final_proj

Me

Today

```
library(caret)
library(mlbench)
library(pdp)
library(vip)
library(AppliedPredictiveModeling)
library(tidyverse)
library(klaR)
library(MASS)
library(corrplot)
library(plotmo)
library(ggplot2)
library(pls)
library(ggpubr)
library(factoextra)
library(gridExtra)
library(corrplot)
library(RColorBrewer)
library(gplots)
library(jpeg)
library(rpart.plot)
library(randomForest)
library(ranger)
library(gbm)
library(pROC)
```

```
# import and subset data
load("./recovery.RData")
set.seed(5095)
dat.1 = dat[sample(1:10000, 2000),]

set.seed(5296)
dat.2 = dat[sample(1:10000, 2000),]

dat.all = rbind(dat.1, dat.2)%>%
  unique.array()

# transform variables as needed
dat1 = dat.all[2:16] %>%
  mutate(gender = as.factor(gender),
         race = as.factor(race),
         smoking = as.factor(smoking),
```

```
         hypertension = as.factor(hypertension),
         diabetes = as.factor(diabetes),
         vaccine = as.factor(vaccine),
         severity = as.factor(severity),
         study = as.factor(study))

# transform into matrix
dat2 = model.matrix(recovery_time ~ ., dat1)[ ,-1]

# split data into training set and test set
set.seed(1)
trainRows = createDataPartition(y = dat1$recovery_time, p = 0.8, list = FALSE)
```

```
# extract training data
x.train = dat2[trainRows,]
y.train = dat1$recovery_time[trainRows]

# correlation plot
x_cor = dat2[trainRows, c("age", "height", "weight", "bmi", "SBP", "LDL")]
png(height=1800, width=1800, units = "px", file="corrplot.png", res = 200)
corrplot::corrplot(cor(x_cor), method = "circle", type = "full")
dev.off()
```

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

```
#library("PerformanceAnalytics")
#chart.Correlation(x, histogram=TRUE, pch=19)

x.test = dat2[-trainRows,]
y.test = dat1$recovery_time[-trainRows]

# plot numeric variables
theme1 <- trellis.par.get()
theme1$plot.symbol$col <- rgb(.2, .4, .2, .5)
theme1$plot.symbol$pch <- 16
theme1$plot.line$col <- rgb(.8, .1, .1, 1)
theme1$plot.line$lwd <- 2
theme1$strip.background$col <- rgb(.0, .2, .6, .2)
trellis.par.set(theme1)

png(height=1800, width=1800, units = "px", file="featureplot.png", res = 200)
p1 = featurePlot(x.train[,c(1,8, 9, 10, 13, 14)], y.train, plot = "scatter", labels = c("","Y"),
            type = c("p"), layout = c(3, 2))
p1
dev.off()
```

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

```
# plot categorical variables
p2 = ggplot(dat1, aes(y = recovery_time, x = gender))+
  geom_boxplot()
p3 = ggplot(dat1, aes(y = recovery_time, x = race))+
  geom_boxplot()
p4 = ggplot(dat1, aes(y = recovery_time, x = smoking))+
  geom_boxplot()
p5 = ggplot(dat1, aes(y = recovery_time, x = hypertension))+
  geom_boxplot()
p6 = ggplot(dat1, aes(y = recovery_time, x = diabetes))+
  geom_boxplot()
p7 = ggplot(dat1, aes(y = recovery_time, x = vaccine))+
  geom_boxplot()
p8 = ggplot(dat1, aes(y = recovery_time, x = severity))+
  geom_boxplot()
p9 = ggplot(dat1, aes(y = recovery_time, x = study))+
  geom_boxplot()

arrange = ggarrange(p2, p3, p4, p5, p6, p7, p8, p9, ncol = 4, nrow = 2)
ggsave("arrangedplot.png", arrange)
```

```
## Saving 6.5 x 4.5 in image
```

```
ctrl1 = trainControl(method = "cv")
```

Linear regression

```
set.seed(1)
lm.fit <- train(x.train, y.train,
                method = "lm",
                trControl = ctrl1)
summary(lm.fit)
```

```
##
## Call:
## lm(formula = .outcome ~ ., data = dat)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -91.266 -14.386  -1.309  10.491 249.295
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -2.765e+03  1.328e+02 -20.816  < 2e-16 ***
## age            5.418e-02  1.163e-01   0.466   0.6413
## gender1       -4.167e+00  9.375e-01  -4.445 9.13e-06 ***
## race2          8.711e-01  2.085e+00   0.418   0.6761
## race3         -2.596e+00  1.195e+00  -2.173   0.0299 *
## race4         -2.298e+00  1.582e+00  -1.453   0.1464
## smoking1       5.844e+00  1.056e+00   5.536 3.38e-08 ***
```

```
## smoking2       7.779e+00  1.579e+00   4.926 8.87e-07 ***
## height         1.613e+01  7.826e-01  20.605  < 2e-16 ***
## weight        -1.751e+01  8.287e-01 -21.125  < 2e-16 ***
## bmi            5.288e+01  2.364e+00  22.366  < 2e-16 ***
## hypertension1  3.605e+00  1.589e+00   2.268   0.0234 *
## diabetes1     -8.238e-01  1.292e+00  -0.638   0.5238
## SBP            1.935e-02  1.046e-01   0.185   0.8533
## LDL           -5.858e-02  2.480e-02  -2.362   0.0183 *
## vaccine1      -7.888e+00  9.610e-01  -8.208 3.37e-16 ***
## severity1      8.905e+00  1.522e+00   5.852 5.40e-09 ***
## studyB         5.322e+00  1.207e+00   4.411 1.07e-05 ***
## studyC        -1.153e+00  1.453e+00  -0.794   0.4274
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 25.08 on 2863 degrees of freedom
## Multiple R-squared:  0.2776, Adjusted R-squared:  0.2731
## F-statistic: 61.12 on 18 and 2863 DF,  p-value: < 2.2e-16
```

Ridge

```
set.seed(1)
ridge.fit <- train(x.train, y.train,
                   method = "glmnet",
                   tuneGrid = expand.grid(alpha = 0,
                                          lambda = exp(seq(10, -5, length=200))),
                   preProc = c("center", "scale"),
                   trControl = ctrl1)
```

```
## Warning in nominalTrainWorkflow(x = x, y = y, wts = weights, info = trainInfo,
## : There were missing values in resampled performance measures.
```

```
png(file="ridge.tiff", height=1800, width=1800, units = "px", res=200)
plot(ridge.fit, xTrans = log)
dev.off()
```

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

```
ridge.fit$bestTune
```

```
##    alpha    lambda
## 65     0 0.8387191
```

```
# coefficients in the final model
coef(ridge.fit$finalModel, s = ridge.fit$bestTune$lambda)
```

```
## 19 x 1 sparse Matrix of class "dgCMatrix"
##                       s1
```

```
## (Intercept)   43.1384455
## age            0.2316867
## gender1       -2.1774835
## race2          0.4152253
## race3         -1.0194303
## race4         -0.9515189
## smoking1       2.5563613
## smoking2       2.2580929
## height         2.3521736
## weight        -5.6570081
## bmi           14.1549514
## hypertension1  1.3789345
## diabetes1     -0.1003691
## SBP            0.5960578
## LDL           -0.9994673
## vaccine1      -3.8355786
## severity1      2.7137367
## studyB         2.8016358
## studyC        -0.2768422
```

Lasso

```
set.seed(1)
lasso.fit <- train(x.train, y.train,
                   method = "glmnet",
                   tuneGrid = expand.grid(alpha = 1,
                                          lambda = exp(seq(10, -5, length =200))),
                   trControl = ctrl1)
```

```
## Warning in nominalTrainWorkflow(x = x, y = y, wts = weights, info = trainInfo,
## : There were missing values in resampled performance measures.
```

```
png(file="lasso.png", height=1800, width=1800, units = "px", res=200)
plot(lasso.fit, xTrans = log)
dev.off()
```

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

```
lasso.fit$bestTune
```

```
##   alpha      lambda
## 1     1 0.006737947
```

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

```
## 19 x 1 sparse Matrix of class "dgCMatrix"
##                            s1
## (Intercept)   -2.659526e+03
## age            5.288381e-02
```

```
## gender1       -4.166055e+00
## race2          8.874830e-01
## race3         -2.577262e+00
## race4         -2.309793e+00
## smoking1       5.823620e+00
## smoking2       7.746311e+00
## height         1.550239e+01
## weight        -1.684532e+01
## bmi            5.100002e+01
## hypertension1  3.568911e+00
## diabetes1     -7.834496e-01
## SBP            2.097807e-02
## LDL           -5.789145e-02
## vaccine1      -7.882531e+00
## severity1      8.888889e+00
## studyB         5.339616e+00
## studyC        -1.117748e+00
```

Elastic net

```
set.seed(1)
enet.fit <- train(x.train, y.train,
                  method = "glmnet",
                  tuneGrid = expand.grid(alpha = seq(0, 1, length = 21),
                                         lambda = exp(seq(2, -2, length = 50))),
                  trControl = ctrl1)
enet.fit$bestTune
```

```
##      alpha    lambda
## 1001     1 0.1353353
```

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

png(file="enet.png", height=1800, width=1800, units = "px", res=200)
plot(enet.fit, par.settings = myPar)
dev.off()
```

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

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

```
## 19 x 1 sparse Matrix of class "dgCMatrix"
##                            s1
## (Intercept)   -1.350889e+03
## age            2.809390e-02
## gender1       -4.052707e+00
## race2          9.488674e-01
```

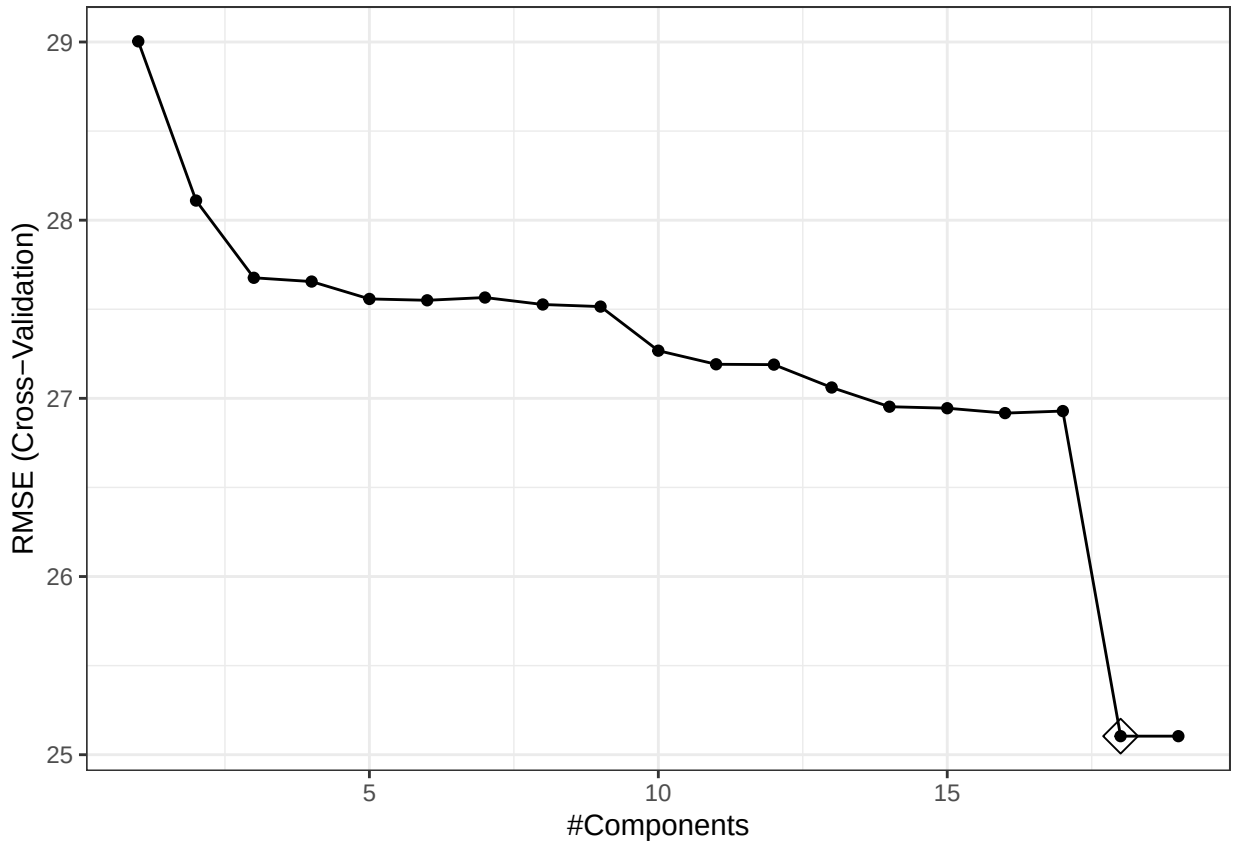
```
## race3         -2.193139e+00
## race4         -2.278903e+00
## smoking1       5.441868e+00
## smoking2       7.128083e+00
## height         7.753069e+00
## weight        -8.628636e+00
## bmi            2.754474e+01
## hypertension1  3.074113e+00
## diabetes1     -1.468496e-01
## SBP            3.786311e-02
## LDL           -4.603493e-02
## vaccine1      -7.719121e+00
## severity1      8.543192e+00
## studyB         5.482654e+00
## studyC        -6.157684e-01
```

PCR

```
set.seed(1)
pcr.fit <- train(x.train, y.train,
                 method = "pcr",
                 tuneGrid  = data.frame(ncomp = 1:19),
                 trControl = ctrl1,
                 preProcess = c("center", "scale"))
summary(pcr.fit)
```

```
## Data:    X dimension: 2882 18
##  Y dimension: 2882 1
## Fit method: svdpc
## Number of components considered: 18
## TRAINING: % variance explained
##           1 comps  2 comps  3 comps  4 comps  5 comps  6 comps  7 comps
## X         12.2664   22.254    31.12    38.15    44.79    51.42    57.61
## .outcome   0.5074    7.019    10.27    10.47    10.53    11.47    11.53
##           8 comps  9 comps  10 comps  11 comps  12 comps  13 comps  14 comps
## X           63.38    68.91     74.34     79.65     84.44     88.73     92.86
## .outcome    11.82    11.83     13.69     13.91     13.92     15.01     15.73
##           15 comps  16 comps  17 comps  18 comps
## X            96.84     98.95     99.99    100.00
## .outcome     15.82     16.01     16.01     27.76
```

```
ggplot(pcr.fit, highlight = TRUE) + theme_bw()
```



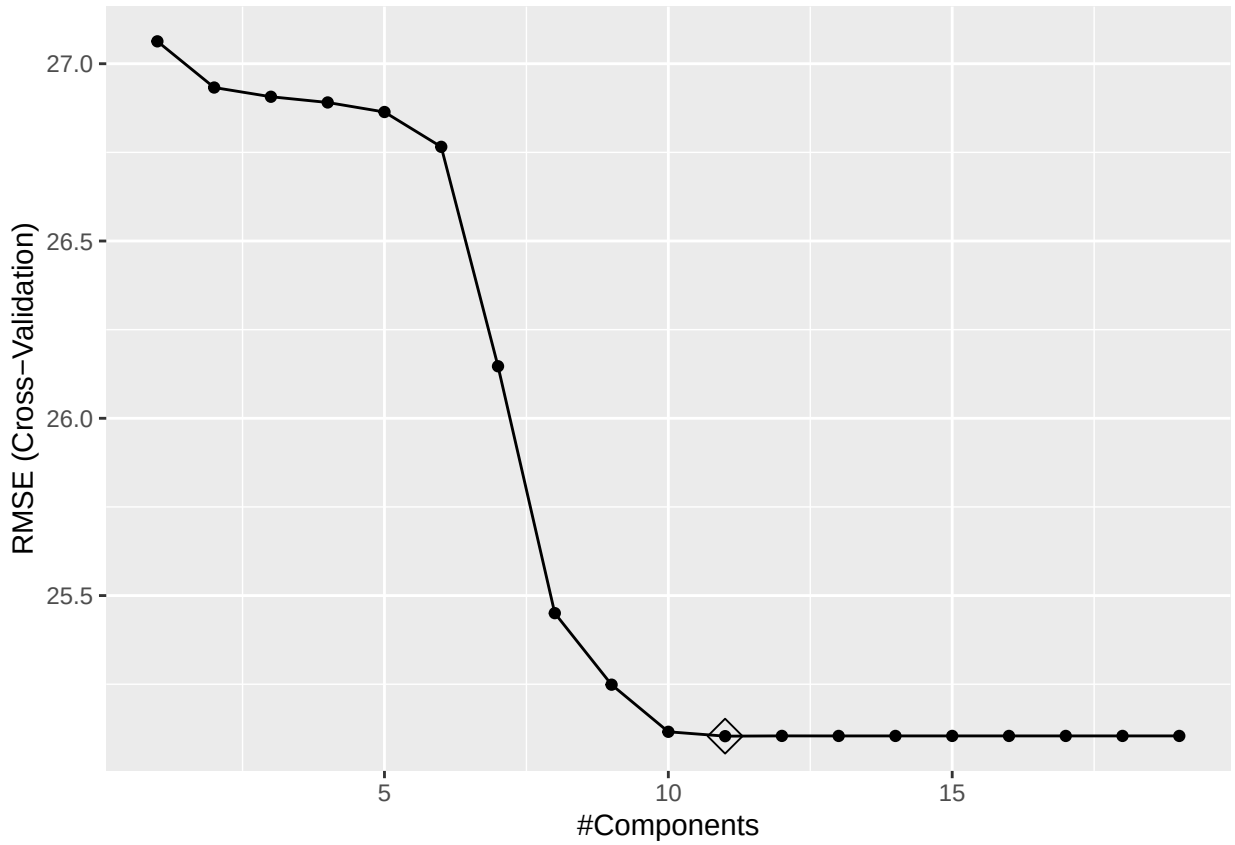

```
ggsave("pcr.tiff", dpi="print")
```

```
## Saving 6.5 x 4.5 in image
```

PLS

```
set.seed(1)
pls.fit <- train(x.train, y.train,
                 method = "pls",
                 tuneGrid = data.frame(ncomp = 1:19),
                 trControl = ctrl1,
                 preProcess = c("center", "scale"))

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




```
ggsave("pls.tiff", dpi="print")
```

```
## Saving 6.5 x 4.5 in image
```

GAM model

```
set.seed(1)
gam.fit <- train(x.train, y.train,
                 method = "gam",
                 tuneGrid = data.frame(method = "GCV.Cp", select = c(TRUE,FALSE)),
                 trControl = ctrl1)
```

```
## 载入需要的程辑包：mgcv
```

```
## 载入需要的程辑包：nlme
```

```
##
## 载入程辑包：'nlme'
```

```
## The following object is masked from 'package:dplyr':
##
##     collapse
```

```
## This is mgcv 1.8-42. For overview type 'help("mgcv-package")'.
```

```
summary(gam.fit)
```

```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## .outcome ~ gender1 + race2 + race3 + race4 + smoking1 + smoking2 +
##     hypertension1 + diabetes1 + vaccine1 + severity1 + studyB +
##     studyC + s(age) + s(SBP) + s(LDL) + s(bmi) + s(height) +
##     s(weight)
##
## Parametric coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)    43.2570     1.2848  33.668  < 2e-16 ***
## gender1        -4.7965     0.8214  -5.839 5.84e-09 ***
## race2           0.6993     1.8250   0.383    0.702
## race3          -1.0536     1.0464  -1.007    0.314
## race4          -2.0949     1.3842  -1.513    0.130
## smoking1        4.9659     0.9242   5.373 8.37e-08 ***
## smoking2        7.8849     1.3829   5.702 1.31e-08 ***
## hypertension1   3.4663     0.8248   4.203 2.72e-05 ***
## diabetes1      -0.9107     1.1309  -0.805    0.421
## vaccine1       -8.0399     0.8415  -9.555  < 2e-16 ***
## severity1       9.4416     1.3296   7.101 1.56e-12 ***
## studyB          4.8228     1.0562   4.566 5.17e-06 ***
## studyC         -0.9022     1.2719  -0.709    0.478
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                 edf Ref.df       F p-value
## s(age)    5.732e-09      9   0.000   0.960
## s(SBP)    7.785e-09      9   0.000   0.757
## s(LDL)    2.455e-01      9   0.036   0.253
## s(bmi)    8.737e+00      9 222.822  <2e-16 ***
## s(height) 2.090e-08      9   0.000   0.408
## s(weight) 1.895e-08      9   0.000   0.446
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.444   Deviance explained = 44.8%
## GCV = 484.97  Scale est. = 481.27    n = 2882
```

```
gam.fit$bestTune
```

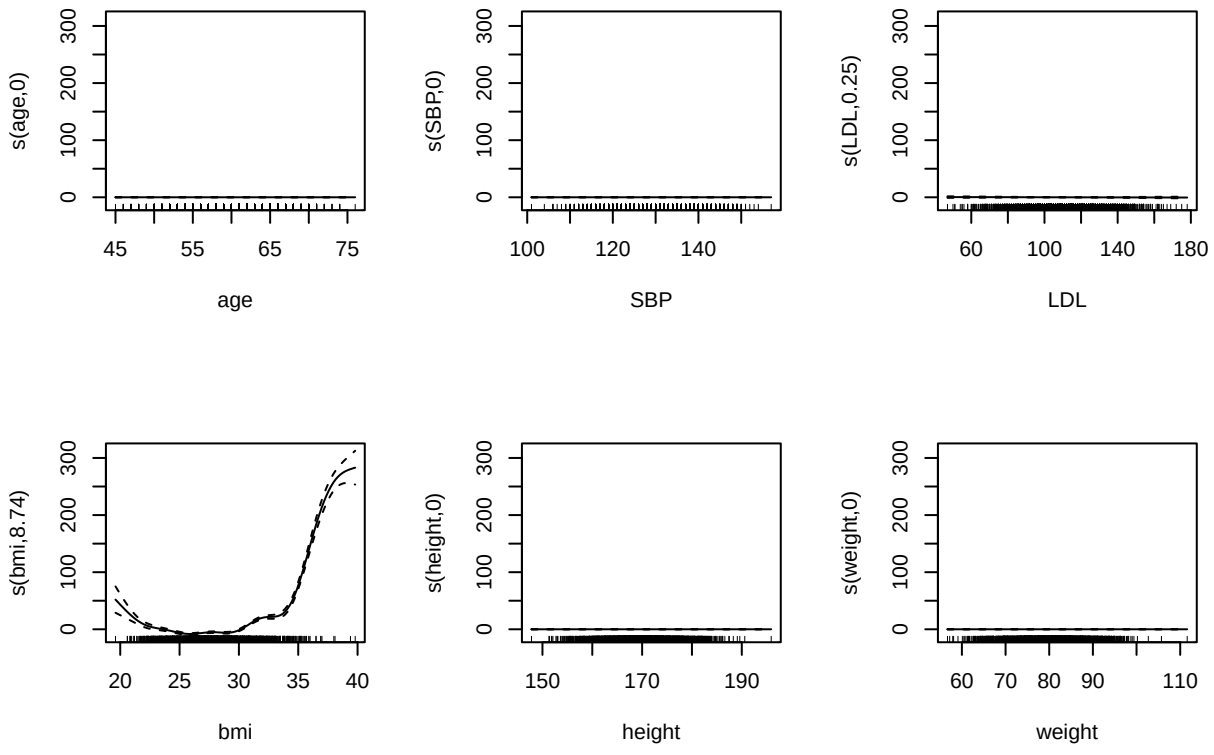
```
##   select method
## 2   TRUE GCV.Cp
```

```
gam.fit$finalModel
```

```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## .outcome ~ gender1 + race2 + 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 0.000 0.245 8.737 0.000 0.000  total = 21.98
##
## GCV score: 484.9695
```

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

plot(gam.fit$finalModel)
```



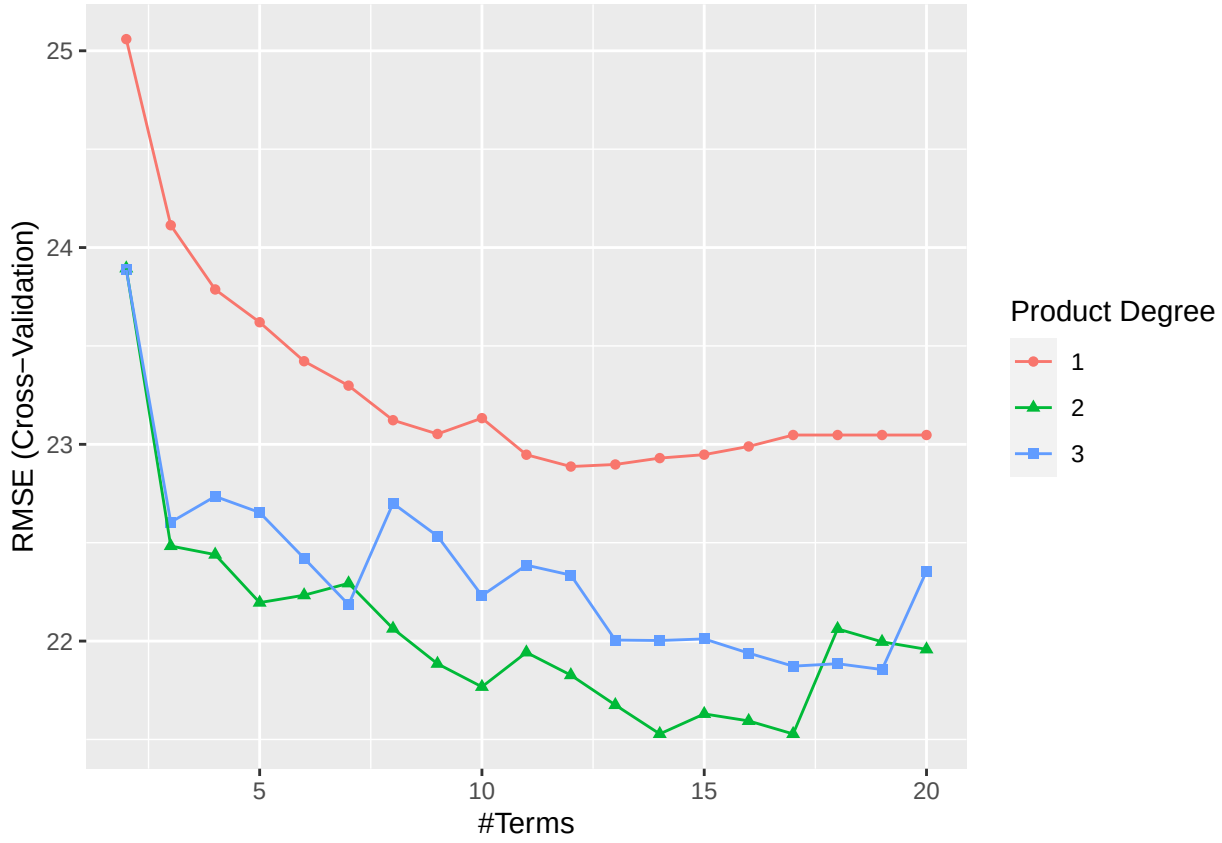
MARS model

```
mars_grid <- expand.grid(degree = 1:3,
                         nprune = 2:20)

set.seed(1)
mars.fit <- train(x.train, y.train,
                  method = "earth",
                  tuneGrid = mars_grid,
                  trControl = ctrl1)
```

```
## 载入需要的程辑包：earth
```

```
ggplot(mars.fit)
```




```
mars.fit$bestTune
```

```
##    nprune degree
## 35     17      2
```

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

```
##              (Intercept)              h(33.3-bmi)     h(bmi-33.3) * studyB
##              -26.8275772                7.5229372               35.5992024
##                  vaccine1     h(bmi-28.5) * studyB      race4 * h(bmi-33.3)
##                -7.5760327                6.7123484              -60.2055112
##  h(bmi-28.5) * severity1   smoking1 * h(bmi-33.3)                  gender1
##                 6.4214446                5.5093431               -4.9104162
##              h(bmi-23.9) h(bmi-28.5) * h(SBP-138) h(bmi-28.5) * h(SBP-128)
##                 6.9086839               -1.3269459                0.5530760
##                  smoking1   smoking2 * h(bmi-33.3) h(bmi-33.3) * h(LDL-115)
##                 4.7734050              -54.9024634                0.8394659
## h(bmi-33.3) * h(115-LDL)   smoking2 * h(bmi-28.5)
##                 0.5197540                8.2746042
```

```
summary(mars.fit)
```

```
## Call: earth(x=matrix[2882,18], y=c(56,44,53,51,3...), keepxy=TRUE, degree=2,
##             nprune=17)
##
##                            coefficients
## (Intercept)                  -26.827577
## gender1                       -4.910416
## smoking1                       4.773405
## vaccine1                      -7.576033
## h(bmi-23.9)                    6.908684
## h(33.3-bmi)                    7.522937
## race4 * h(bmi-33.3)          -60.205511
## smoking1 * h(bmi-33.3)         5.509343
## smoking2 * h(bmi-33.3)       -54.902463
## smoking2 * h(bmi-28.5)         8.274604
## h(bmi-28.5) * severity1        6.421445
## h(bmi-28.5) * studyB           6.712348
## h(bmi-33.3) * studyB          35.599202
## h(bmi-28.5) * h(SBP-138)      -1.326946
## h(bmi-28.5) * h(SBP-128)       0.553076
## h(bmi-33.3) * h(LDL-115)       0.839466
## h(bmi-33.3) * h(115-LDL)       0.519754
##
## Selected 17 of 22 terms, and 10 of 18 predictors (nprune=17)
## Termination condition: Reached nk 37
## Importance: bmi, studyB, vaccine1, severity1, race4, SBP, gender1, ...
## Number of terms at each degree of interaction: 1 5 11
## GCV 397.1968    RSS 1112383    GRSq 0.5411432    RSq 0.5537964
```

```
png(file="mars.png", height=1800, width=1800, units = "px", res=200)
p1 <- pdp::partial(mars.fit, pred.var = c("bmi"), grid.resolution = 10) %>% autoplot()
p2 <- pdp::partial(mars.fit, pred.var = c("height"), grid.resolution = 10) %>% autoplot()
p3 <- pdp::partial(mars.fit, pred.var = c("weight"), grid.resolution = 10) %>% autoplot()
p4 <- pdp::partial(mars.fit, pred.var = c("bmi", "height"),
                   grid.resolution = 10) %>%
      pdp::plotPartial(levelplot = FALSE, zlab = "yhat", drape = TRUE,
                       screen = list(z = 20, x = -60))

grid.arrange(p1, p2, p3, p4, ncol = 2, nrow = 2)
dev.off()
```

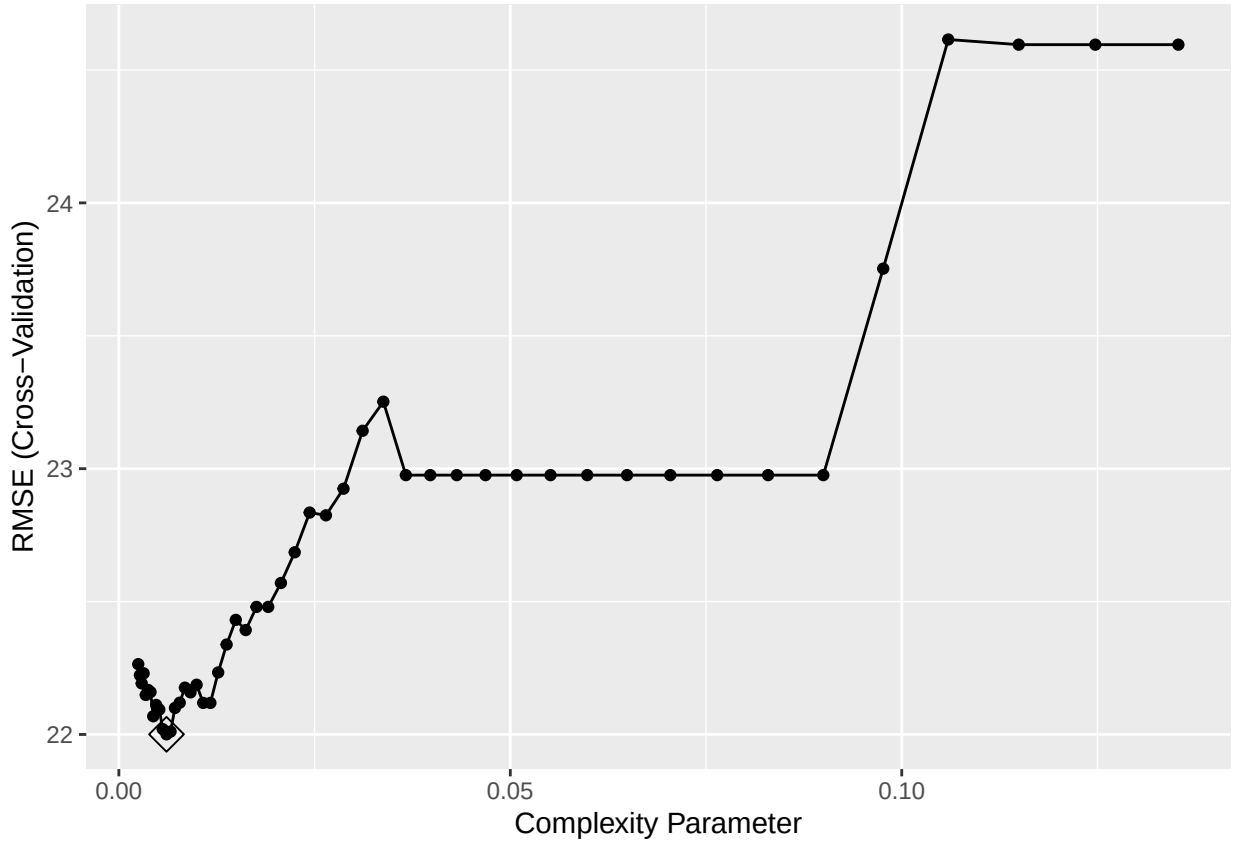
```
## pdf
##   2
```

Regression Tree

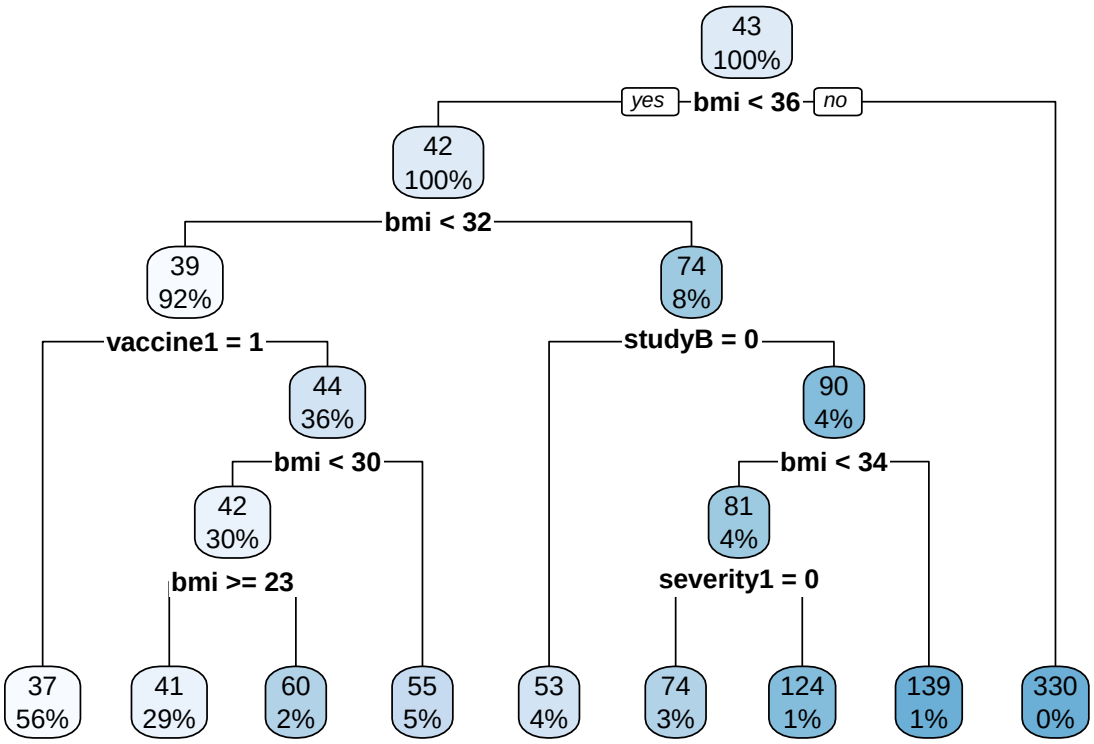
```
set.seed(1)
rpart.fit <- train(x=x.train,
                   y = y.train,
                   method = "rpart",
                    tuneGrid = data.frame(cp = exp(seq(-6,-2, length = 50))),
                    trControl = ctrl1)
```

```
## Warning in nominalTrainWorkflow(x = x, y = y, wts = weights, info = trainInfo,
## : There were missing values in resampled performance measures.
```

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




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



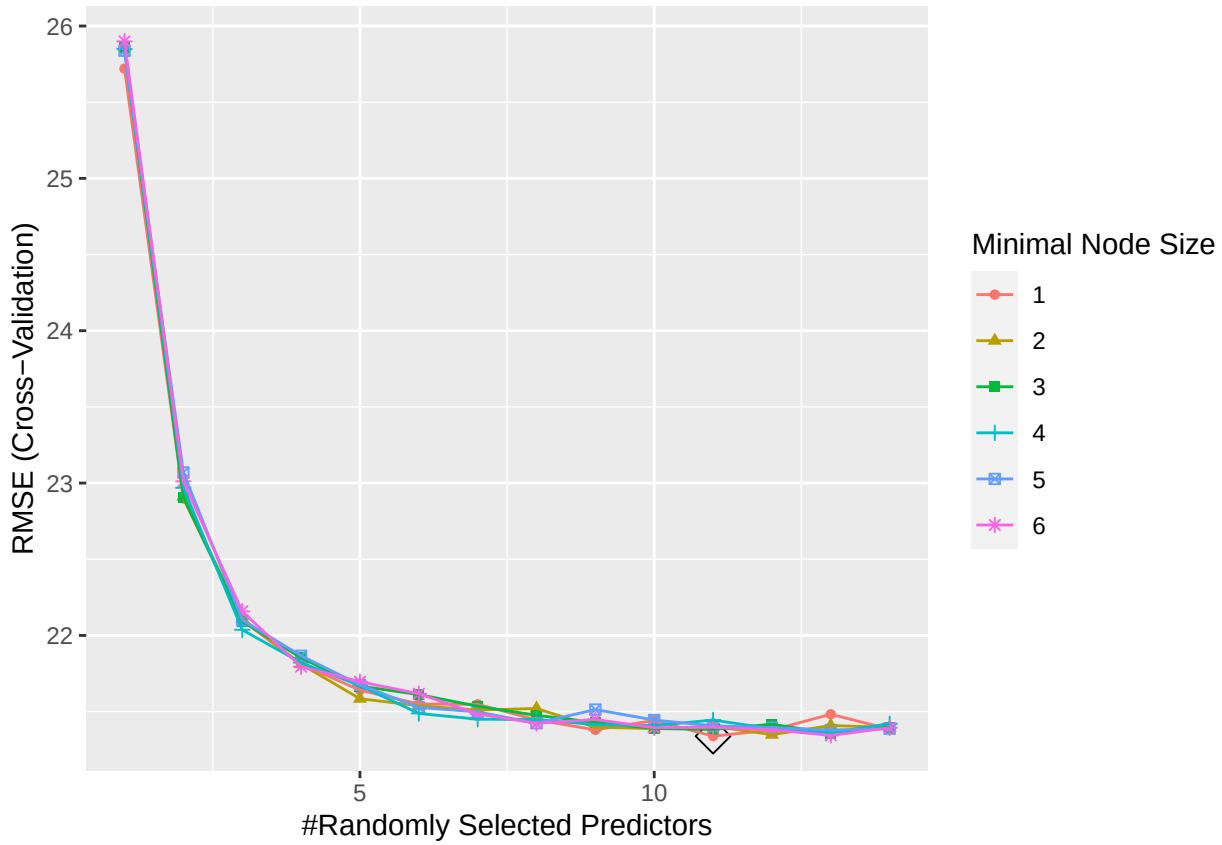
random forest

```
# Try more if possible
rf.grid <- expand.grid(mtry = 1:14,
splitrule = "variance",
min.node.size = 1:6)
set.seed(1)
rf.fit <- train(x.train,
                y.train,
method = "ranger",
tuneGrid = rf.grid,
trControl = ctrl1)
```

```
rf.fit$bestTune
```

```
##    mtry splitrule min.node.size
## 61   11  variance             1
```

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

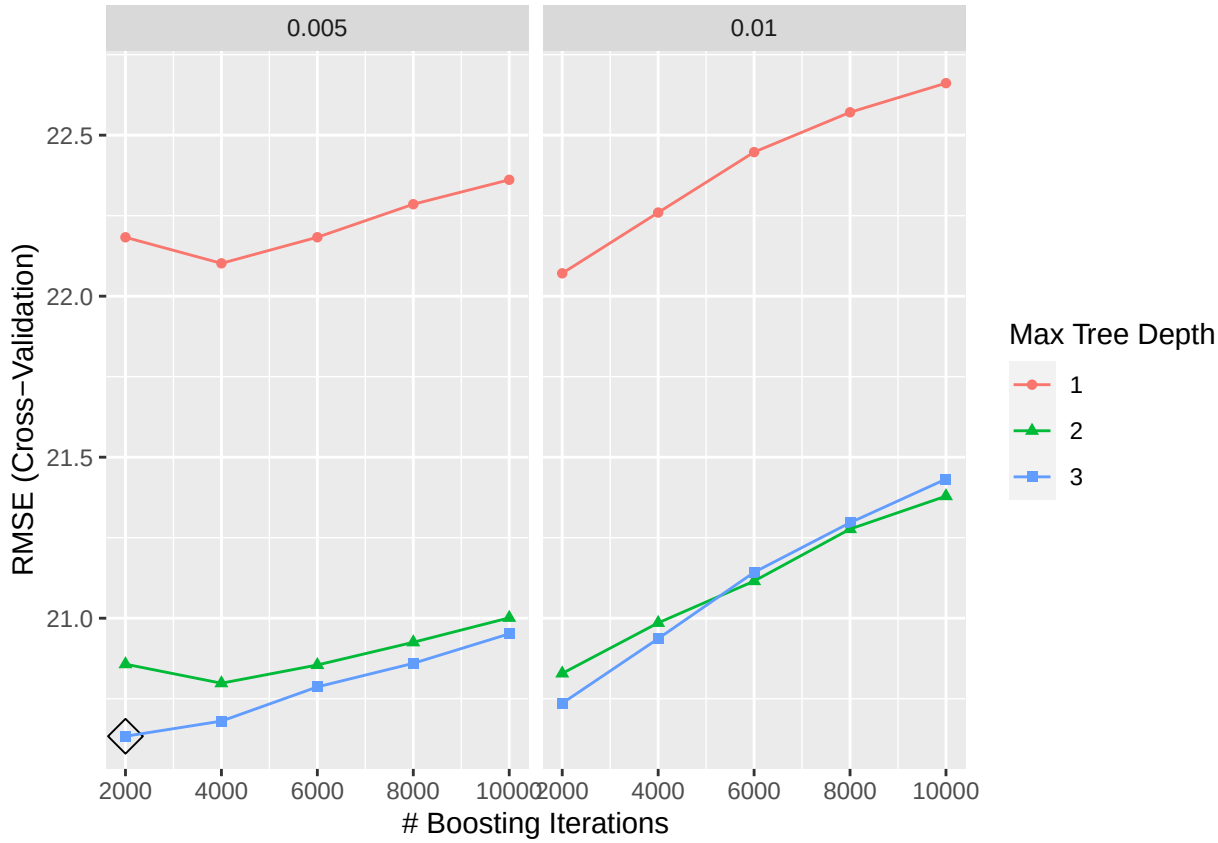



```
rf.pred <- predict(rf.fit, newdata = x.test)
mean((y.test-rf.pred)^2)
```

```
## [1] 512.5156
```

```
gbm.grid <- expand.grid(n.trees = c(2000,4000,6000,8000,10000),
interaction.depth = 1:3,
shrinkage = c(0.005,0.01),
n.minobsinnode = c(1))
set.seed(1)
gbm.fit <- train(x.train,y.train,
                 method = "gbm",
                 tuneGrid = gbm.grid,
                 trControl = ctrl1,
                 verbose = FALSE)
```

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




```
gbm.fit$bestTune
```

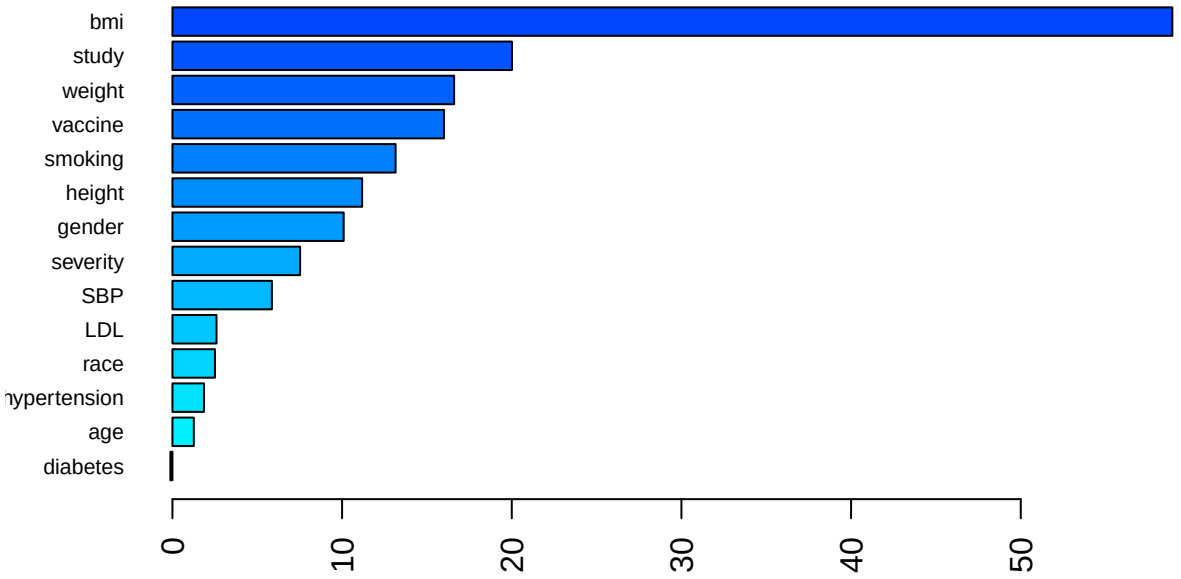
```
##    n.trees interaction.depth shrinkage n.minobsinnode
## 11    2000                 3     0.005              1
```

```
gbm.pred <- predict(gbm.fit, newdata = x.test)
mean((y.test-gbm.pred)^2)
```

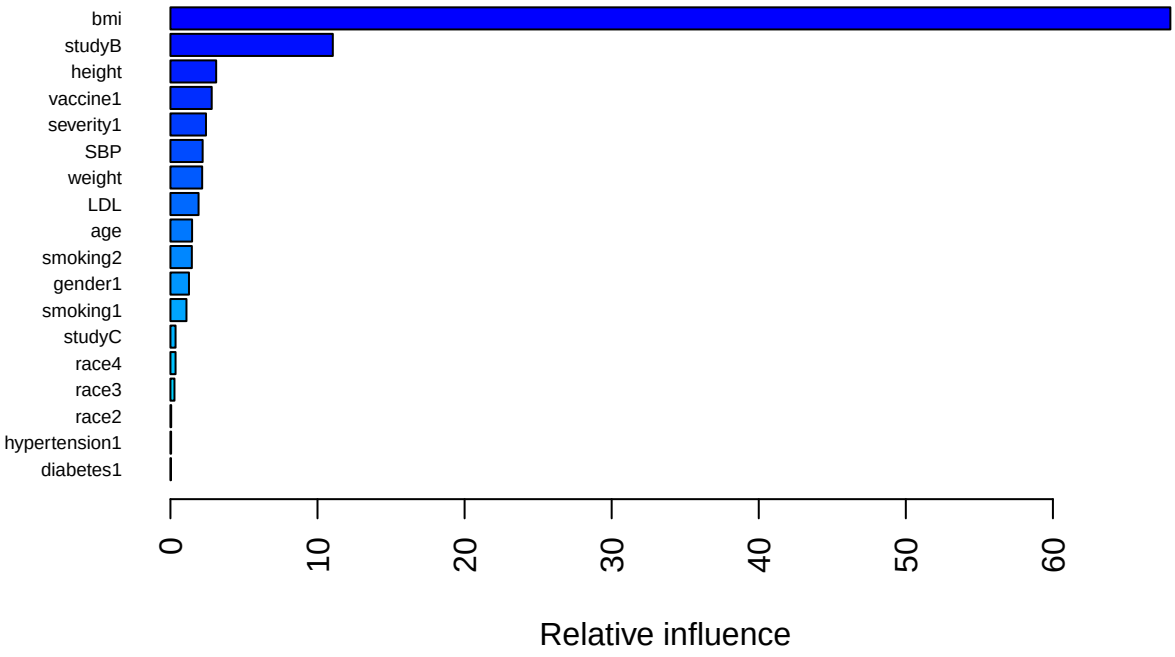
```
## [1] 487.4652
```

```
set.seed(1)
rf2.final.per <- ranger(recovery_time~., dat1[trainRows,],
                        mtry = rf.fit$bestTune[[1]],
                        splitrule = "variance",
                        min.node.size = rf.fit$bestTune[[3]],
                        importance = "permutation",
                         scale.permutation.importance = TRUE)

barplot(sort(ranger::importance(rf2.final.per), decreasing = FALSE),
las = 2, horiz = TRUE, cex.names = 0.7,
col = colorRampPalette(colors = c("cyan","blue"))(19))
```




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




```
##                          var     rel.inf
## bmi                      bmi 67.98507215
## studyB                studyB 11.04019125
## height                height  3.11027713
## vaccine1           vaccine1  2.80598010
## severity1         severity1  2.41754331
## SBP                     SBP  2.19109833
## weight               weight  2.15794966
## LDL                     LDL  1.91344748
## age                     age  1.47161785
## smoking2           smoking2  1.45559538
## gender1             gender1  1.25955715
## smoking1           smoking1  1.09018405
## studyC               studyC  0.34773985
## race4                 race4  0.34765420
## race3                 race3  0.27311430
## race2                 race2  0.05118855
## hypertension1 hypertension1  0.04612109
## diabetes1         diabetes1  0.03566815
```

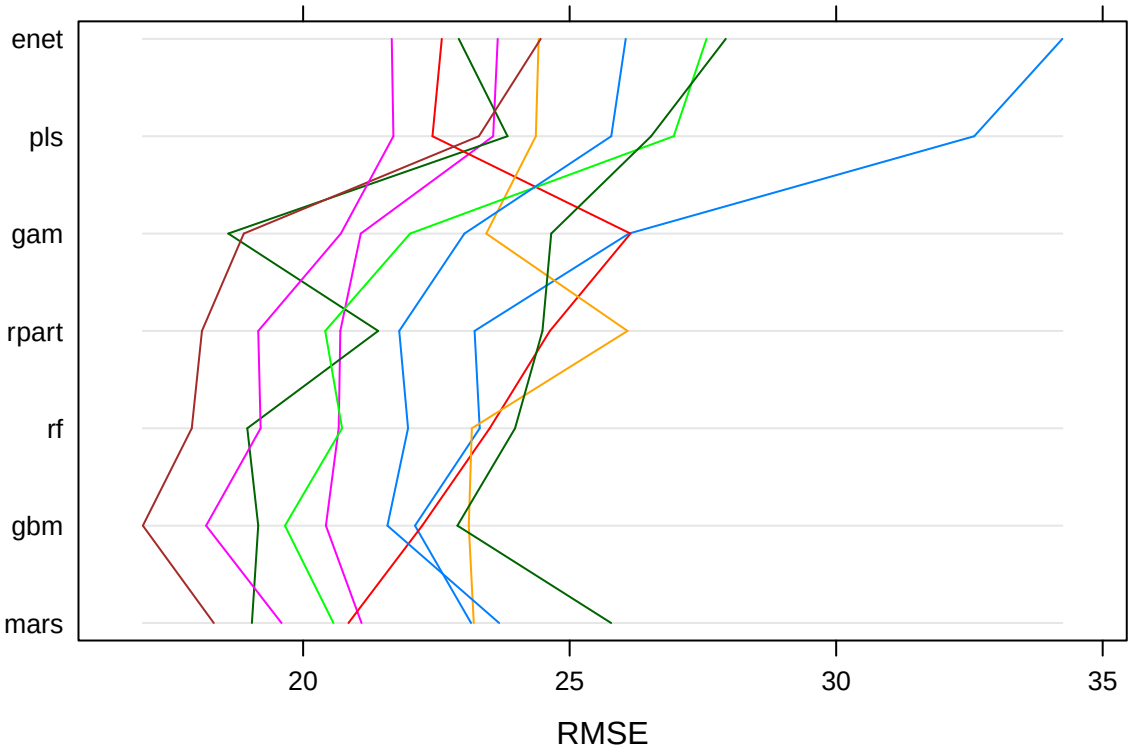
Comparing different models

```
set.seed(1)
resamp = resamples(list(enet = enet.fit, pls = pls.fit, gam = gam.fit, mars = mars.fit,rf = rf.fit,gbm =
```

```
summary(resamp)
```

```
##
## Call:
## summary.resamples(object = resamp)
##
## Models: enet, pls, gam, mars, rf, gbm, rpart
## Number of resamples: 10
##
## MAE
##           Min.  1st Qu.   Median     Mean  3rd Qu.     Max. NA's
## enet  14.89563 15.41241 16.31429 16.48704 17.18978 18.68102    0
## pls   14.88596 15.73014 16.78619 16.77285 17.65509 18.70689    0
## gam   13.63349 14.66753 15.56539 15.39251 16.01871 16.82288    0
## mars  13.57177 14.17293 14.70892 14.88652 15.85824 16.12610    0
## rf    13.34452 13.71658 14.81148 14.75197 15.67082 16.18638    0
## gbm   12.80459 13.54969 14.46672 14.36228 15.21148 15.78439    0
## rpart 13.57200 14.43384 15.08326 15.06314 15.64389 16.76941    0
##
## RMSE
##           Min.  1st Qu.   Median     Mean  3rd Qu.     Max. NA's
## enet  21.66236 23.10295 24.43842 25.55056 27.18938 34.24423    0
## pls   21.69353 23.36433 24.10026 25.10344 26.34144 32.59019    0
## gam   18.59663 20.80165 22.51682 22.46502 24.35001 26.14106    0
## mars  18.32398 19.83786 20.97298 21.52795 23.18857 25.77849    0
## rf    17.91126 19.56908 21.34942 21.33878 23.27605 23.97571    0
## gbm   16.99334 19.28323 21.00432 20.63349 22.20037 23.10783    0
## rpart 18.10205 20.48515 21.60586 22.00056 24.17166 26.08592    0
##
## Rsquared
##             Min.   1st Qu.    Median      Mean   3rd Qu.      Max. NA's
## enet  0.08983837 0.1977097 0.2506698 0.2393136 0.2882582 0.3466723    0
## pls   0.11783579 0.2047681 0.2671251 0.2632351 0.3365684 0.3870614    0
## gam   0.14925569 0.3053848 0.4458158 0.4177506 0.5275640 0.6443694    0
## mars  0.14582135 0.3633383 0.4571700 0.4526473 0.5790718 0.6588231    0
## rf    0.14785585 0.3680986 0.4628669 0.4531400 0.5706298 0.6700218    0
## gbm   0.14759097 0.4206024 0.4852933 0.4842539 0.6221652 0.7058248    0
## rpart 0.02935530 0.3516698 0.4622695 0.4285523 0.5761503 0.6673153    0
```

```
parallelplot(resamp, metric = "RMSE")
```




```
png(file="comparison.png", height=1800, width=1800, units = "px", res=200)
bwplot(resamp, metric = "RMSE")
```

```
png(file="VIP.png", height=1800, width=1800, units = "px", res=200)
p1 <- vip(mars.fit, num_features = 40, bar = FALSE, value = "gcv") + ggtitle("GCV")
p2 <- vip(mars.fit, num_features = 40, bar = FALSE, value = "rss") + ggtitle("RSS")

gridExtra::grid.arrange(p1, p2, ncol = 2)
dev.off()
```

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

Prediction

```
predy2.pls = predict(lm.fit, newdata = x.test)
mean((y.test-predy2.pls)^2)
```

```
## [1] 652.6144
```

```
predy2.pls = predict(ridge.fit, newdata = x.test)
mean((y.test-predy2.pls)^2)
```

```
## [1] 745.3525
```

```
predy2.pls = predict(enet.fit, newdata = x.test)
mean((y.test-predy2.pls)^2)
```

```
## [1] 677.4994
```

```
predy2.pls = predict(pls.fit, newdata = x.test)
mean((y.test-predy2.pls)^2)
```

```
## [1] 652.476
```

```
predy2.pcr = predict(pcr.fit, newdata = x.test)
mean((y.test-predy2.pcr)^2)
```

```
## [1] 652.6144
```

```
predy2.mars = predict(mars.fit, newdata = x.test)
mean((y.test-predy2.mars)^2)
```

```
## [1] 439.1718
```

```
predy2.lasso = predict(lasso.fit, newdata = x.test)
mean((y.test-predy2.lasso)^2)
```

```
## [1] 652.7542
```

```
predy2.gam = predict(gam.fit, newdata = x.test)
mean((y.test-predy2.gam)^2)
```

```
## [1] 486.8146
```