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

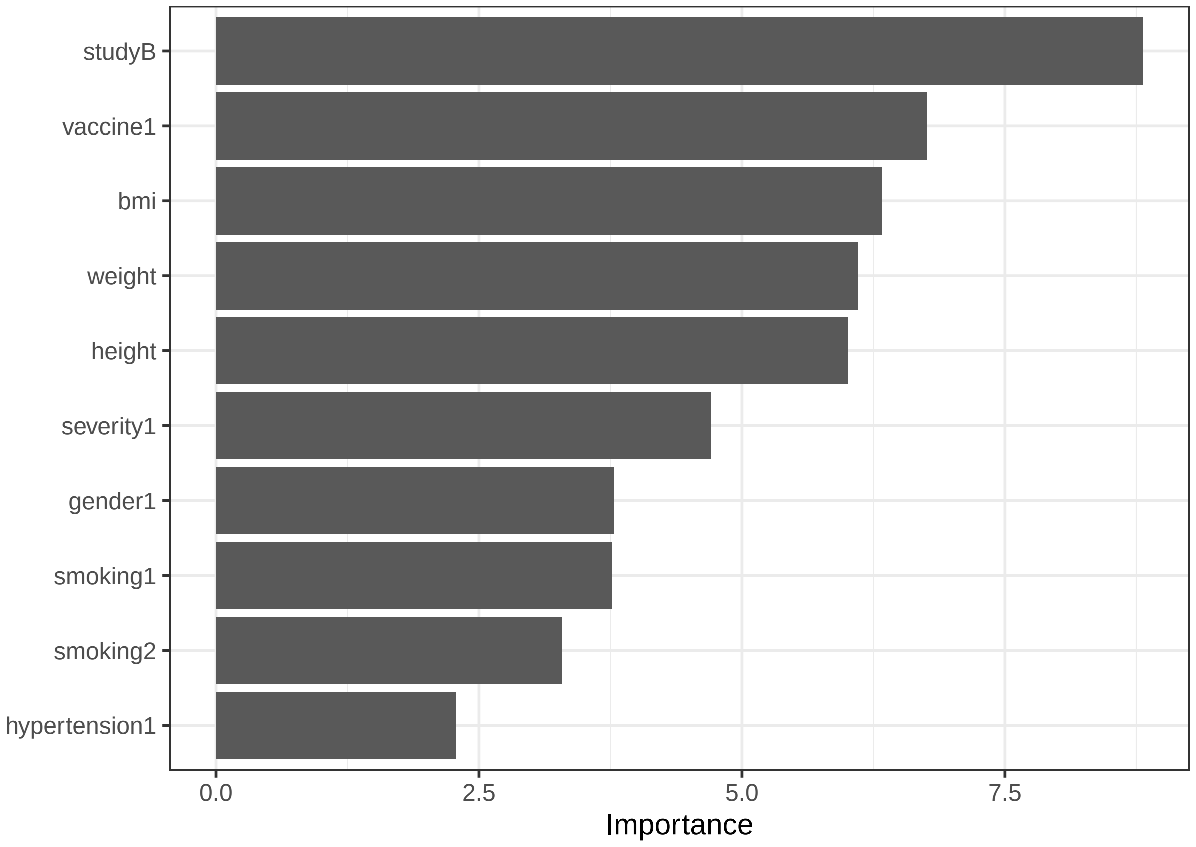
```
ctrl1 <- trainControl(method = "cv", number = 10)
```

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()
```

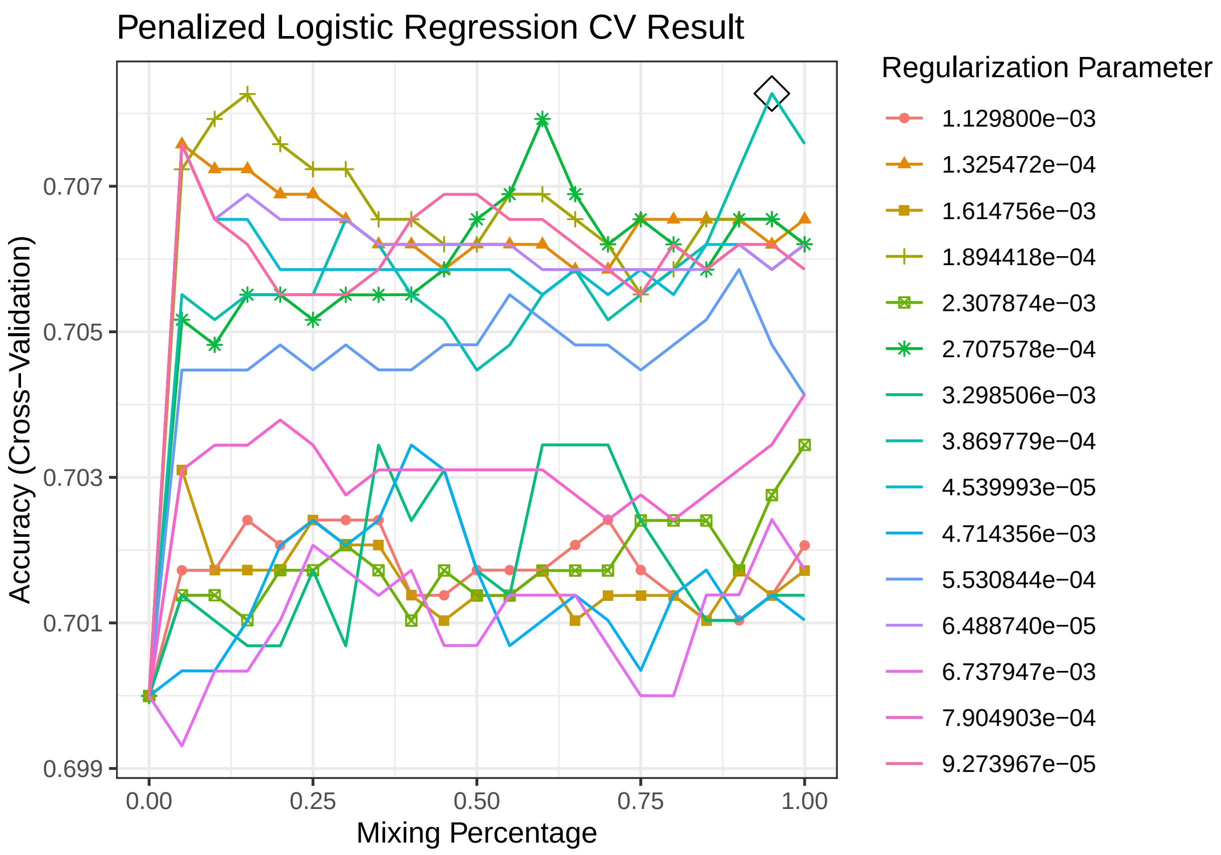


1.1.2 Penalized Logistic Regression

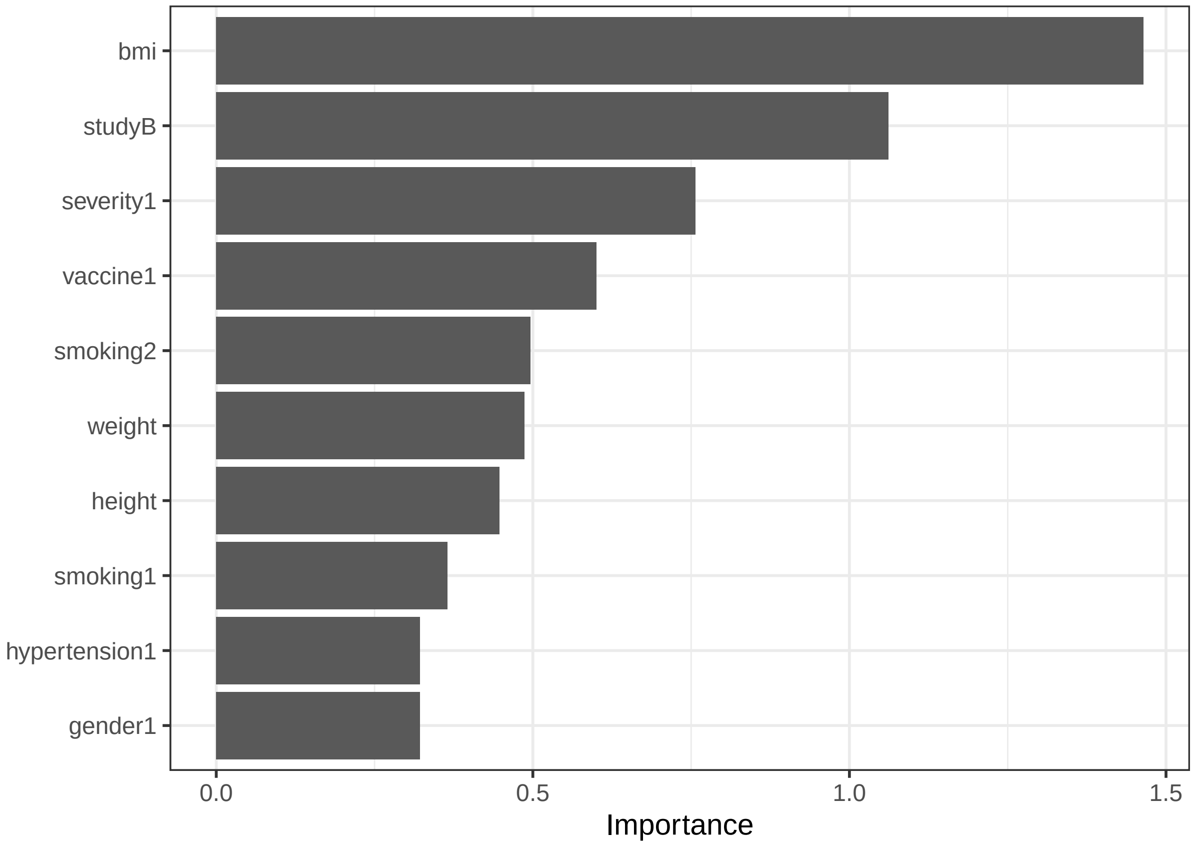
```
glmnGrid <- expand.grid(.alpha = seq(0, 1, length = 21),
                        .lambda = exp(seq(-10, -5, length = 15)))
set.seed(2023)
glmn.fit <- train(train.x,
                  train.bin.y,
                  method = 'glmnet',
                  tuneGrid = glmnGrid,
                  trControl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

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

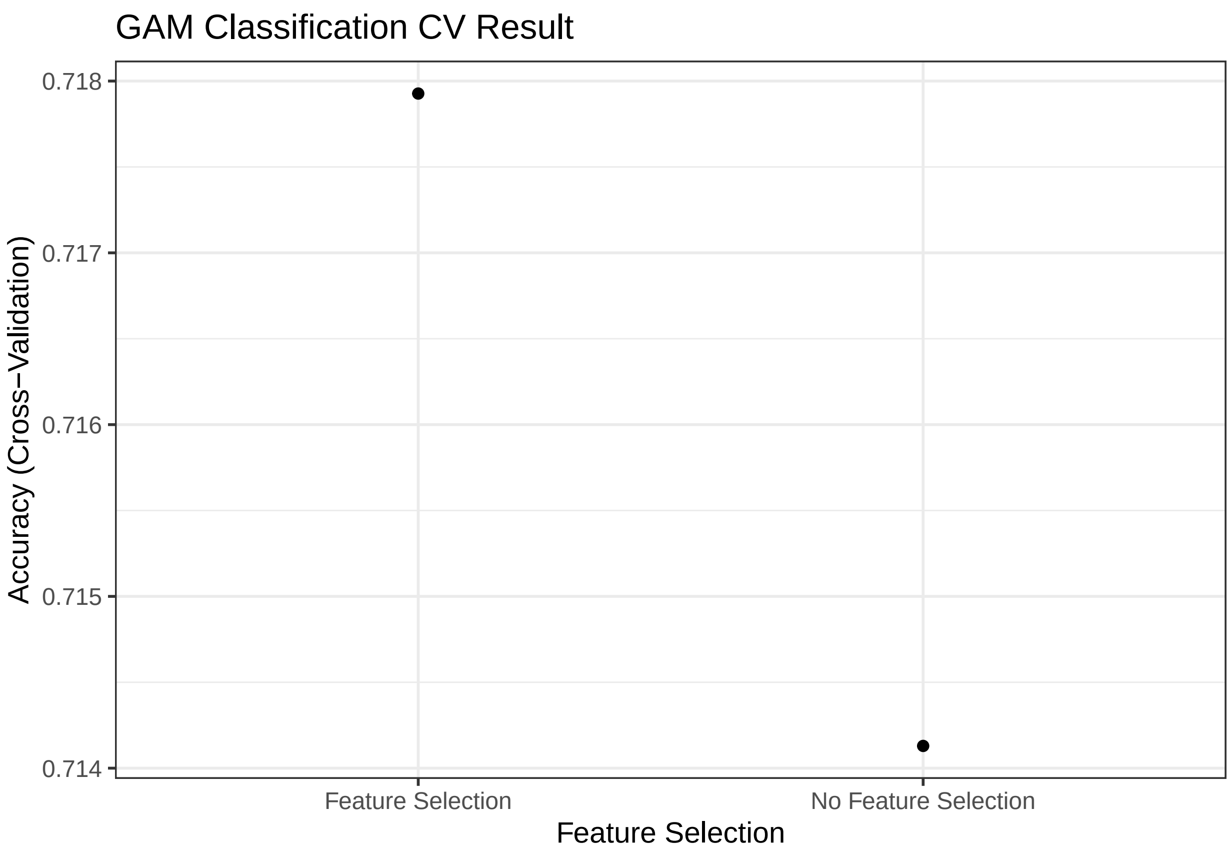


```r
ggsave("./figure/penal_logi_cv.jpeg", dpi = 500)

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



1.1.3 Generalized Additive Model (GAM) for classification

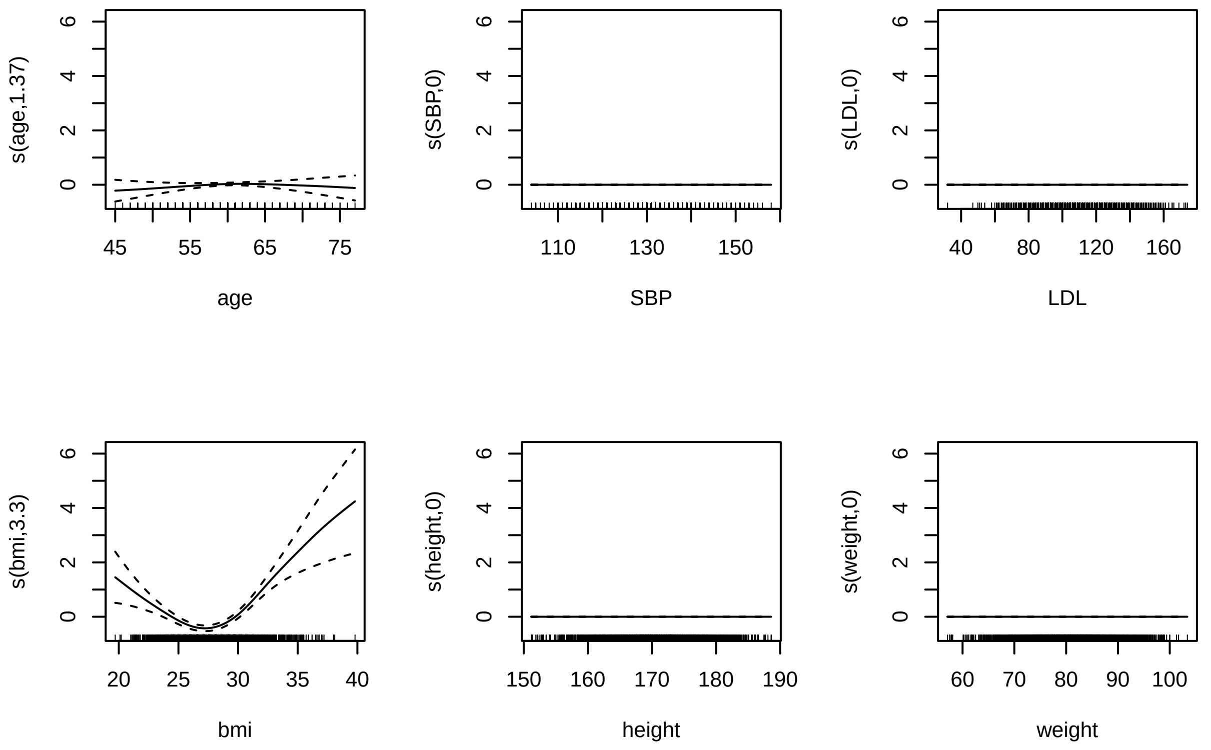
```
set.seed(2023)
gam.bin.fit <- train(train.x,
                     train.bin.y,
                     method = "gam",
                     trControl = ctrl1)

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



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

gam.bin.fit$bestTune
```

```
##   select method
## 2   TRUE GCV.Cp
```

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



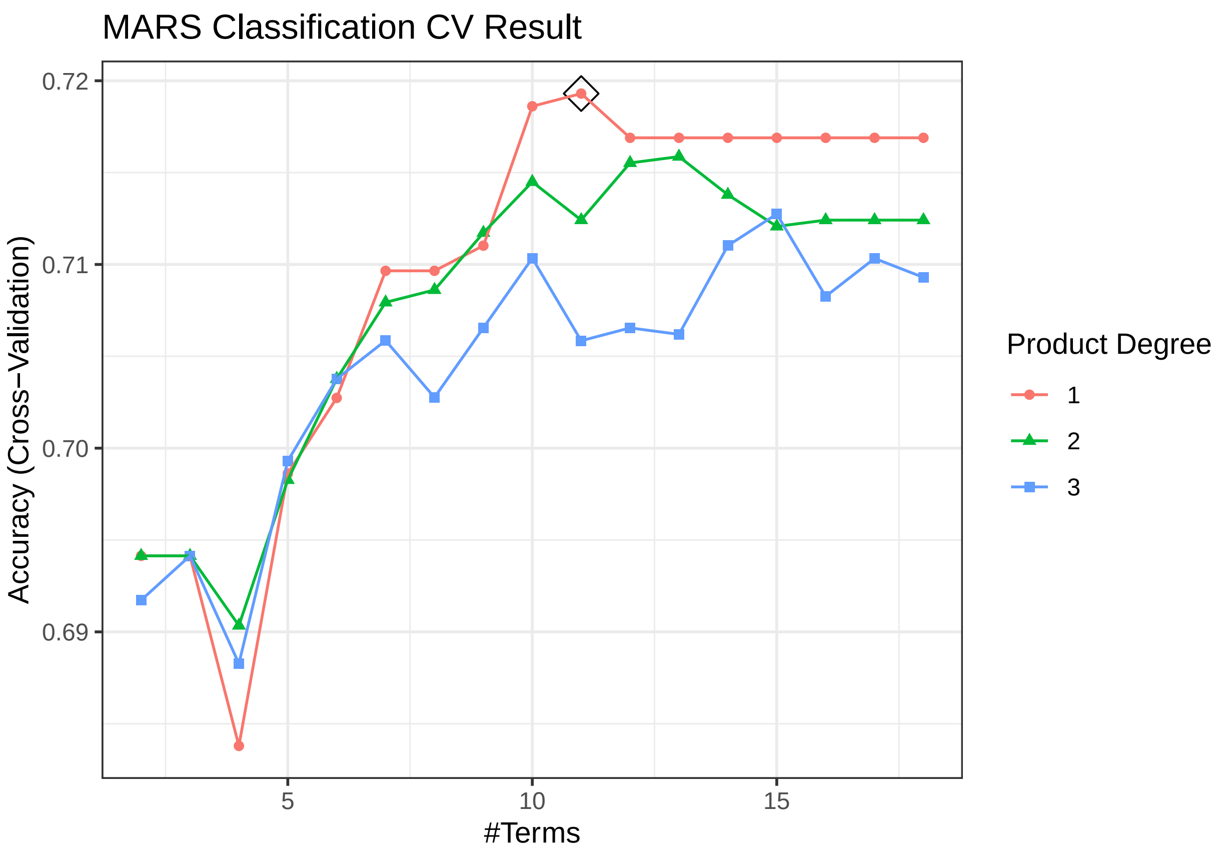
```r
par(mfrow=c(1, 1))
```

1.1.4 Multivariate Adaptive Regression Splines (MARS) for classification

```r
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
```

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



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

mars.bin.fit$bestTune
```

```
##    nprune degree
## 10     11      1
```

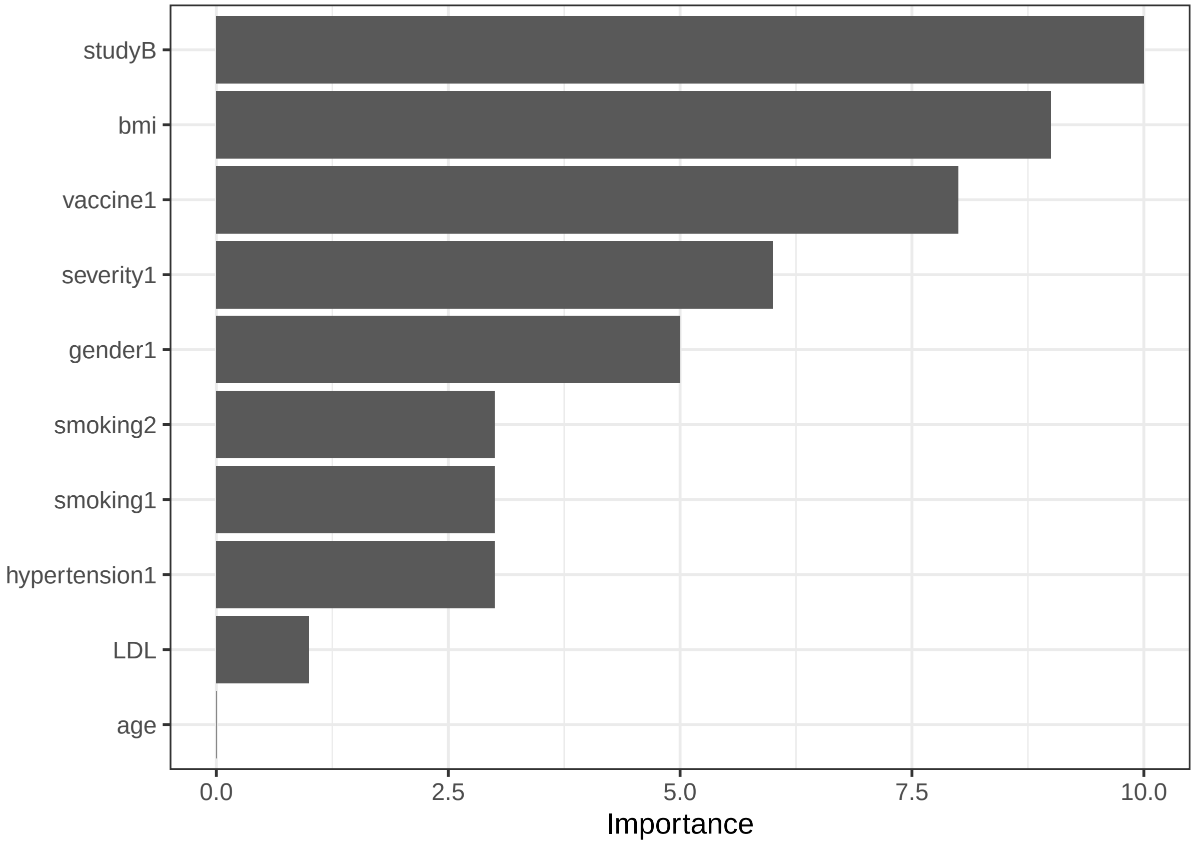
```r
coef(mars.bin.fit$finalModel) %>%
  broom::tidy() %>%
  knitr::kable()
```

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

```r
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)

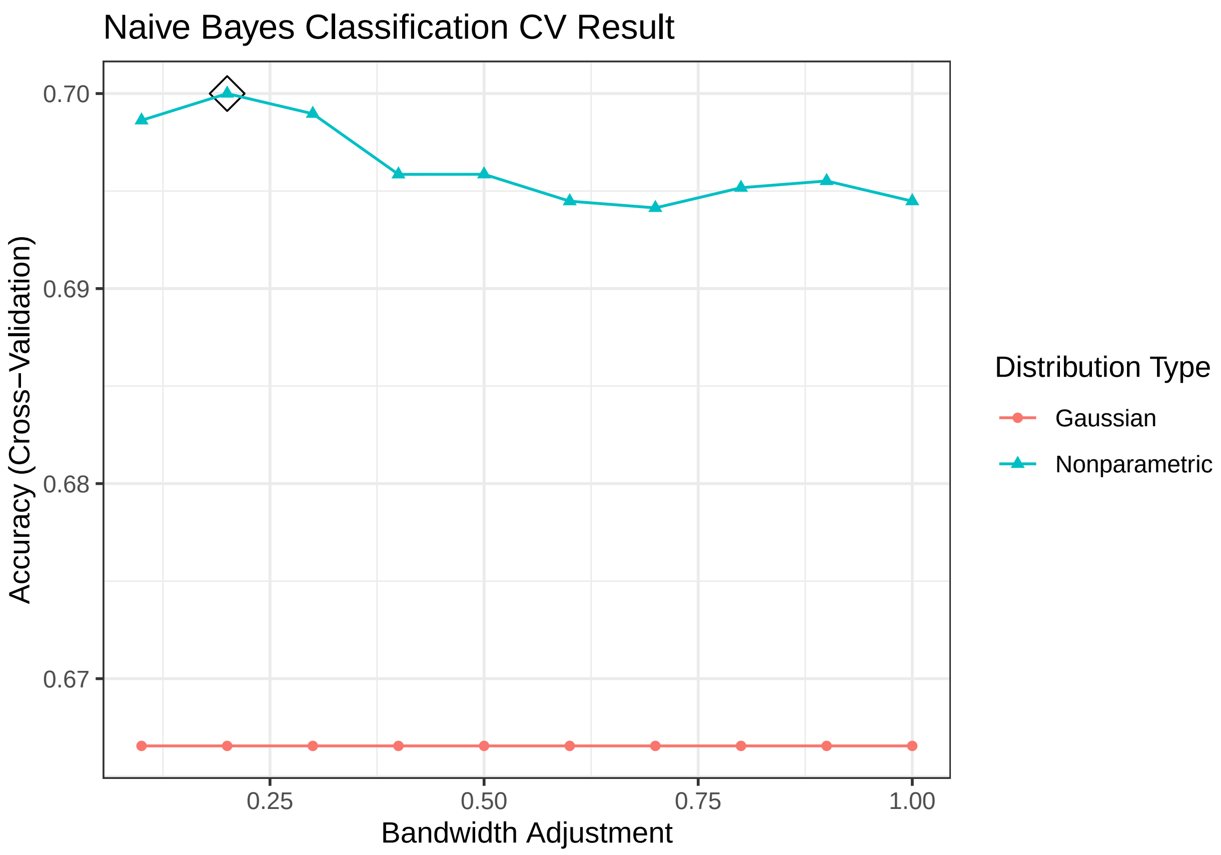
```
set.seed(2023)
qda.fit <- train(train.x,
                   train.bin.y,
                   method = "qda",
                   trControl = ctrl1)
```

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()
```



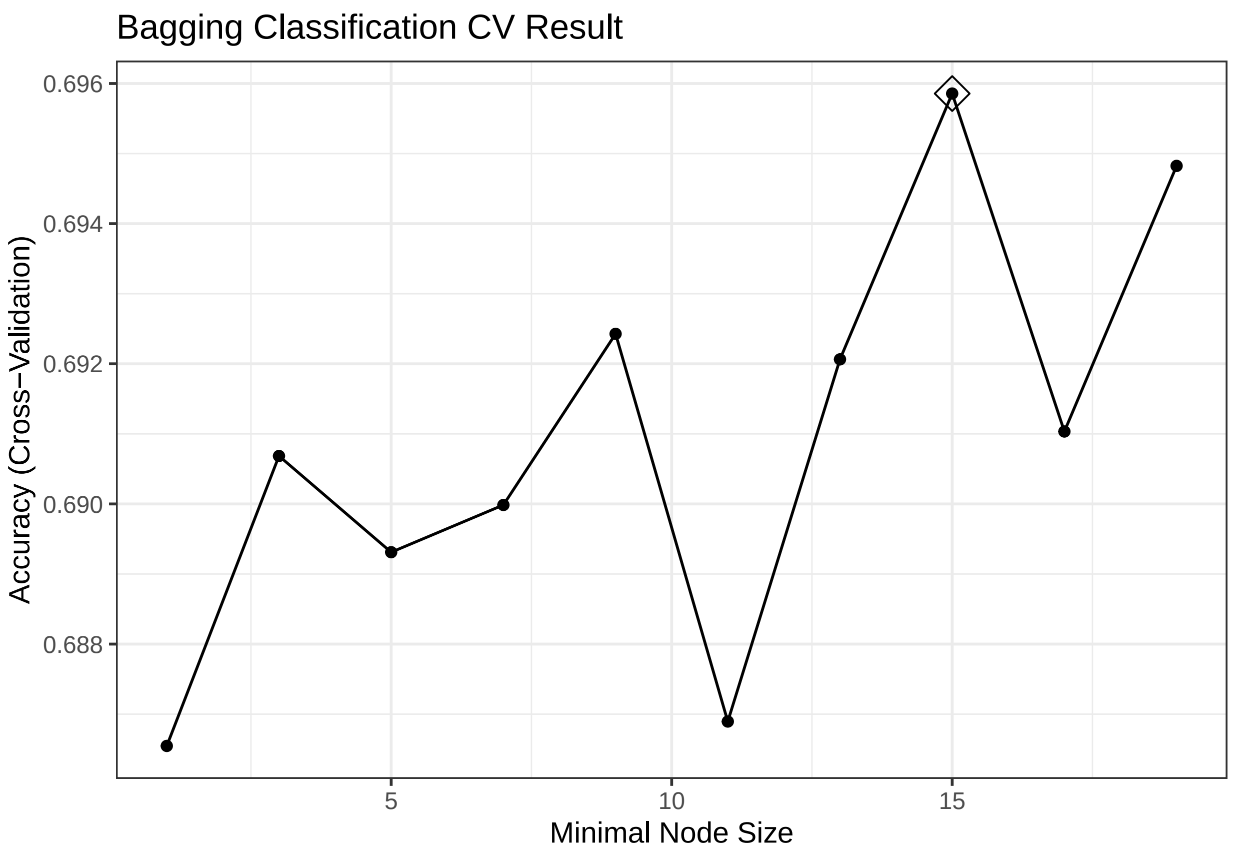
```r
ggsave("./figure/nb_cv.jpeg", dpi = 500)
```

1.1.8 Bagging

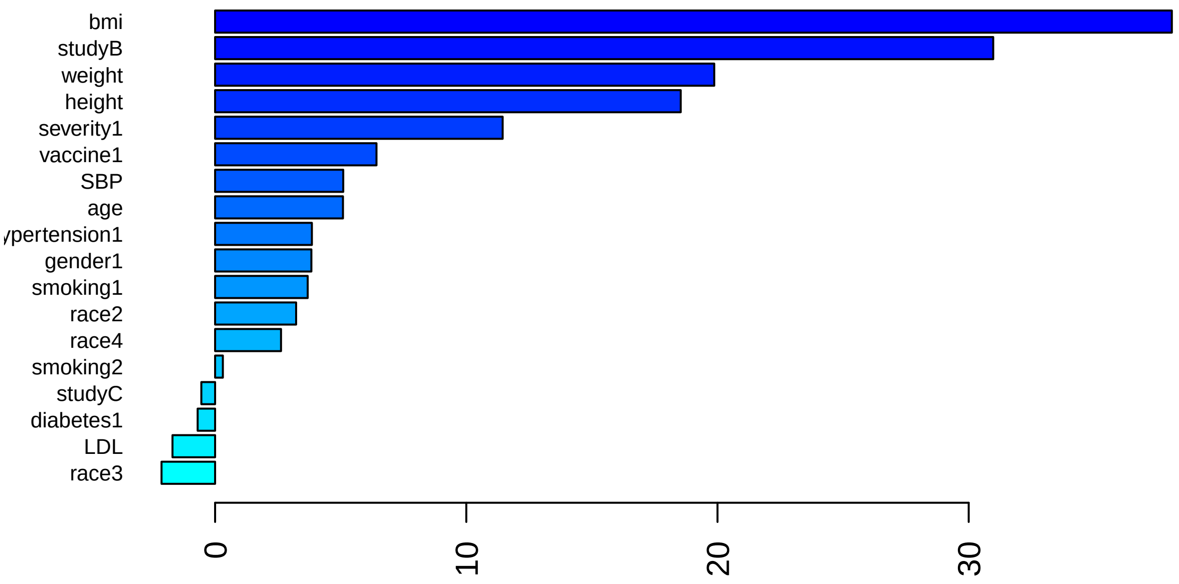
```r
bag.grid2 <- expand.grid(mtry = ncol(train.x),
                         splitrule = "gini",
                         min.node.size = seq(1, 19, by = 2))
set.seed(2023)
bag.fit2 <- train(train.x,
                  train.bin.y,
                  method = "ranger",
                  tuneGrid = bag.grid2,
                  trControl = ctrl1)

bag.fit2$bestTune
```

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

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



```r
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)))
```

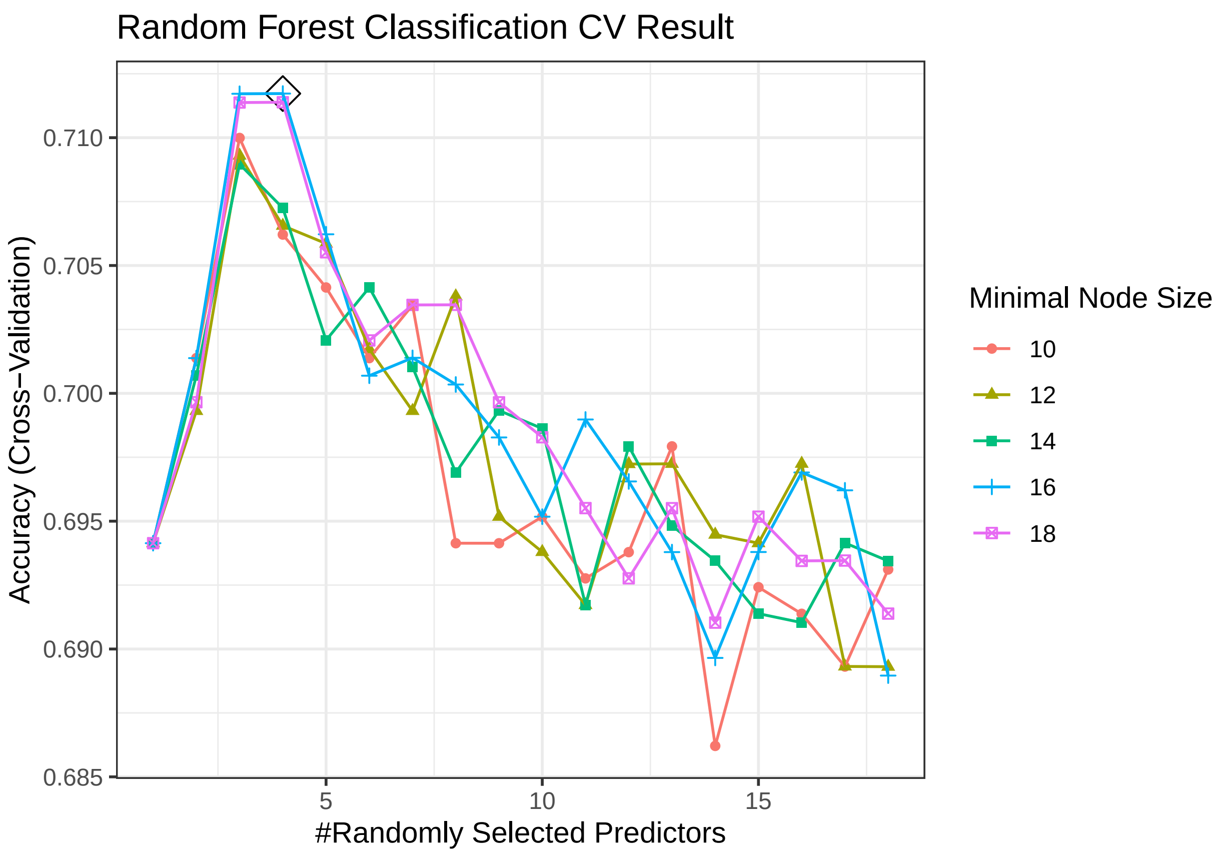


1.1.9 Random Forest

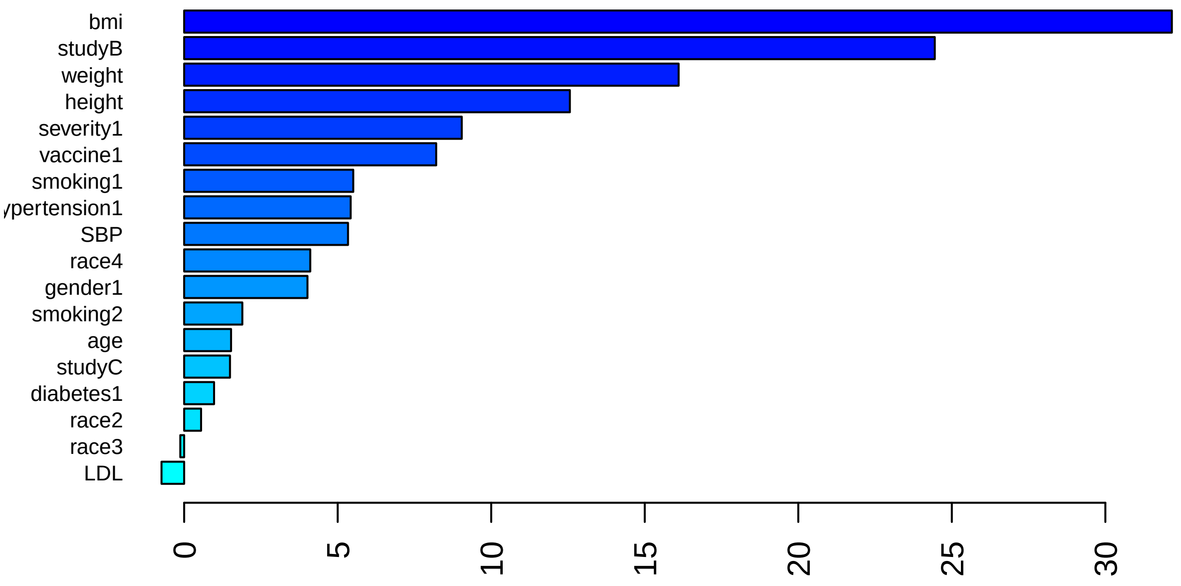
```
rf.grid2 <- expand.grid(mtry = 1:ncol(train.x),
                        splitrule = "gini",
                        min.node.size = seq(10, 18, by = 2))
set.seed(2023)
rf.fit2 <- train(train.x,
                train.bin.y,
                method = "ranger",
                tuneGrid = rf.grid2,
                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()
```



```r
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)))
```

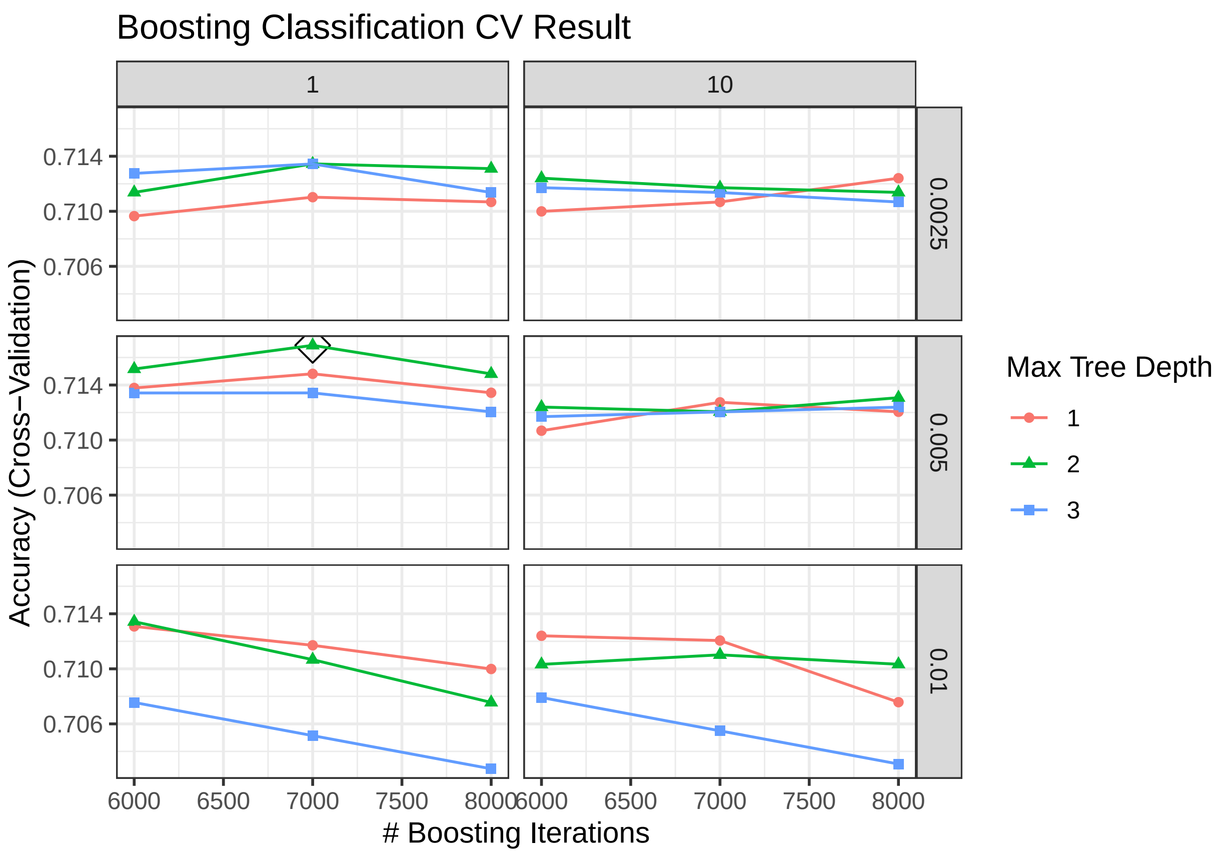


1.1.10 Boosting

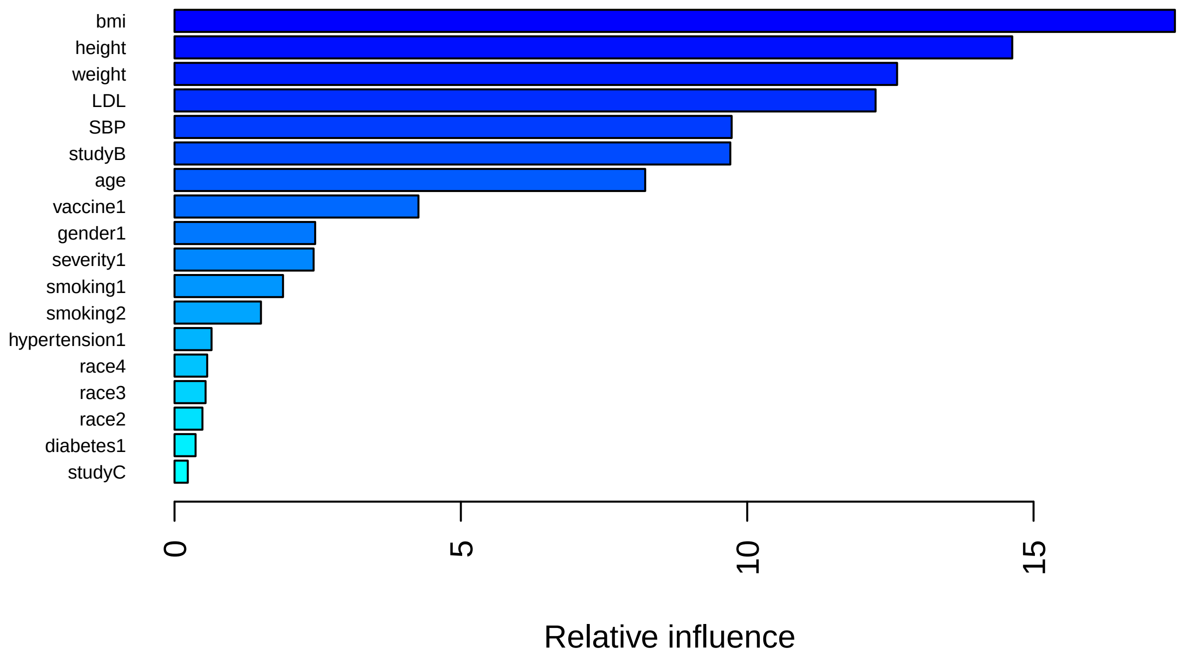
```r
set.seed(2023)
bst.grid2 <- expand.grid(n.trees = c(6000, 7000, 8000),
                        interaction.depth = 1:3,
                        shrinkage = c(0.0025, 0.005, 0.01),
                        n.minobsinnode = c(1,10))

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
## 26    7000                 2     0.005              1
```

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



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

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



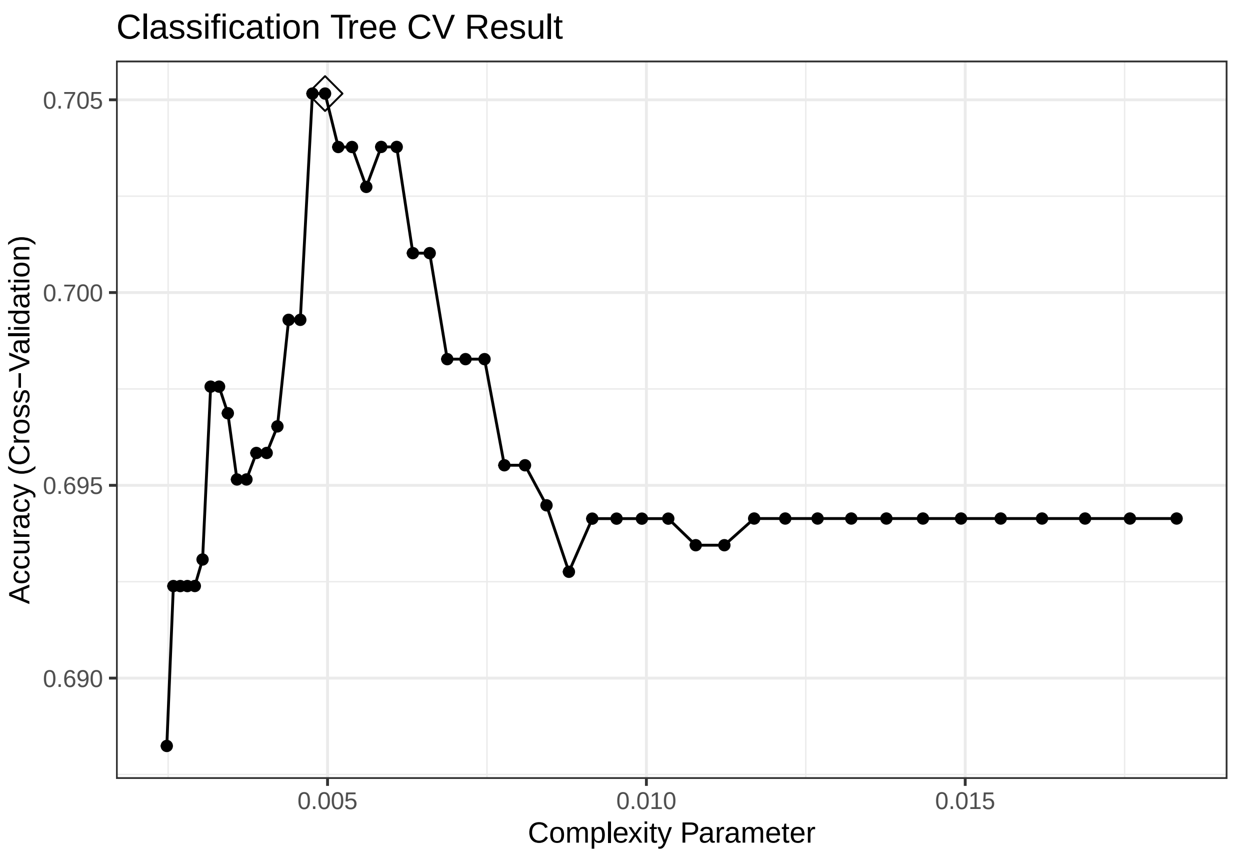
```
##                                 var     rel.inf
## bmi                       bmi 17.4678617
## height                 height 14.6274336
## weight                 weight 12.6168495
## LDL                       LDL 12.2417343
## SBP                       SBP  9.7283254
## studyB                 studyB  9.7051849
## age                       age  8.2186384
## vaccine1             vaccine1  4.2592937
## gender1               gender1  2.4561002
## severity1           severity1  2.4286230
## smoking1             smoking1  1.8945366
## smoking2             smoking2  1.5093649
## hypertension1 hypertension1  0.6466999
## race4                   race4  0.5705586
## race3                   race3  0.5423003
## race2                   race2  0.4871927
## diabetes1           diabetes1  0.3675255
## studyC                 studyC  0.2317767
```

1.1.11 Classification Trees

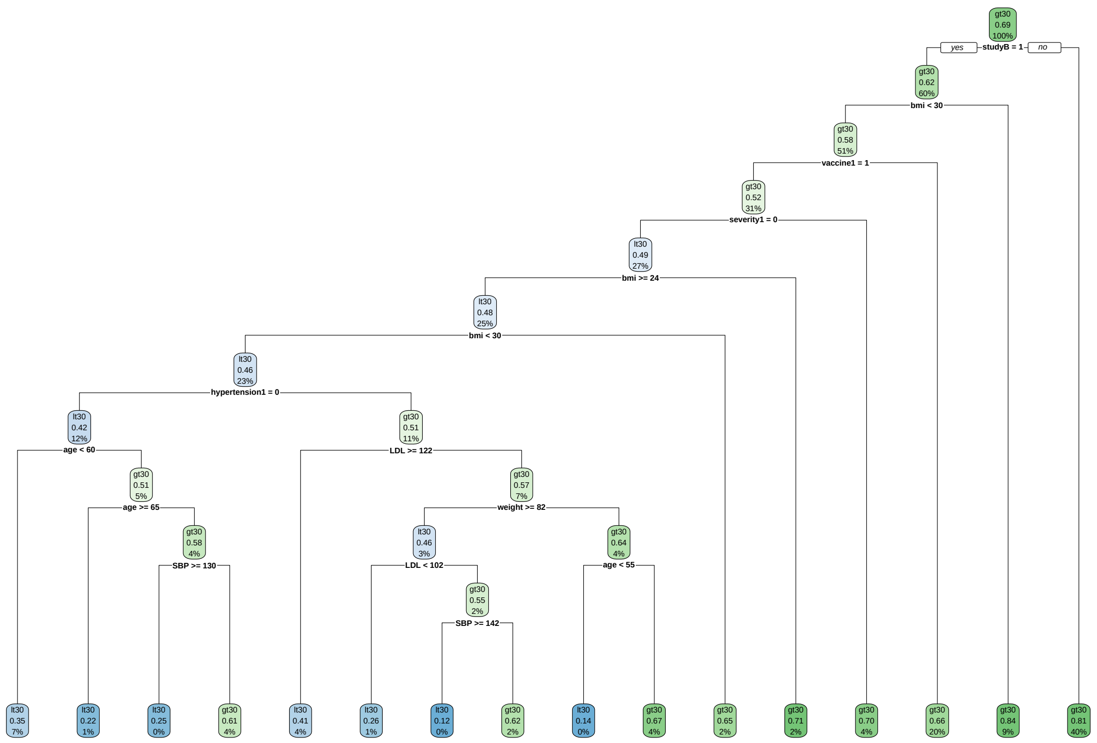
```
rpart.grid = expand.grid(cp = exp(seq(-6,-4, len = 50)))
set.seed(2023)
rpart.fit2 <- train(train.x,
                   train.bin.y,
                   method = "rpart",
                   tuneGrid = rpart.grid,
                   trControl = ctrl1)

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)
```

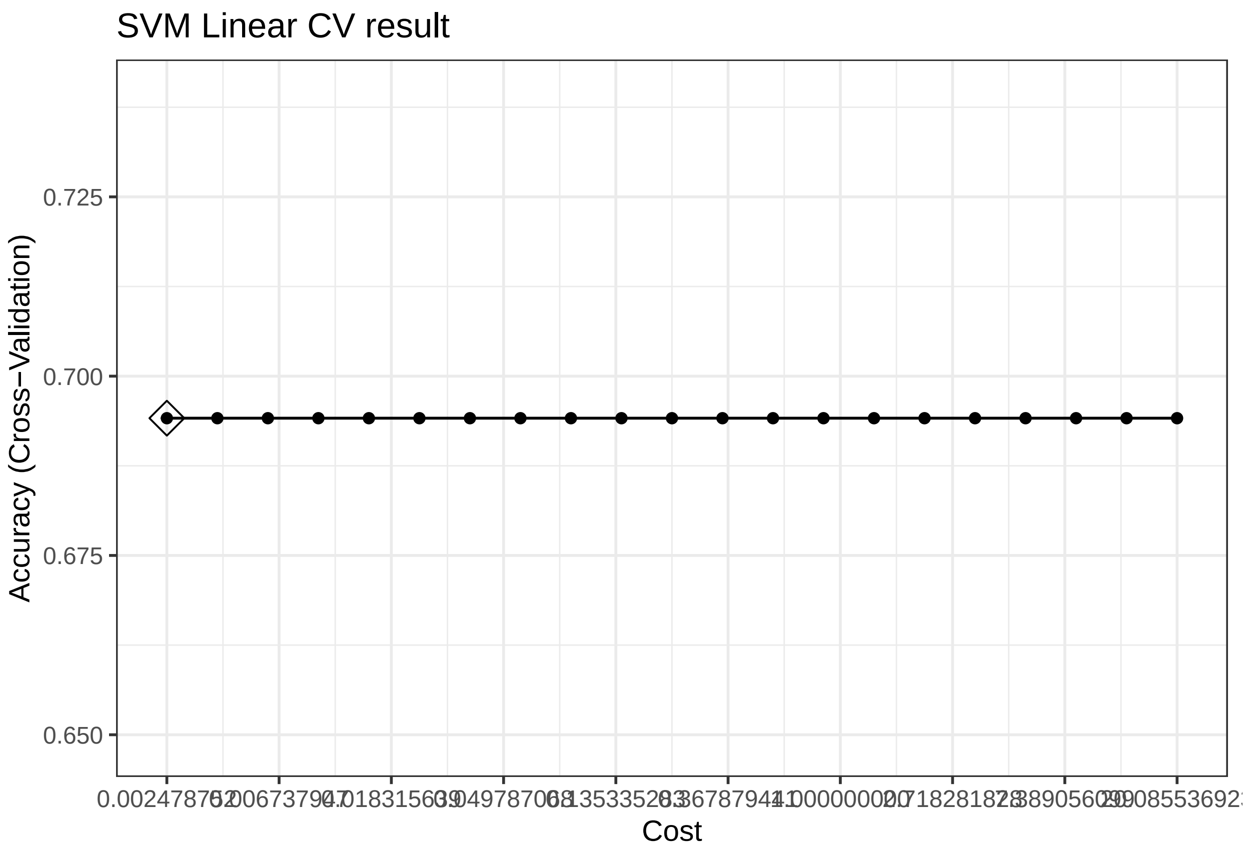


```
jpeg("./figure/rpart2.jpeg", width = 8, height = 6, units="in", res=500)
rpart.plot(rpart.fit2$finalModel)
dev.off()
```

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

1.1.12 Support Vector Machine (SVM)

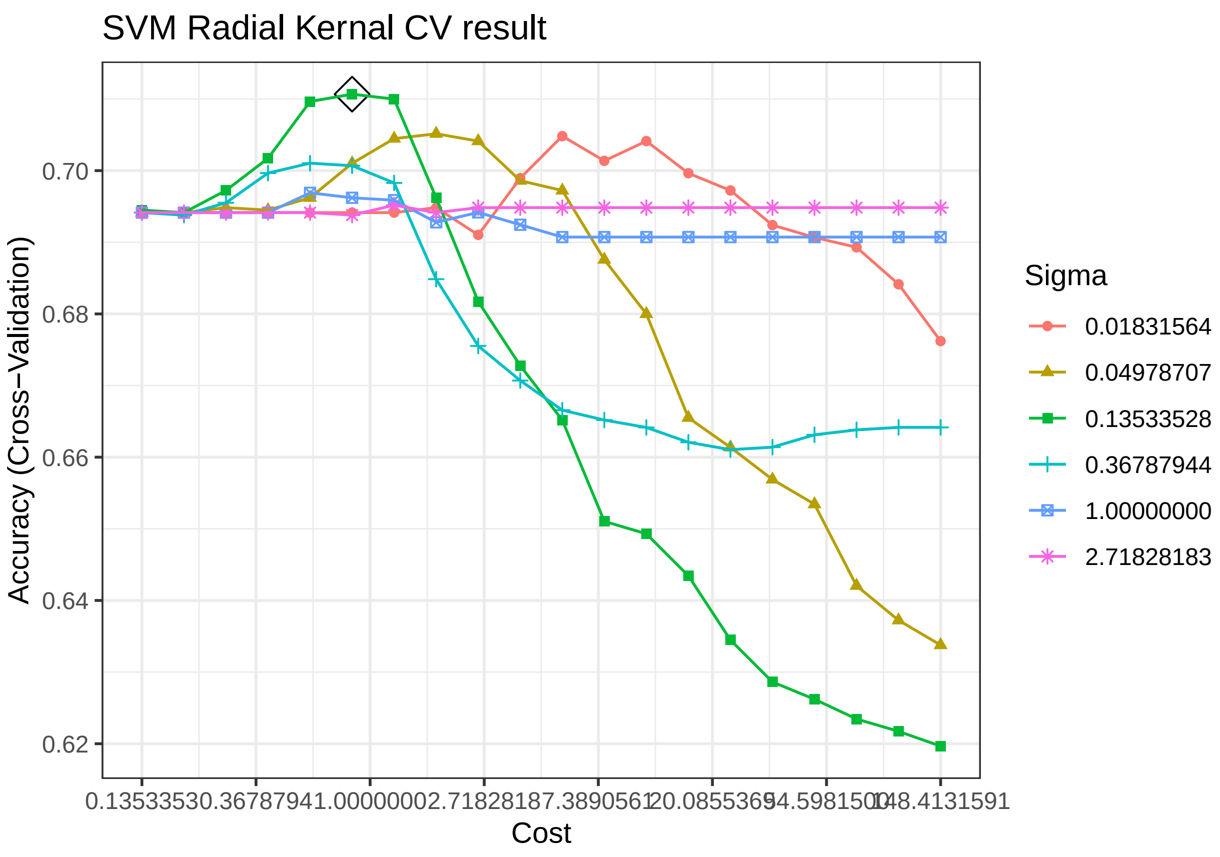
```
set.seed(2023)
svml.fit <- train(train.x,
                  train.bin.y,
                  method = "svmLinear",
                  tuneGrid = data.frame(C = exp(seq(-6, 3, len = 21))),
                  trControl = ctrl1)
ggplot(svml.fit, highlight = TRUE) +
  scale_x_continuous(trans='log',n.breaks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



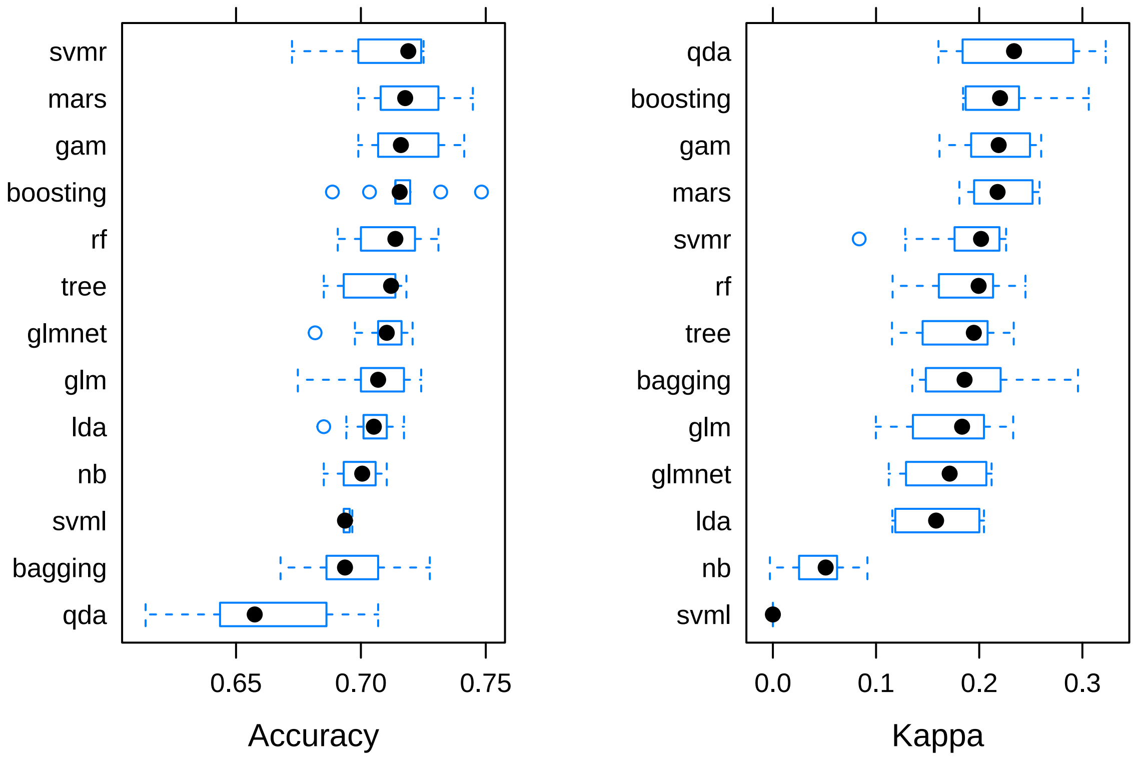
```
ggsave("./figure/svmr_cv.jpeg", dpi = 500)
```

1.2 Model Selection

```
set.seed(2023)
resamp2 <- resamples(list(glm = glm.fit,
                          glmnet = glmn.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,
                          svml = svml.fit,
                          svmr = svmr.fit))

summary(resamp2)
```

```
##
## Call:
## summary.resamples(object = resamp2)
##
## Models: glm, glmnet, gam, mars, lda, qda, nb, bagging, rf, boosting, tree, svml, 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 0.6885813 0.7137931 0.7155172 0.7168821 0.7193457 0.7482759    0
## tree     0.6851211 0.6939655 0.7120715 0.7051615 0.7137931 0.7182131    0
## svml     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  0.184344290 0.19435635 0.22020503 0.22719300 0.23638392 0.30622010
## tree      0.115434149 0.15719160 0.19478063 0.18525932 0.20594295 0.23344205
## svml      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
## svml         0
## svmr         0
```

```
p1=bwplot(resamp2, metric = "Accuracy")
p2=bwplot(resamp2, metric = "Kappa")
grid.arrange(p1, p2 ,ncol=2)
```



```
jpeg("./figure/resample2.jpeg", width = 8, height=6, units="in", res=500)
p1=bwplot(resamp2, metric = "Accuracy")
p2=bwplot(resamp2, metric = "Kappa")
grid.arrange(p1, p2, ncol=2)
dev.off()
```

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

1.3 Training / Testing Error

```
# svmr error
# training
pred.svmr.train <- predict(svmr.fit, newdata = train.x)
confusionMatrix(data = pred.svmr.train, reference = train.bin.y)
```

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

```
##           Reference
## Prediction lt30 gt30
##       lt30  373   90
##       gt30  514 1923
##
##                Accuracy : 0.7917
##                  95% CI : (0.7765, 0.8064)
##     No Information Rate : 0.6941
##     P-Value [Acc > NIR] : < 2.2e-16
##
##                   Kappa : 0.4338
##
##  Mcnemar's Test P-Value : < 2.2e-16
##
##             Sensitivity : 0.4205
##             Specificity : 0.9553
##          Pos Pred Value : 0.8056
##          Neg Pred Value : 0.7891
##              Prevalence : 0.3059
##          Detection Rate : 0.1286
##    Detection Prevalence : 0.1597
##       Balanced Accuracy : 0.6879
##
##        'Positive' Class : lt30
##
```

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