

Final Primary 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 Primary Analysis

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

1.1.1 Linear Model

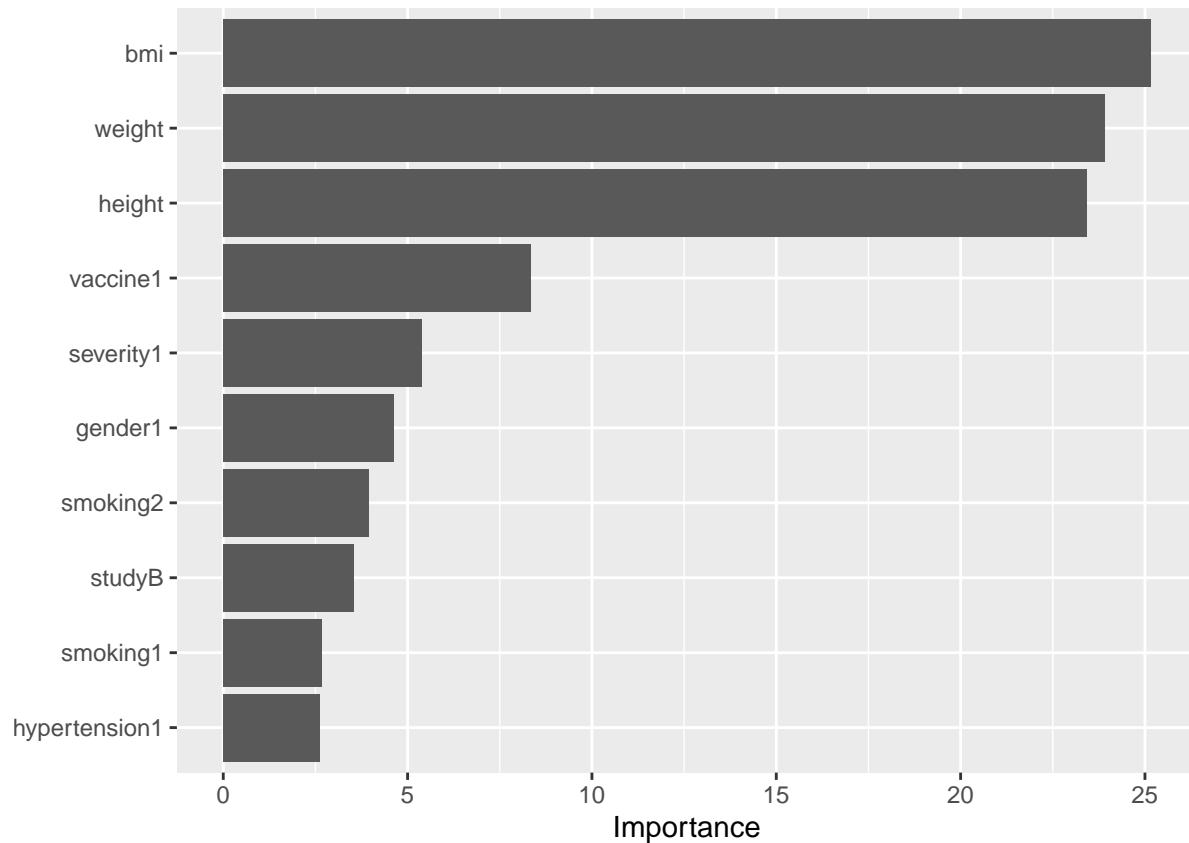
```
set.seed(2023)

lm.fit <- train(train.x, train.y,
               method = "lm",
               trControl = ctrl1)

coef(lm.fit$finalModel)

##      (Intercept)          age      gender1      race2      race3
## -3.190120e+03  1.163953e-01 -4.443893e+00  2.189010e+00 -6.599719e-01
##           race4      smoking1      smoking2      height      weight
## -1.156806e+00  2.905693e+00  6.427376e+00  1.866280e+01 -2.014323e+01
##           bmi hypertension1      diabetes1      SBP      LDL
##  6.056969e+01  4.165589e+00 -1.152370e+00 -7.863399e-02 -4.215262e-02
##           vaccine1      severity1      studyB      studyC
## -8.133542e+00  8.747096e+00  4.368587e+00 -6.869681e-01

vip(lm.fit$finalModel)
```



1.1.2 LASSO

```
set.seed(2023)
lasso.fit <- train(train.x, train.y,
  method = "glmnet",
  tuneGrid = expand.grid(
    alpha = 1,
    lambda = exp(seq(0, -7, length=100))),
  trControl = ctrl1)
```

```
lasso.fit$bestTune
```

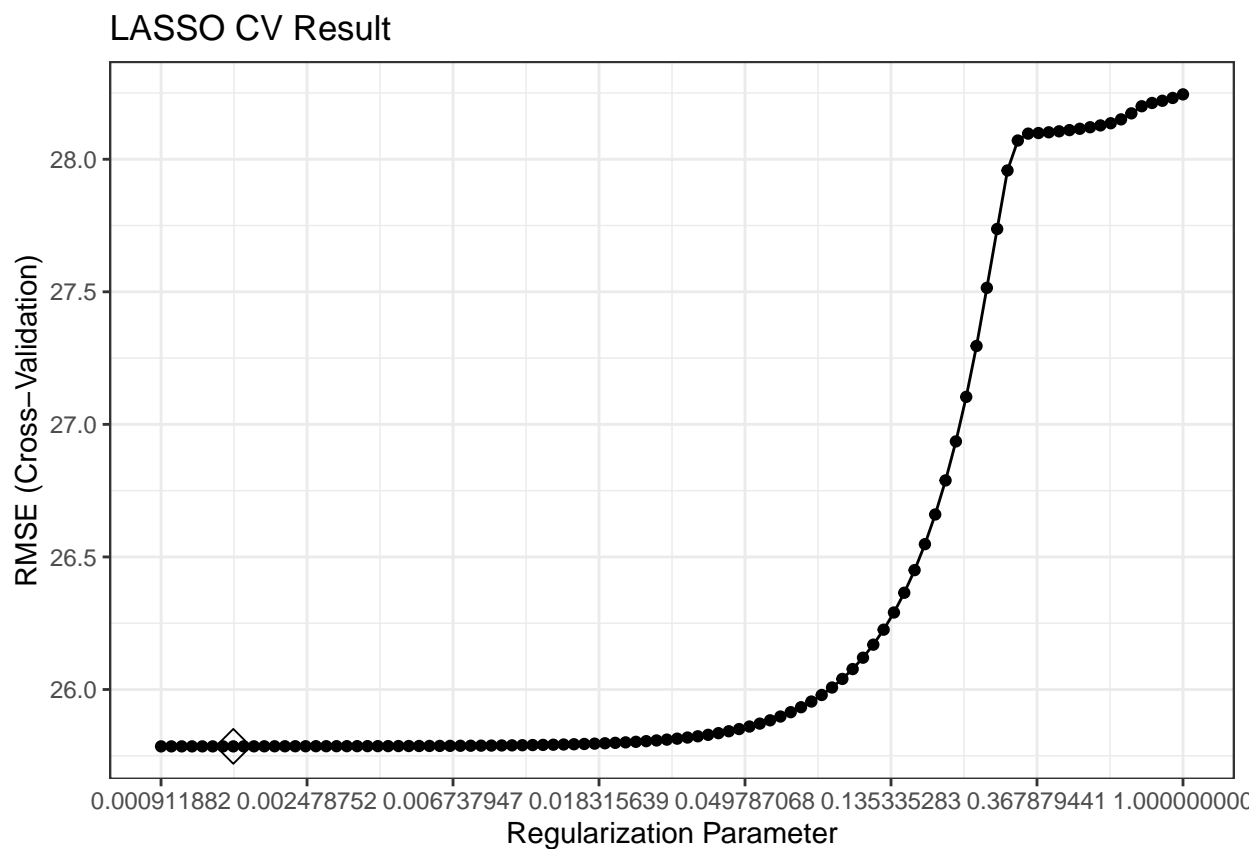
```
##   alpha      lambda
## 8      1 0.001495865
```

```
coef(lasso.fit$finalModel, s = lasso.fit$bestTune$lambda)
```

```
## 19 x 1 sparse Matrix of class "dgCMatrix"
##              s1
## (Intercept) -3.134172e+03
## age         1.153955e-01
## gender1     -4.441866e+00
## race2       2.191861e+00
## race3      -6.681255e-01
## race4      -1.149670e+00
## smoking1    2.901232e+00
## smoking2    6.400802e+00
```

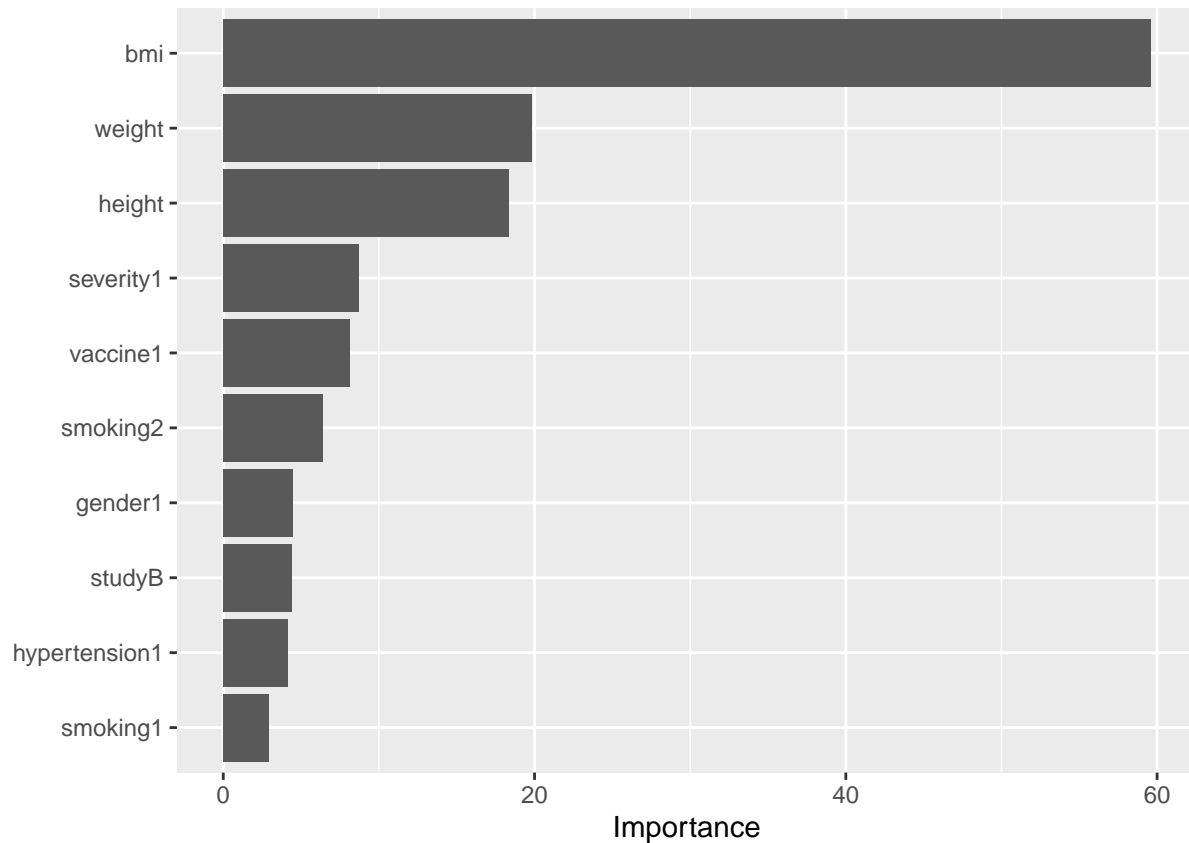
```
## height      1.833161e+01
## weight     -1.979266e+01
## bmi        5.956877e+01
## hypertension1 4.150461e+00
## diabetes1  -1.160249e+00
## SBP        -7.746419e-02
## LDL        -4.212203e-02
## vaccine1   -8.147730e+00
## severity1   8.730928e+00
## studyB      4.369356e+00
## studyC     -6.781352e-01
```

```
ggplot(lasso.fit, highlight = TRUE) +
  labs(title="LASSO CV Result") +
  scale_x_continuous(trans='log', n.breaks = 10) +
  theme_bw()
```



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

vip(lasso.fit$finalModel)
```



1.1.3 Ridge

```
set.seed(2023)
ridge.fit <- train(train.x, train.y,
  method = "glmnet",
  tuneGrid = expand.grid(alpha = 0,
    lambda = exp(seq(1, -5, length=100))),
  trControl = ctrl1)

ridge.fit$bestTune
```

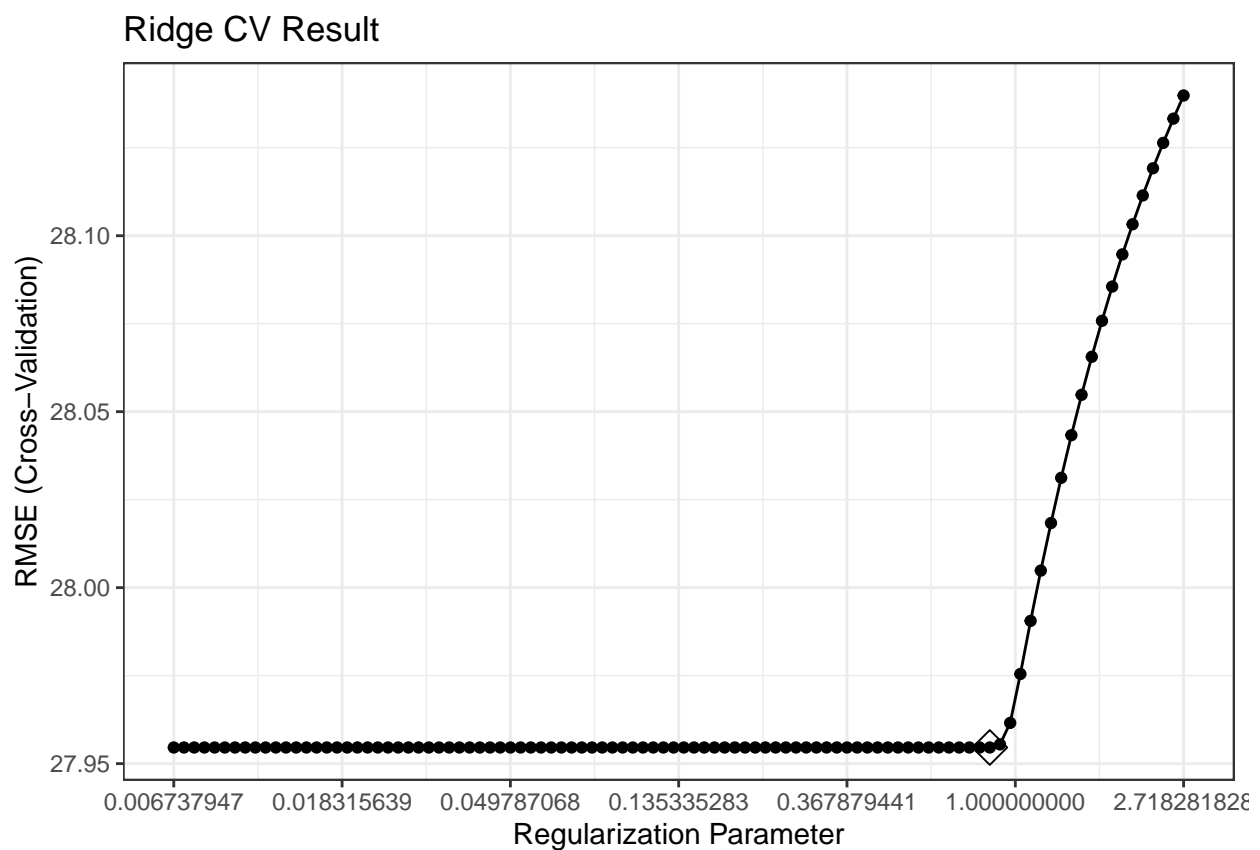
```
##      alpha      lambda
## 81      0 0.8594049
```

```
coef(ridge.fit$finalModel, s = ridge.fit$bestTune$lambda)
```

```
## 19 x 1 sparse Matrix of class "dgCMatrix"
##              s1
## (Intercept) -131.33806374
## age         0.09731228
## gender1     -4.40320528
## race2       2.66527141
## race3      -1.32710400
## race4      -1.12570977
## smoking1    2.82624366
## smoking2    5.18400128
## height     0.60404463
```

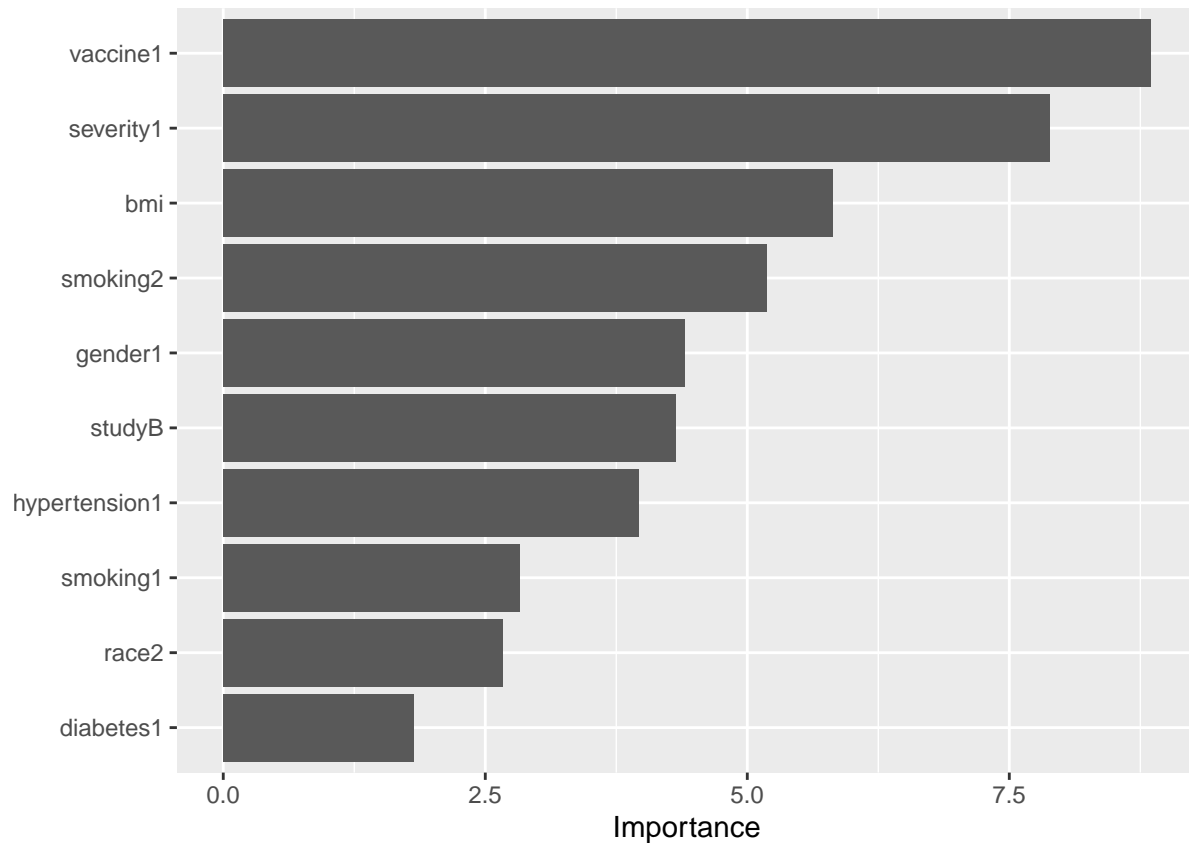
```
## weight      -1.01341715
## bmi         5.81922510
## hypertension1 3.96367066
## diabetes1   -1.81677375
## SBP        -0.06303616
## LDL        -0.04440780
## vaccine1    -8.84608080
## severity1   7.88676978
## studyB      4.32156225
## studyC     -0.51357417
```

```
ggplot(ridge.fit, highlight = TRUE) +
  scale_x_continuous(trans='log', n.breaks = 6) +
  labs(title="Ridge CV Result") +
  theme_bw()
```



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

```
vip(ridge.fit$finalModel)
```



1.1.4 Elastic Net

```
set.seed(2023)
enet.fit <- train(train.x, train.y,
  method = "glmnet",
  tuneGrid = expand.grid(
    alpha = seq(0, 1, length = 11),
    lambda = exp(seq(0, -8, length = 50))),
  trControl = ctrl1)

enet.fit$bestTune
```

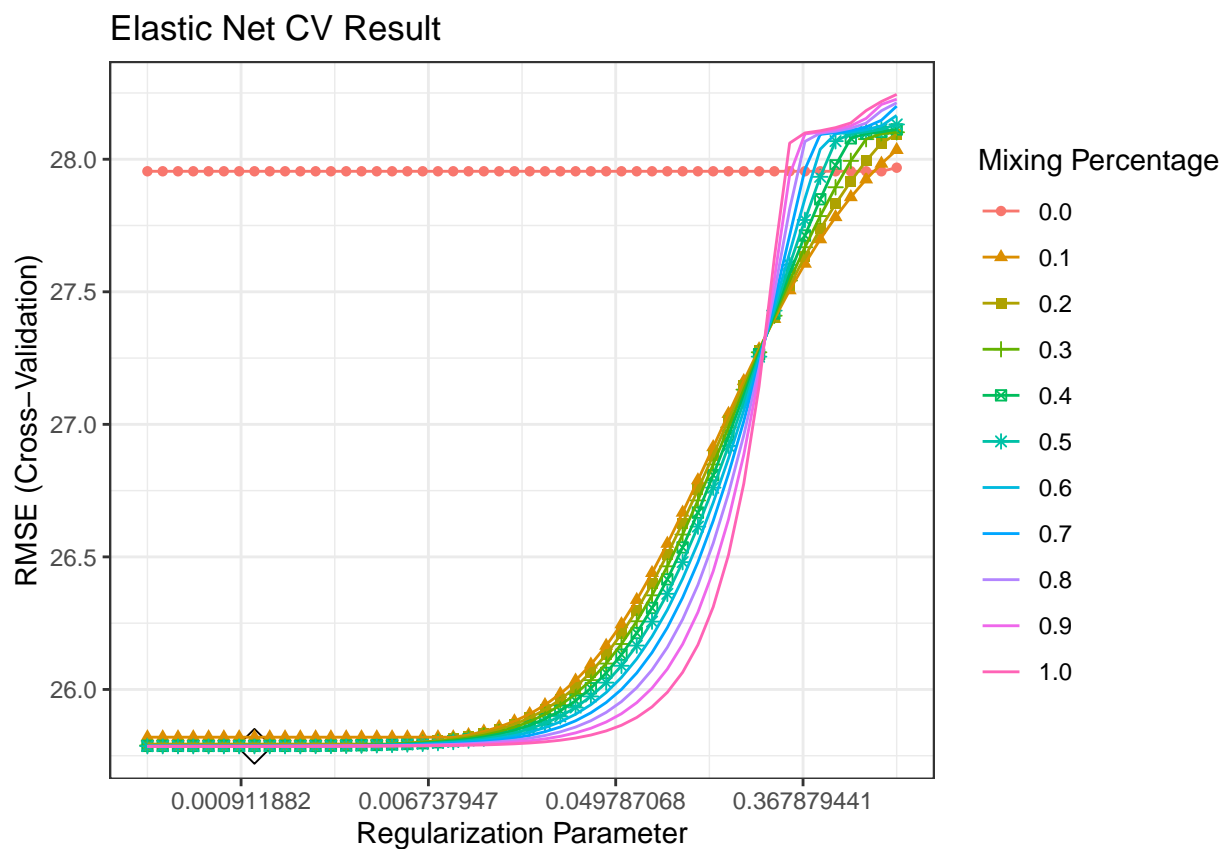
```
##      alpha      lambda
## 458    0.9 0.001051915
```

```
coef(enet.fit$finalModel, enet.fit$bestTune$lambda)
```

```
## 19 x 1 sparse Matrix of class "dgCMatrix"
##              s1
## (Intercept) -3.133363e+03
## age          1.156446e-01
## gender1      -4.443015e+00
## race2         2.194049e+00
## race3        -6.697538e-01
## race4        -1.151993e+00
## smoking1      2.902929e+00
## smoking2      6.403008e+00
```

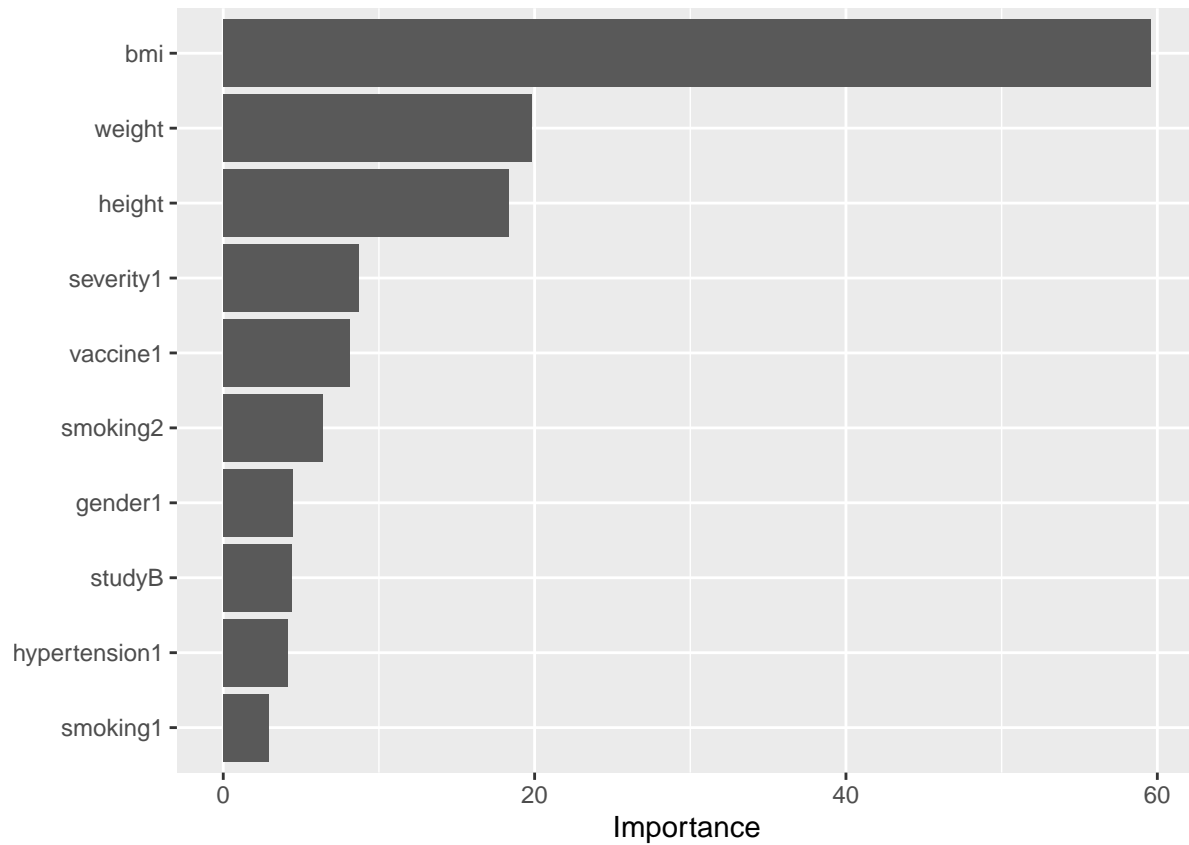
```
## height      1.832705e+01
## weight     -1.978780e+01
## bmi        5.955488e+01
## hypertension1 4.156169e+00
## diabetes1  -1.161920e+00
## SBP        -7.786025e-02
## LDL        -4.215546e-02
## vaccine1   -8.149202e+00
## severity1   8.732536e+00
## studyB      4.370077e+00
## studyC     -6.790033e-01
```

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



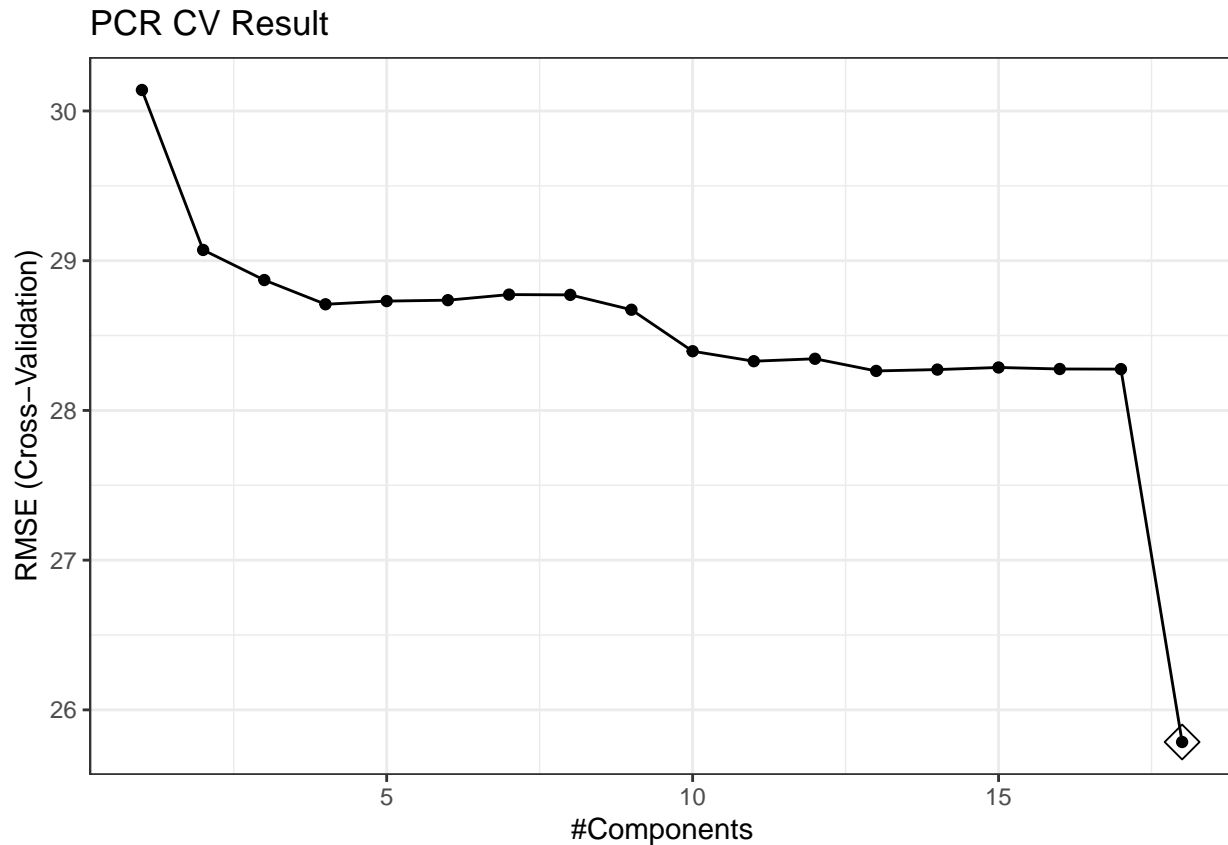
```
ggsave("./figure/enet_cv.jpeg", dpi = 500)
```

```
vip(enet.fit$finalModel)
```

1.1.5 Principal components regression (PCR)

```
set.seed(2023)
pcr.fit <- train(train.x,
                 train.y,
                 method = "pcr",
                 tuneGrid = data.frame(ncomp = 1:ncol(train.x)),
                 trControl = ctrl1,
                 preProcess = c("center", "scale"))
ggplot(pcr.fit, highlight = TRUE) +
  labs(title = "PCR CV Result") +
  theme_bw()
```



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

```
pcr.fit$bestTune
```

```
##      ncomp
## 18      18
```

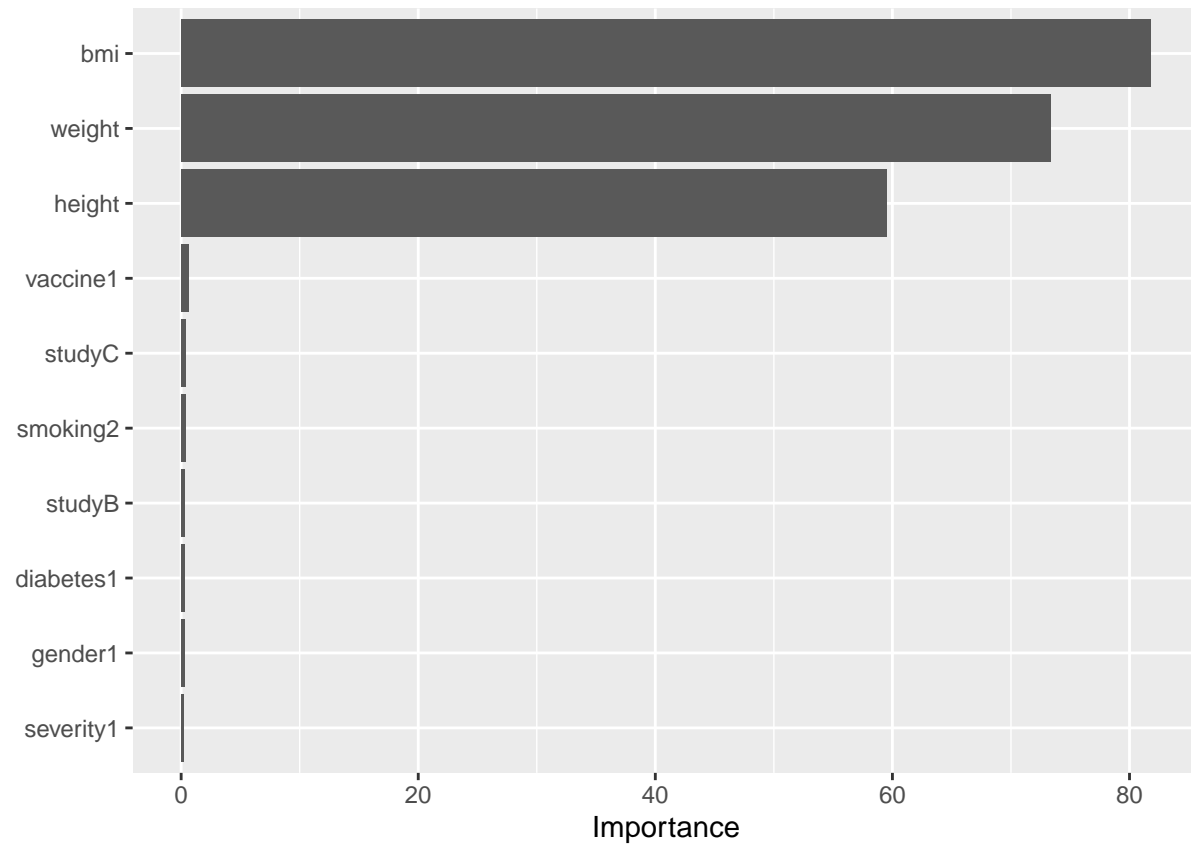
```
coef(pcr.fit$finalModel)
```

```
## , , 18 comps
```

```
##
##      .outcome
## age      0.5252538
## gender1  -2.2221586
## race2     0.4563464
## race3    -0.2619635
## race4    -0.3476329
## smoking1  1.3205684
## smoking2  1.9344423
## height   112.6936931
## weight   -141.0001175
## bmi      165.1518985
## hypertension1  2.0811234
## diabetes1 -0.4188178
## SBP      -0.6356938
## LDL      -0.8376686
## vaccine1 -4.0025673
## severity1  2.5879846
```

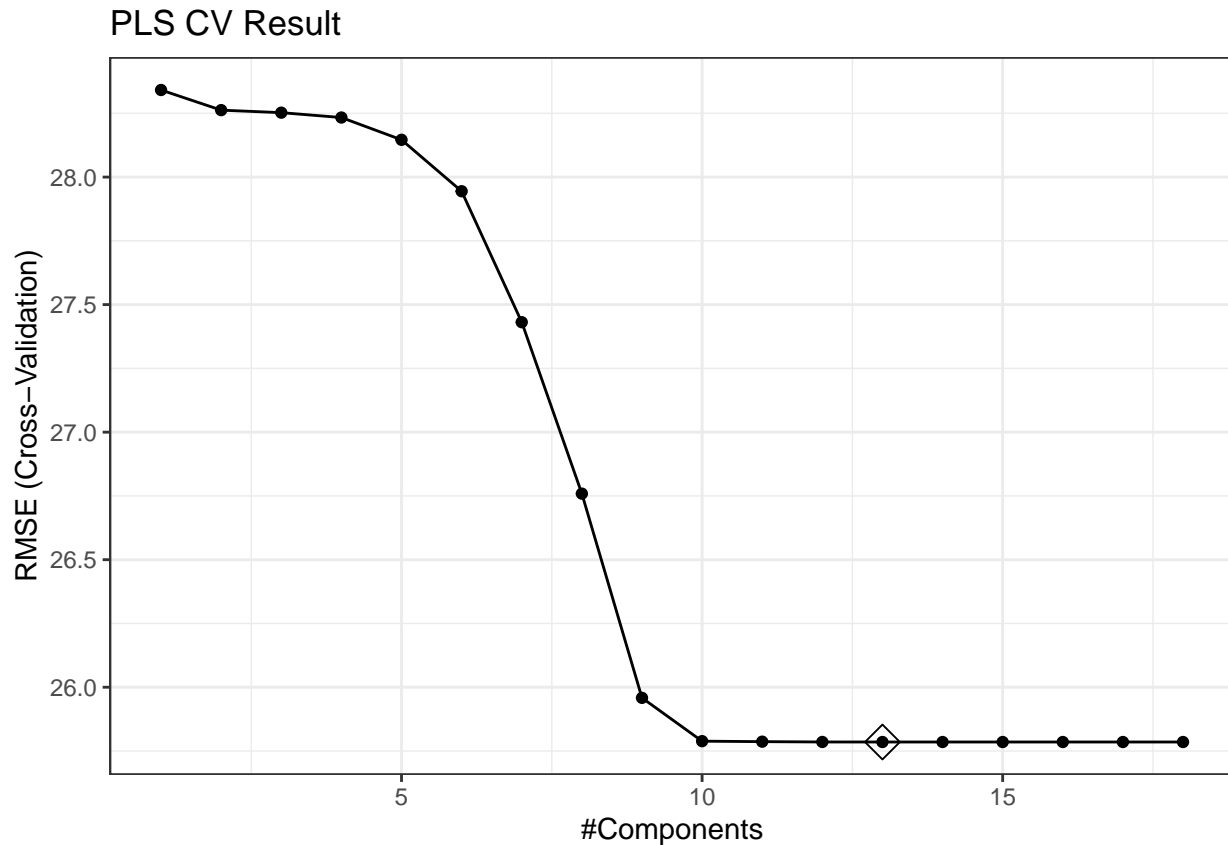
```
## studyB      2.1374000
## studyC     -0.2730416
```

```
vip(pcr.fit$finalModel)
```



1.1.6 Partial Least Squares (PLS)

```
set.seed(2023)
pls.fit <- train(train.x,
                 train.y,
                 method = "pls",
                 tuneGrid = data.frame(ncomp = 1:ncol(train.x)),
                 trControl = ctrl1,
                 preProcess = c("center", "scale"))
ggplot(pls.fit, highlight = TRUE) +
  labs(title = "PLS CV Result") +
  theme_bw()
```



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

```
pls.fit$bestTune
```

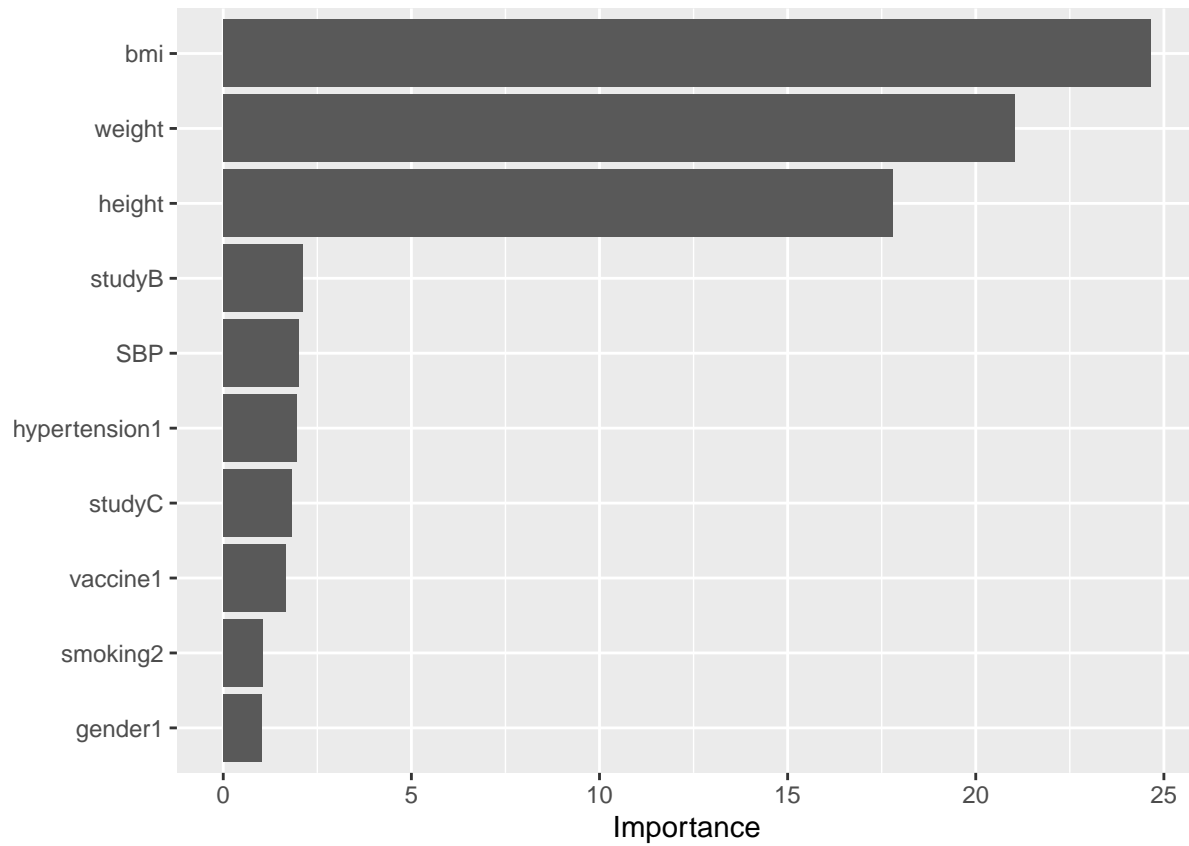
```
##      ncomp
## 13      13
```

```
coef(pls.fit$finalModel)
```

```
## , , 13 comps
##
##               .outcome
## age           0.5253162
## gender1       -2.2224171
## race2         0.4564699
## race3        -0.2616135
## race4        -0.3472528
## smoking1      1.3206873
## smoking2      1.9344789
## height       112.6936914
## weight       -141.0001239
## bmi          165.1518926
## hypertension1 2.0811255
## diabetes1     -0.4187817
## SBP          -0.6356784
## LDL          -0.8377705
## vaccine1     -4.0025291
## severity1     2.5877989
```

```
## studyB      2.1374098
## studyC     -0.2730417
```

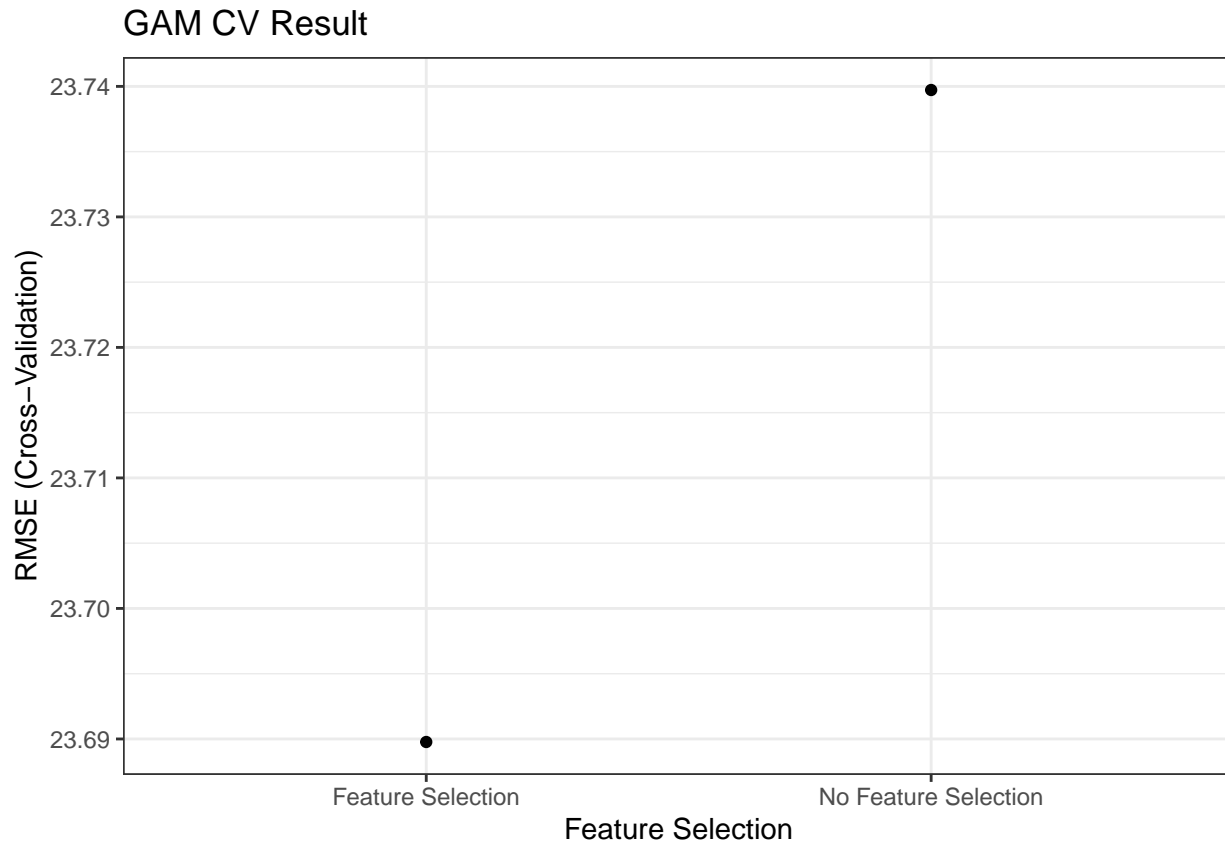
```
vip(pls.fit$finalModel)
```



1.1.7 Generalized Additive Model (GAM)

```
set.seed(2023)
gam.fit <- train(train.x,
                 train.y,
                 method = "gam",
                 tuneGrid = data.frame(select = c(TRUE, FALSE),
                                       method = "GCV.Cp"),
                 trControl = ctrl1)

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



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

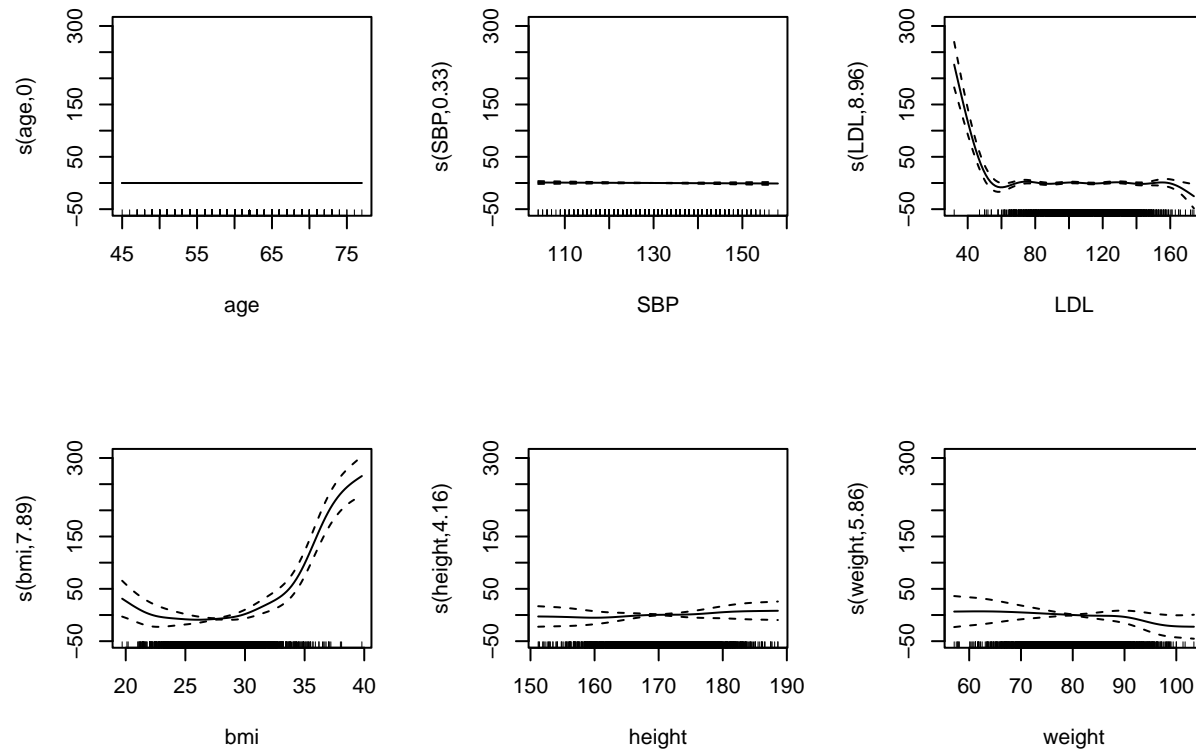
```
gam.fit$bestTune
```

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

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

```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## .outcome ~ gender1 + race3 + race4 + smoking1 + smoking2 + hypertension1 +
## diabetes1 + vaccine1 + severity1 + studyB + studyC + s(age) +
## s(SBP) + s(LDL) + s(bmi) + s(height) + s(weight)
##
## Estimated degrees of freedom:
## 0.000 0.329 8.959 7.893 4.163 5.856 total = 39.2
##
## GCV score: 524.051
```

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

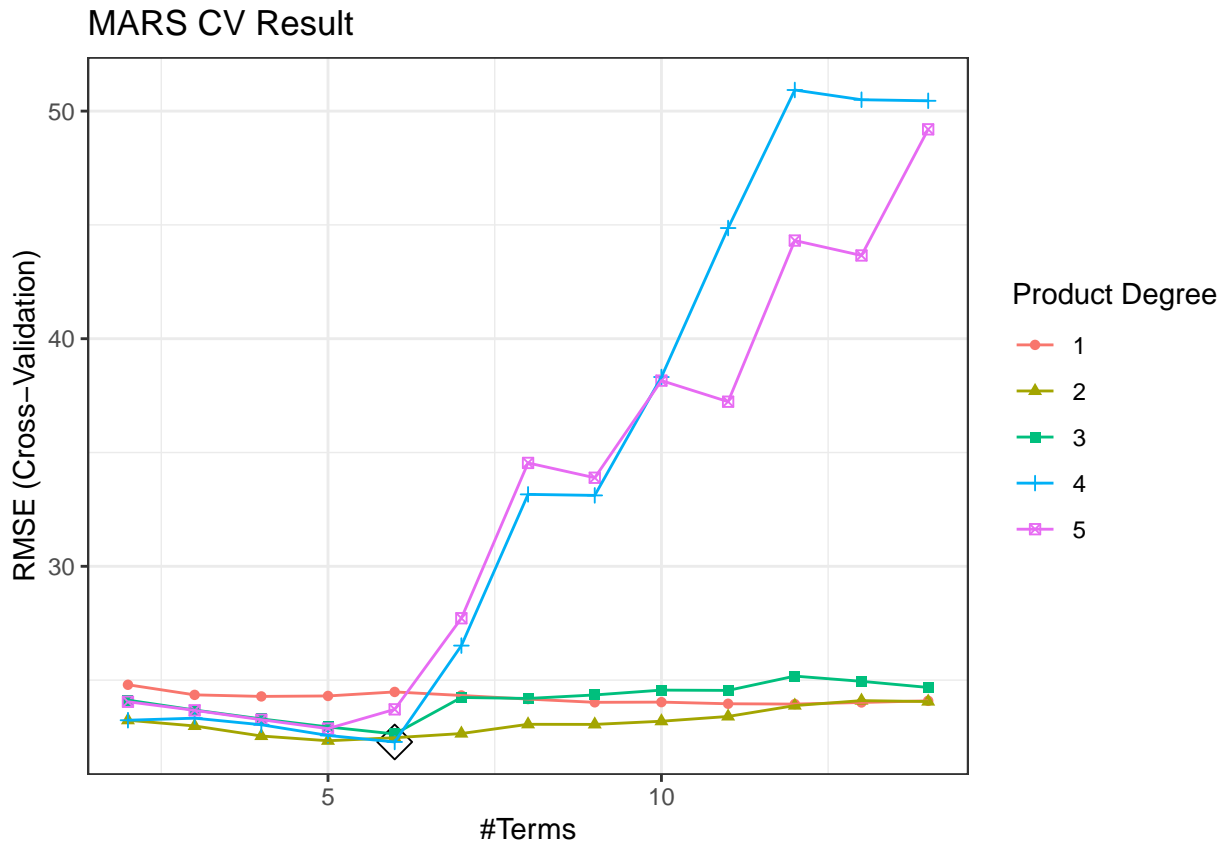


```
par(mfrow=c(1, 1))
```

1.1.8 Multivariate Adaptive Regression Splines (MARS)

```
mars.grid <- expand.grid(degree = 1:5,
                        nprune = 2:14)
set.seed(2023)
mars.fit <- train(train.x,
                  train.y,
                  method = "earth",
                  tuneGrid = mars.grid,
                  trControl = ctrl1)

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



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

```
mars.fit$bestTune
```

```
##      nprune degree
## 44         6      4
```

```
coef(mars.fit$finalModel)
```

```
##              (Intercept)                h(31.7-bmi)
##              19.332680                3.707079
##              h(bmi-31.7) * studyB          h(bmi-26.8)
##              39.317768                6.812493
## h(bmi-31.7) * h(LDL-115) * studyB          vaccine1
##              -1.309903                -7.855865
```

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

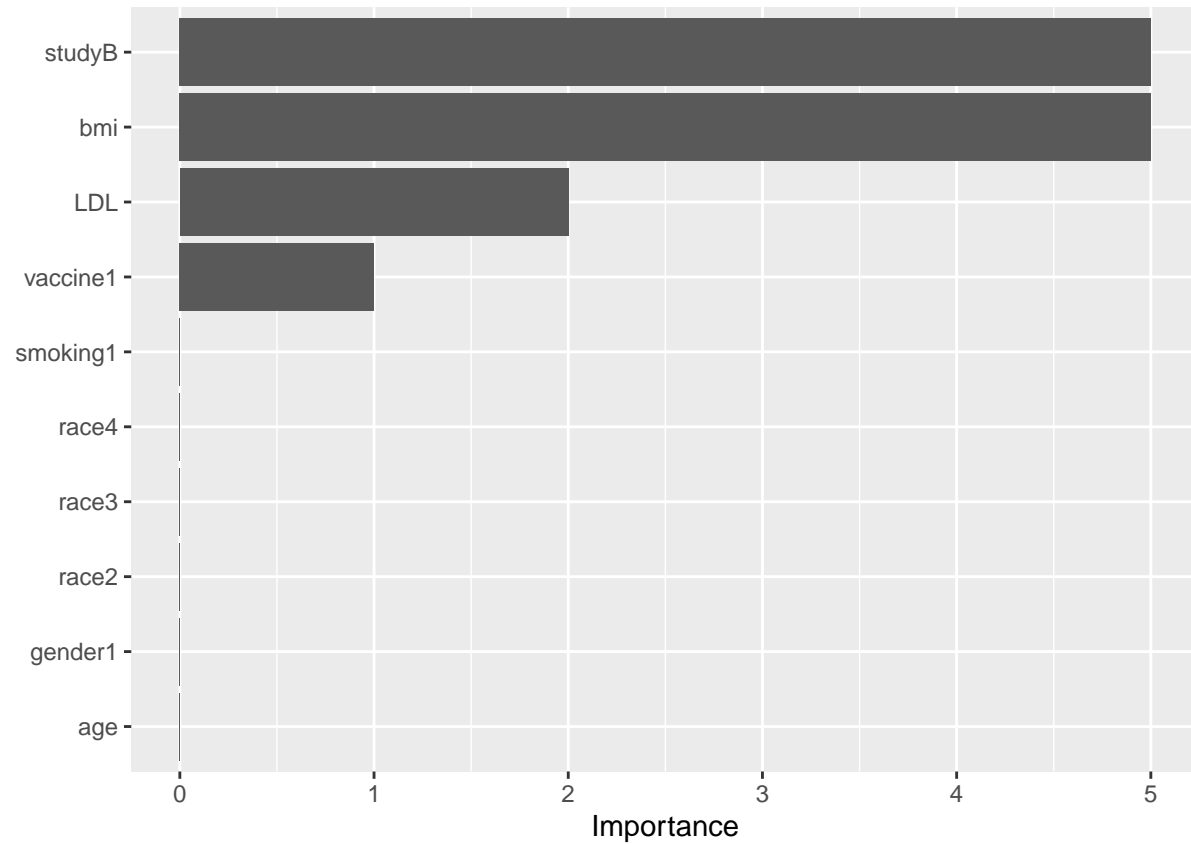
```
## Call: earth(x=matrix[2900,18], y=c(40,34,31,50,3...), keepxy=TRUE, degree=4,
##              nprune=6)
```

```
##
##              coefficients
## (Intercept)                19.332680
## vaccine1                   -7.855865
## h(bmi-26.8)                 6.812493
## h(31.7-bmi)                 3.707079
## h(bmi-31.7) * studyB        39.317768
## h(bmi-31.7) * h(LDL-115) * studyB -1.309903
##
```



```
## Selected 6 of 26 terms, and 4 of 18 predictors (nprune=6)
## Termination condition: Reached nk 37
## Importance: bmi, studyB, LDL, vaccine1, age-unused, gender1-unused, ...
## Number of terms at each degree of interaction: 1 3 1 1
## GCV 474.177    RSS 1362340    GRSq 0.4906252    RSq 0.4950084
```

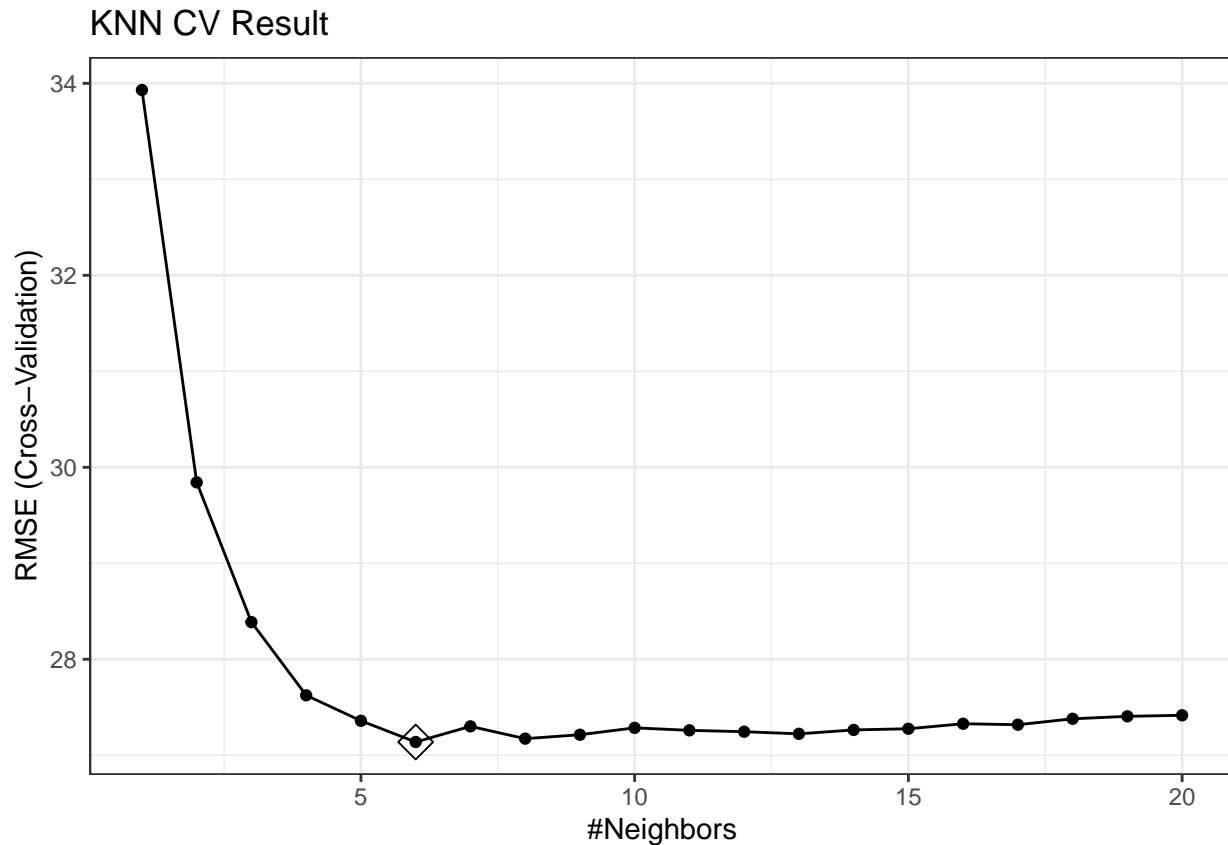
```
vip(mars.fit$finalModel)
```



1.1.9 K-Nearest Neighbour (KNN)

```
set.seed(2023)
knn.fit <- train(train.x,
                 train.y,
                 tuneGrid = data.frame(k = 1:20),
                 method = "knn",
                 trControl = ctrl1)

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



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

```
knn.fit$bestTune
```

```
## k
## 6 6
```

1.1.10 Bagging

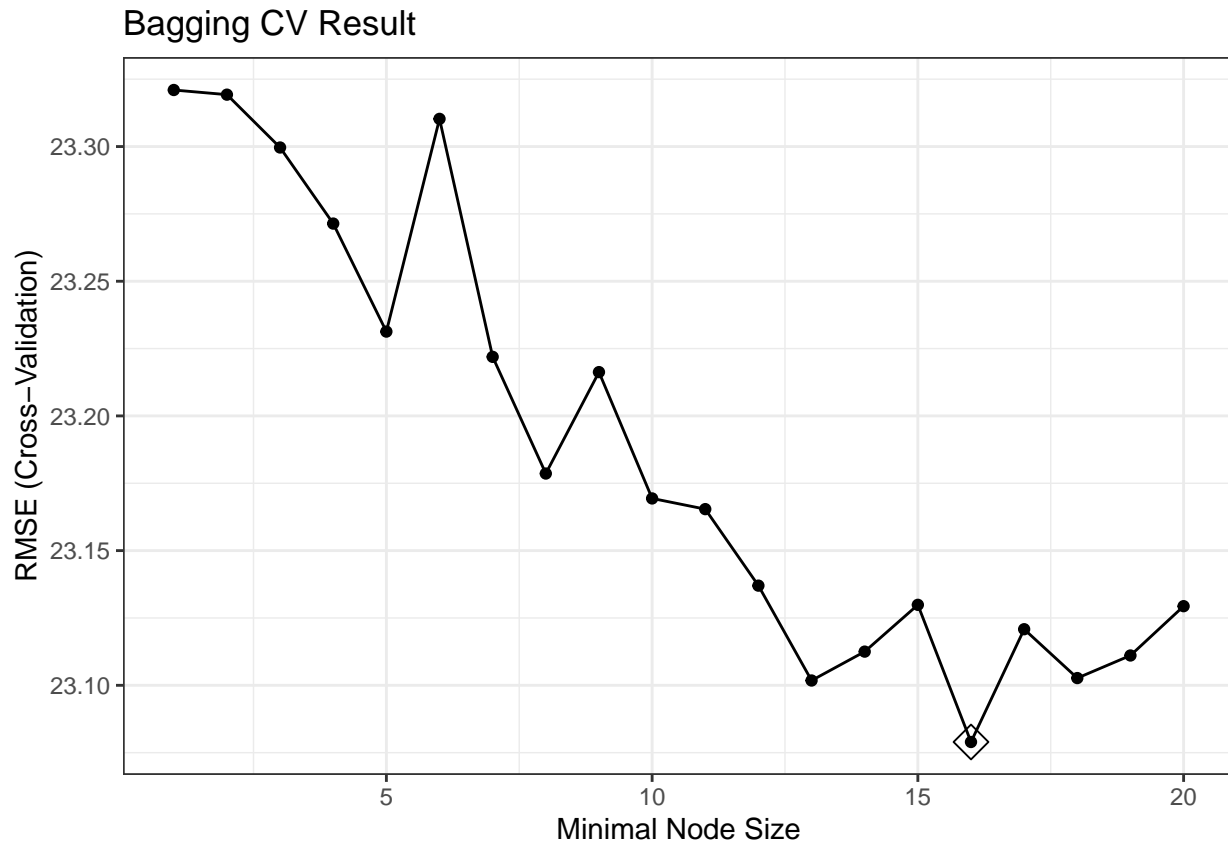
```
bag.grid <- expand.grid(mtry = ncol(train.x),
                      splitrule = "variance",
                      min.node.size = 1:20)
```

```
set.seed(2023)
bag.fit <- train(train.x,
                train.y,
                method = "ranger",
                tuneGrid = bag.grid,
                trControl = ctrl1)
```

```
bag.fit$bestTune
```

```
## mtry splitrule min.node.size
## 16 18 variance 16
```

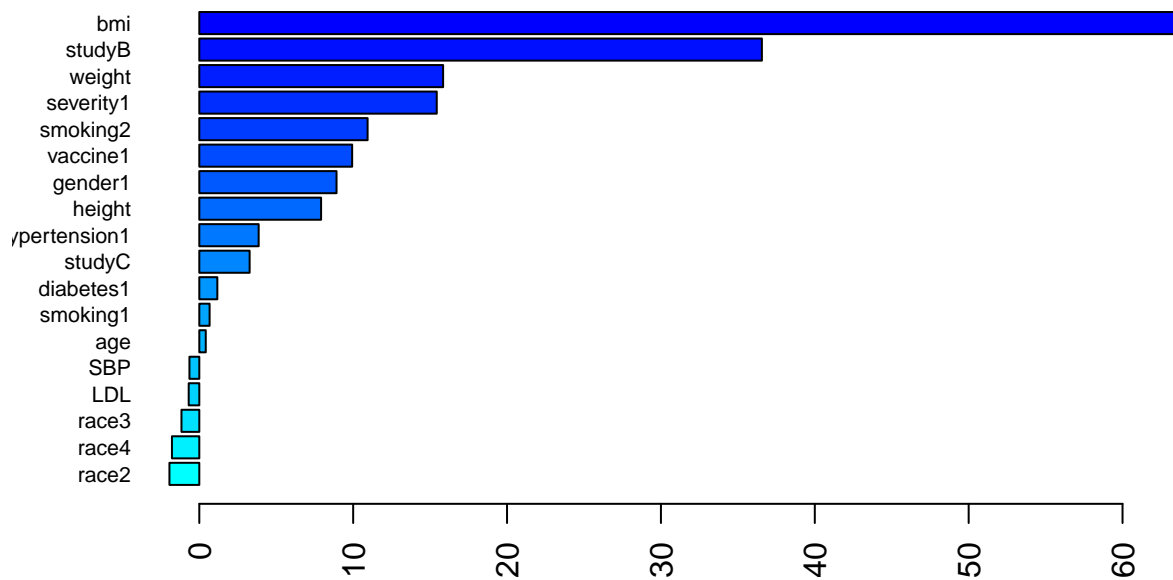
```
ggplot(bag.fit, highlight = TRUE) +
  labs(title = "Bagging CV Result") +
  theme_bw()
```



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

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

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



```
# p1 <- pdp::partial(
#   bag.fit,
#   pred.var = "Lot_Area",
#   grid.resolution = 20
# ) %>%
#   autoplot()
# p2 <- pdp::partial(
#   bag.fit,
#   pred.var = "Lot_Frontage",
#   grid.resolution = 20
# ) %>%
#   autoplot()
# gridExtra::grid.arrange(p1, p2, nrow = 1)
```

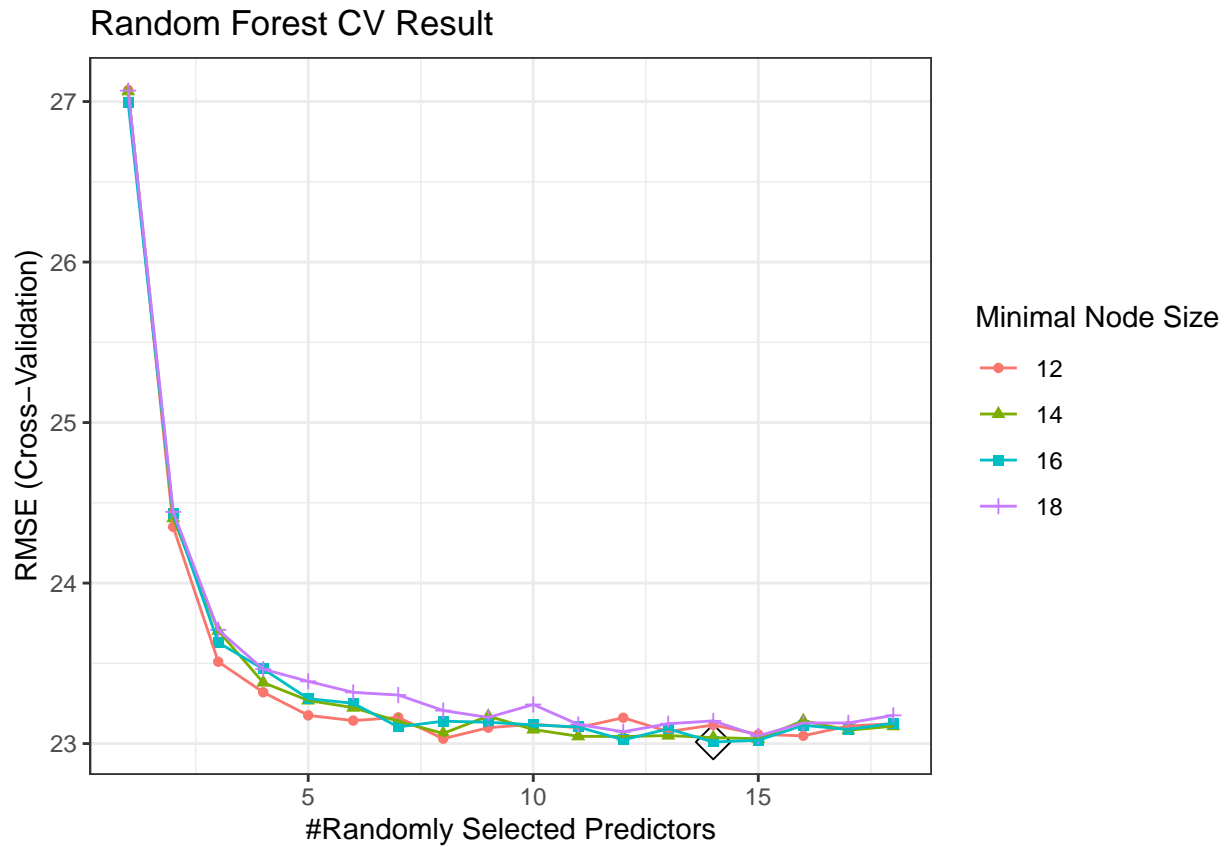
1.1.11 Random Forest

```
rf.grid <- expand.grid(mtry = 1:ncol(train.x),
                      splitrule = "variance",
                      min.node.size = seq(12, 18, by = 2))
set.seed(2023)
rf.fit <- train(train.x,
                train.y,
                method = "ranger",
                tuneGrid = rf.grid,
                trControl = ctrl1)

rf.fit$bestTune
```

```
##   mtry splitrule min.node.size
## 55   14  variance             16

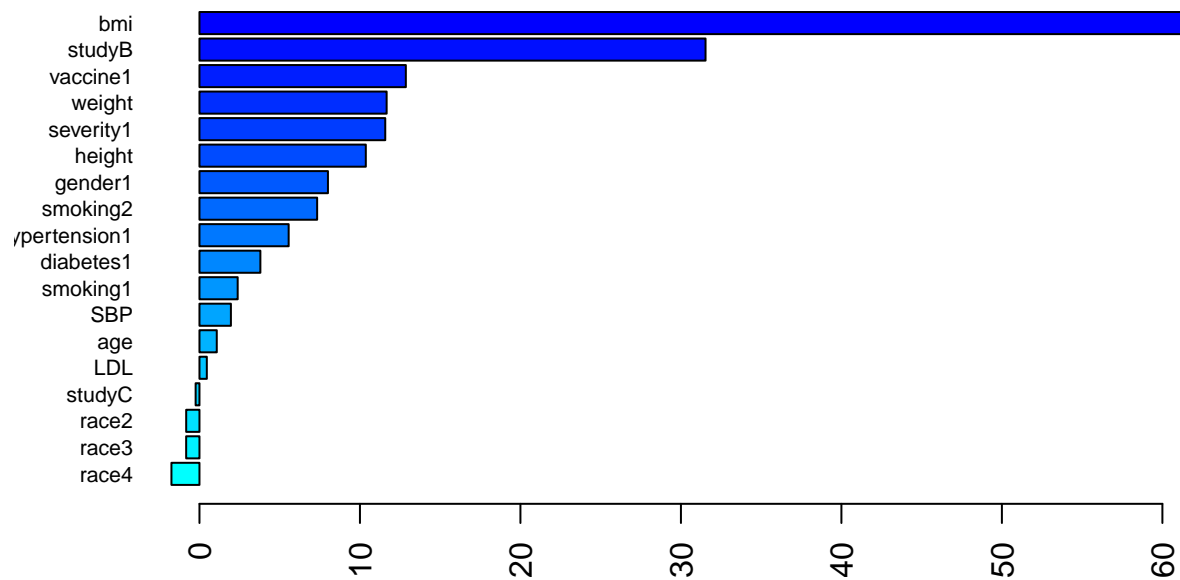
ggplot(rf.fit, highlight = TRUE) +
  labs(title = "Random Forest CV Result") +
  theme_bw()
```



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

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

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



1.1.12 Boosting

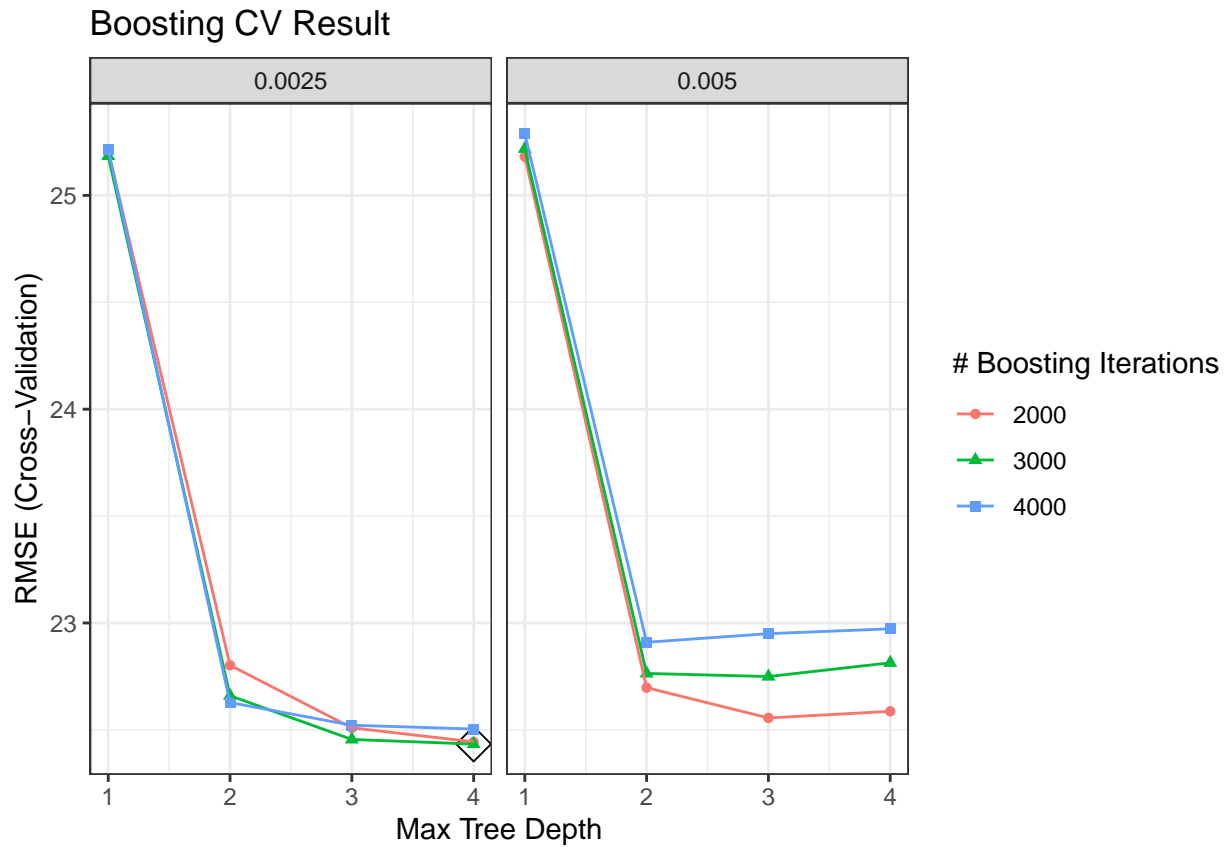
```
set.seed(2023)
bst.grid <- expand.grid(n.trees = c(2000, 3000, 4000),
                      interaction.depth = 1:4,
                      shrinkage = c(0.0025, 0.005),
                      n.minobsinnode = c(1))

bst.fit <- train(train.x,
                train.y,
                method = "gbm",
                tuneGrid = bst.grid,
                trControl = ctrl1,
                verbose = FALSE)

bst.fit$bestTune

##      n.trees interaction.depth shrinkage n.minobsinnode
## 11      3000                4    0.0025                1

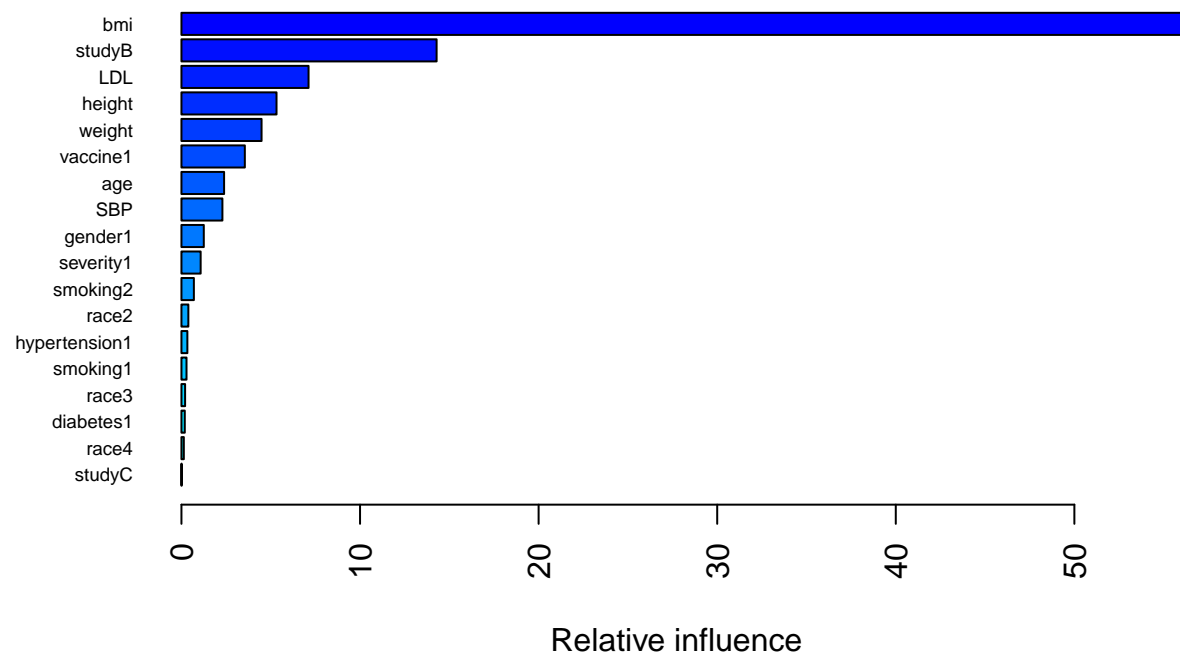
ggplot(bst.fit, highlight = TRUE) +
  labs(title = "Boosting CV Result") +
  theme_bw()
```



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

```
# Variable Importance
```

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



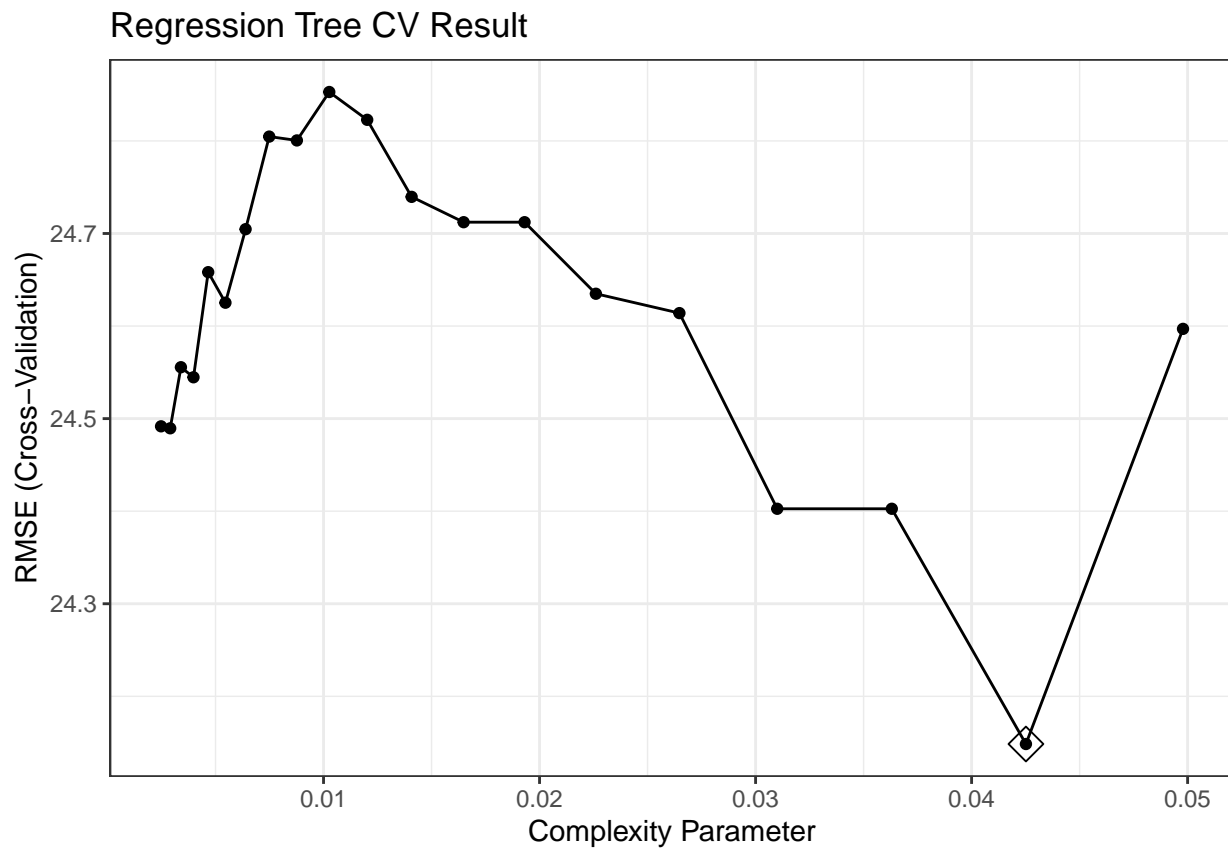
```
##          var      rel.inf
```

```
## bmi                bmi 55.99388120
## studyB             studyB 14.28732491
## LDL                LDL 7.11711346
## height             height 5.32395384
## weight             weight 4.48605845
## vaccine1           vaccine1 3.54931355
## age                age 2.38824261
## SBP                SBP 2.29301728
## gender1            gender1 1.25177144
## severity1          severity1 1.07498927
## smoking2           smoking2 0.69541862
## race2              race2 0.38716069
## hypertension1      hypertension1 0.33152029
## smoking1           smoking1 0.28428517
## race3              race3 0.20519173
## diabetes1          diabetes1 0.18728012
## race4              race4 0.13299757
## studyC             studyC 0.01047981
```

1.1.13 Regression Trees

```
rpart.grid <- expand.grid(cp = exp(seq(-6,-3, length = 20)))
set.seed(2023)
rpart.fit1 <- train(train.x,
                    train.y,
                    method = "rpart",
                    tuneGrid = rpart.grid,
                    trControl = ctrl1)

ggplot(rpart.fit1, highlight = TRUE) +
  labs(title = "Regression Tree CV Result") +
  theme_bw()
```

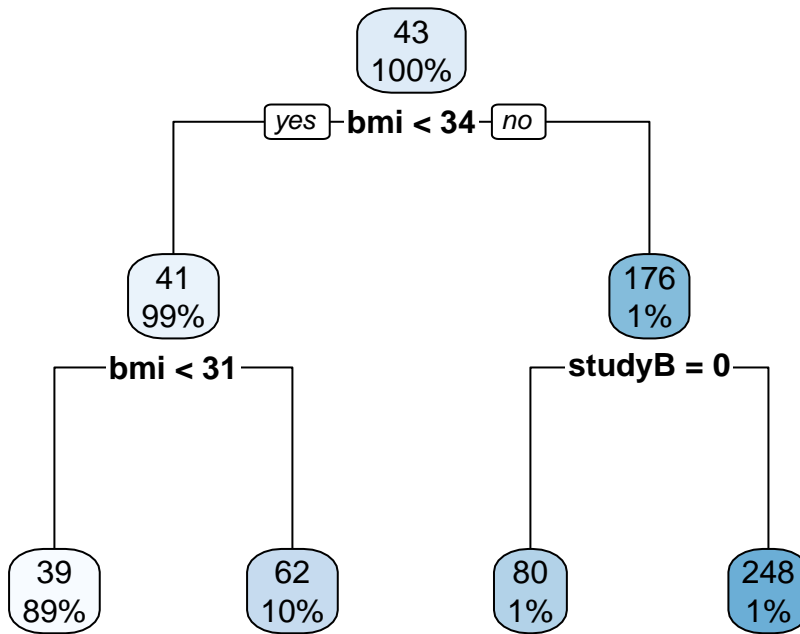



```
ggsave("./figure/rpart1_cv.jpeg", dpi = 500)
```

```
rpart.fit1$bestTune
```

```
##           cp  
## 19 0.04251515
```

```
rpart.plot(rpart.fit1$finalModel)
```



```
jpeg("./figure/rpart1.jpeg", width = 8, height = 6, units="in", res=500)
rpart.plot(rpart.fit1$finalModel)
dev.off()
```

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

```
library(patchwork)
lasso <- ggplot(lasso.fit, highlight = TRUE) +
  labs(title="LASSO CV Result") +
  scale_x_continuous(trans='log', n.breaks = 10) +
  theme_bw()
```

```
ridge <- ggplot(ridge.fit, highlight = TRUE) +
  scale_x_continuous(trans='log', n.breaks = 6) +
  labs(title="Ridge CV Result") +
  theme_bw()
```

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

```
pcr <- ggplot(pcr.fit, highlight = TRUE) +
  labs(title="PCR CV Result") +
  theme_bw()
```

```
pls <- ggplot(pls.fit, highlight = TRUE) +
  labs(title="PLS CV Result") +
  theme_bw()
```

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

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

knn <- ggplot(knn.fit, highlight = TRUE) +
  labs(title = "KNN CV Result") +
  theme_bw()

bagging <- ggplot(bag.fit, highlight = TRUE) +
  labs(title = "Bagging CV Result") +
  theme_bw()

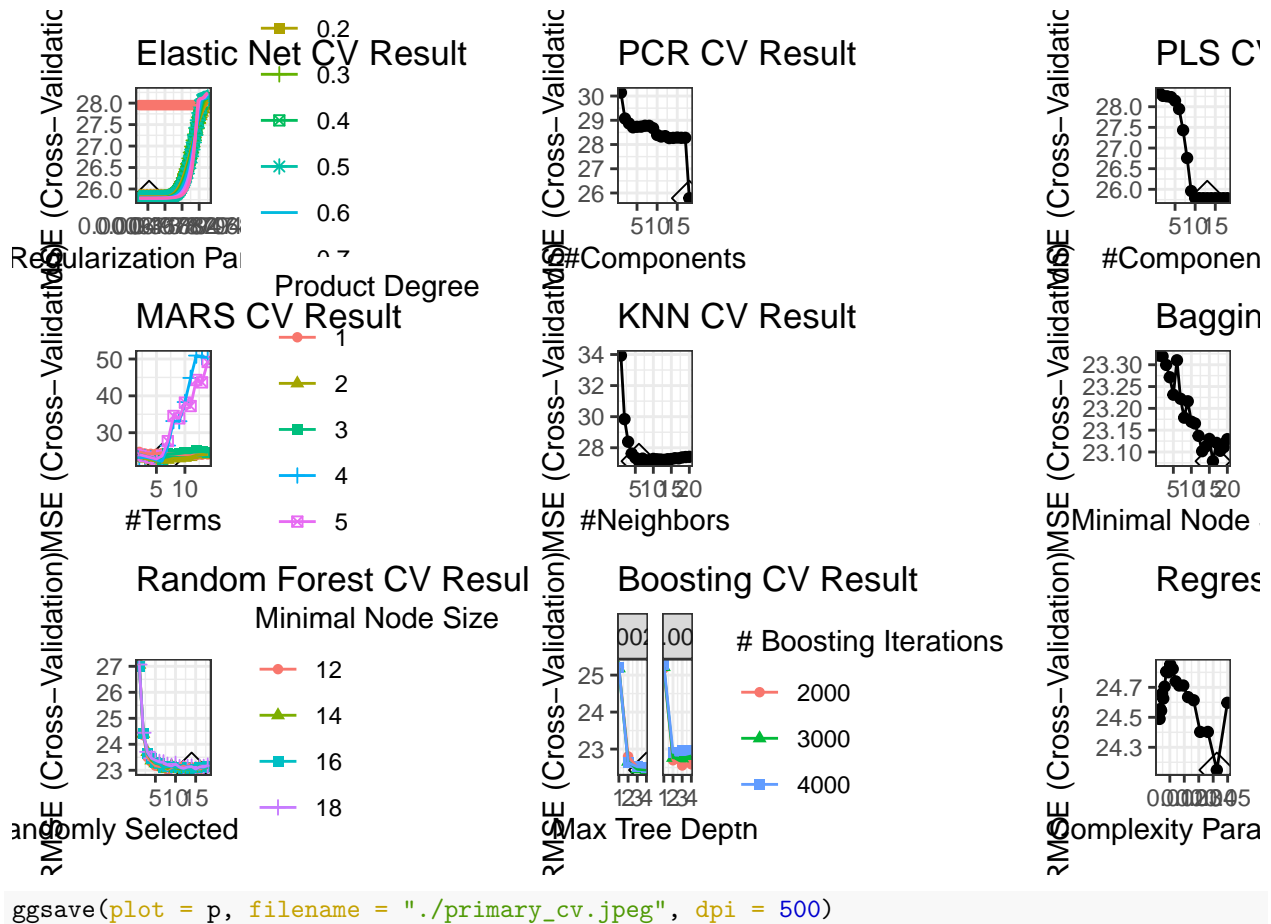
rf <- ggplot(rf.fit, highlight = TRUE) +
  labs(title = "Random Forest CV Result") +
  theme_bw()

boosting <- ggplot(bst.fit, highlight = TRUE) +
  labs(title = "Boosting CV Result") +
  theme_bw()

tree <- ggplot(rpart.fit1, highlight = TRUE) +
  labs(title = "Regression Tree CV Result") +
  theme_bw()

p <- wrap_plots(enet, pcr,
               pls,
               mars, knn,
               bagging, rf, boosting, tree,
               ncol = 3)

p
```



1.2 Model Selection

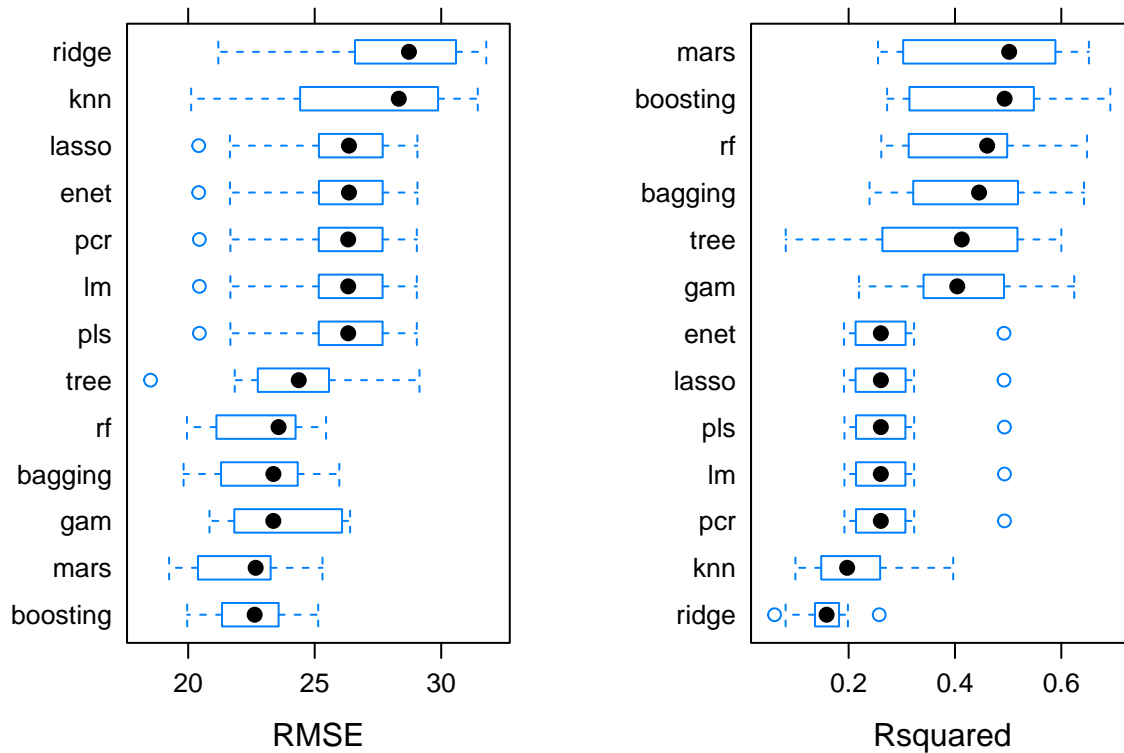
```
set.seed(2023)
resamp <- resamples(list(lm = lm.fit,
                        lasso = lasso.fit,
                        ridge = ridge.fit,
                        enet = enet.fit,
                        pcr = pcr.fit,
                        pls = pls.fit,
                        gam = gam.fit,
                        mars = mars.fit,
                        knn = knn.fit,
                        bagging = bag.fit,
                        rf = rf.fit,
                        boosting = bst.fit,
                        tree = rpart.fit1))

summary(resamp)

##
## Call:
## summary.resamples(object = resamp)
##
## Models: lm, lasso, ridge, enet, pcr, pls, gam, mars, knn, bagging, rf, boosting, tree
```

```
## Number of resamples: 10
##
## MAE
##           Min.   1st Qu.   Median     Mean   3rd Qu.     Max. NA's
## lm       15.54483 15.80758 16.63529 16.59842 17.13204 18.12333    0
## lasso    15.51069 15.78658 16.61245 16.57052 17.09219 18.09015    0
## ridge    15.34004 16.62387 16.79935 16.84047 17.23997 18.17959    0
## enet     15.51026 15.78694 16.61217 16.57069 17.09223 18.09088    0
## pcr      15.54483 15.80758 16.63529 16.59842 17.13204 18.12333    0
## pls      15.54482 15.80753 16.63528 16.59840 17.13208 18.12332    0
## gam      14.60392 14.76502 15.40409 15.42678 15.78762 17.02963    0
## mars     13.99273 14.46938 14.98372 14.92537 15.32753 15.89972    0
## knn      14.43602 16.28400 16.79135 16.77166 17.45629 18.38966    0
## bagging  14.22336 14.45336 15.13841 15.11634 15.80201 15.93486    0
## rf       14.25716 14.38885 15.08343 15.06824 15.64831 16.12144    0
## boosting 13.69309 14.20488 14.59800 14.60751 15.08662 15.39300    0
## tree     13.85891 15.27840 15.72822 15.63398 16.07374 16.57189    0
##
## RMSE
##           Min.   1st Qu.   Median     Mean   3rd Qu.     Max. NA's
## lm       20.44180 25.16612 26.32308 25.78528 27.58385 29.03646    0
## lasso    20.41446 25.16779 26.35443 25.78553 27.58286 29.05994    0
## ridge    21.18921 26.76934 28.72409 27.95459 30.39855 31.78080    0
## enet     20.41395 25.16792 26.35390 25.78540 27.58280 29.06018    0
## pcr      20.44180 25.16612 26.32308 25.78528 27.58385 29.03646    0
## pls      20.44179 25.16611 26.32305 25.78526 27.58386 29.03644    0
## gam      20.84135 22.00149 23.36475 23.68977 25.89070 26.39798    0
## mars     19.24575 20.68200 22.66604 22.28254 23.25541 25.30793    0
## knn      20.11678 25.01933 28.32298 27.13762 29.65682 31.44427    0
## bagging  19.81748 21.50728 23.36814 23.07896 24.24524 25.97220    0
## rf       19.95074 21.25601 23.57112 23.00997 24.19683 25.45015    0
## boosting 19.95912 21.38359 22.62738 22.43370 23.50567 25.13742    0
## tree     18.51152 23.03638 24.36887 24.14847 25.41831 29.14098    0
##
## Rsquared
##           Min.   1st Qu.   Median     Mean   3rd Qu.     Max. NA's
## lm       0.19215021 0.2201628 0.2605519 0.2764092 0.3001496 0.4930552    0
## lasso    0.19133277 0.2196625 0.2606385 0.2763222 0.3004686 0.4921785    0
## ridge    0.06069200 0.1374835 0.1585905 0.1552980 0.1812584 0.2575556    0
## enet     0.19132111 0.2196526 0.2606417 0.2763214 0.3004556 0.4921930    0
## pcr      0.19215021 0.2201628 0.2605519 0.2764092 0.3001496 0.4930552    0
## pls      0.19215072 0.2201634 0.2605543 0.2764103 0.3001491 0.4930584    0
## gam      0.21948254 0.3453667 0.4042745 0.4084093 0.4864782 0.6243131    0
## mars     0.25523324 0.3327875 0.5019111 0.4666544 0.5812142 0.6518673    0
## knn      0.09988269 0.1495740 0.1971881 0.2119237 0.2570144 0.3966191    0
## bagging  0.23926439 0.3254906 0.4452885 0.4315122 0.5070804 0.6426996    0
## rf       0.26142227 0.3159714 0.4605716 0.4347653 0.4923031 0.6483873    0
## boosting 0.27236258 0.3582823 0.4933617 0.4727917 0.5472122 0.6921047    0
## tree     0.08170188 0.2889918 0.4127453 0.3758431 0.4958400 0.6000578    0

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



```
jpeg("./figure/resample1.jpeg", width = 8, height=6, units="in", res=500)
p1=bwplot(resamp, metric = "RMSE")
p2=bwplot(resamp, metric = "Rsquared")
grid.arrange(p1, p2, ncol=2)
dev.off()
```

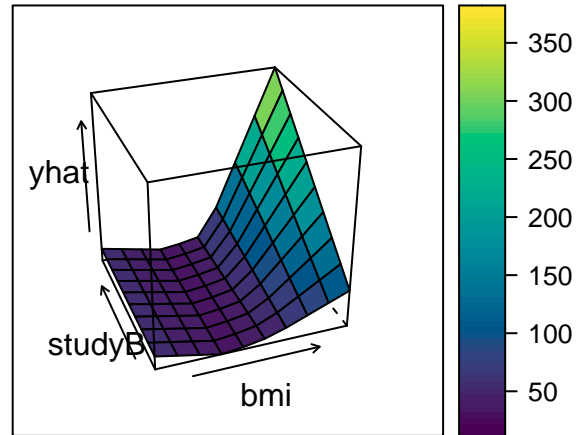
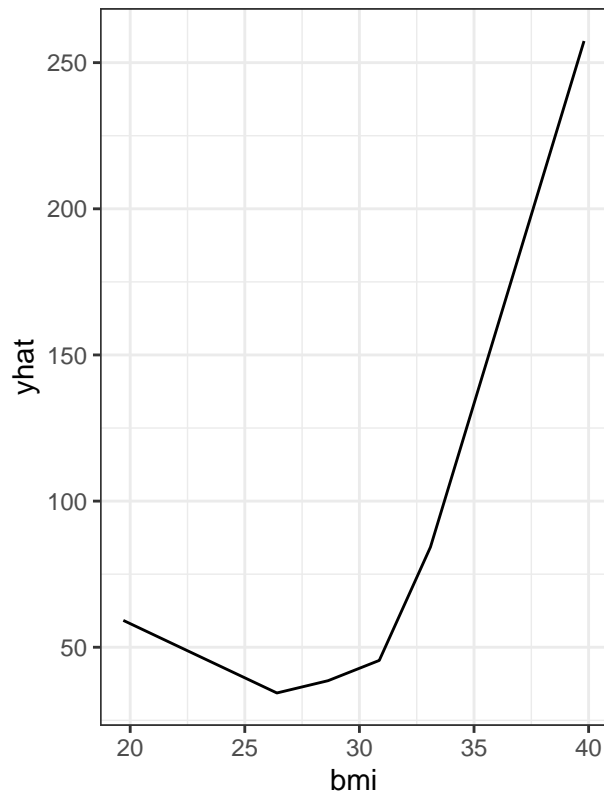
```
## pdf
## 2
```

```
p1<- pdp::partial(mars.fit, pred.var = c("bmi"), grid.resolution = 10) %>% autoplot() +
  theme_bw()+
  labs(title = "Partial Dependence Plots of MARS Model")
```

```
p2 <-pdp::partial(mars.fit, pred.var = c("bmi", "studyB"),
  grid.resolution = 10) %>%
  pdp::plotPartial(levelplot = FALSE, zlab = "yhat", drape = TRUE,
    screen = list(z = 20, x = -60))
```

```
# jpeg("./figure/partial_dependence.jpeg", width = 8, height=6, units="in", res=500)
gridExtra::grid.arrange(p1, p2, ncol = 2)
```

Partial Dependence Plots of MARS Model



```
# dev.off()

# Important variables
varImp(mars.fit$finalModel)
```

```
##           Overall
## bmi      100.00000
## studyB   100.00000
## LDL      26.01105
## vaccine1 17.64446
```

1.3 Training / Testing Error

```
# training error
mars.train.pred = predict(mars.fit, newdata = train.x)
RMSE(train.y, mars.train.pred)
```

```
## [1] 21.67424
```

```
# testing error
mars.pred = predict(mars.fit, newdata = test.x)
RMSE(test.y, mars.pred)
```

```
## [1] 23.63736
```