha = 0.5) +
    labs(title = paste("Density plot of", var, "by Severity"), x = var,
 y = "Density") +
    scale_fill_manual(values = c("not_severe" = "#66C2A5", "severe" = "
#FC8D62")) +
    theme_minimal()
})
```

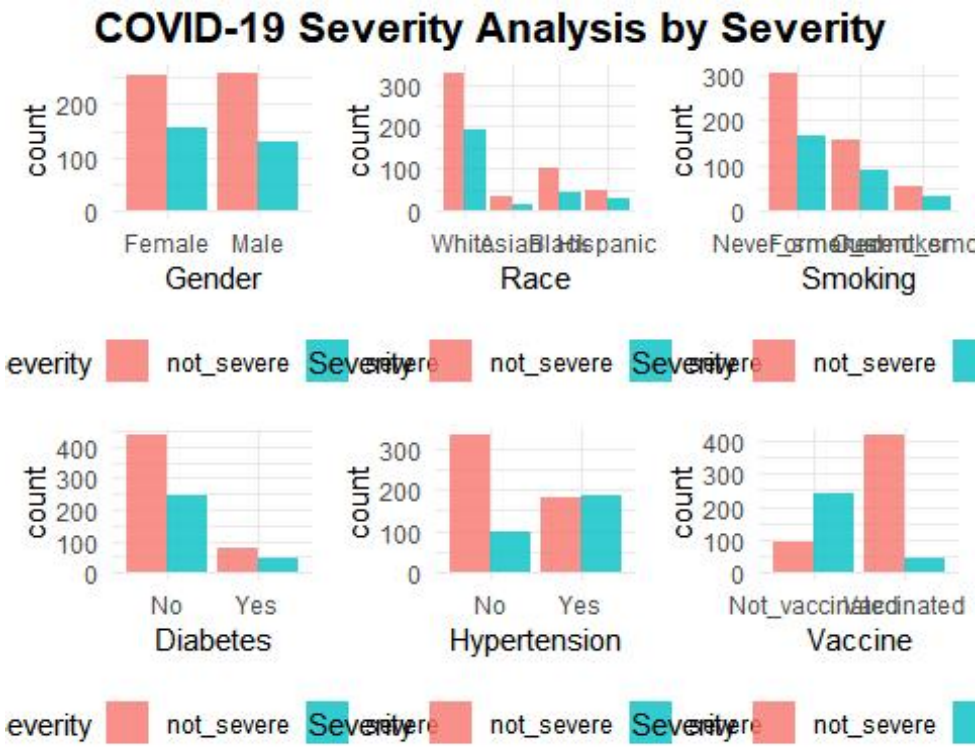
```r
# Display all plots in a grid
gridExtra::grid.arrange(grobs = plot_con_severity, nrow = 2, ncol = 4)
```



categorical variable

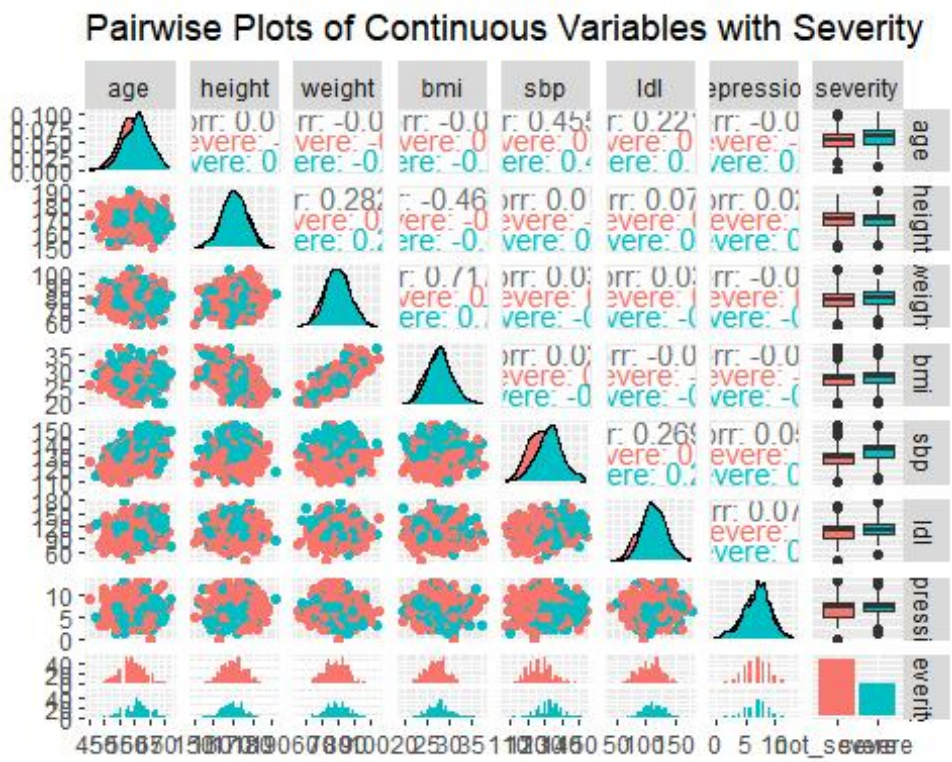
```r
# Bar Chart
gender_bar = trainData |>
  ggplot(aes(x = gender, fill = severity)) +
  geom_bar(stat = "count",
           position = "dodge",
           alpha = 0.8) +
  labs(x = "Gender", fill = "Severity") +
  theme_minimal() +
  theme(legend.position = "bottom")

race_bar = trainData |>
  ggplot(aes(x = race, fill = severity)) +
  geom_bar(stat = "count",
           position = "dodge",
           alpha = 0.8) +
  labs(x = "Race", fill = "Severity") +
  theme_minimal() +
  theme(legend.position = "bottom")

smoking_bar = trainData |>
  ggplot(aes(x = smoking, fill = severity)) +
```

```r
  geom_bar(stat = "count",
           position = "dodge",
           alpha = 0.8) +
  labs(x = "Smoking", fill = "Severity") +
  theme_minimal() +
  theme(legend.position = "bottom")

diabetes_bar = trainData |>
  ggplot(aes(x = diabetes, fill = severity)) +
  geom_bar(stat = "count",
           position = "dodge",
           alpha = 0.8) +
  labs(x = "Diabetes", fill = "Severity") +
  theme_minimal() +
  theme(legend.position = "bottom")

hypertension_bar = trainData |>
  ggplot(aes(x = hypertension, fill = severity)) +
  geom_bar(stat = "count",
           position = "dodge",
           alpha = 0.8) +
  labs(x = "Hypertension", fill = "Severity") +
  theme_minimal() +
  theme(legend.position = "bottom")

vaccine_bar = trainData |>
  ggplot(aes(x = vaccine, fill = severity)) +
  geom_bar(stat = "count",
           position = "dodge",
           alpha = 0.8) +
  labs(x = "Vaccine", fill = "Severity") +
  theme_minimal() +
  theme(legend.position = "bottom")

library(gridExtra)
library(grid)
grid.arrange(
  arrangeGrob(
    gender_bar, race_bar, smoking_bar,
    diabetes_bar, hypertension_bar, vaccine_bar,
    ncol = 3, nrow = 2
  ),
  top = textGrob("COVID-19 Severity Analysis by Severity", gp = gpar(fo
ntsize = 16, fontface = "bold"))
)
```

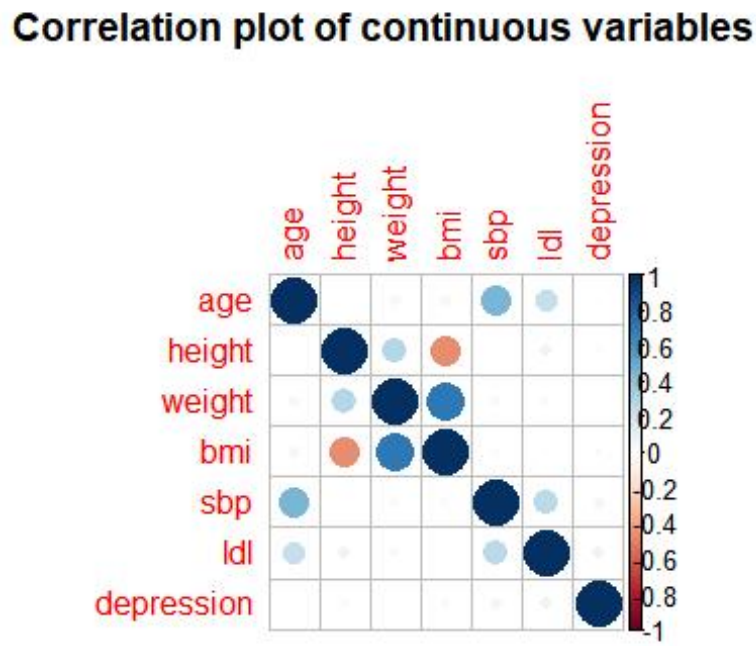


correlation

```
ggpairs(trainData[, c(con_var, "severity")],
        mapping = aes(color = severity),
        title = "Pairwise Plots of Continuous Variables with Severity")
```




```
ggsave("./figure/plot_corr1.jpeg", dpi = 500)

corrplot(cor(trainData[,con_var]), method = "circle", type = "full",
         title = "Correlation plot of continuous variables",
         mar = c(2, 2, 4, 2))
```




```
ggsave("./figure/plot_corr2.jpeg", dpi = 500)
```

Model training

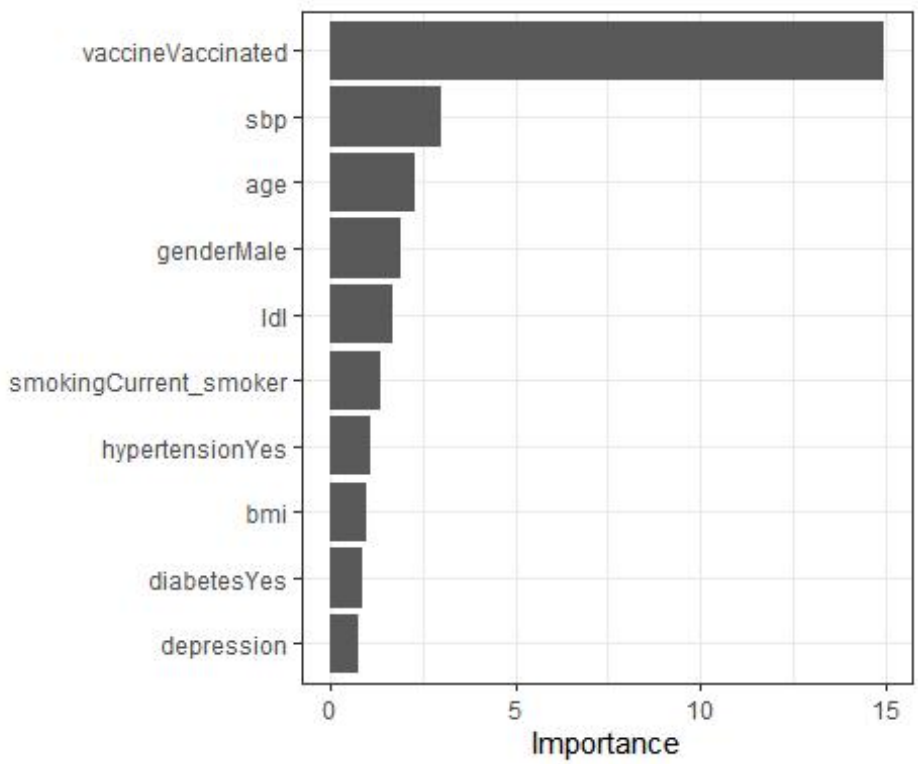
```
x = model.matrix(severity ~ . , trainData)[, -1]
y = trainData[, "severity"]

x2 = model.matrix(severity ~ . , testData)[, -1]
y2 = testData$severity

# cv
set.seed(3731)
ctrl = trainControl(method = "cv",
                    number = 10,
                    classProbs = TRUE,
                    allowParallel = TRUE,
                    summaryFunction = twoClassSummary,
                    savePredictions = "final")
```

Logistic Regression

```
set.seed(3731)
glm.fit = train(x,
                y,
                method = 'glm',
                trControl = ctrl)
coef(glm.fit$finalModel)
```

```
##           (Intercept)                   age            genderMale
##          -36.14267644            0.06479499           -0.40913157
##             raceAsian             raceBlack          raceHispanic
##           -0.20261995            0.01737165           -0.17462048
##  smokingFormer_smoker smokingCurrent_smoker                height
##            0.02496598            0.49239971            0.11171808
##                weight                   bmi           diabetesYes
##           -0.13337473            0.53758507            0.25302775
##       hypertensionYes                   sbp                   ldl
##            0.38092720            0.07081051            0.01002248
##     vaccineVaccinated            depression
##           -3.61798671           -0.03796927
```

```
vip(glm.fit$finalModel) + theme_bw()
```



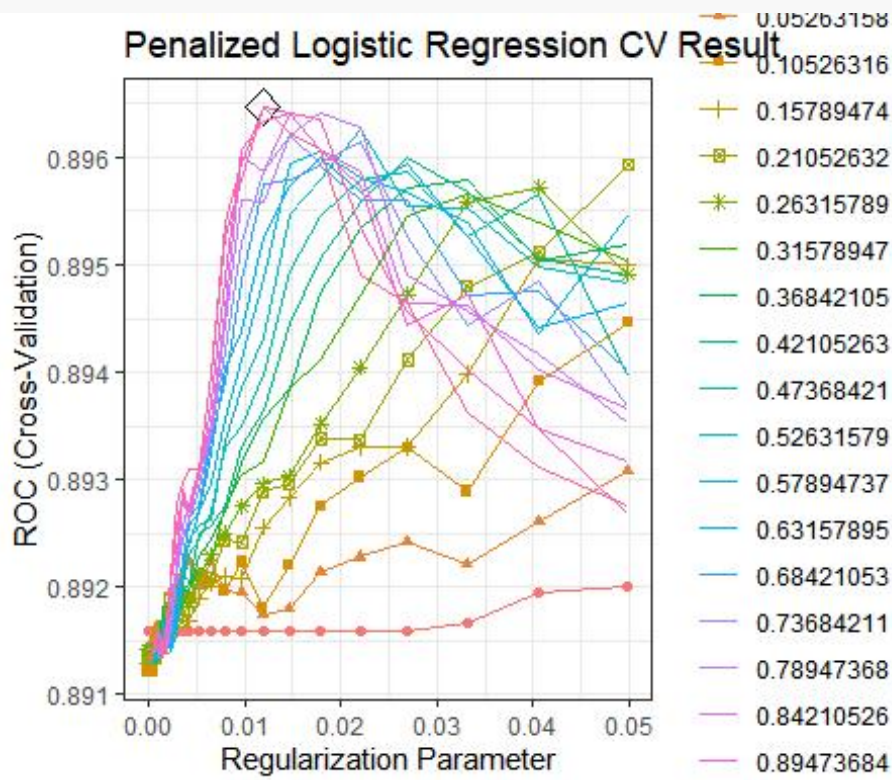

```
#max(glm.fit$results$Accuracy)
```

Penalized logistic regression

Penalized logistic regression can be fitted using `glmnet`. We use the `train` function to select the optimal tuning parameters.

```
glmnGrid = expand.grid(.alpha = seq(0, 1, length = 20),
                       .lambda = exp(seq(-13, -3, length = 50)))
set.seed(3731)
glmn.fit = train(severity ~ .,
                 data = trainData,
```

```
                  method = "glmnet",
                  tuneGrid = glmnGrid,
                  trControl = ctrl)

glmn.fit$bestTune

##     alpha     lambda
## 993     1 0.01193152

# plot
myCol = rainbow(25)
myPar = list(superpose.symbol = list(col = myCol),
             superpose.line = list(col = myCol))
ggplot(glmn.fit, highlight = TRUE) +
  labs(title="Penalized Logistic Regression CV Result") +
  theme_bw()
```

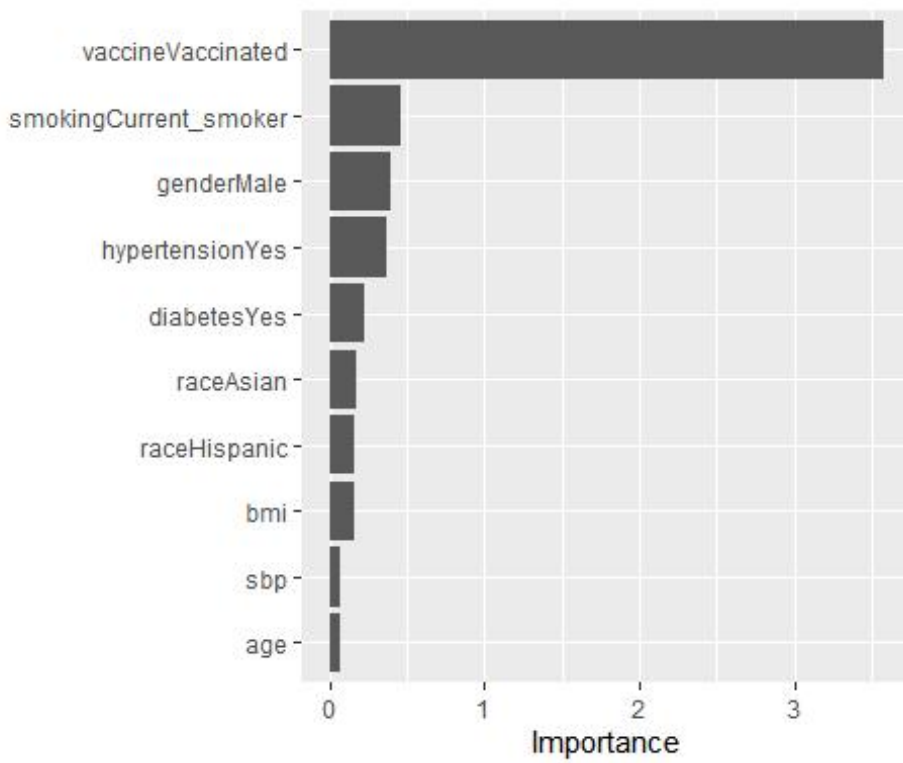



```
ggsave("./figure/penal_logi_cv.jpeg", dpi = 500)

# # Confusion matrix
# glmn.pred.prob = predict(glmn.fit, newdata = testData, type = "prob")
# glmn.pred = rep("not_severe", nrow(testData))
# glmn.pred[glmn.pred.prob[, "severe"] > 0.5] = "severe"
#
# confusionMatrix(data = as.factor(glmn.pred),
#                 reference = y2,
#                 positive = "severe")
```

```r
# Coefficients
coef(glmn.fit$finalModel, glmn.fit$bestTune$lambda)
```

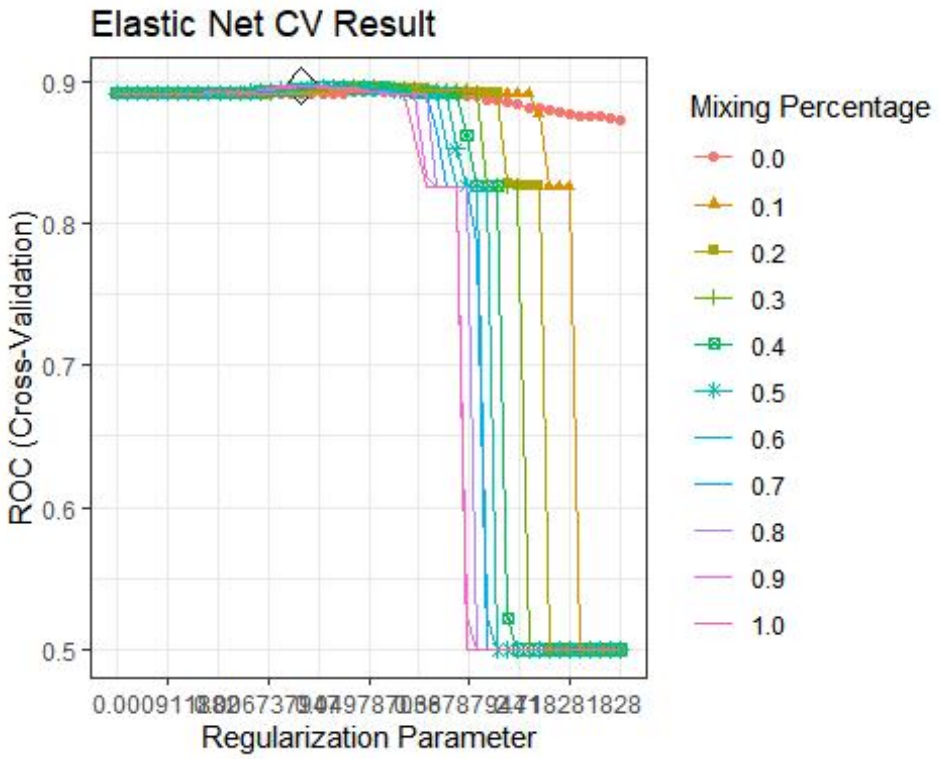
```
## 17 x 1 sparse Matrix of class "dgCMatrix"
##                                   s1
## (Intercept)           -13.748527613
## age                     0.048124759
## genderMale             -0.195662915
## raceAsian               .
## raceBlack               .
## raceHispanic            .
## smokingFormer_smoker    .
## smokingCurrent_smoker   0.077493852
## height                  .
## weight                  .
## bmi                     0.117063103
## diabetesYes             .
## hypertensionYes         0.290951440
## sbp                     0.061655434
## ldl                     0.004234011
## vaccineVaccinated      -3.169495661
## depression              .
```

```r
vip(glmn.fit$finalModel)
```

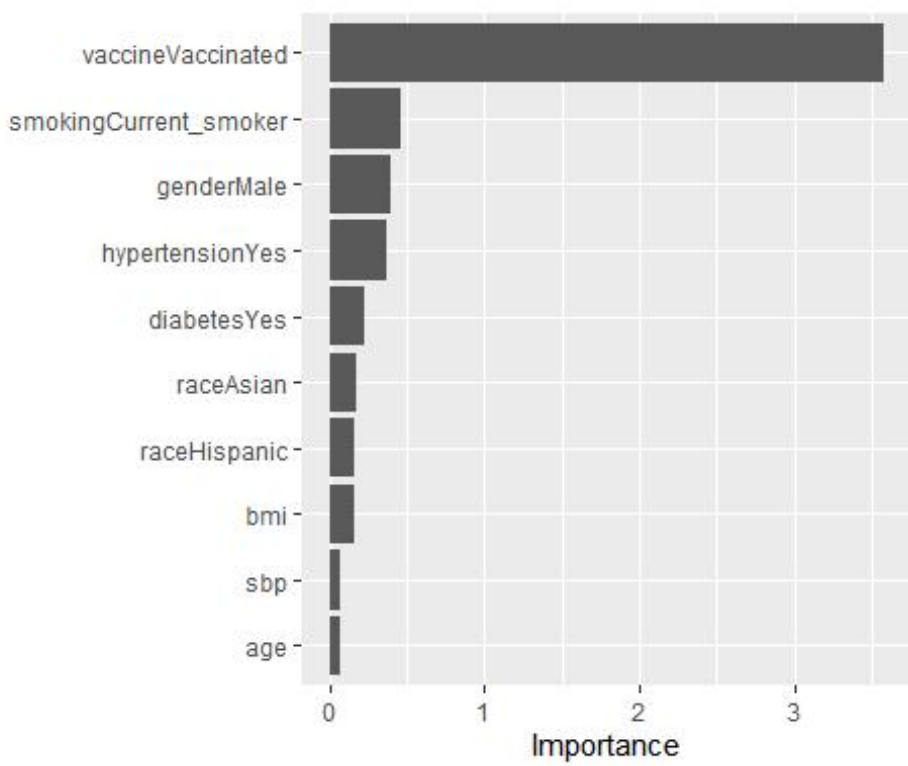


Elastic Net

```
set.seed(3731)
enet.fit = train(x,
                 y,
                 method = "glmnet",
                 tuneGrid = expand.grid(alpha = seq(0, 1, length = 11),
                                        lambda = exp(seq(2,-8, length =
 50))),
                 trControl = ctrl)

enet.fit$bestTune

##     alpha     lambda
## 519     1 0.01321331

# Coefficients
coef(enet.fit$finalModel, enet.fit$bestTune$lambda)

## 17 x 1 sparse Matrix of class "dgCMatrix"
##                                   s1
## (Intercept)           -13.377273440
## age                     0.046336268
## genderMale             -0.175609847
## raceAsian               .
## raceBlack               .
## raceHispanic            .
## smokingFormer_smoker    .
## smokingCurrent_smoker   0.042685195
## height                  .
## weight                  .
## bmi                     0.112075355
## diabetesYes             .
## hypertensionYes         0.281618275
## sbp                     0.060939569
## ldl                     0.003798565
## vaccineVaccinated      -3.133379258
## depression              .

# plot
ggplot(enet.fit, highlight = TRUE) +
  scale_x_continuous(trans='log', n.breaks = 6) +
  labs(title ="Elastic Net CV Result") +
  theme_bw()
```

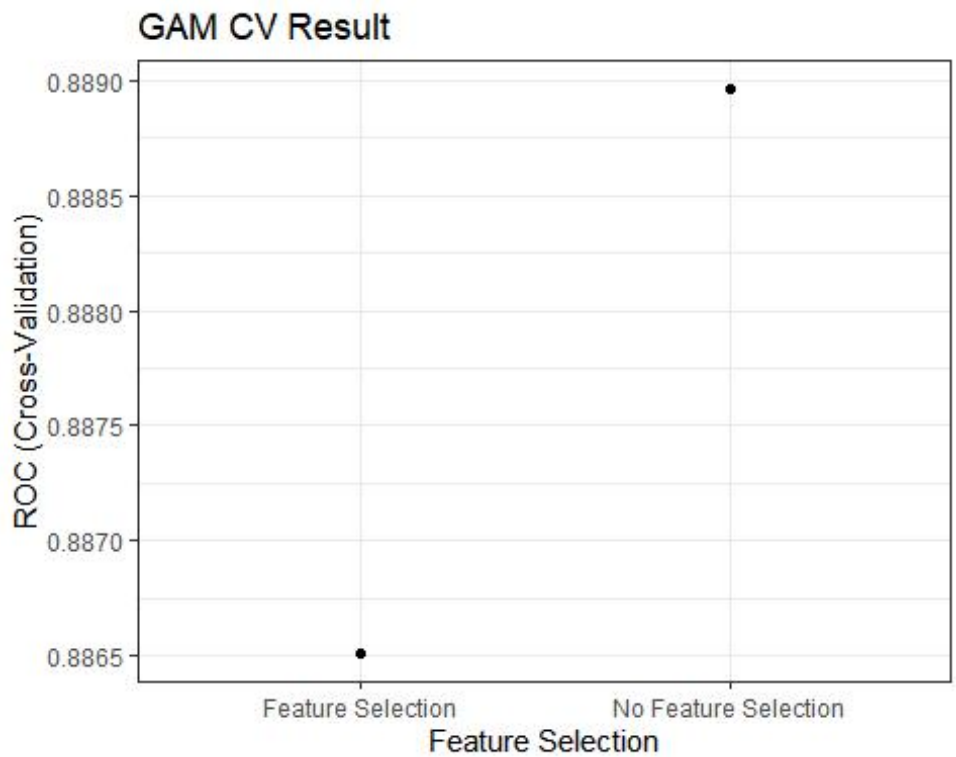



```r
ggsave("./figure/enet_cv.jpeg", dpi = 500)

vip(enet.fit$finalModel)
```



Generalized Additive Model (GAM)

```
set.seed(3731)
gam.fit = train(x,
                y,
                method = "gam",
                metric = "ROC",
                trControl = ctrl)
gam.fit$bestTune

##   select method
## 1  FALSE GCV.Cp

ggplot(gam.fit) +
  labs(title = "GAM CV Result") +
  theme_bw()
```



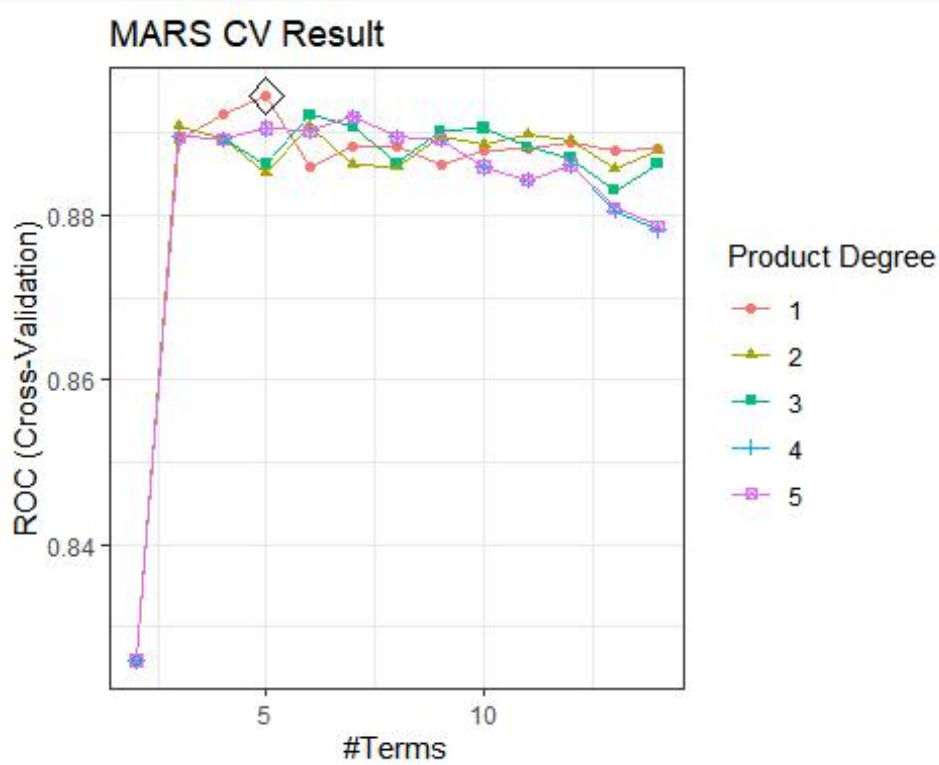

```
ggsave("./figure/gam_cv.jpeg", dpi = 500)

# coef(gam.fit$finalModel)
gam.fit$finalModel

##
## Family: binomial
## Link function: logit
##
## Formula:
## .outcome ~ genderMale + raceAsian + raceBlack + raceHispanic +
```

```
##     smokingFormer_smoker + smokingCurrent_smoker + diabetesYes +
##     hypertensionYes + vaccineVaccinated + s(depression) + s(age) +
##     s(sbp) + s(ldl) + s(bmi) + s(height) + s(weight)
##
## Estimated degrees of freedom:
## 1.00 1.06 3.47 1.74 1.00 7.69 1.00
##  total = 26.97
##
## UBRE score: -0.2345662
```

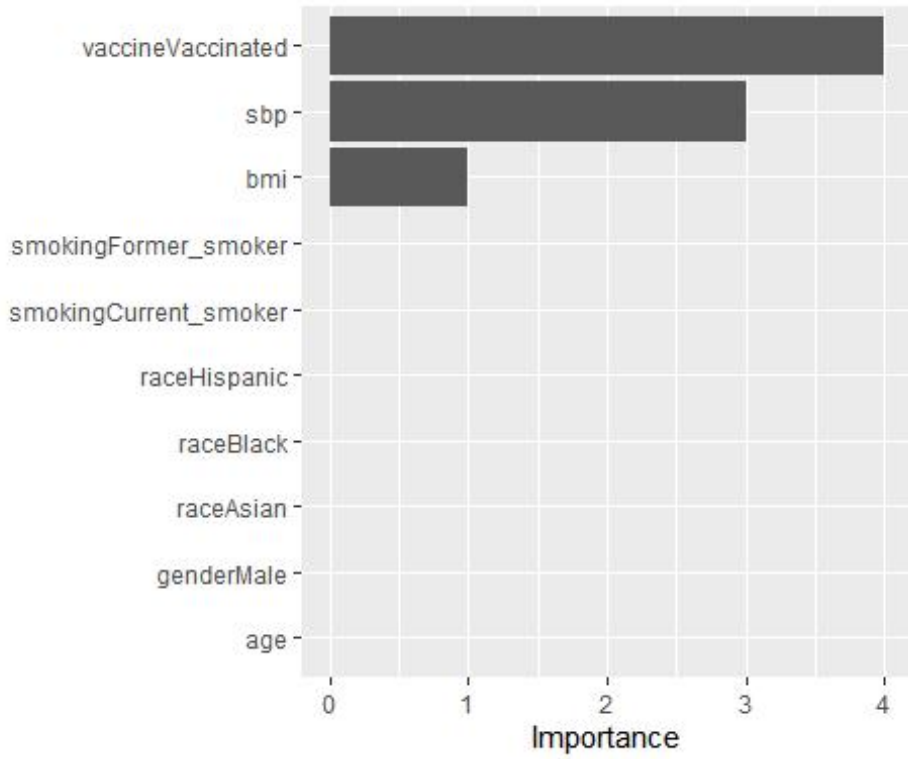
```
# par(mfrow=c(2, 3))
# plot(gam.fit$finalModel)
# par(mfrow=c(1, 1))
```

Multivariate Adaptive Regression Splines (MARS)

```
mars.grid = expand.grid(degree = 1:5,
                        nprune = 2:14)
set.seed(3731)
mars.fit = train(x,
                 y,
                 method = "earth",
                 tuneGrid = mars.grid,
                 trControl = ctrl)

ggplot(mars.fit, highlight = TRUE)+
  labs(title  ="MARS CV Result") +
  theme_bw()
```



```r
ggsave("./figure/mars_cv.jpeg", dpi = 500)

mars.fit$bestTune

##   nprune degree
## 4      5      1

coef(mars.fit$finalModel)

##       (Intercept) vaccineVaccinated        h(sbp-139)        h(139-s
bp)
##        1.98341761       -3.50798169       -0.01515556       -0.13557
595
##         h(bmi-27)
##        0.24293455

summary(mars.fit$finalModel)

## Call: earth(x=matrix[800,16], y=factor.object, keepxy=TRUE,
##             glm=list(family=function.object, maxit=100), degree=1, n
prune=5)
##
## GLM coefficients
##                       severe
## (Intercept)        1.9834176
## vaccineVaccinated -3.5079817
## h(bmi-27)          0.2429345
## h(139-sbp)        -0.1355759
## h(sbp-139)        -0.0151556
##
## GLM (family binomial, link logit):
##  nulldev  df       dev  df   devratio     AIC iters converged
##  1043.15 799   605.753 795      0.419   615.8     5         1
##
## Earth selected 5 of 24 terms, and 3 of 16 predictors (nprune=5)
## Termination condition: Reached nk 33
## Importance: vaccineVaccinated, sbp, bmi, age-unused, genderMale-unus
ed, ...
## Number of terms at each degree of interaction: 1 4 (additive model)
## Earth GCV 0.1246822    RSS 97.51412    GRSq 0.4585368    RSq 0.46932
54

vip(mars.fit$finalModel)
```



Linear Discriminant Analysis (LDA)

```
set.seed(3731)
lda.fit = train(x,
                y,
                method = "lda",
                metric = "ROC",
                trControl = ctrl)
```

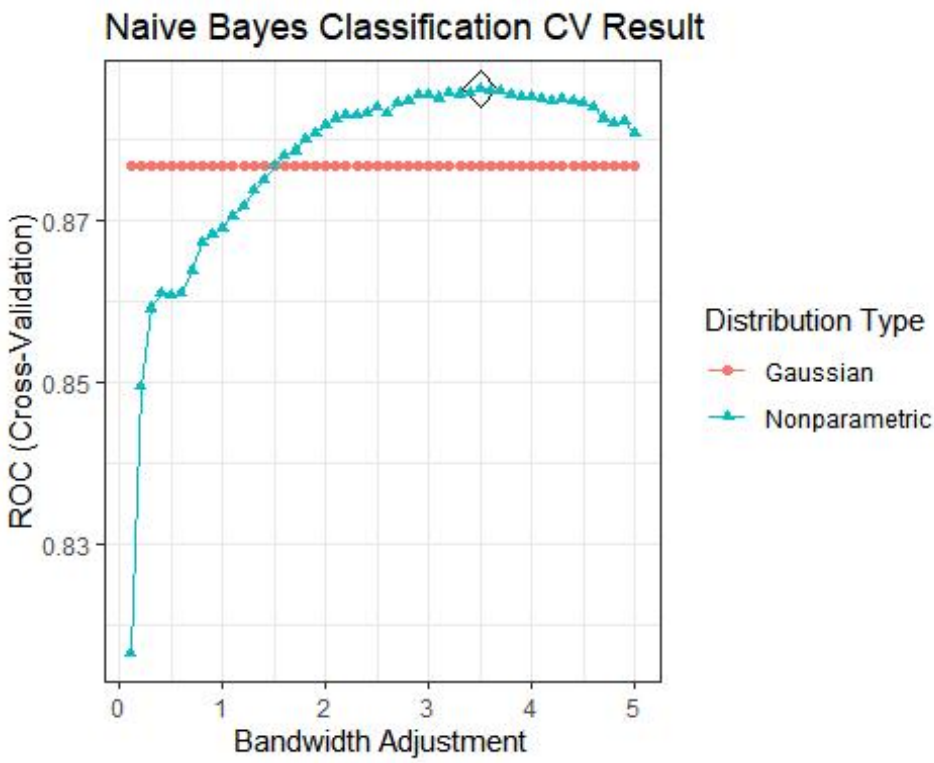
Quadratic Discriminant Analysis (QDA)

```
set.seed(3731)
qda.fit = train(x,
                y,
                method = "qda",
                metric = "ROC",
                trControl = ctrl)
```

Naive Bayes (NB)

```
nbGrid = expand.grid(usekernel = c(FALSE,TRUE),
                     fL = 1,
                     adjust = seq(0.1, 5, by = .1))
set.seed(3731)
nb.fit = train(x,
               y,
               method = "nb",
               tuneGrid = nbGrid,
               metric = "ROC",
```

```
                trControl = ctrl)
nb.fit$bestTune

##    fL usekernel adjust
## 85  1      TRUE    3.5

ggplot(nb.fit, highlight = TRUE) +
  labs(title  ="Naive Bayes Classification CV Result") +
  theme_bw()
```

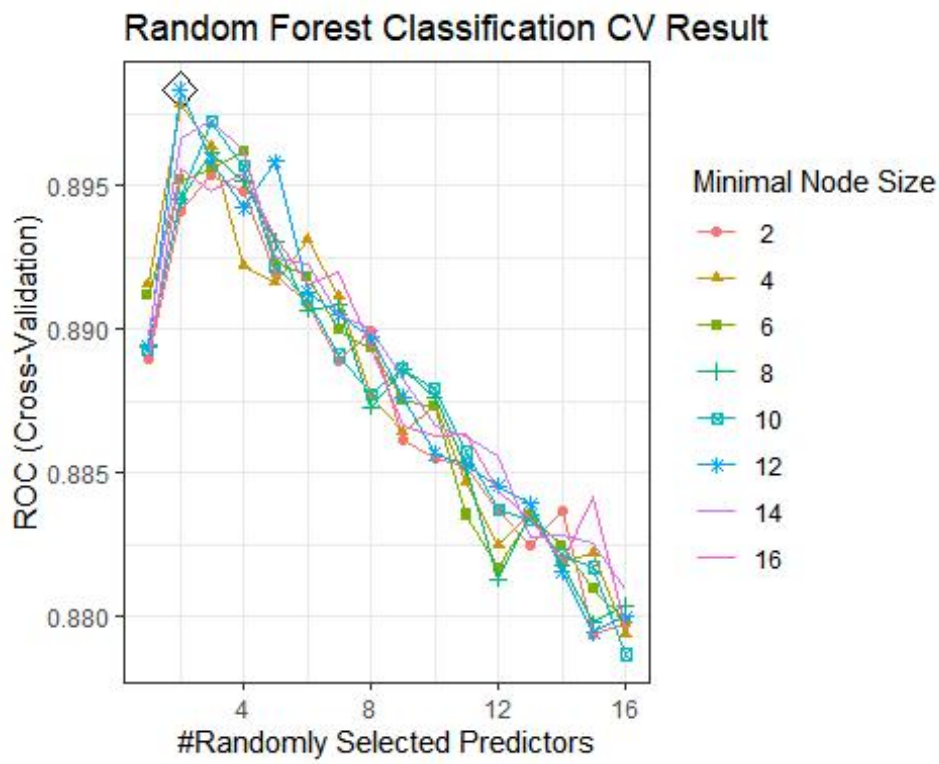



```
ggsave("./figure/nb_cv.jpeg", dpi = 500)
```

Random Forest

```
rf.grid2 = expand.grid(mtry = 1:ncol(x),
                       splitrule = "gini",
                       min.node.size = seq(from = 2, to = 16, by = 2))
set.seed(3731)
rf.fit2 = train(x,
                y,
                method = "ranger",
                tuneGrid = rf.grid2,
                trControl = ctrl)

rf.fit2$bestTune

##    mtry splitrule min.node.size
## 14    2      gini            12
```

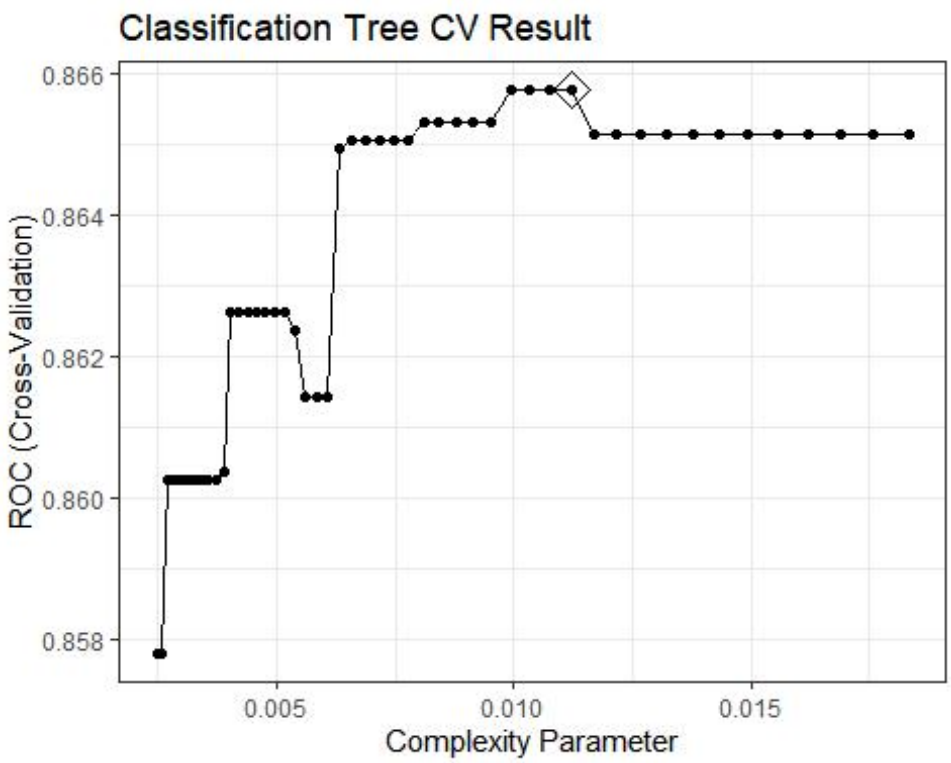
```r
ggplot(rf.fit2, highlight = TRUE) +
  labs(title = "Random Forest Classification CV Result") +
  theme_bw()
```




```r
ggsave("./figure/rf_classification_cv.jpeg", dpi = 500)
```

Classification Trees

```r
rpart.grid = expand.grid(cp = exp(seq(-6,-4, len = 50)))
set.seed(3731)
rpart.fit = train(x,
                  y,
                  method = "rpart",
                  tuneGrid = rpart.grid,
                  trControl = ctrl)

rpart.fit$bestTune

##             cp
## 38 0.01122293

ggplot(rpart.fit, highlight = TRUE) +
  labs(title = "Classification Tree CV Result") +
  theme_bw()
```

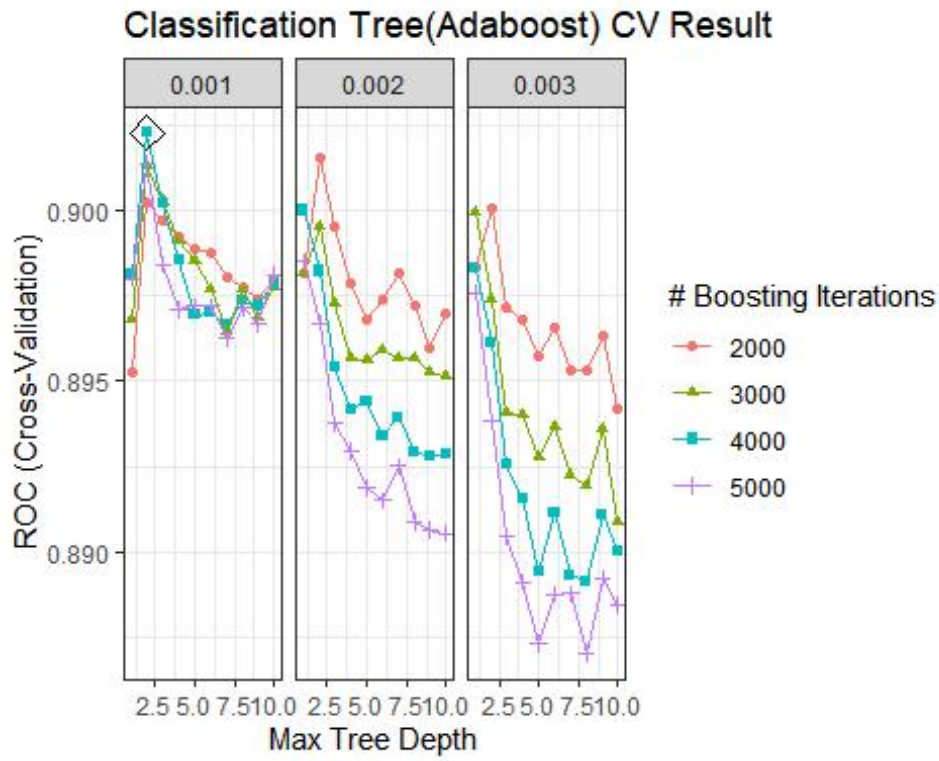



```
# ggsave("./figure/rpart_cv.jpeg", dpi = 500)
#
# rpart.plot(rpart.fit$finalModel)
#
# jpeg("./figure/rpart.jpeg", width = 8, height = 6, units="in", res=50
0)
# rpart.plot(rpart.fit$finalModel)
# dev.off()
```

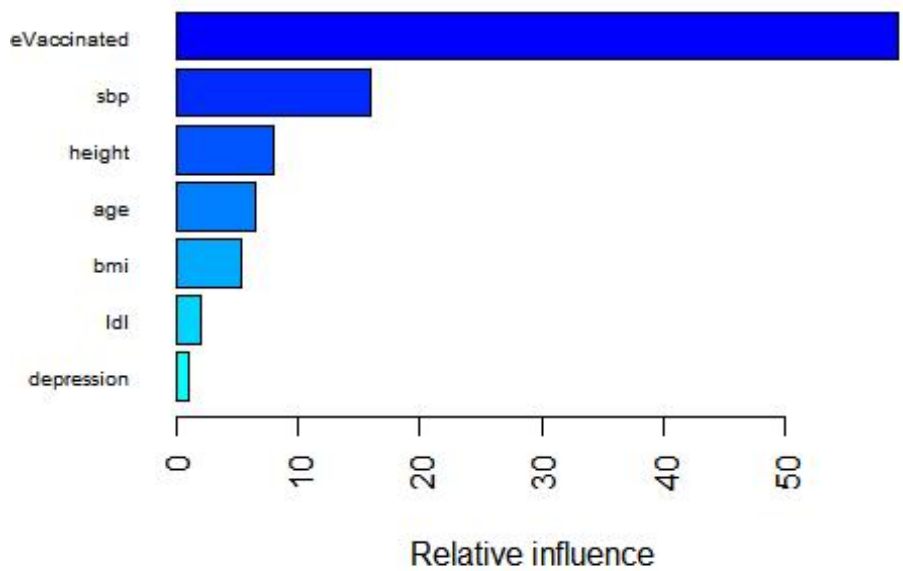
Adaboost

```
gbmA.grid = expand.grid(n.trees = c(2000, 3000, 4000, 5000),
                        interaction.depth = 1:10,
                        shrinkage = c(0.001, 0.002, 0.003),
                        n.minobsinnode = 1)
set.seed(3731)
gbmA.fit = train(x,
                 y,
                 method = "gbm",
                 tuneGrid = gbmA.grid,
                 trControl = ctrl,
                 distribution = "adaboost",
                 verbose = FALSE)
gbmA.fit$bestTune

##   n.trees interaction.depth shrinkage n.minobsinnode
## 7    4000                 2     0.001              1
```

```r
# plot
ggplot(gbmA.fit, highlight = TRUE) +
  labs(title = "Classification Tree(Adaboost) CV Result") +
  theme_bw()
```




```r
ggsave("./figure/gbmA_cv.jpeg", dpi = 500)

# Variable importance
summary(gbmA.fit$finalModel, las = 2, cBars = 7, cex.names = 0.6)
```

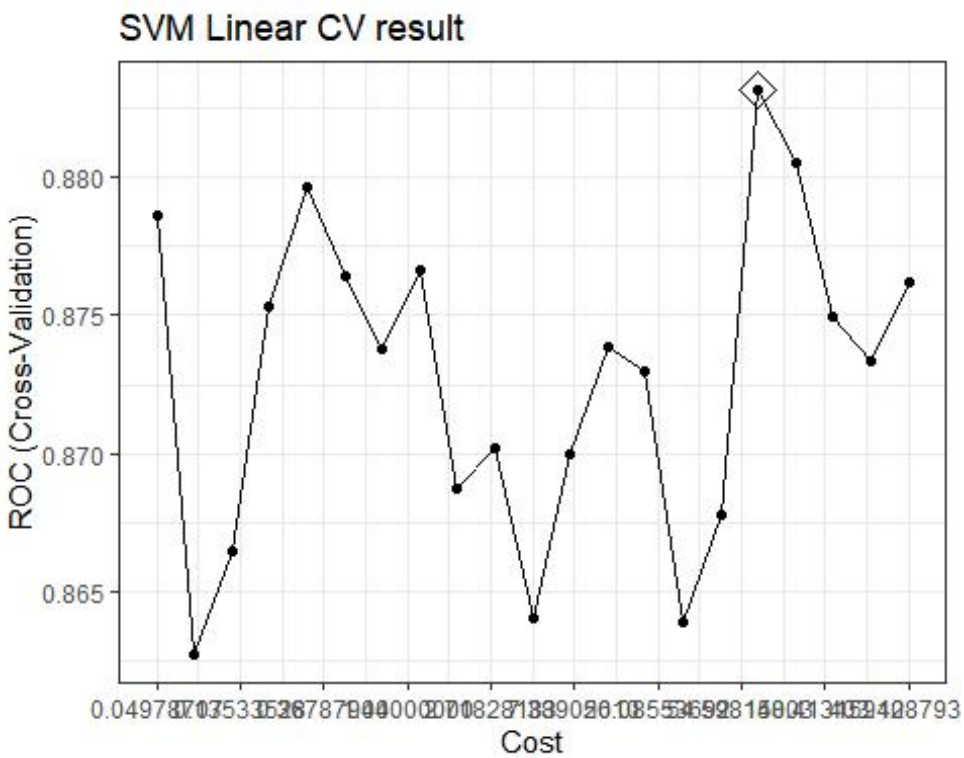



```
##                                          var      rel.inf
## vaccineVaccinated         vaccineVaccinated 59.244643505
## sbp                                     sbp 15.984611726
## height                               height  7.934349106
## age                                     age  6.450499807
## bmi                                     bmi  5.273480867
## ldl                                     ldl  1.994823637
## depression                       depression  1.067582456
## weight                               weight  0.970517584
## hypertensionYes             hypertensionYes  0.514722903
## genderMale                       genderMale  0.276478309
## smokingCurrent_smoker smokingCurrent_smoker  0.258412504
## raceAsian                         raceAsian  0.010638798
## diabetesYes                     diabetesYes  0.008363645
## smokingFormer_smoker   smokingFormer_smoker  0.008324171
## raceHispanic                   raceHispanic  0.002550982
## raceBlack                         raceBlack  0.000000000
```

Support Vector Machine (SVM)

```
set.seed(3731)
svml.fit = train(x,
                 y,
                 method = "svmLinear",
                 tuneGrid = data.frame(C = exp(seq(-3, 6, len = 21))),
                 trControl = ctrl)

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

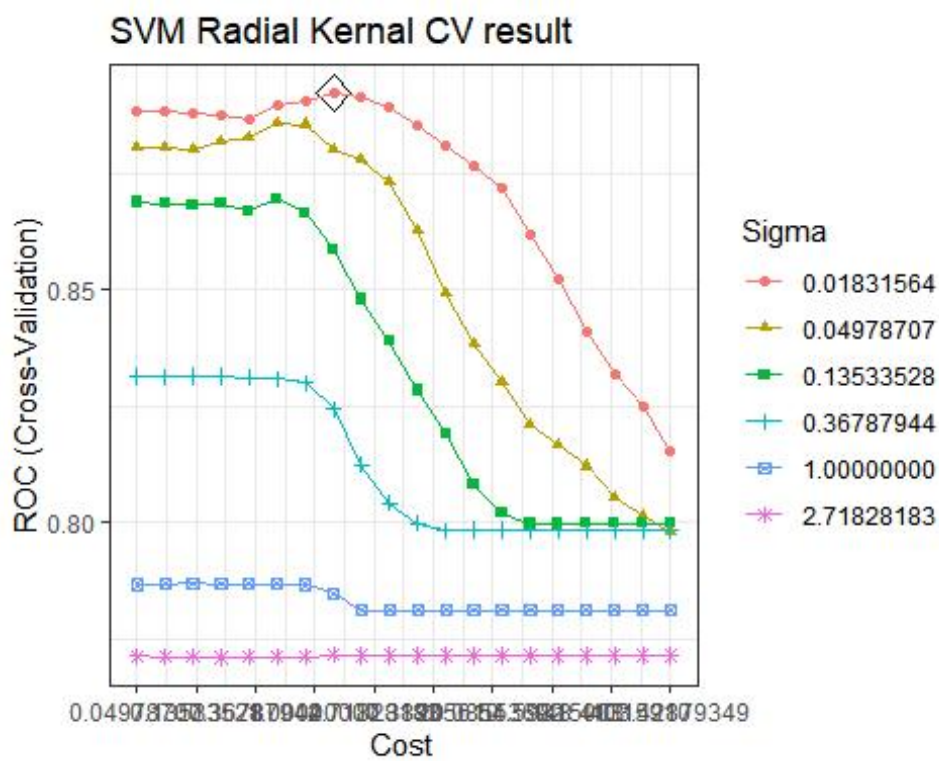
```
  scale_x_continuous(trans='log',n.breaks = 10) +
  labs(title = "SVM Linear CV result") +
  theme_bw()
```




```
ggsave("./figure/svml_cv.jpeg", dpi = 500)

svmr.grid = expand.grid(C = exp(seq(-3, 6, len = 20)),
                        sigma = exp(seq(-4, 1, len = 6)))

set.seed(3731)
svmr.fit = train(x,
                 y,
                 method = "svmRadialSigma",
                 tuneGrid = svmr.grid,
                 trControl = ctrl)
```

```
## maximum number of iterations reached 0.001555028 0.001526522maximum
number of iterations reached 0.0001049961 0.0001003757maximum number of
 iterations reached 0.001565161 0.00152748maximum number of iterations
reached 0.0001555562 0.0001484596maximum number of iterations reached 0.
001624193 0.00158779maximum number of iterations reached 0.001008161 0.
0009672123maximum number of iterations reached 9.968407e-06 9.252759e-0
6maximum number of iterations reached 0.002522674 0.002475664maximum nu
mber of iterations reached 5.77933e-05 5.52207e-05maximum number of ite
rations reached 0.001071575 0.001035467maximum number of iterations rea
ched 0.0002230658 0.0002129264maximum number of iterations reached 0.00
05720601 0.0005568371maximum number of iterations reached 7.043732e-05
```

```
6.734821e-05maximum number of iterations reached 0.001051966 0.00102525
maximum number of iterations reached 0.001943041 0.001873563maximum num
ber of iterations reached 0.002437711 0.002383565maximum number of iter
ations reached 0.0001147904 0.0001097216maximum number of iterations re
ached 0.001801172 0.0017537maximum number of iterations reached 0.00062
63894 0.0005984378maximum number of iterations reached 0.0002870176 0.0
00267116maximum number of iterations reached 0.002676939 0.00261618maxi
mum number of iterations reached 0.0004819192 0.0004611776maximum numbe
r of iterations reached 1.891896e-05 1.755898e-05

svmr.fit$bestTune

##         sigma        C
## 43 0.01831564 1.371342

# plot
myCol= rainbow(25)
myPar = list(superpose.symbol = list(col = myCol),
             superpose.line = list(col = myCol))
ggplot(svmr.fit, highlight = TRUE, par.settings = myPar) +
  scale_x_continuous(trans='log',n.breaks = 10) +
  labs(title = "SVM Radial Kernal CV result") +
  theme_bw()
```




```
ggsave("./figure/svmr_cv.jpeg", dpi = 500)
```

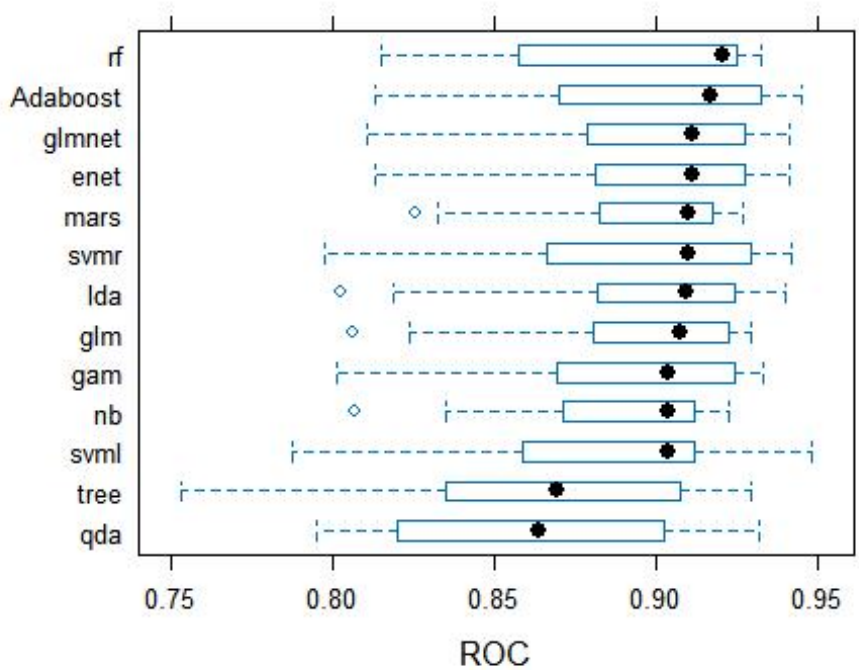
Model Selection

```
set.seed(3731)
resamp = resamples(list(glm = glm.fit,
                        glmnet = glmn.fit,
                        enet = enet.fit,
                        gam = gam.fit,
                        mars = mars.fit,
                        lda = lda.fit,
                        qda = qda.fit,
                        nb = nb.fit,
                        rf = rf.fit2,
                        tree = rpart.fit,
                        Adaboost = gbmA.fit,
                        svml = svml.fit,
                        svmr = svmr.fit))

summary(resamp)
```

```
##
## Call:
## summary.resamples(object = resamp)
##
## Models: glm, glmnet, enet, gam, mars, lda, qda, nb, rf, tree, Adaboo
st, svml, svmr
## Number of resamples: 10
##
## ROC
##               Min.   1st Qu.    Median      Mean   3rd Qu.      Max.
 NA's
## glm      0.8060224 0.8812879 0.9072129 0.8906537 0.9220274 0.9290061
    0
## glmnet   0.8109244 0.8846213 0.9112446 0.8964676 0.9254202 0.9409814
    0
## enet     0.8130252 0.8865160 0.9109195 0.8965507 0.9254202 0.9409814
    0
## gam      0.8011204 0.8721921 0.9038824 0.8889628 0.9231874 0.9330629
    0
## mars     0.8256303 0.8868742 0.9100563 0.8944594 0.9167082 0.9267241
    0
## lda      0.8025210 0.8843786 0.9088911 0.8929675 0.9238808 0.9396552
    0
## qda      0.7948179 0.8237412 0.8637593 0.8613904 0.8976164 0.9316976
    0
## nb       0.8067227 0.8739816 0.9038462 0.8862909 0.9111610 0.9222448
    0
## rf       0.8151261 0.8692951 0.9201681 0.8983231 0.9247347 0.9323867
    0
## tree     0.7535497 0.8387100 0.8693634 0.8657576 0.9045346 0.9290451
    0
## Adaboost 0.8130252 0.8804103 0.9166119 0.9022879 0.9320292 0.9449602
```

```
    0
## svml     0.7876944 0.8673622 0.9035666 0.8831536 0.9103641 0.9476127
    0
## svmr     0.7976190 0.8741684 0.9096119 0.8924048 0.9263016 0.9416446
    0
##
## Sens
##               Min.   1st Qu.    Median      Mean   3rd Qu.      Max.
 NA's
## glm      0.8431373 0.8486991 0.8921569 0.8811840 0.9033748 0.9230769
    0
## glmnet   0.8235294 0.8503017 0.8823529 0.8792232 0.9033748 0.9230769
    0
## enet     0.8039216 0.8503017 0.8725490 0.8753017 0.9033748 0.9230769
    0
## gam      0.8431373 0.8627451 0.8834842 0.8869910 0.9171380 0.9230769
    0
## mars     0.8235294 0.8627451 0.8823529 0.8850679 0.9171380 0.9423077
    0
## lda      0.7843137 0.8116516 0.8446456 0.8442308 0.8647247 0.9230769
    0
## qda      0.8269231 0.8438914 0.8627451 0.8638009 0.8781109 0.9230769
    0
## nb       0.9038462 0.9414593 0.9607843 0.9553167 0.9756787 0.9807692
    0
## rf       0.8846154 0.9276018 0.9411765 0.9397059 0.9607843 0.9807692
    0
## tree     0.8627451 0.8745287 0.9127074 0.9104827 0.9366516 0.9615385
    0
## Adaboost 0.8627451 0.8921569 0.9215686 0.9142911 0.9371229 0.9615385
    0
## svml     0.7647059 0.7730015 0.8137255 0.8130845 0.8461538 0.8653846
    0
## svmr     0.8627451 0.8696267 0.9019608 0.8948341 0.9033748 0.9423077
    0
##
## Spec
##               Min.   1st Qu.    Median      Mean   3rd Qu.      Max.
 NA's
## glm      0.6551724 0.6964286 0.7931034 0.7827586 0.8620690 0.8928571
    0
## glmnet   0.6206897 0.7500000 0.8103448 0.8038177 0.8851601 0.9310345
    0
## enet     0.6206897 0.7500000 0.8103448 0.8038177 0.8851601 0.9310345
    0
## gam      0.6206897 0.6875000 0.7758621 0.7513547 0.7931034 0.8620690
    0
## mars     0.5517241 0.7321429 0.7931034 0.7726601 0.8275862 0.8928571
    0
## lda      0.6551724 0.7857143 0.8602217 0.8352217 0.8965517 0.9310345
```

```
    0
## qda      0.6206897 0.6813424 0.7543103 0.7584975 0.8411330 0.8965517
    0
## nb       0.3928571 0.4482759 0.5178571 0.5379310 0.6083744 0.7931034
    0
## rf       0.5517241 0.6160714 0.7241379 0.7094828 0.7844828 0.8928571
    0
## tree     0.5862069 0.7142857 0.7758621 0.7584975 0.8275862 0.8571429
    0
## Adaboost 0.5862069 0.6785714 0.7758621 0.7548030 0.8275862 0.8928571
    0
## svml     0.6206897 0.7857143 0.8774631 0.8386700 0.8965517 0.9655172
    0
## svmr     0.6206897 0.7500000 0.8275862 0.8038177 0.8620690 0.9310345
    0

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



Because the Adaboost model shows the highest median ROC value according to the resampling outcomes reflecting our models' performance on the training group, my choice for predicting the `severity` response variable would be the **Adaboost** model.

Training / Testing Error

```
# Adaboost error
# training
pred.gbmA.train = predict(gbmA.fit, newdata = x)
```

```r
confusionMatrix(data = pred.gbmA.train, reference = y, positive = "seve
re")
```

```
## Confusion Matrix and Statistics
##
##             Reference
## Prediction   not_severe severe
##   not_severe        481     66
##   severe             33    220
##
##                Accuracy : 0.8762
##                  95% CI : (0.8514, 0.8983)
##     No Information Rate : 0.6425
##     P-Value [Acc > NIR] : < 2.2e-16
##
##                   Kappa : 0.7235
##
##  Mcnemar's Test P-Value : 0.001299
##
##             Sensitivity : 0.7692
##             Specificity : 0.9358
##          Pos Pred Value : 0.8696
##          Neg Pred Value : 0.8793
##              Prevalence : 0.3575
##          Detection Rate : 0.2750
##    Detection Prevalence : 0.3162
##       Balanced Accuracy : 0.8525
##
##        'Positive' Class : severe
##
```

```r
##Accuracy : 0.8762; Kappa : 0.7235

# test
pred.gbmA.test = predict(gbmA.fit, newdata = x2)
confusionMatrix(data = pred.gbmA.test, reference = y2, positive = "seve
re")
```

```
## Confusion Matrix and Statistics
##
##             Reference
## Prediction   not_severe severe
##   not_severe        126     18
##   severe              9     47
##
##                Accuracy : 0.865
##                  95% CI : (0.8097, 0.9091)
##     No Information Rate : 0.675
##     P-Value [Acc > NIR] : 5.597e-10
##
```

```
##                   Kappa : 0.6809
##
##  Mcnemar's Test P-Value : 0.1237
##
##             Sensitivity : 0.7231
##             Specificity : 0.9333
##          Pos Pred Value : 0.8393
##          Neg Pred Value : 0.8750
##              Prevalence : 0.3250
##          Detection Rate : 0.2350
##    Detection Prevalence : 0.2800
##       Balanced Accuracy : 0.8282
##
##        'Positive' Class : severe
##

##Accuracy : 0.865; Kappa : 0.6809
```

AUC

```
# AUC test
glm.pred = predict(glm.fit, newdata = x2, type = "prob")[, 2]
glmn.pred = predict(glmn.fit, newdata = testData, type = "prob")[, 2]
enet.pred = predict(enet.fit, newdata = x2, type = "prob")[, 2]
gam.pred = predict(gam.fit, newdata = x2, type = "prob")[, 2]
mars.pred = predict(mars.fit, newdata = x2, type = "prob")[, 2]
lda.pred = predict(lda.fit, newdata = x2, type = "prob")[, 2]
qda.pred = predict(qda.fit, newdata = x2, type = "prob")[, 2]
nb.pred = predict(nb.fit, newdata = x2, type = "prob")[, 2]
rf.pred = predict(rf.fit2, newdata = x2, type = "prob")[, 2]
rpart.pred = predict(rpart.fit, newdata = x2, type = "prob")[, 2]
gbmA.pred = predict(gbmA.fit, newdata = testData, type = "prob")[, 2]
svml.pred = predict(svml.fit, newdata = x2, type = "prob")[, 2]
svmr.pred = predict(svmr.fit, newdata = x2, type = "prob")[, 2]


roc.glm = roc(y2, glm.pred)
roc.glmn = roc(y2, glmn.pred)
roc.enet = roc(y2, enet.pred)
roc.gam = roc(y2, gam.pred)
roc.mars = roc(y2, mars.pred)
roc.lda = roc(y2, lda.pred)
roc.qda = roc(y2, qda.pred)
roc.nb = roc(y2, nb.pred)
roc.rf = roc(y2, rf.pred)
roc.rpart = roc(y2, rpart.pred)
roc.gbmA = roc(y2, gbmA.pred)
roc.svml = roc(y2, svml.pred)
roc.svmr = roc(y2, svmr.pred)
```

```r
auc = c(roc.glm$auc,
        roc.glmn$auc,
        roc.enet$auc,
        roc.gam$auc,
        roc.mars$auc,
        roc.lda$auc,
        roc.qda$auc,
        roc.nb$auc,
        roc.rf$auc,
        roc.rpart$auc,
        roc.gbmA$auc,
        roc.svml$auc,
        roc.svmr$auc)

names(auc) = c("GLM", "GLMnet", "ENet", "GAM", "MARS", "LDA", "QDA", "N
B", "RF", "RPART", "GBM", "SVML", "SVMR")
auc
```

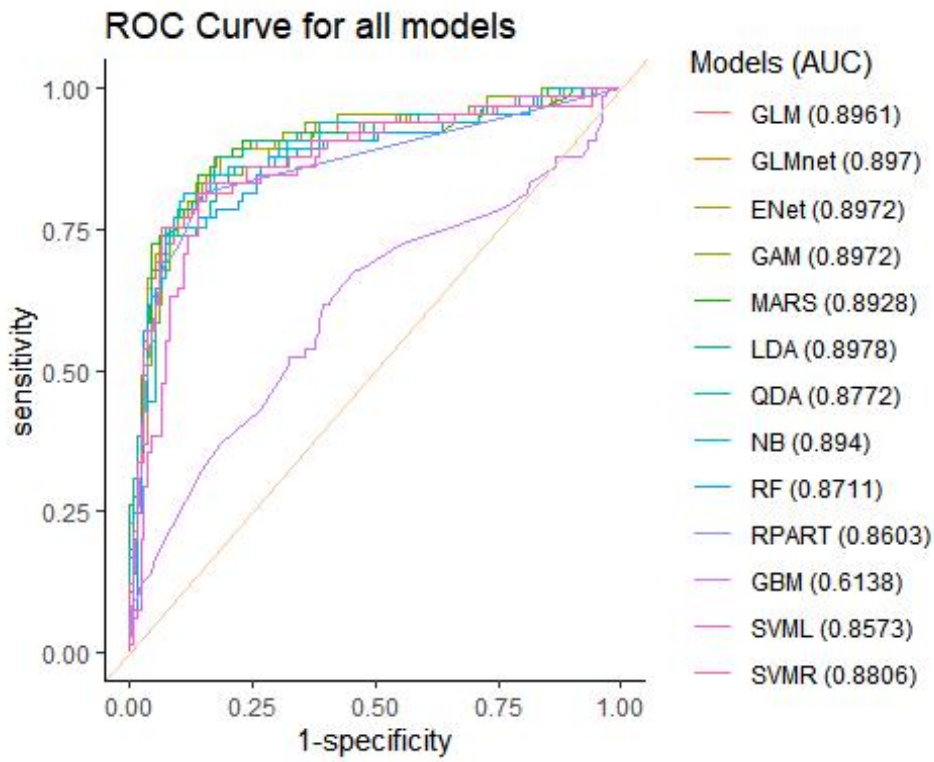
```
##       GLM    GLMnet      ENet       GAM      MARS       LDA       QD
A        NB
## 0.8960684 0.8969801 0.8972080 0.8972080 0.8927635 0.8977778 0.877151
0 0.8940171
##        RF     RPART       GBM      SVML      SVMR
## 0.8711111 0.8602849 0.6137892 0.8573219 0.8805698
```

```r
modelNames = c("GLM", "GLMnet", "ENet", "GAM", "MARS", "LDA", "QDA", "N
B", "RF", "RPART", "GBM", "SVML", "SVMR")
# order auc
auc_data = data.frame(model = modelNames,
                      auc = auc)
auc_data[order(-auc_data$auc), ]
```

```
##         model       auc
## LDA       LDA 0.8977778
## GAM       GAM 0.8972080
## ENet     ENet 0.8972080
## GLMnet GLMnet 0.8969801
## GLM       GLM 0.8960684
## NB         NB 0.8940171
## MARS     MARS 0.8927635
## SVMR     SVMR 0.8805698
## QDA       QDA 0.8771510
## RF         RF 0.8711111
## RPART   RPART 0.8602849
## SVML     SVML 0.8573219
## GBM       GBM 0.6137892
```

```r
# plot auc
ggroc(list(roc.glm, roc.glmn, roc.enet, roc.gam, roc.mars, roc.lda, roc.
qda, roc.nb, roc.rf, roc.rpart, roc.gbmA, roc.svml, roc.svmr), legacy.a
xes = TRUE) +
```

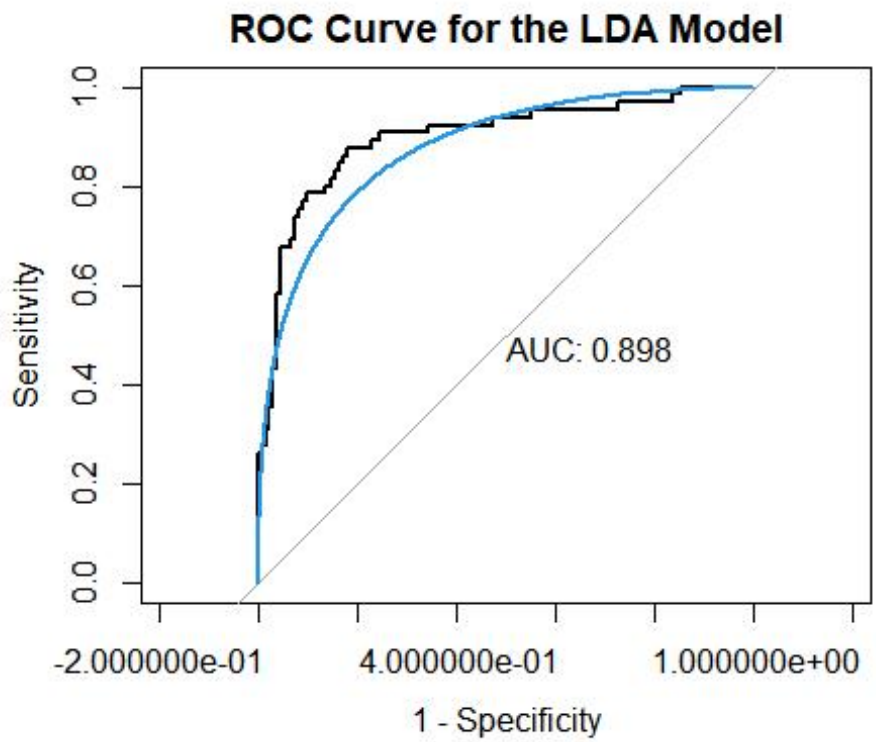
```
  scale_color_discrete(labels = paste0(modelNames, " (", round(auc, 4),
")"),
                       name = "Models (AUC)") +
  geom_abline(intercept = 0, slope = 1, color = "#f9cb9c") +
  theme_classic() +
  labs(title = "ROC Curve for all models")
```




```
ggsave("./figure/roc_test.jpeg", dpi = 500)
```

According to the model, the LDA model also has the highest auc value(**0.8977778**) among all the models. Thus, I prefer to choose the **LDA** model.

```
plot(roc.lda,
     legacy.axes = TRUE,
     print.auc = TRUE,
     main = "ROC Curve for the LDA Model")
plot(smooth(roc.mars), col = 4, add = TRUE)
```




```
# test data
test.pred.prob = predict(lda.fit, newdata = x2, type = "prob")[, 2]
test.pred = rep("not_severe", length(test.pred.prob))
test.pred[test.pred.prob > 0.5] = "severe"
res = confusionMatrix(data = factor(test.pred, levels = c("not_severe",
 "severe")),
                      reference = y2,
                      positive = "severe")
res

## Confusion Matrix and Statistics
##
##              Reference
## Prediction   not_severe severe
##   not_severe        115     13
##   severe             20     52
##
##                Accuracy : 0.835
##                  95% CI : (0.7762, 0.8836)
##     No Information Rate : 0.675
##     P-Value [Acc > NIR] : 2.442e-07
##
##                   Kappa : 0.6341
##
##  Mcnemar's Test P-Value : 0.2963
##
##             Sensitivity : 0.8000
```

```
##             Specificity : 0.8519
##          Pos Pred Value : 0.7222
##          Neg Pred Value : 0.8984
##              Prevalence : 0.3250
##          Detection Rate : 0.2600
##    Detection Prevalence : 0.3600
##       Balanced Accuracy : 0.8259
##
##        'Positive' Class : severe
##
```

```
1-0.835
```

```
## [1] 0.165
```

Also, the value of Accuracy is 0.835 and Kappa is 0.6341 in LDA for test data. In addition, we can obtain the misclassification error rate is 16.5% (1-0.835 = 0.165).