

Final Secondary Analysis

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```
library(tidyverse)
library(summarytools)
library(corrplot)
library(caret)
library(vip)
library(rpart.plot)
library(ranger)
```

1 Model Training

1.1 Secondary Analysis

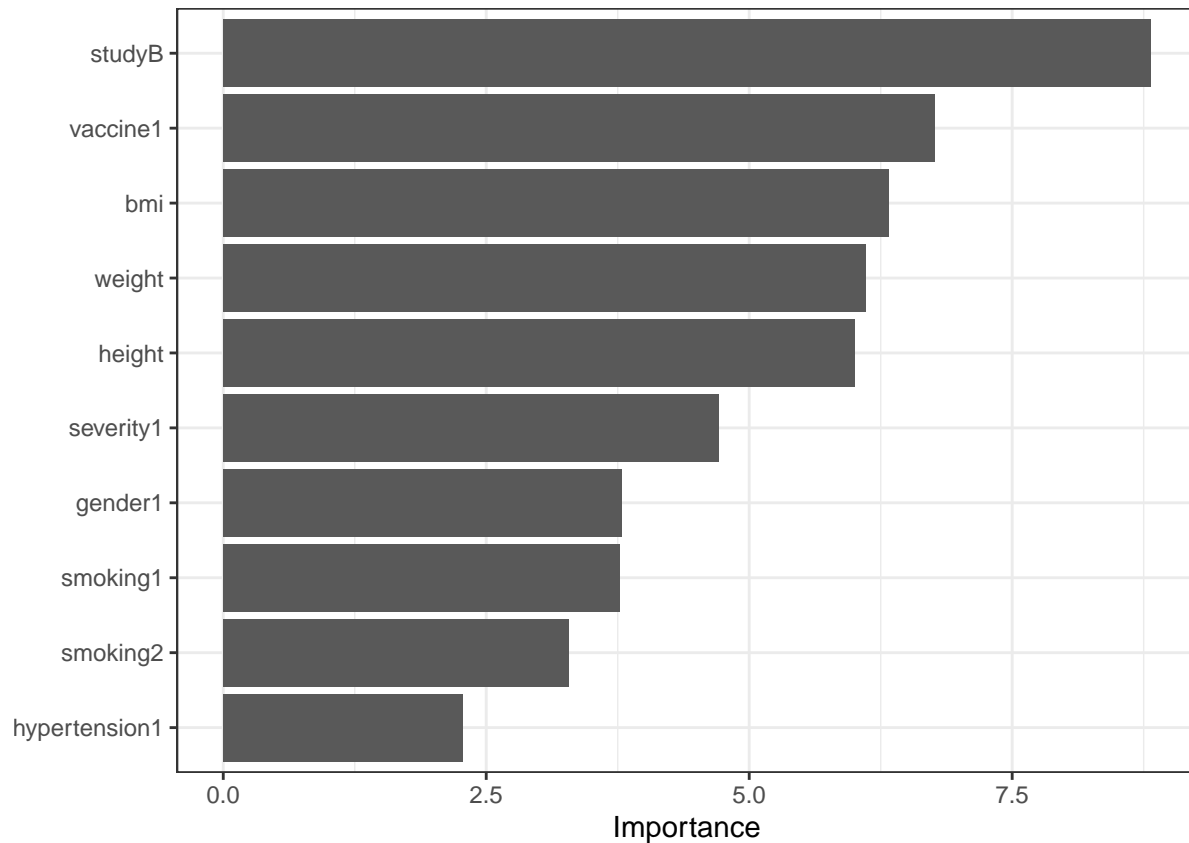
```
ctrl1 <- trainControl(method = "cv", number = 10)
```

1.1.1 Logistic Regression

```
set.seed(2023)
glm.fit <- train(x = train.x,
                 y = train.bin.y,
                 method = 'glm',
                 trControl = ctrl1)
coef(glm.fit$finalModel)
```

```
##      (Intercept)          age      gender1      race2      race3
## -85.313351100    0.014271893  -0.323467202  -0.104376256  -0.039351201
##           race4      smoking1      smoking2      height      weight
##   0.003550318    0.367190652    0.502782618    0.502637208  -0.545510559
##           bmi hypertension1    diabetes1      SBP      LDL
##   1.634689792    0.325697328  -0.070567897  -0.005832901  -0.001829020
##      vaccine1      severity1      studyB      studyC
##  -0.600151829    0.761039467  -1.066825060  -0.031460504
```

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



1.1.2 Penalized Logistic Regression

```

glmnetGrid <- expand.grid(.alpha = seq(0, 1, length = 21),
                        .lambda = exp(seq(-10, -5, length = 15)))
set.seed(2023)
glmnet.fit <- train(train.x,
                   train.bin.y,
                   method = 'glmnet',
                   tuneGrid = glmnetGrid,
                   trControl = ctrl1)

glmnet.fit$bestTune

```

```

##      alpha      lambda
## 292  0.95 0.0003869779

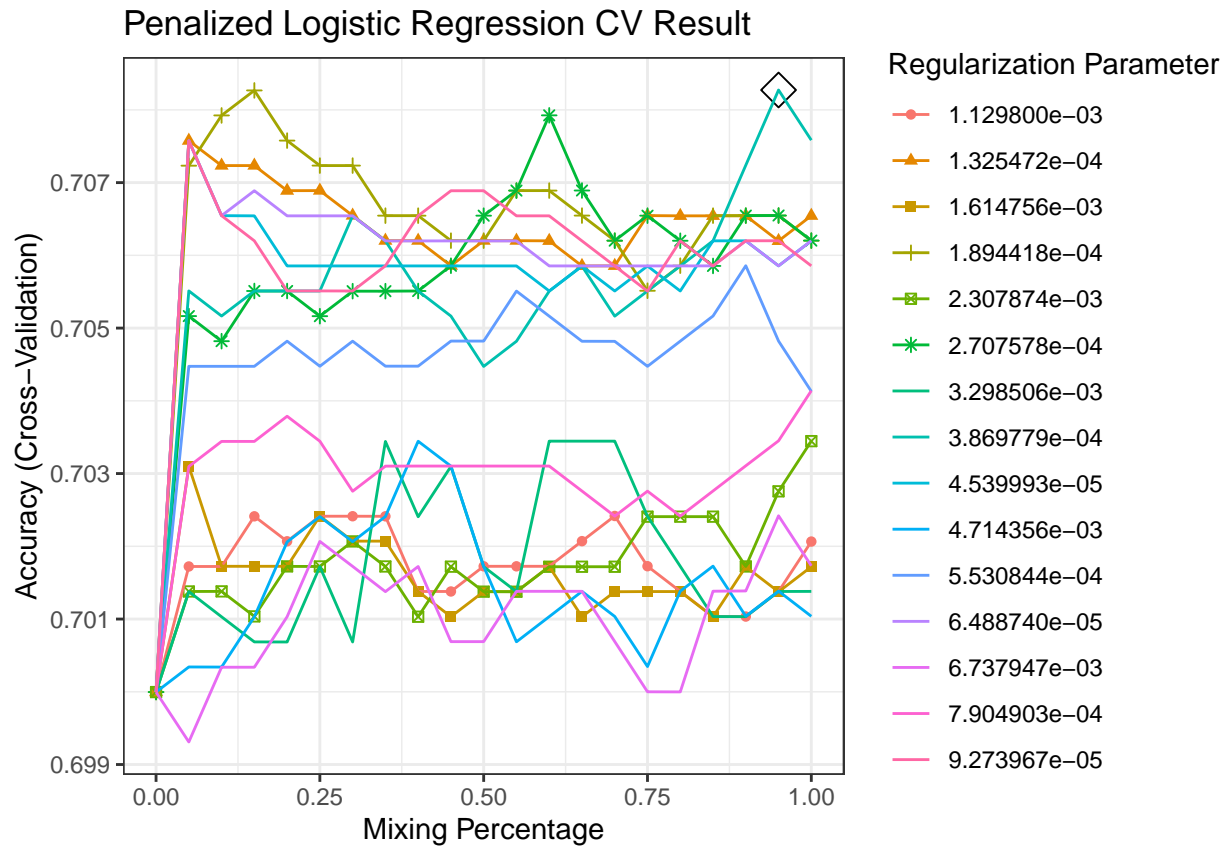
```

```

myCol <- rainbow(25)
myPar <- list(superpose.symbol = list(col = myCol),
             superpose.line = list(col = myCol))

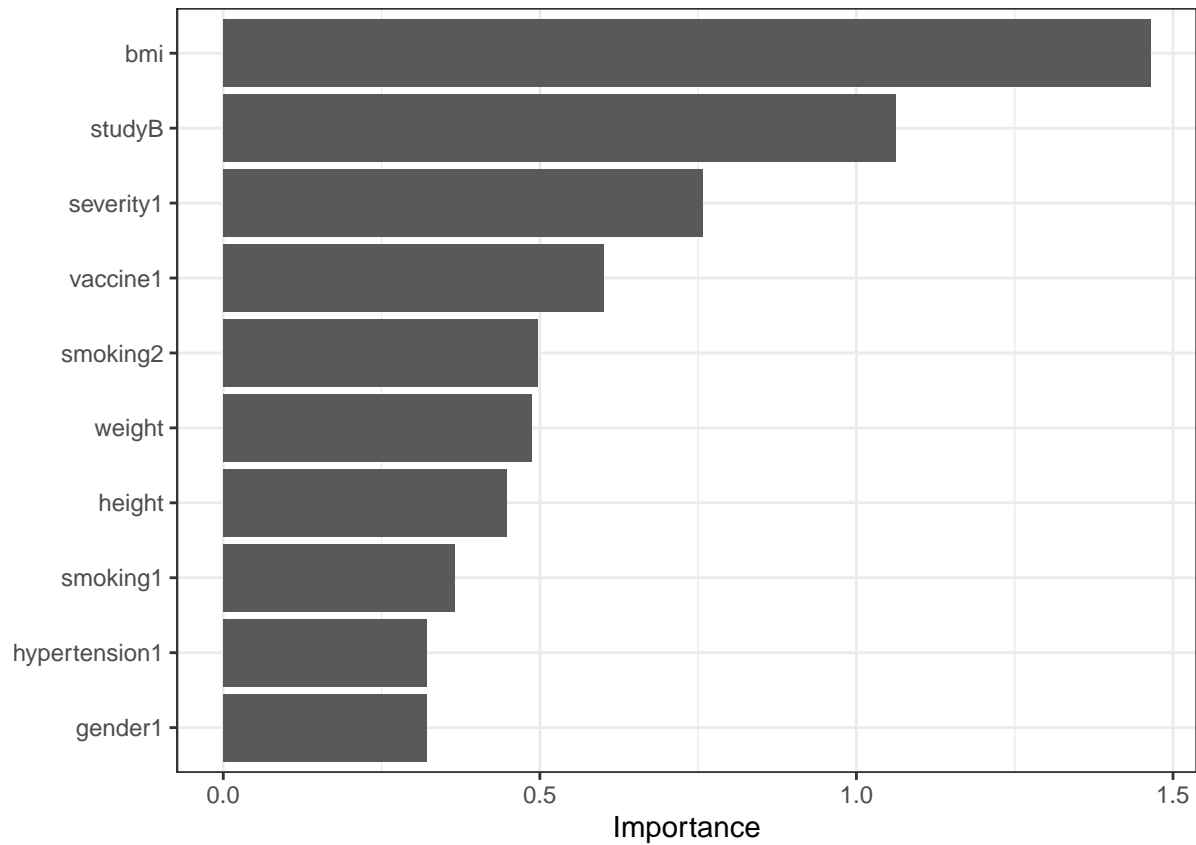
ggplot(glmnet.fit, highlight = TRUE) +
  labs(title="Penalized Logistic Regression CV Result") +
  theme_bw()

```



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

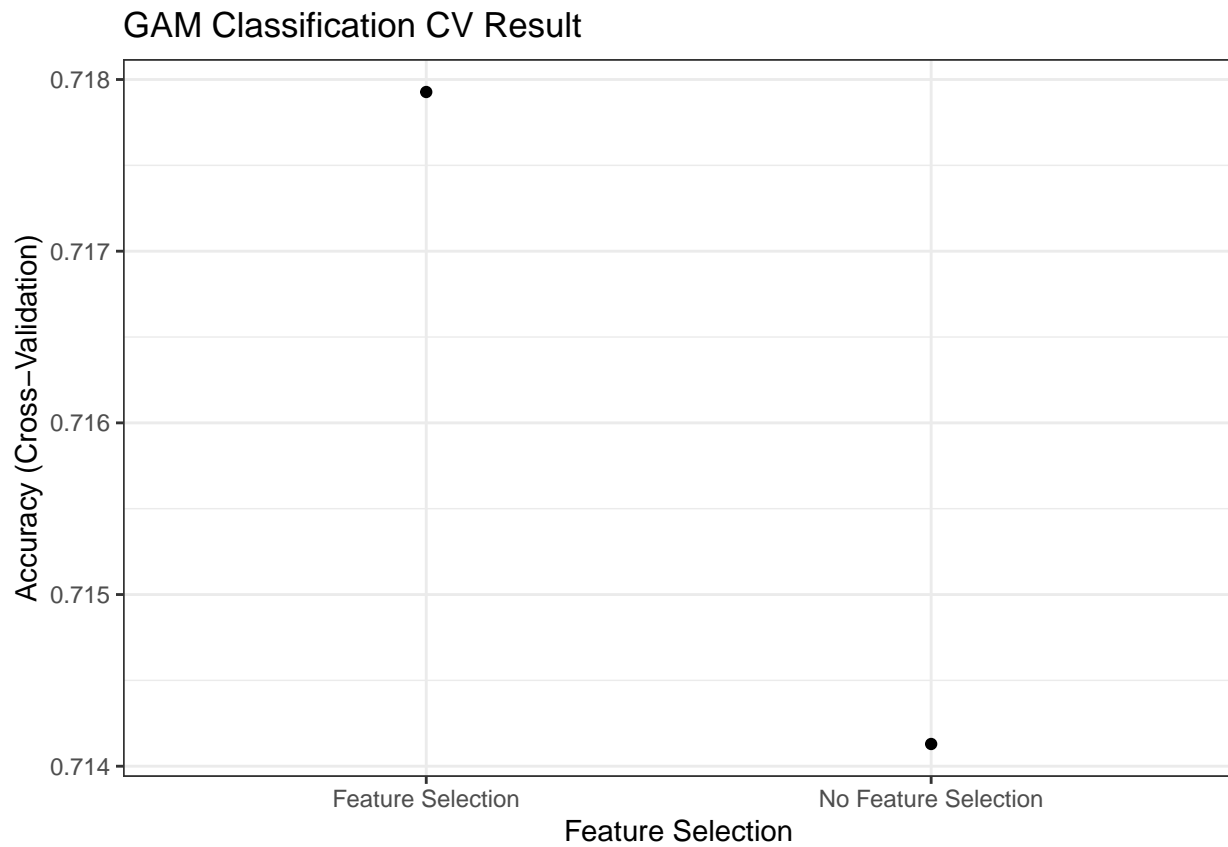
```
#coef(glmn.fit$finalModel)
vip(glmn.fit$finalModel) + theme_bw()
```



1.1.3 Generalized Additive Model (GAM) for classification

```
set.seed(2023)
gam.bin.fit <- train(train.x,
                     train.bin.y,
                     method = "gam",
                     trControl = ctrl1)

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



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

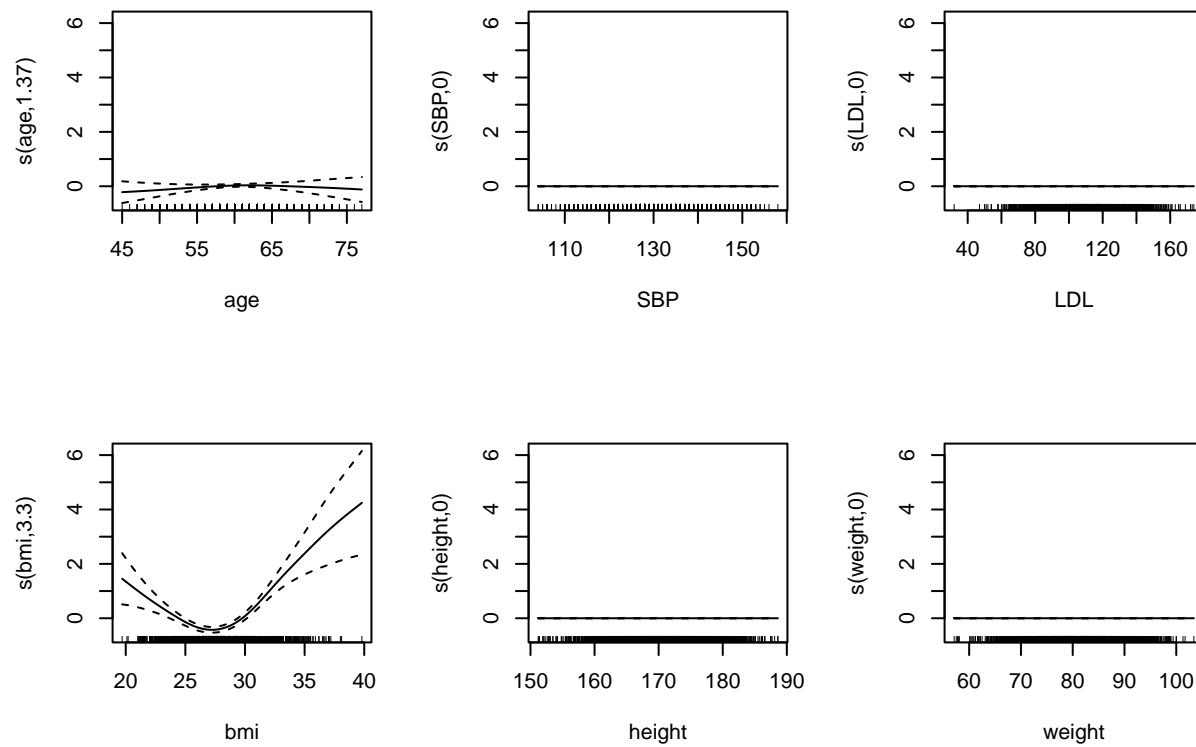
```
gam.bin.fit$bestTune
```

```
## select method
```

```
## 2 TRUE GCV.Cp
```

```
par(mfrow=c(2, 3))
```

```
plot(gam.bin.fit$finalModel)
```



```
par(mfrow=c(1, 1))
```

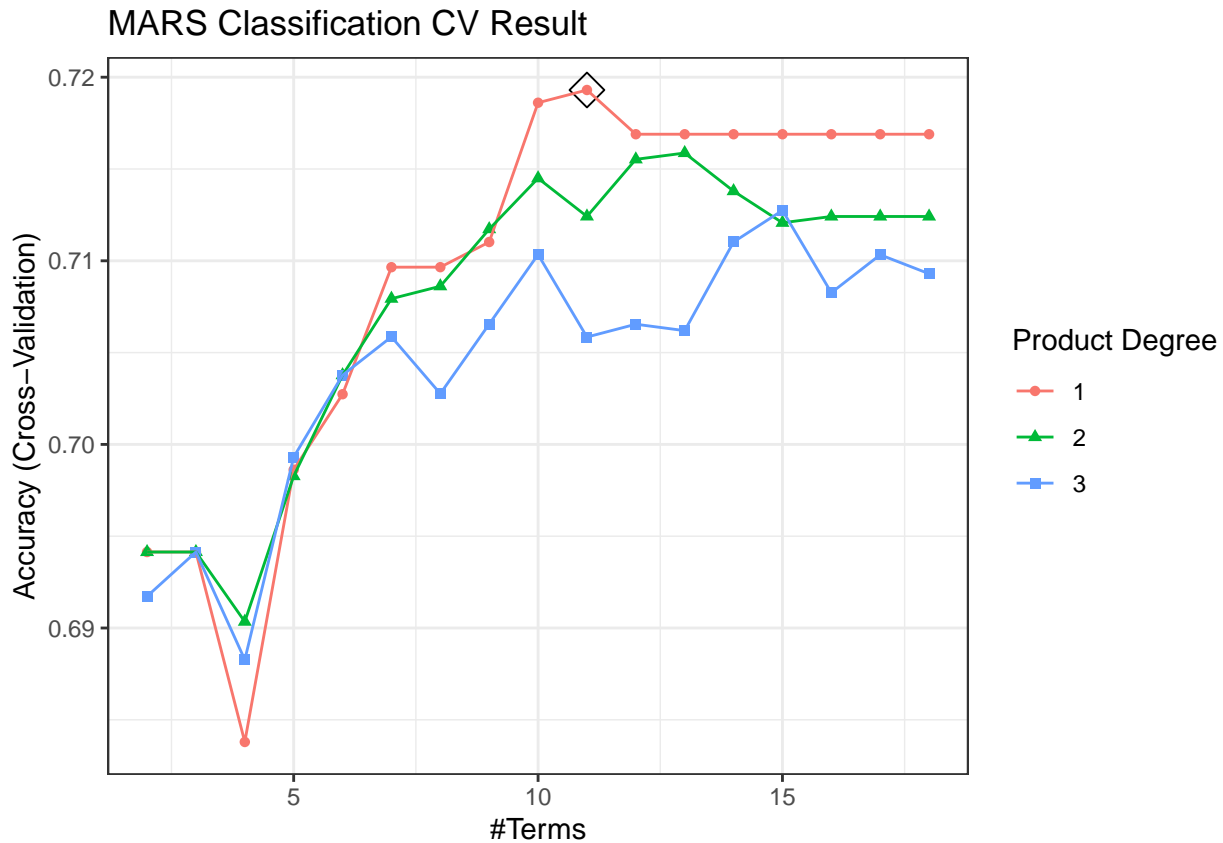
1.1.4 Multivariate Adaptive Regression Splines (MARS) for classification

```
set.seed(2023)
mars.bin.fit <- train(train.x,
                      train.bin.y,
                      method = "earth",
                      tuneGrid = expand.grid(degree = 1:3,
                                             nprune = 2:ncol(train.x)),
                      trControl = ctrl1)

mars.bin.fit$bestTune

##      nprune degree
## 10       11      1

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



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

```
mars.bin.fit$bestTune
```

```
##      nprune degree
```

```
## 10      11      1
```

```
coef(mars.bin.fit$finalModel) %>%
```

```
  broom::tidy() %>%
```

```
  knitr::kable()
```

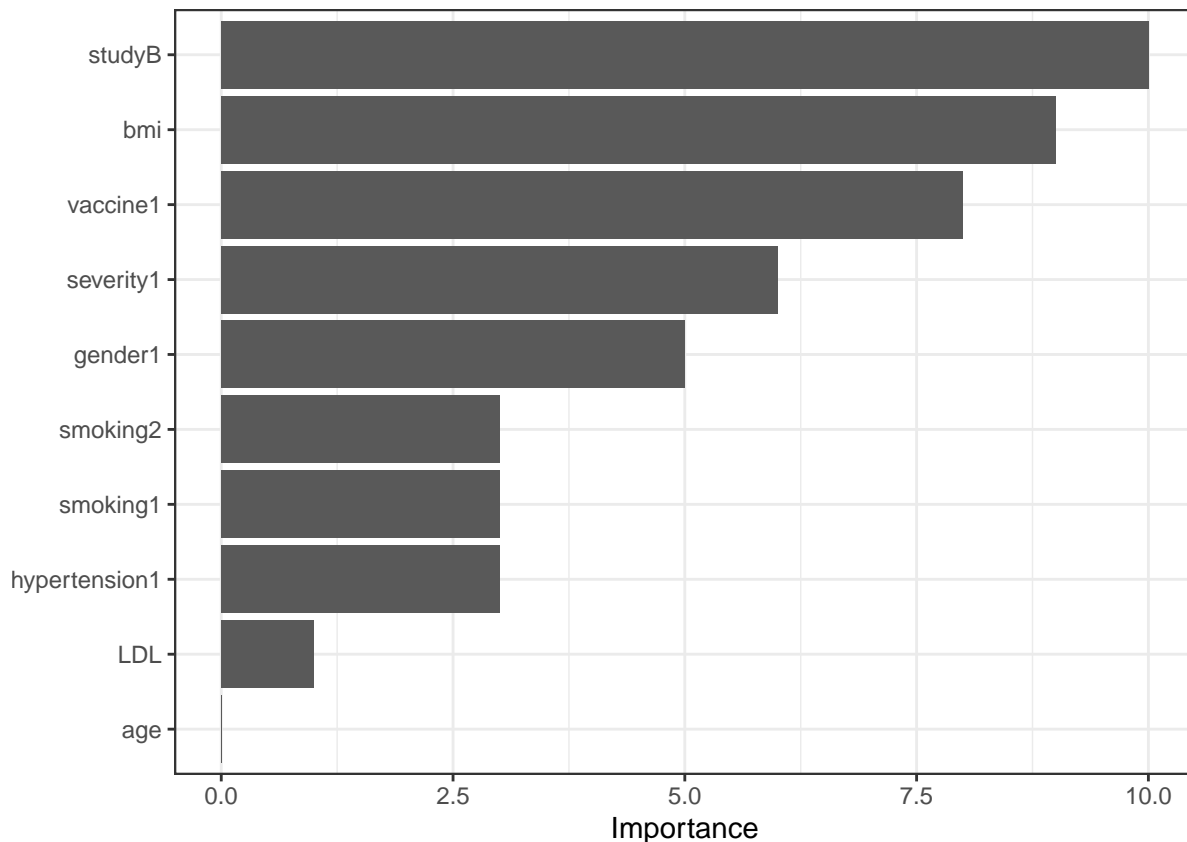
names	x
(Intercept)	1.1011705
studyB	-1.0779091
h(bmi-26.9)	0.2900212
h(26.9-bmi)	0.2935615
vaccine1	-0.6217928
severity1	0.7969230
gender1	-0.3261333
hypertension1	0.3099788
smoking1	0.3912885
smoking2	0.5358382
h(LDL-157)	-0.1512777

```
summary(mars.bin.fit$finalModel)
```

```
## Call: earth(x=matrix[2900,18], y=factor.object, keepxy=TRUE,
```



```
##          glm=list(family=function.object, maxit=100), degree=1, nprune=11)
##
## GLM coefficients
##          gt30
## (Intercept)  1.1011705
## gender1      -0.3261333
## smoking1      0.3912885
## smoking2      0.5358382
## hypertension1 0.3099788
## vaccine1     -0.6217928
## severity1     0.7969230
## studyB       -1.0779090
## h(26.9-bmi)   0.2935615
## h(bmi-26.9)   0.2900212
## h(LDL-157)    -0.1512777
##
## GLM (family binomial, link logit):
## nulldev  df      dev  df  devratio    AIC iters converged
## 3571.35 2899  3204.42 2889    0.103   3226    4          1
##
## Earth selected 11 of 14 terms, and 9 of 18 predictors (nprune=11)
## Termination condition: RSq changed by less than 0.001 at 14 terms
## Importance: studyB, bmi, vaccine1, severity1, gender1, smoking1, smoking2, ...
## Number of terms at each degree of interaction: 1 10 (additive model)
## Earth GCV 0.1906834  RSS 545.0022  GRSq 0.1024844  RSq 0.1148255
vip(mars.bin.fit$finalModel) + theme_bw()
```



1.1.5 Linear Discriminant Analysis (LDA)

```
set.seed(2023)
lda.fit <- train(train.x,
                 train.bin.y,
                 method = "lda",
                 trControl = ctrl1)
```

1.1.6 Quadratic Discriminant Analysis (QDA)

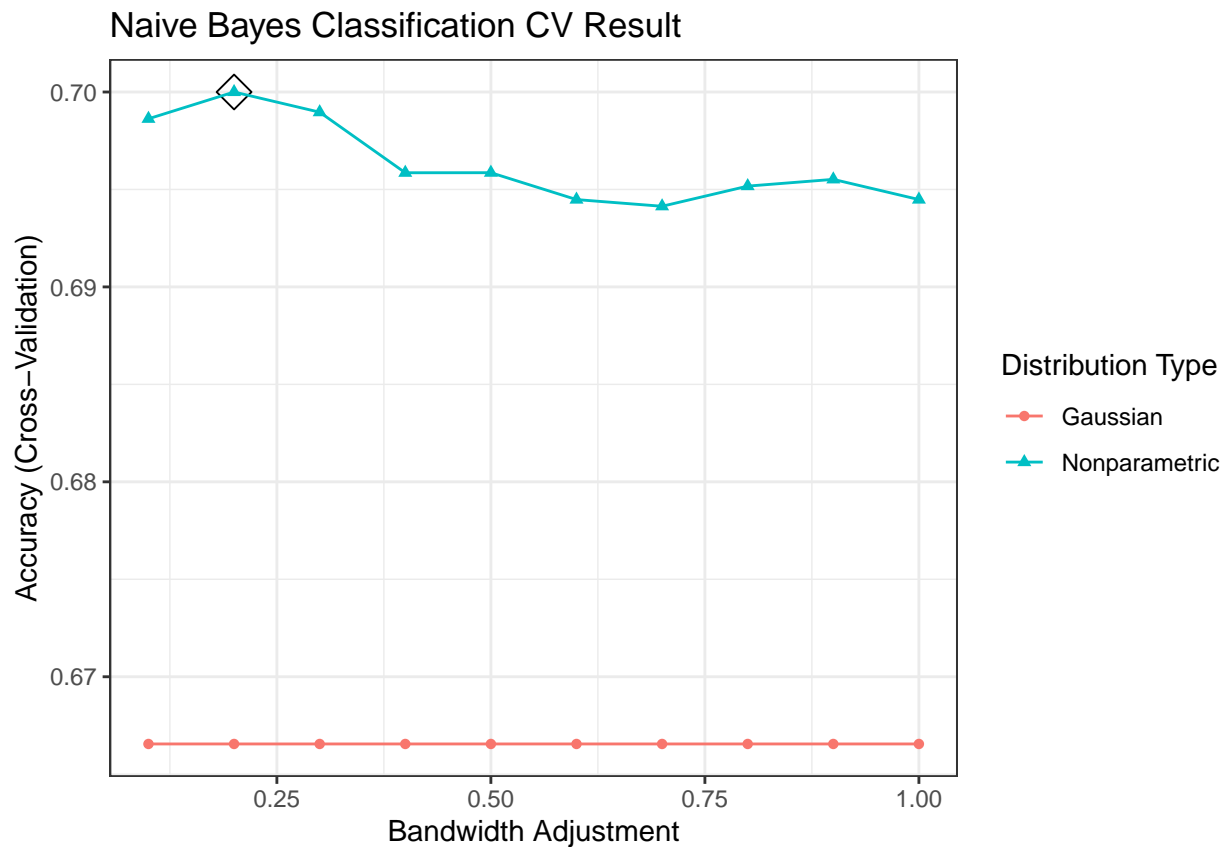
```
set.seed(2023)
qda.fit <- train(train.x,
                 train.bin.y,
                 method = "qda",
                 trControl = ctrl1)
```

1.1.7 Naive Bayes (NB)

```
nbGrid <- expand.grid(usekernel = c(FALSE, TRUE),
                    fL = 1,
                    adjust = seq(0.1, 1, by = .1))
set.seed(2023)
nb.fit <- train(train.x,
               train.bin.y,
               method = "nb",
               tuneGrid = nbGrid,
               trControl = ctrl1)
nb.fit$bestTune

##    fL usekernel adjust
## 12 1         TRUE  0.2

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



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

1.1.8 Bagging

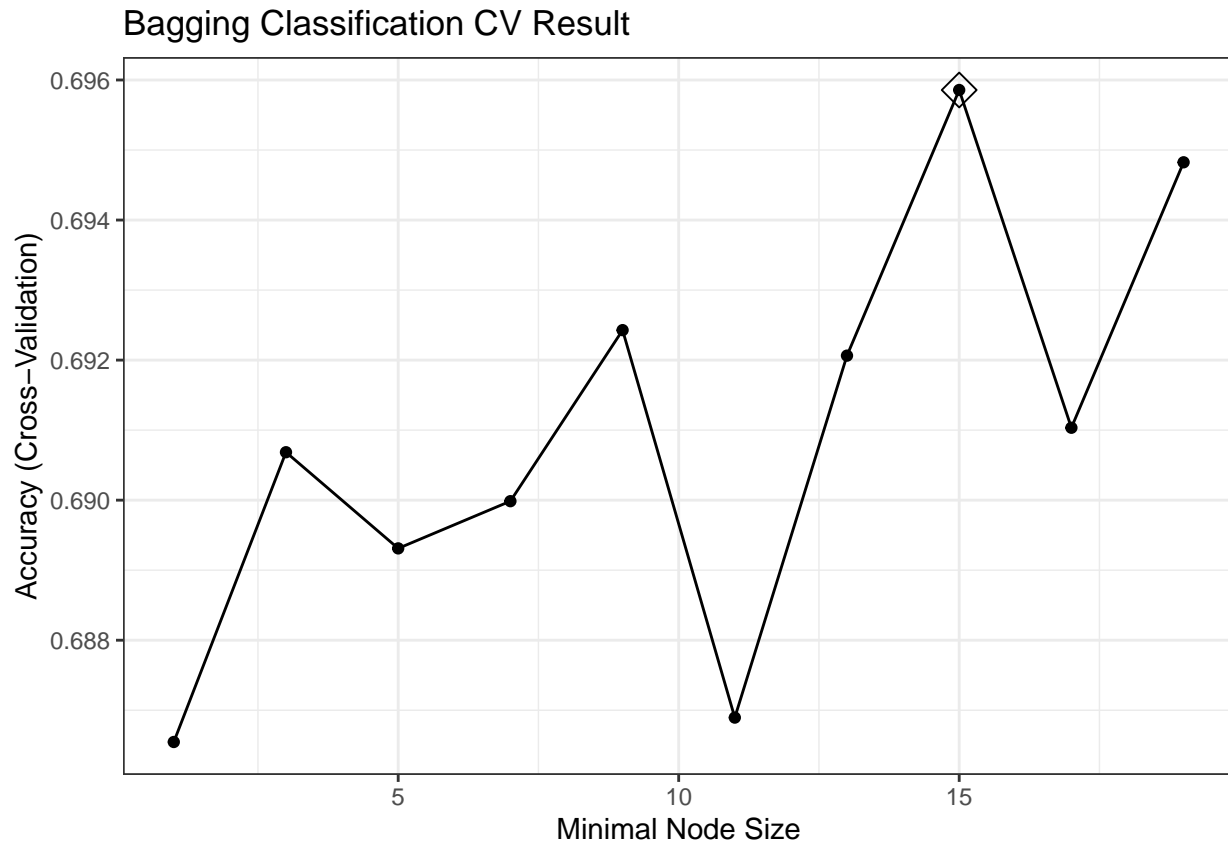
```
bag.grid2 <- expand.grid(mtry = ncol(train.x),
                        splitrule = "gini",
                        min.node.size = seq(1, 19, by = 2))

set.seed(2023)
bag.fit2 <- train(train.x,
                  train.bin.y,
                  method = "ranger",
                  tuneGrid = bag.grid2,
                  trControl = ctrl1)

bag.fit2$bestTune

##   mtry splitrule min.node.size
##  8    18      gini           15

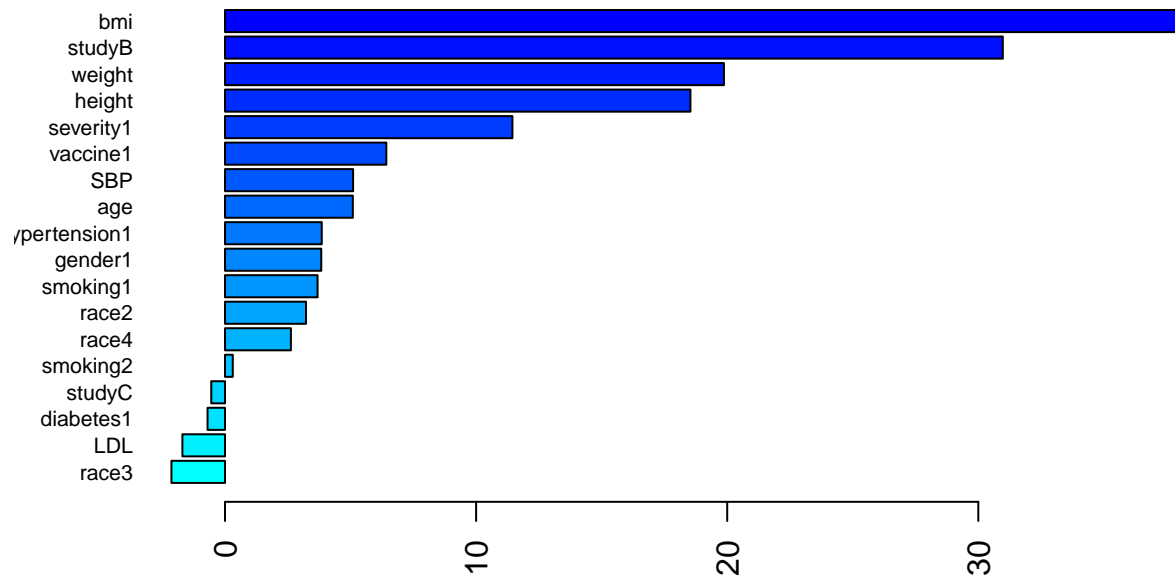
ggplot(bag.fit2, highlight = TRUE) +
  labs(title = "Bagging Classification CV Result") +
  theme_bw()
```



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

```
bag.final.per2 <- ranger(recovery_time ~ .,
  data = train.bin.dat.matrix,
  mtry = ncol(train.x),
  splitrule = "gini",
  min.node.size = bag.fit2$bestTune[[3]],
  importance = "permutation",
  scale.permutation.importance = TRUE)
```

```
barplot(sort(ranger::importance(bag.final.per2),
  decreasing = FALSE),
  las = 2, horiz = TRUE, cex.names = 0.7,
  col = colorRampPalette(colors = c("cyan", "blue"))(ncol(train.x)))
```



1.1.9 Random Forest

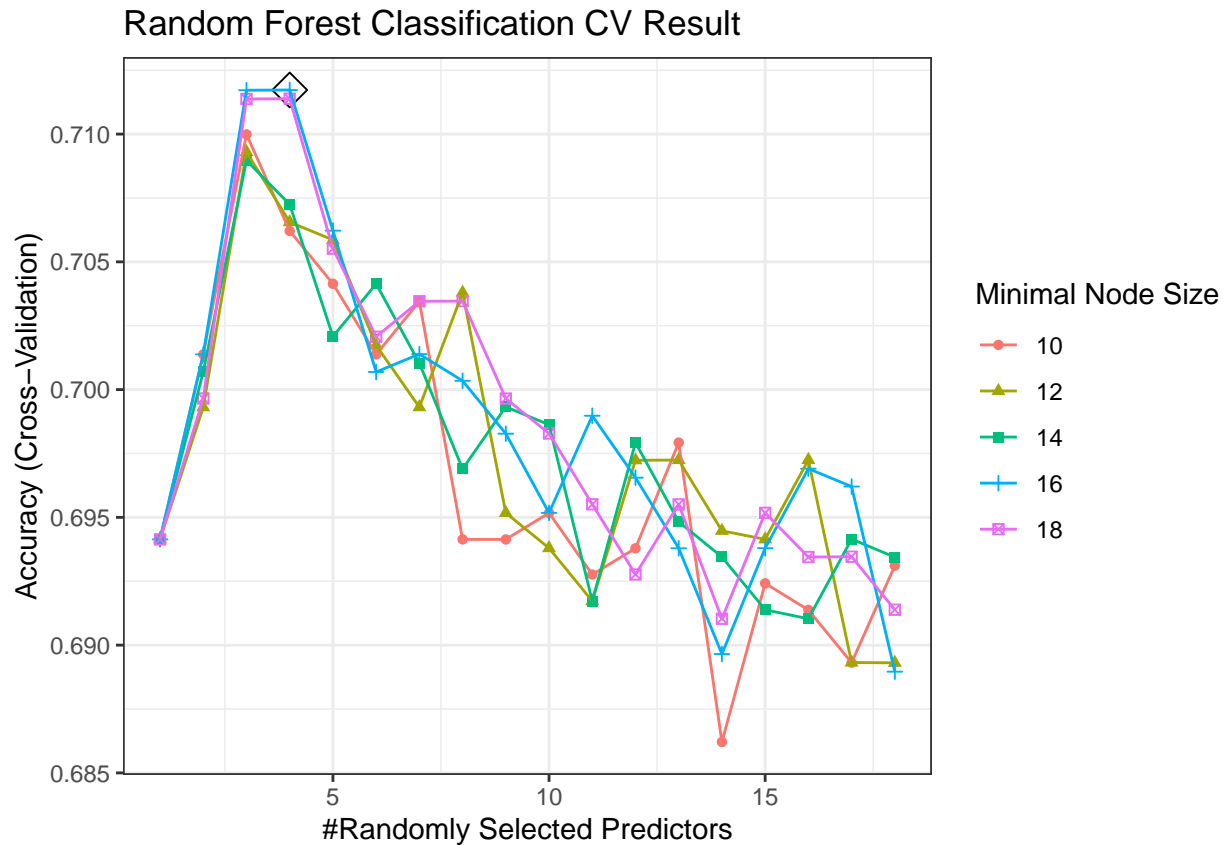
```
rf.grid2 <- expand.grid(mtry = 1:ncol(train.x),
  splitrule = "gini",
  min.node.size = seq(10, 18, by = 2))

set.seed(2023)
rf.fit2 <- train(train.x,
  train.bin.y,
  method = "ranger",
  tuneGrid = rf.grid2,
  trControl = ctrl1)

rf.fit2$bestTune

##      mtry splitrule min.node.size
## 19      4      gini             16

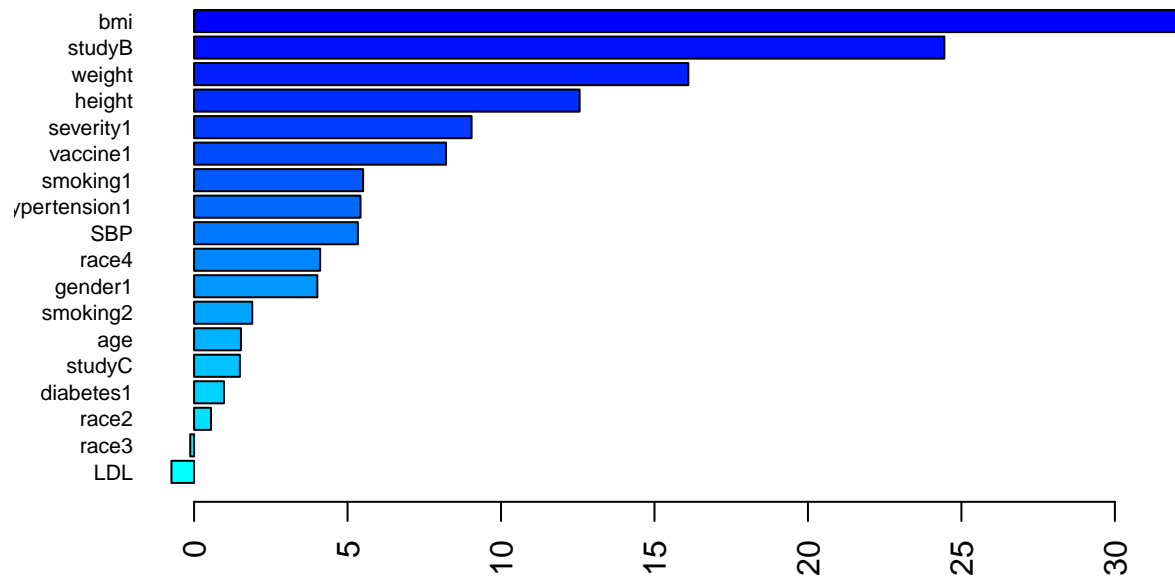
ggplot(rf.fit2, highlight = TRUE) +
  labs(title = "Random Forest Classification CV Result") +
  theme_bw()
```



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

rf.final.per2 <- ranger(recovery_time ~ .,
  data = train.bin.dat.matrix,
  mtry = rf.fit2$bestTune[[1]],
  splitrule = "gini",
  min.node.size = rf.fit2$bestTune[[3]],
  importance = "permutation",
  scale.permutation.importance = TRUE)

barplot(sort(ranger::importance(rf.final.per2), decreasing = FALSE),
  las = 2, horiz = TRUE, cex.names = 0.7,
  col = colorRampPalette(colors = c("cyan", "blue"))(ncol(train.x)))
```



1.1.10 Boosting

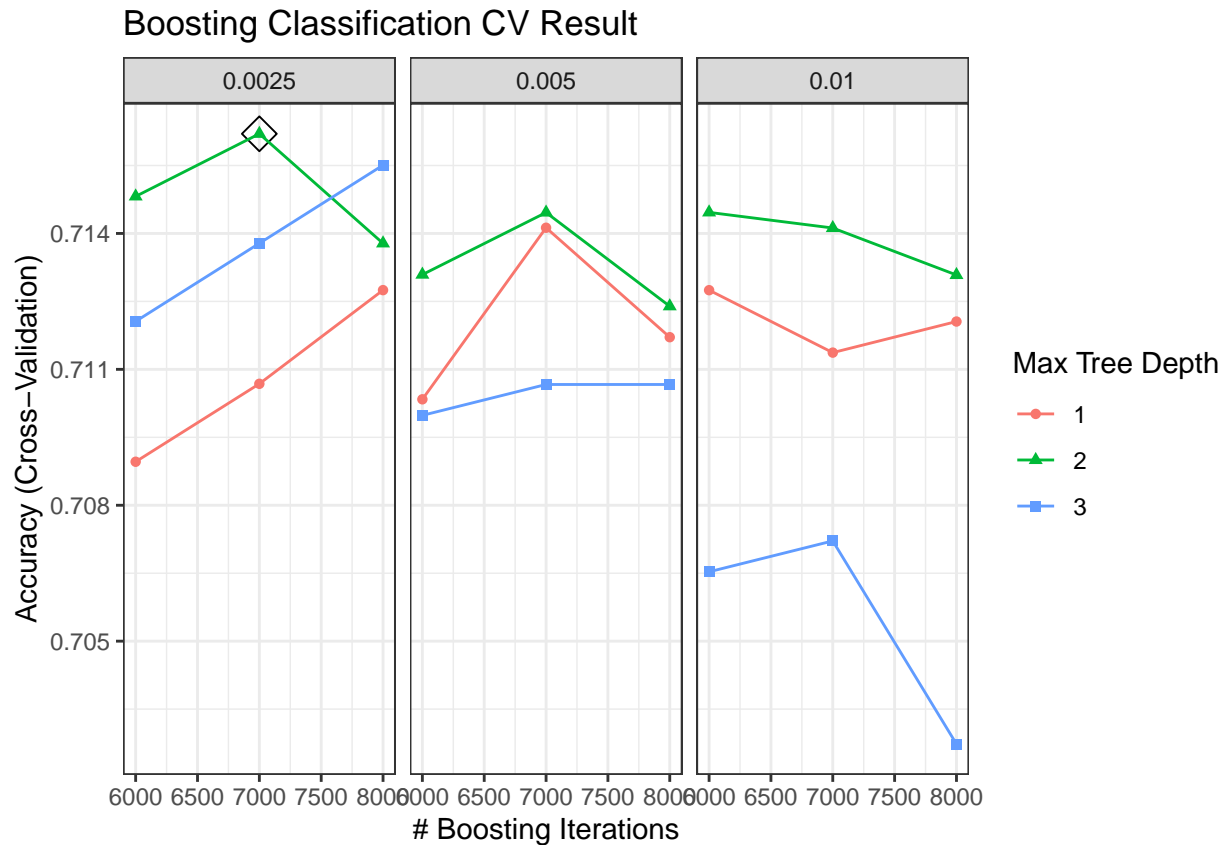
```
set.seed(2023)
bst.grid2 <- expand.grid(n.trees = c(6000, 7000, 8000),
                        interaction.depth = 1:3,
                        shrinkage = c(0.0025, 0.005, 0.01),
                        n.minobsinnode = c(1))

bst.fit2 <- train(train.x,
                  train.bin.y,
                  method = "gbm",
                  tuneGrid = bst.grid2,
                  trControl = ctrl1,
                  verbose = FALSE)

bst.fit2$bestTune

##   n.trees interaction.depth shrinkage n.minobsinnode
## 5    7000                2    0.0025              1

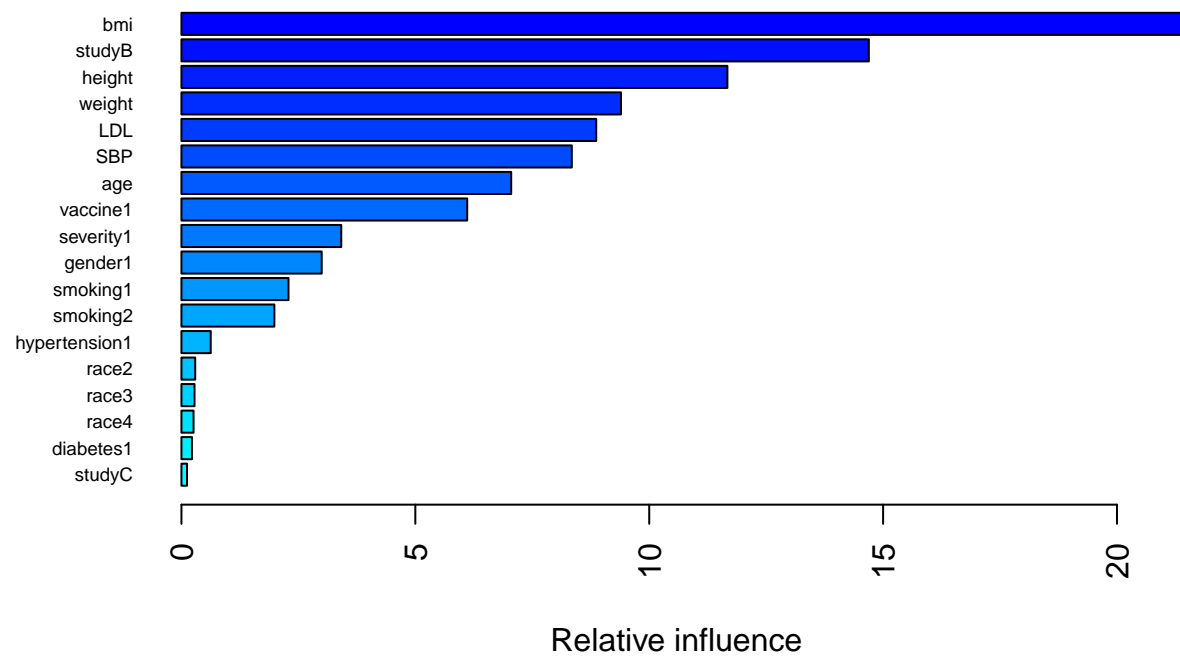
ggplot(bst.fit2, highlight = TRUE) +
  labs(title = "Boosting Classification CV Result") +
  theme_bw()
```



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

```
# Variable Importance
```

```
summary(bst.fit2$finalModel, las = 2, cBars = ncol(train.x), cex.names = 0.6)
```



```
## var rel.inf
```



```
## bmi                bmi 21.3771761
## studyB             studyB 14.6951389
## height             height 11.6710328
## weight             weight 9.3956406
## LDL                LDL 8.8668553
## SBP                SBP 8.3449683
## age                age 7.0495783
## vaccine1           vaccine1 6.1085301
## severity1          severity1 3.4158576
## gender1            gender1 2.9981363
## smoking1           smoking1 2.2884025
## smoking2           smoking2 1.9870804
## hypertension1      hypertension1 0.6262043
## race2              race2 0.2943443
## race3              race3 0.2793109
## race4              race4 0.2588588
## diabetes1          diabetes1 0.2245058
## studyC             studyC 0.1183788
```

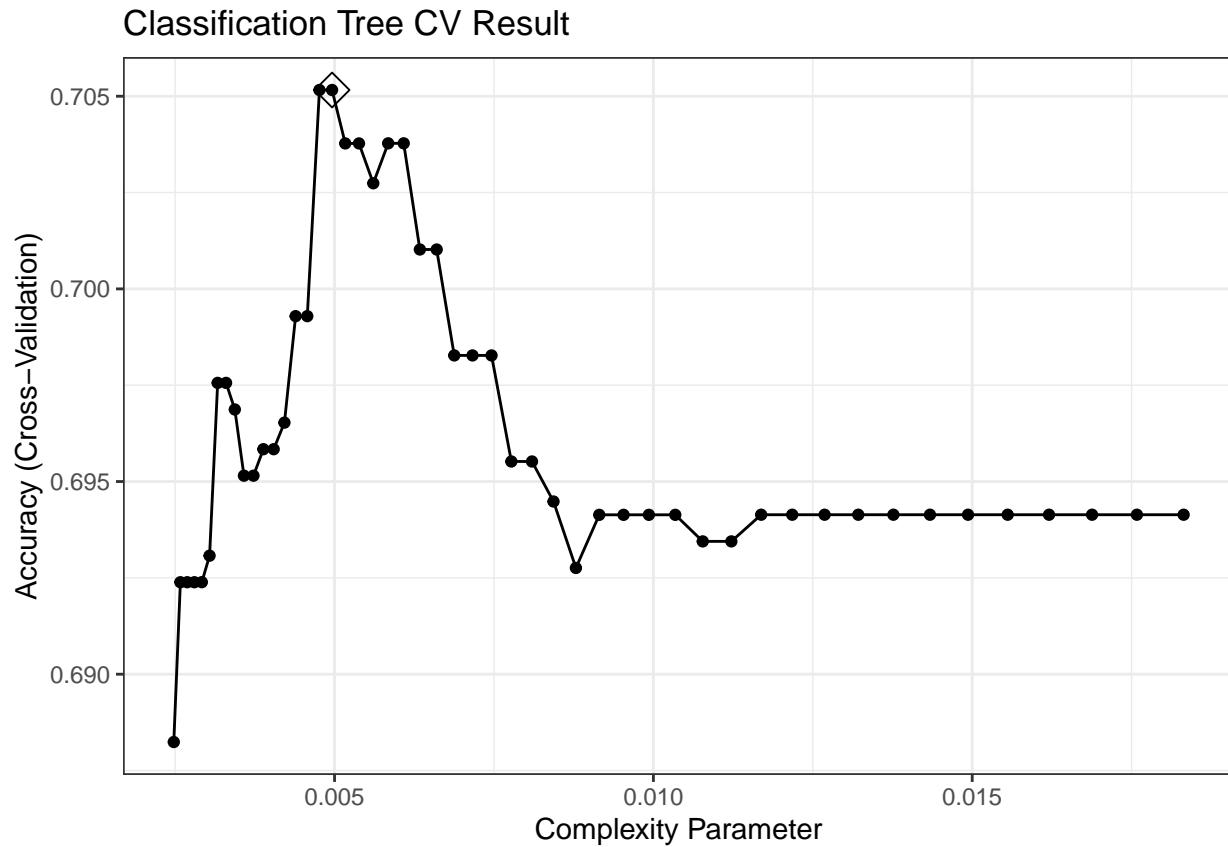
1.1.11 Classification Trees

```
rpart.grid = expand.grid(cp = exp(seq(-6,-4, len = 50)))
set.seed(2023)
rpart.fit2 <- train(train.x,
                    train.bin.y,
                    method = "rpart",
                    tuneGrid = rpart.grid,
                    trControl = ctrl1)

rpart.fit2$bestTune
```

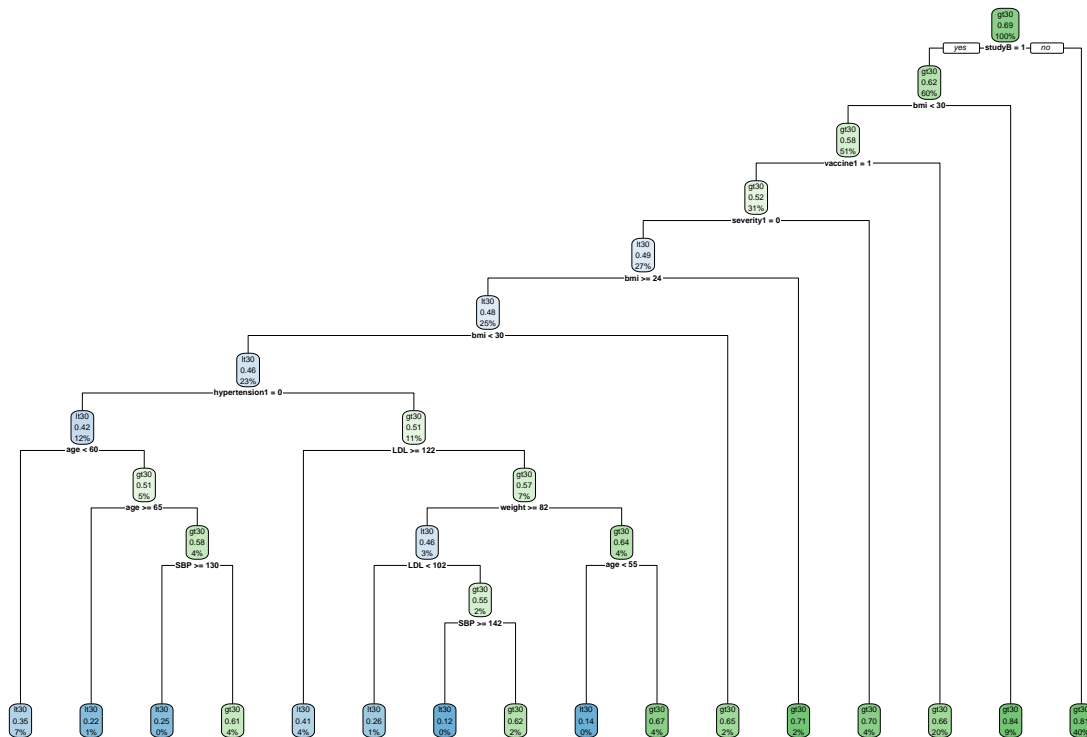
```
##                cp
## 18 0.004961126

ggplot(rpart.fit2, highlight = TRUE) +
  labs(title = "Classification Tree CV Result") +
  theme_bw()
```



```
ggsave("./figure/rpart2_cv.jpeg", dpi = 500)
```

```
rpart.plot(rpart.fit2$finalModel)
```

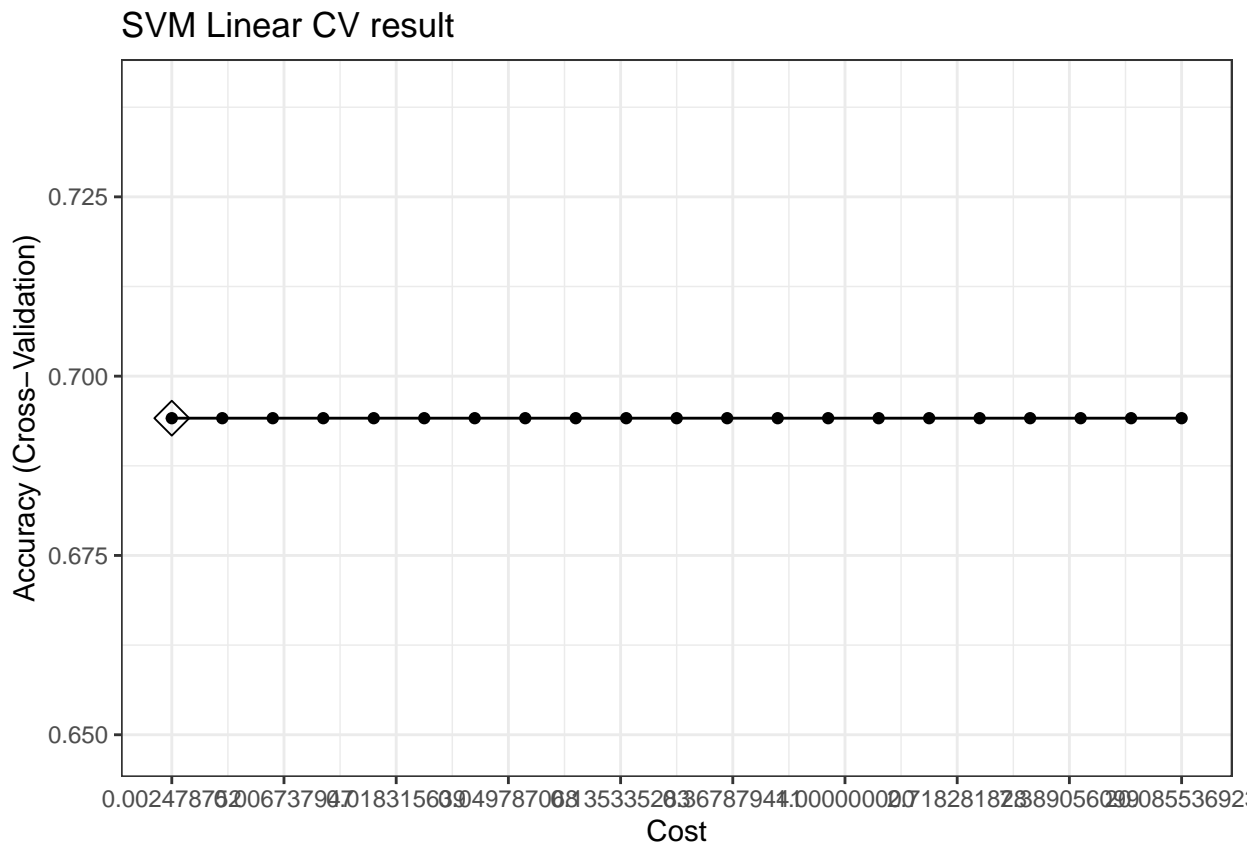


```
jpeg("./figure/rpart2.jpeg", width = 8, height = 6, units="in", res=500)
rpart.plot(rpart.fit2$finalModel)
dev.off()
```

```
## pdf
## 2
```

1.1.12 Support Vector Machine (SVM)

```
set.seed(2023)
svml.fit <- train(train.x,
                  train.bin.y,
                  method = "svmLinear",
                  tuneGrid = data.frame(C = exp(seq(-6, 3, len = 21))),
                  trControl = ctrl1)
ggplot(svml.fit, highlight = TRUE) +
  scale_x_continuous(trans='log', n.breaks = 10) +
  labs(title = "SVM Linear CV result") +
  theme_bw()
```



```
svmr.grid <- expand.grid(C = exp(seq(-2, 5, len = 20)),
                        sigma = exp(seq(-4, 1, len = 6)))
```

```
set.seed(2023)
svmr.fit <- train(train.x,
                  train.bin.y,
                  method = "svmRadialSigma",
```

```

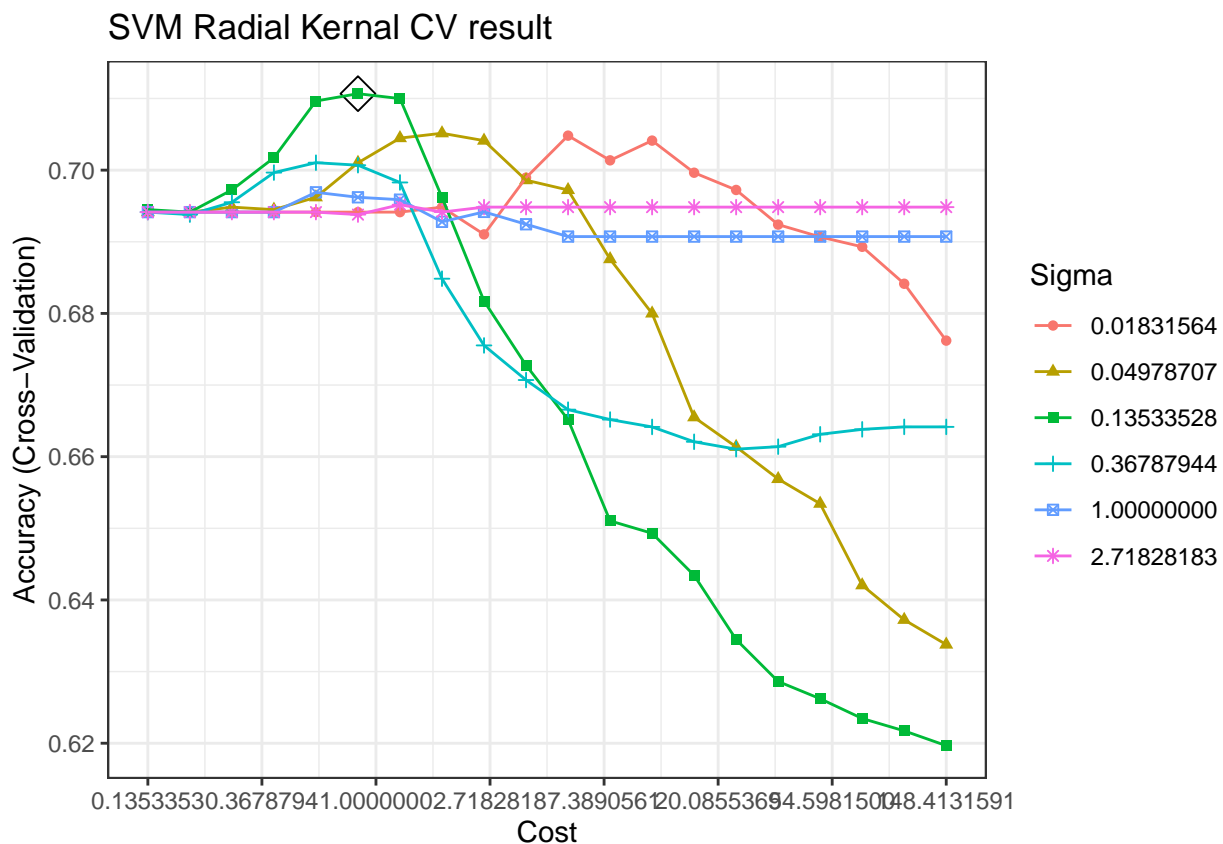
tuneGrid = svmr.grid,
trControl = ctrl1)

svmr.fit$bestTune

##      sigma      C
## 33 0.1353353 0.8539397

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 Kernel CV result") +
  theme_bw()

```



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

```
confusionMatrix(svmr.fit)
```

```

## Cross-Validated (10 fold) Confusion Matrix
##
## (entries are percentual average cell counts across resamples)
##
##      Reference
## Prediction lt30 gt30
##      lt30  7.2  5.6
##      gt30 23.3 63.8

```

```
##
## Accuracy (average) : 0.7107
```

1.2 Model Selection

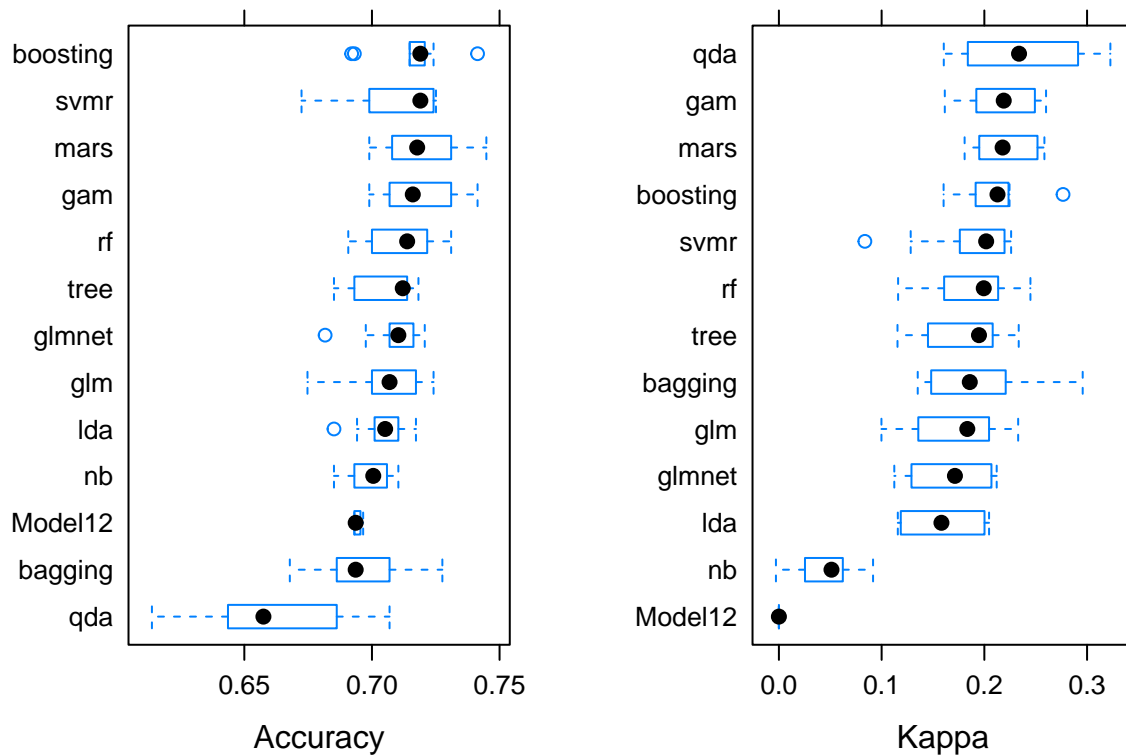
```
set.seed(2023)
resamp <- resamples(list(glm = glm.fit,
                        glmnet = glmnet.fit,
                        gam = gam.bin.fit,
                        mars = mars.bin.fit,
                        lda = lda.fit,
                        qda = qda.fit,
                        nb = nb.fit,
                        bagging = bag.fit2,
                        rf = rf.fit2,
                        boosting = bst.fit2,
                        tree = rpart.fit2,
                        svm1 <- svm1.fit,
                        svmr = svmr.fit))

summary(resamp)
```

```
##
## Call:
## summary.resamples(object = resamp)
##
## Models: glm, glmnet, gam, mars, lda, qda, nb, bagging, rf, boosting, tree, Model12, svmr
## Number of resamples: 10
##
## Accuracy
##           Min.   1st Qu.   Median     Mean   3rd Qu.     Max. NA's
## glm       0.6747405 0.7008621 0.7068966 0.7062019 0.7157661 0.7241379    0
## glmnet    0.6816609 0.7071484 0.7103448 0.7082733 0.7156455 0.7206897    0
## gam       0.6989619 0.7075081 0.7160031 0.7179273 0.7301724 0.7413793    0
## mars      0.6989619 0.7085140 0.7177272 0.7193030 0.7293103 0.7448276    0
## lda       0.6851211 0.7016353 0.7051724 0.7041377 0.7100943 0.7172414    0
## qda       0.6137931 0.6456300 0.6574831 0.6617249 0.6830401 0.7068966    0
## nb        0.6851211 0.6948276 0.7005155 0.6999997 0.7052738 0.7103448    0
## bagging   0.6678201 0.6868005 0.6936308 0.6958570 0.7060345 0.7275862    0
## rf        0.6907216 0.7025862 0.7137931 0.7117251 0.7214095 0.7310345    0
## boosting  0.6920415 0.7153928 0.7189681 0.7161996 0.7206897 0.7413793    0
## tree      0.6851211 0.6939655 0.7120715 0.7051615 0.7137931 0.7182131    0
## Model12   0.6931034 0.6931034 0.6936308 0.6941389 0.6951658 0.6965517    0
## svmr      0.6724138 0.7000835 0.7189655 0.7106728 0.7235158 0.7250859    0
##
## Kappa
##           Min.   1st Qu.   Median     Mean   3rd Qu.     Max.
## glm       0.099807807 0.13883240 0.18339368 0.17256251 0.20348169 0.23291936
## glmnet    0.112313034 0.13880153 0.17136252 0.16787994 0.19888520 0.21200875
## gam       0.161494386 0.19398754 0.21887062 0.21564943 0.24436296 0.26005307
## mars      0.180770377 0.19596335 0.21778595 0.22123773 0.25078783 0.25846579
## lda       0.115743112 0.12766456 0.15822405 0.15973057 0.19212331 0.20459740
## qda       0.160506591 0.18959640 0.23375702 0.23794797 0.28596378 0.32268598
## nb       -0.002898219 0.02675247 0.05118034 0.04369503 0.06220707 0.09165486
```

```
## bagging 0.135151078 0.15295507 0.18580343 0.19152328 0.21778297 0.29572702
## rf      0.116038882 0.16147317 0.19942793 0.19013744 0.21328968 0.24484209
## boosting 0.160322728 0.19228241 0.21278228 0.20874763 0.22299842 0.27659150
## tree    0.115434149 0.15719160 0.19478063 0.18525932 0.20594295 0.23344205
## Model12 0.000000000 0.00000000 0.00000000 0.00000000 0.00000000 0.00000000
## svmr    0.083682565 0.17761275 0.20175711 0.18642362 0.21956318 0.22606383
##          NA's
## glm      0
## glmnet   0
## gam      0
## mars     0
## lda      0
## qda      0
## nb       0
## bagging  0
## rf       0
## boosting  0
## tree     0
## Model12  0
## svmr     0
```

```
p1=bwplot(resamp, metric = "Accuracy")
p2=bwplot(resamp, metric = "Kappa")
grid.arrange(p1, p2, ncol=2)
```



```
jpeg("./figure/resample2.jpeg", width = 8, height=6, units="in", res=500)
p1=bwplot(resamp, metric = "Accuracy")
p2=bwplot(resamp, metric = "Kappa")
grid.arrange(p1, p2, ncol=2)
dev.off()
```

```
## pdf
## 2
```

1.3 Training / Testing Error

```
pred.svmr <- predict(svmr.fit, newdata = test.x)
confusionMatrix(data = pred.svmr, reference = test.bin.y)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction lt30 gt30
##      lt30   62   39
##      gt30  153  469
##
##           Accuracy : 0.7344
##           95% CI : (0.7006, 0.7663)
##      No Information Rate : 0.7026
##      P-Value [Acc > NIR] : 0.03255
##
##           Kappa : 0.2498
##
##  Mcnemar's Test P-Value : 3.49e-16
##
##           Sensitivity : 0.28837
##           Specificity : 0.92323
##      Pos Pred Value : 0.61386
##      Neg Pred Value : 0.75402
##           Prevalence : 0.29737
##      Detection Rate : 0.08575
##      Detection Prevalence : 0.13970
##      Balanced Accuracy : 0.60580
##
##      'Positive' Class : lt30
##
```