# Final Project Code

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## Contents

**1 Data Import 3**

**2 Data partition 5**

**3 Primary Analysis 5**
3.1 Exploratory analysis and data visualization . . . . . . . . . . . . . . . . . . . . . 5
3.1.1 Data Frame Summary . . . . . . . . . . . . . . . . . . . . . . . . . . . . . 5
3.2 Model Training . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . 12
3.2.1 Linear Model . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . 12
3.2.2 LASSO . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . 12
3.2.3 Ridge . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . 15
3.2.4 Elastic Net . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . 17
3.2.5 Principal components regression (PCR) . . . . . . . . . . . . . . . . . . . 19
3.2.6 Partial Least Squares (PLS) . . . . . . . . . . . . . . . . . . . . . . . . . 21
3.2.7 Generalized Additive Model (GAM) . . . . . . . . . . . . . . . . . . . . . 23
3.2.8 Multivariate Adaptive Regression Splines (MARS) . . . . . . . . . . . . . 25
3.2.9 K-Nearest Neighbour (KNN) . . . . . . . . . . . . . . . . . . . . . . . . . 27
3.2.10 Bagging . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . 28
3.2.11 Random Forest . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . 28
3.2.12 Boosting . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . 28
3.2.13 Regression Trees . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . 28
3.3 Model Selection . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . 28
3.4 Training / Testing Error . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . 31

**4 Secondary Analysis 32**
4.1 Exploratory analysis and data visualization . . . . . . . . . . . . . . . . . . . . . 32
4.1.1 Data Frame Summary . . . . . . . . . . . . . . . . . . . . . . . . . . . . . 32
4.2 Model Training . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . 34
4.2.1 Logistic Regression . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . 34
4.2.2 Penalized Logistic Regression . . . . . . . . . . . . . . . . . . . . . . . . 34
4.2.3 Generalized Additive Model (GAM) for classification . . . . . . . . . . . . 34
4.2.4 Multivariate Adaptive Regression Splines (MARS) for classification . . . . 34
4.2.5 Linear Discriminant Analysis (LDA) . . . . . . . . . . . . . . . . . . . . . 34
4.2.6 Quadratic Discriminant Analysis (QDA) . . . . . . . . . . . . . . . . . . . 34
4.2.7 Naive Bayes (NB) . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . 34
4.2.8 Bagging . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . 34
4.2.9 Random Forest . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . 34
4.2.10 Boosting . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . 34
4.2.11 Classification Trees . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . 34
4.2.12 Support Vector Machine (SVM) . . . . . . . . . . . . . . . . . . . . . . . 34
4.2.13 Hierarchical Clustering . . . . . . . . . . . . . . . . . . . . . . . . . . . . 34
4.2.14 Principal Component Analysis (PCA) . . . . . . . . . . . . . . . . . . . . 34

4.3 Model Selection . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . 34
4.4 Training / Testing Error . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . 34

```
library(tidyverse)
library(summarytools)
library(corrplot)
library(caret)
library(vip)
```

# 1 Data Import

```
# import data
load("./recovery.RData")

set.seed(3196)
lts.dat <- dat[sample(1:10000, 2000),]
set.seed(2575)
lincole.dat <- dat[sample(1:10000, 2000),]
set.seed(5509)
amy.dat <- dat[sample(1:10000, 2000),]

dat1 <- lts.dat %>%
  merge(lincole.dat, all = TRUE) %>%
  na.omit() %>%
  select(-id) %>%
  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))

dat2 <- lts.dat %>%
  merge(amy.dat, all = TRUE) %>%
  na.omit() %>%
  select(-id) %>%
  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))

dat3 <- lincole.dat %>%
  merge(amy.dat, all = TRUE) %>%
  na.omit() %>%
  select(-id) %>%
  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))

dat <- dat1
summary(dat)
```

```
##       age         gender   race     smoking      height          weight
##  Min.   :45.00   0:1842   1:2372   0:2223   Min.   :151.2   Min.   : 56.70
##  1st Qu.:57.00   1:1781   2: 172   1:1034   1st Qu.:166.2   1st Qu.: 75.40
##  Median :60.00            3: 716   2: 366   Median :170.2   Median : 80.20
##  Mean   :60.06            4: 363            Mean   :170.2   Mean   : 80.13
##  3rd Qu.:63.00                              3rd Qu.:174.2   3rd Qu.: 84.80
##  Max.   :77.00                              Max.   :188.6   Max.   :103.40
##       bmi         hypertension diabetes      SBP             LDL            vaccine
##  Min.   :19.70   0:1891       0:3065   Min.   :102.0   Min.   : 28.0   0:1469
##  1st Qu.:25.80   1:1732       1: 558   1st Qu.:125.0   1st Qu.: 97.0   1:2154
##  Median :27.60                         Median :130.0   Median :110.0
##  Mean   :27.73                         Mean   :130.2   Mean   :110.5
##  3rd Qu.:29.40                         3rd Qu.:136.0   3rd Qu.:124.0
##  Max.   :39.80                         Max.   :158.0   Max.   :174.0
##  severity study    recovery_time
##  0:3289   A: 728   Min.   :  3.00
##  1: 334   B:2171   1st Qu.: 28.00
##           C: 724   Median : 38.00
##                    Mean   : 42.87
##                    3rd Qu.: 49.00
##                    Max.   :365.00
```

```
bin.dat1 <- dat1 %>%
  mutate(recovery_time = ifelse(recovery_time > 30, 1, 0))

bin.dat2 <- dat2 %>%
  mutate(recovery_time = ifelse(recovery_time > 30, 1, 0))

bin.dat3 <- dat3 %>%
  mutate(recovery_time = ifelse(recovery_time > 30, 1, 0))

bin.dat <- bin.dat1
summary(bin.dat)
```

```
##       age         gender   race     smoking      height          weight
##  Min.   :45.00   0:1842   1:2372   0:2223   Min.   :151.2   Min.   : 56.70
##  1st Qu.:57.00   1:1781   2: 172   1:1034   1st Qu.:166.2   1st Qu.: 75.40
##  Median :60.00            3: 716   2: 366   Median :170.2   Median : 80.20
##  Mean   :60.06            4: 363            Mean   :170.2   Mean   : 80.13
##  3rd Qu.:63.00                              3rd Qu.:174.2   3rd Qu.: 84.80
##  Max.   :77.00                              Max.   :188.6   Max.   :103.40
##       bmi         hypertension diabetes      SBP             LDL            vaccine
##  Min.   :19.70   0:1891       0:3065   Min.   :102.0   Min.   : 28.0   0:1469
##  1st Qu.:25.80   1:1732       1: 558   1st Qu.:125.0   1st Qu.: 97.0   1:2154
##  Median :27.60                         Median :130.0   Median :110.0
##  Mean   :27.73                         Mean   :130.2   Mean   :110.5
##  3rd Qu.:29.40                         3rd Qu.:136.0   3rd Qu.:124.0
##  Max.   :39.80                         Max.   :158.0   Max.   :174.0
##  severity study    recovery_time
##  0:3289   A: 728   Min.   :0.0000
##  1: 334   B:2171   1st Qu.:0.0000
##           C: 724   Median :1.0000
##                    Mean   :0.6958
##                    3rd Qu.:1.0000
##                    Max.   :1.0000
```

# 2 Data partition

```
# data partition
dat.matrix <- model.matrix(recovery_time ~ ., dat)[ ,-1]

set.seed(2023)
trainRows <- createDataPartition(y = dat$recovery_time, p = 0.8, list = FALSE)

train.dat <- dat[trainRows,]
train.bin.dat <- bin.dat[trainRows,]

train.x <- dat.matrix[trainRows,]
train.y <- dat$recovery_time[trainRows]
train.bin.y <- bin.dat$recovery_time[trainRows]

test.x <- dat.matrix[-trainRows,]
test.y <- dat$recovery_time[-trainRows]
test.bin.y <- bin.dat$recovery_time[-trainRows]
```

# 3 Primary Analysis

## 3.1 Exploratory analysis and data visualization

```
# data summary
st_options(plain.ascii = FALSE,
           style = "rmarkdown",
           dfSummary.silent = TRUE,
           footnote = NA,
           subtitle.emphasis = FALSE)
dfSummary(train.dat)
```

### 3.1.1 Data Frame Summary

**train.dat**
**Dimensions:** 2900 x 15
**Duplicates:** 0

| No | Variable | Stats / Values | Freqs (% of Valid) | Graph | Valid | Missing |
|---|---|---|---|---|---|---|
| 1 | age<br>[numeric] | Mean (sd) : 60.1 (4.5)<br>min < med < max:<br>45 < 60 < 77<br>IQR (CV) : 6 (0.1) | 33 distinct values | :<br>:<br>. : :<br>: : : .<br>. : : : : : : . | 2900<br>(100.0%) | 0<br>(0.0%) |
| 2 | gender<br>[factor] | 1. 0<br>2. 1 | 1468 (50.6%)<br>1432 (49.4%) | IIIIIIIIII<br>IIIIIIIII | 2900<br>(100.0%) | 0<br>(0.0%) |
| 3 | race<br>[factor] | 1. 1<br>2. 2<br>3. 3<br>4. 4 | 1909 (65.8%)<br>132 ( 4.6%)<br>568 (19.6%)<br>291 (10.0%) | IIIIIIIIIIIII<br><br>III<br>II | 2900<br>(100.0%) | 0<br>(0.0%) |
| 4 | smoking<br>[factor] | 1. 0<br>2. 1<br>3. 2 | 1763 (60.8%)<br>845 (29.1%)<br>292 (10.1%) | IIIIIIIIIIII<br>IIIII<br>II | 2900<br>(100.0%) | 0<br>(0.0%) |
| 5 | height<br>[numeric] | Mean (sd) : 170.2 (6)<br>min < med < max:<br>151.2 < 170.1 < 188.6<br>IQR (CV) : 8 (0) | 312 distinct values | : :<br>: :<br>. : : .<br>: : : :<br>. : : : : . | 2900<br>(100.0%) | 0<br>(0.0%) |
| 6 | weight<br>[numeric] | Mean (sd) : 80.2 (7)<br>min < med < max:<br>57.1 < 80.3 < 103.4<br>IQR (CV) : 9.5 (0.1) | 361 distinct values | . :<br>. : :<br>: : : :<br>. : : : : .<br>. : : : : : : . | 2900<br>(100.0%) | 0<br>(0.0%) |
| 7 | bmi<br>[numeric] | Mean (sd) : 27.8 (2.7)<br>min < med < max:<br>19.7 < 27.7 < 39.8<br>IQR (CV) : 3.6 (0.1) | 160 distinct values | : .<br>: :<br>: : : .<br>: : : :<br>: : : : : : . | 2900<br>(100.0%) | 0<br>(0.0%) |
| 8 | hypertension<br>[factor] | 1. 0<br>2. 1 | 1514 (52.2%)<br>1386 (47.8%) | IIIIIIIIII<br>IIIIIIIII | 2900<br>(100.0%) | 0<br>(0.0%) |
| 9 | diabetes<br>[factor] | 1. 0<br>2. 1 | 2446 (84.3%)<br>454 (15.7%) | IIIIIIIIIIIIIIII<br>III | 2900<br>(100.0%) | 0<br>(0.0%) |
| 10 | SBP<br>[numeric] | Mean (sd) : 130.2 (8.1)<br>min < med < max:<br>104 < 130 < 158<br>IQR (CV) : 11 (0.1) | 54 distinct values | :<br>: .<br>: : : .<br>. : : : :<br>. : : : : : : | 2900<br>(100.0%) | 0<br>(0.0%) |
| 11 | LDL<br>[numeric] | Mean (sd) : 110.3 (19.9)<br>min < med < max:<br>32 < 110 < 174<br>IQR (CV) : 27 (0.2) | 116 distinct values | . :<br>: : :<br>: : : .<br>: : : : :<br>. : : : : : . | 2900<br>(100.0%) | 0<br>(0.0%) |
| 12 | vaccine<br>[factor] | 1. 0<br>2. 1 | 1192 (41.1%)<br>1708 (58.9%) | IIIIIIII<br>IIIIIIIIIII | 2900<br>(100.0%) | 0<br>(0.0%) |
| 13 | severity<br>[factor] | 1. 0<br>2. 1 | 2619 (90.3%)<br>281 ( 9.7%) | IIIIIIIIIIIIIIIIII<br>I | 2900<br>(100.0%) | 0<br>(0.0%) |
| 14 | study<br>[factor] | 1. A<br>2. B<br>3. C | 580 (20.0%)<br>1750 (60.3%)<br>570 (19.7%) | IIII<br>IIIIIIIIIIII<br>III | 2900<br>(100.0%) | 0<br>(0.0%) |

| No | Variable | Stats / Values | Freqs (% of Valid) | Graph | Valid | Missing |
|---|---|---|---|---|---|---|
| 15 | recovery_time<br>[numeric] | Mean (sd) : 43 (30.5)<br>min < med < max:<br>3 < 38 < 365<br>IQR (CV) : 21 (0.7) | 144 distinct<br>values | :<br>: :<br>: :<br>: :<br>: : . | 2900<br>(100.0%) | 0<br>(0.0%) |

```
skimr::skim_without_charts(train.dat)
```

Table 2: Data summary

| | |
|---|---|
| Name | train.dat |
| Number of rows | 2900 |
| Number of columns | 15 |
| Column type frequency: | |
| factor | 8 |
| numeric | 7 |
| Group variables | None |

**Variable type: factor**

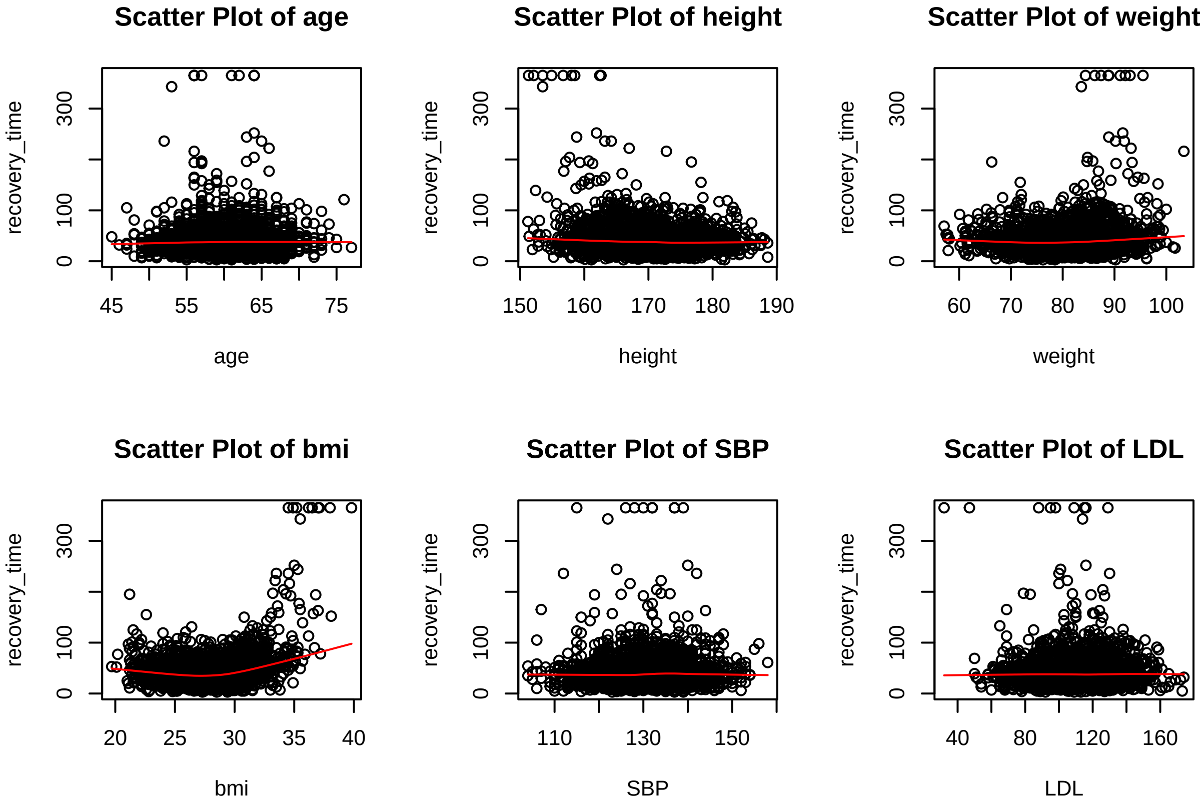
| skim_variable | n_missing | complete_rate | ordered | n_unique | top_counts |
|---|---|---|---|---|---|
| gender | 0 | 1 | FALSE | 2 | 0: 1468, 1: 1432 |
| race | 0 | 1 | FALSE | 4 | 1: 1909, 3: 568, 4: 291, 2: 132 |
| smoking | 0 | 1 | FALSE | 3 | 0: 1763, 1: 845, 2: 292 |
| hypertension | 0 | 1 | FALSE | 2 | 0: 1514, 1: 1386 |
| diabetes | 0 | 1 | FALSE | 2 | 0: 2446, 1: 454 |
| vaccine | 0 | 1 | FALSE | 2 | 1: 1708, 0: 1192 |
| severity | 0 | 1 | FALSE | 2 | 0: 2619, 1: 281 |
| study | 0 | 1 | FALSE | 3 | B: 1750, A: 580, C: 570 |

**Variable type: numeric**

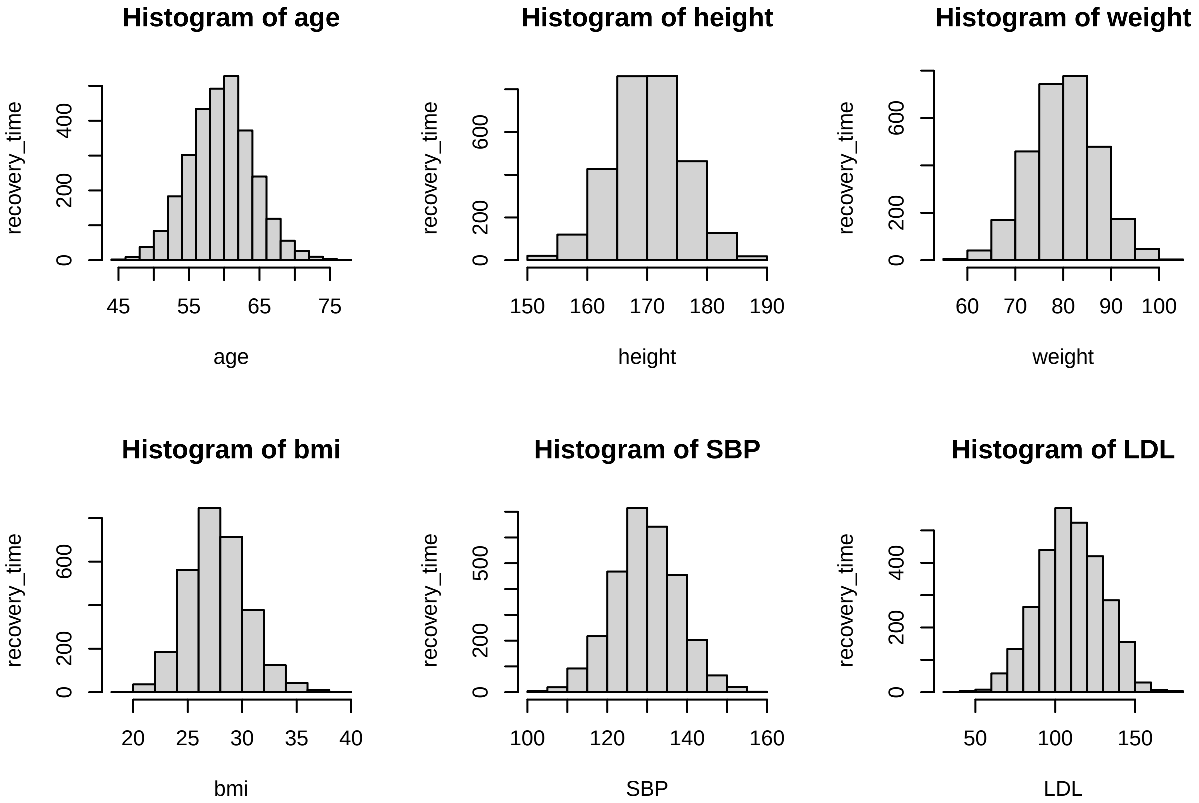
| skim_variable | n_missing | complete_rate | mean | sd | p0 | p25 | p50 | p75 | p100 |
|---|---|---|---|---|---|---|---|---|---|
| age | 0 | 1 | 60.07 | 4.51 | 45.0 | 57.0 | 60.00 | 63.0 | 77.0 |
| height | 0 | 1 | 170.17 | 6.04 | 151.2 | 166.1 | 170.15 | 174.1 | 188.6 |
| weight | 0 | 1 | 80.20 | 7.00 | 57.1 | 75.4 | 80.30 | 84.9 | 103.4 |
| bmi | 0 | 1 | 27.76 | 2.73 | 19.7 | 25.9 | 27.70 | 29.5 | 39.8 |
| SBP | 0 | 1 | 130.19 | 8.08 | 104.0 | 125.0 | 130.00 | 136.0 | 158.0 |
| LDL | 0 | 1 | 110.27 | 19.87 | 32.0 | 97.0 | 110.00 | 124.0 | 174.0 |
| recovery_time | 0 | 1 | 43.02 | 30.51 | 3.0 | 28.0 | 38.00 | 49.0 | 365.0 |

```
##################################################################
## Remember to edit the next chunk if you do any modification here:)
##################################################################
```

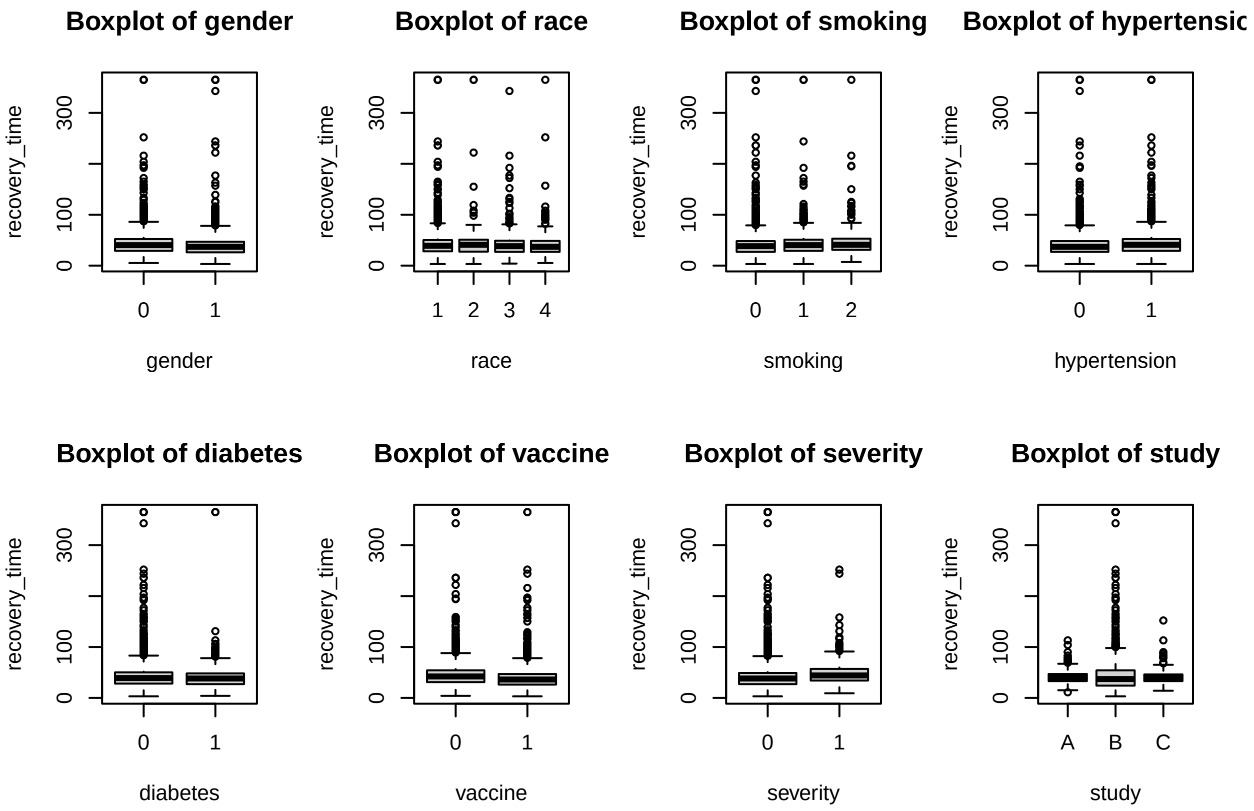
```
# EDA
# library(GGally)
# ggpairs(dat)

cts_var = c("age", "height", "weight", "bmi", "SBP", "LDL")
fct_var = c("gender", "race", "smoking", "hypertension", "diabetes", "vaccine", "severity", "study")
# featurePlot(x = traindataset1[ ,1:14],
#             y = traindataset1[ ,15],
# plot = "scatter",
# span = .5,
# labels = c("Predictors", "Recovery Time"), type = c("p", "smooth"))

# scatter plot of continuous predictors
par(mfrow=c(2, 3))
for (i in 1:length(cts_var)){
  var = cts_var[i]
  plot(recovery_time~train.dat[,var],
       data = train.dat,
       ylab = "recovery_time",
       xlab = var,
       main = str_c("Scatter Plot of ", var))
  lines(stats::lowess(train.dat[,var], train.dat$recovery_time), col = "red", type = "l")
}
```



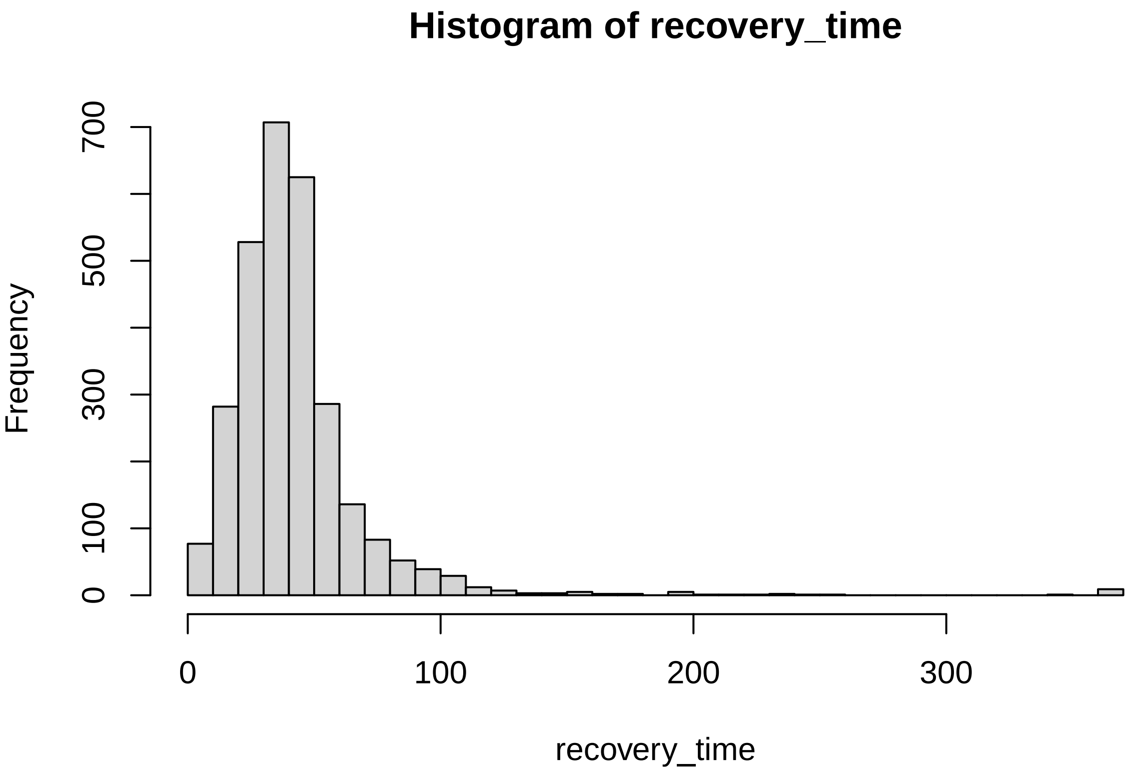
```
for (i in 1:length(cts_var)){
  var = cts_var[i]
  hist(train.dat[,var],
       ylab = "recovery_time",
       xlab = var,
       main = str_c("Histogram of ", var))
}
```



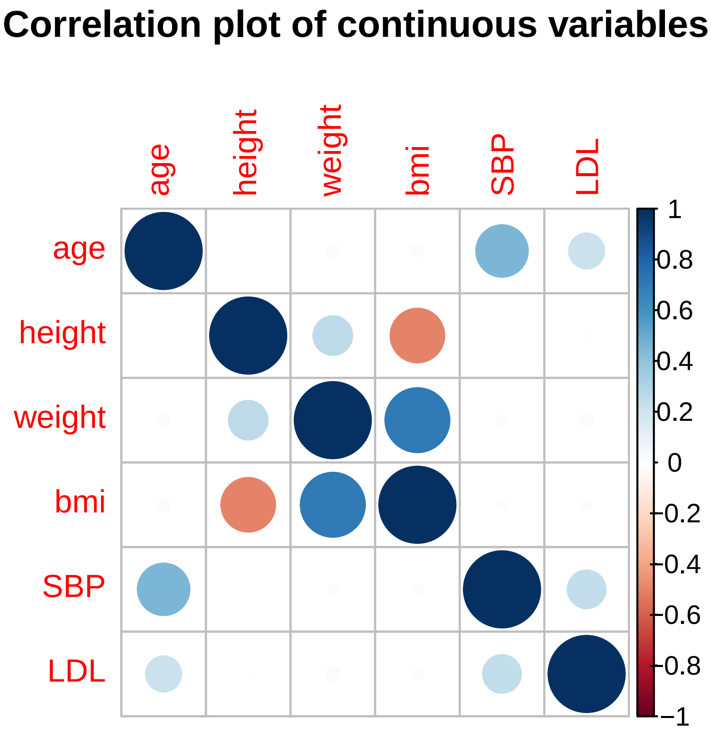
```
# boxplot of categorical predictors
par(mfrow=c(2, 4))
for (i in 1:length(fct_var)){
  var = fct_var[i]
  plot(recovery_time~train.dat[,var],
        data = train.dat,
        ylab = "recovery_time",
        xlab = var,
        main = str_c("Boxplot of ", var))
}
```



```
# histogram of response
par(mfrow=c(1, 1))
hist(train.dat$recovery_time,
     breaks = 50,
     main = "Histogram of recovery_time",
     xlab = "recovery_time")
```



```
# correlation
par(mfrow=c(1, 1))
corrplot(cor(train.dat[,cts_var]), method = "circle", type = "full",
         title = "Correlation plot of continuous variables",
         mar = c(2, 2, 4, 2))
```



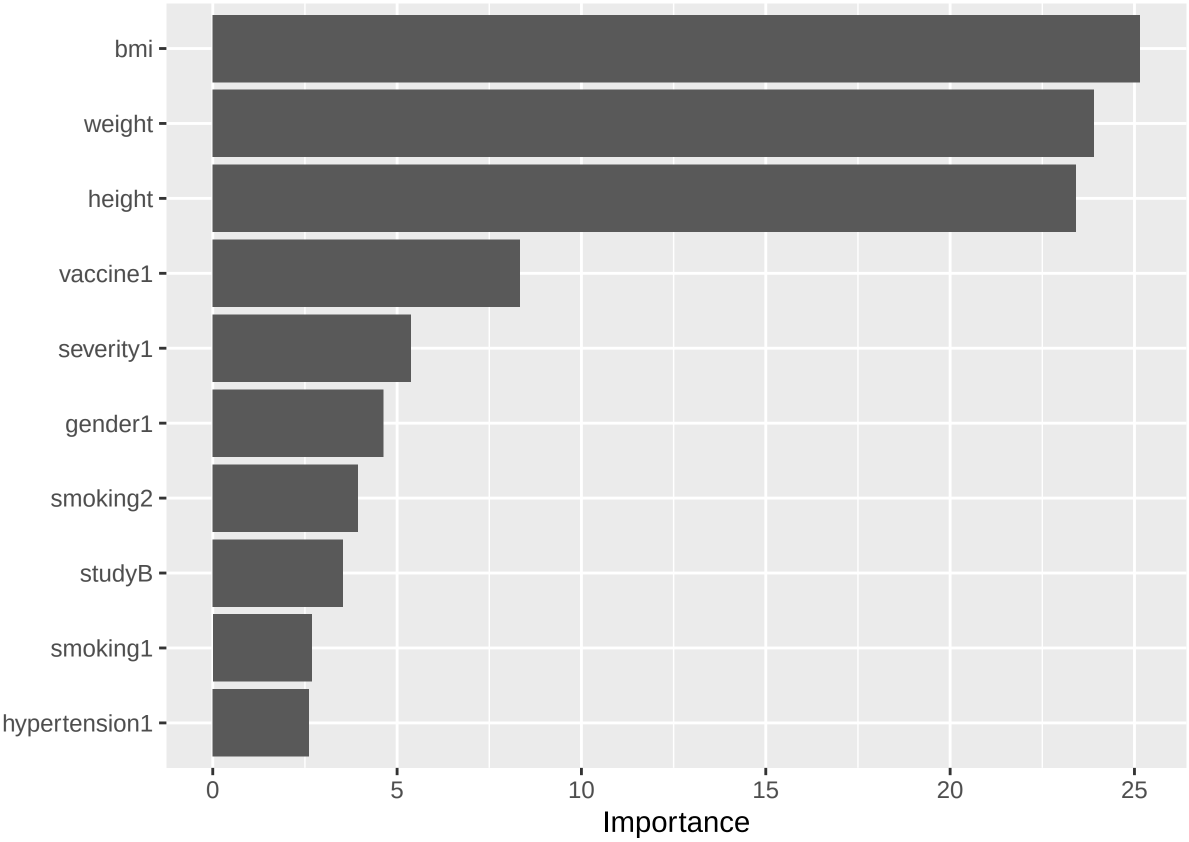
## 3.2 Model Training

### 3.2.1 Linear Model

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



### 3.2.2 LASSO

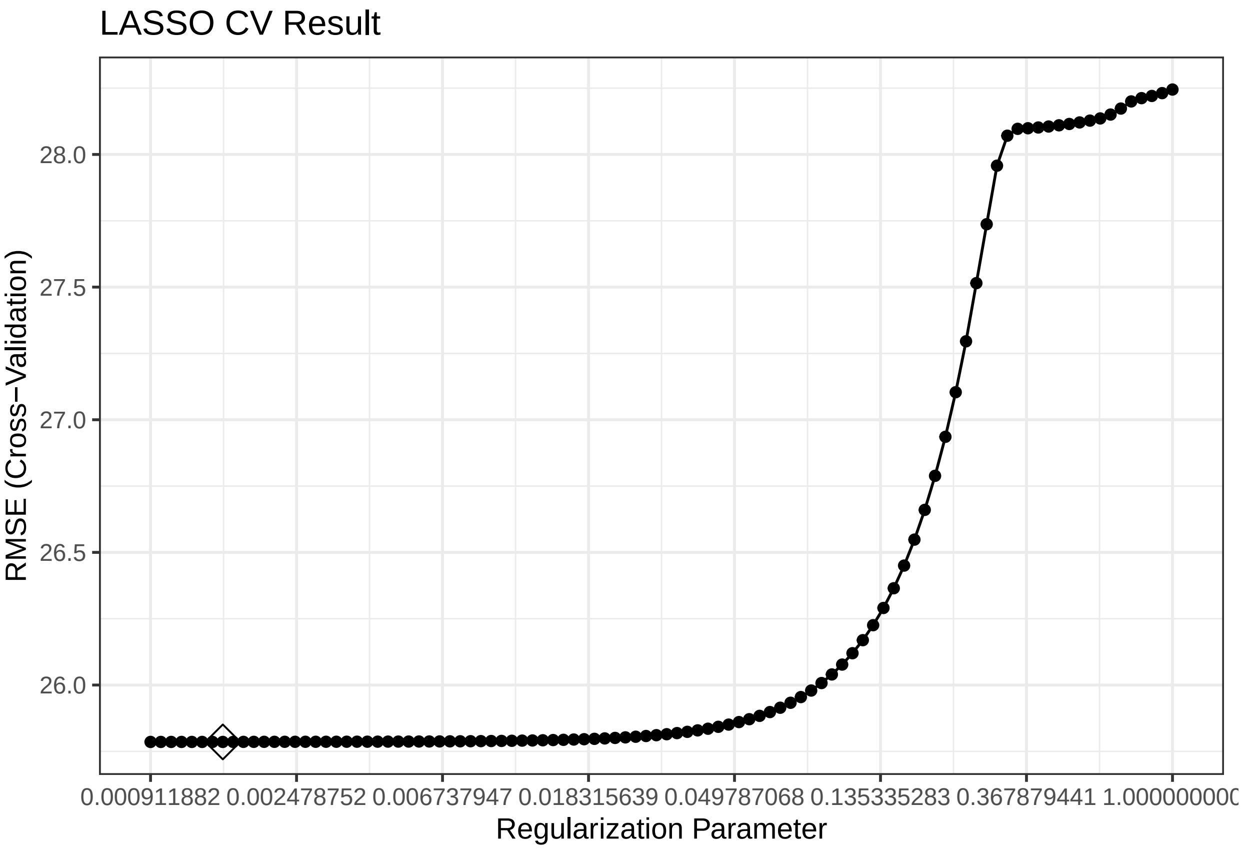
```
set.seed(2023)
lasso.fit <- train(train.x, train.y,
                   method = "glmnet",
                   tuneGrid = expand.grid(
                     alpha = 1,
                     lambda = exp(seq(0, -7, length=100))),
                   trControl = ctrl1)

lasso.fit$bestTune
```

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

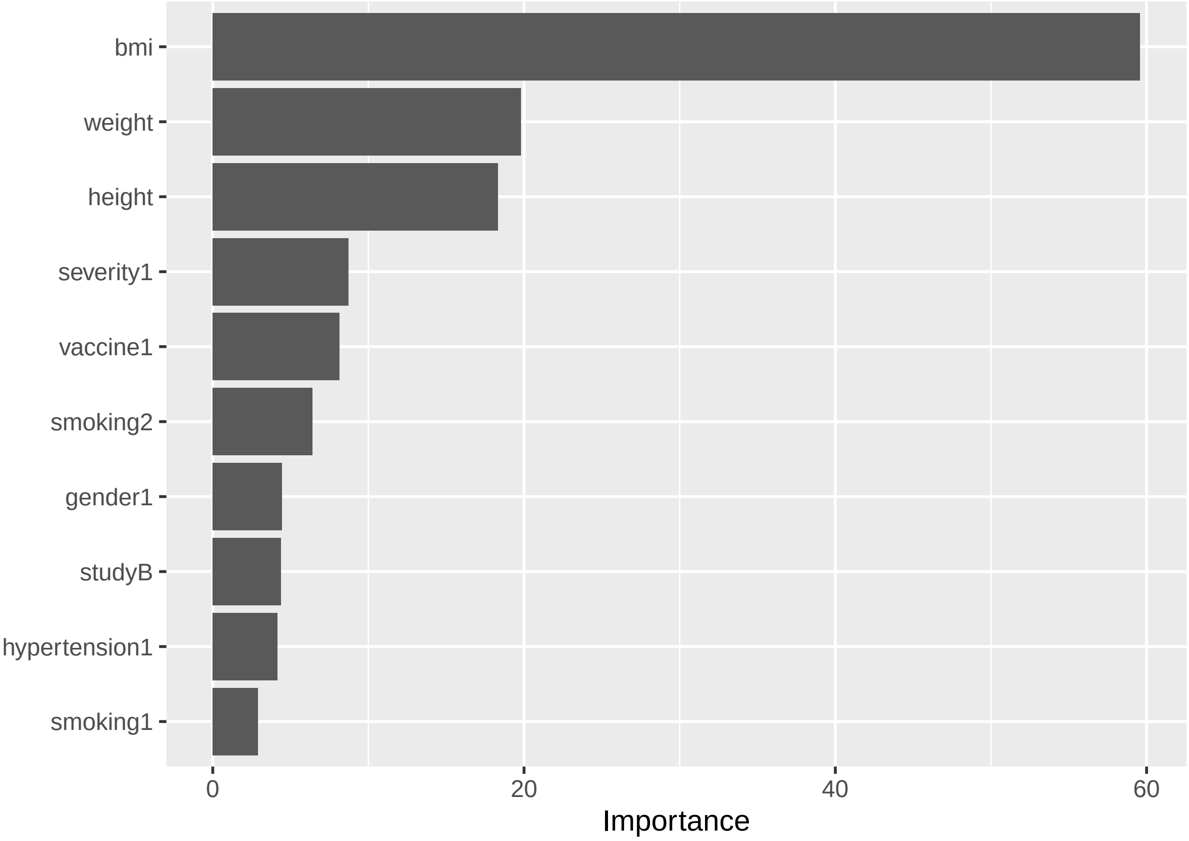
```
coef(lasso.fit$finalModel, s = lasso.fit$bestTune$lambda)
```

```
## 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()
```



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

vip(lasso.fit$finalModel)
```



### 3.2.3 Ridge

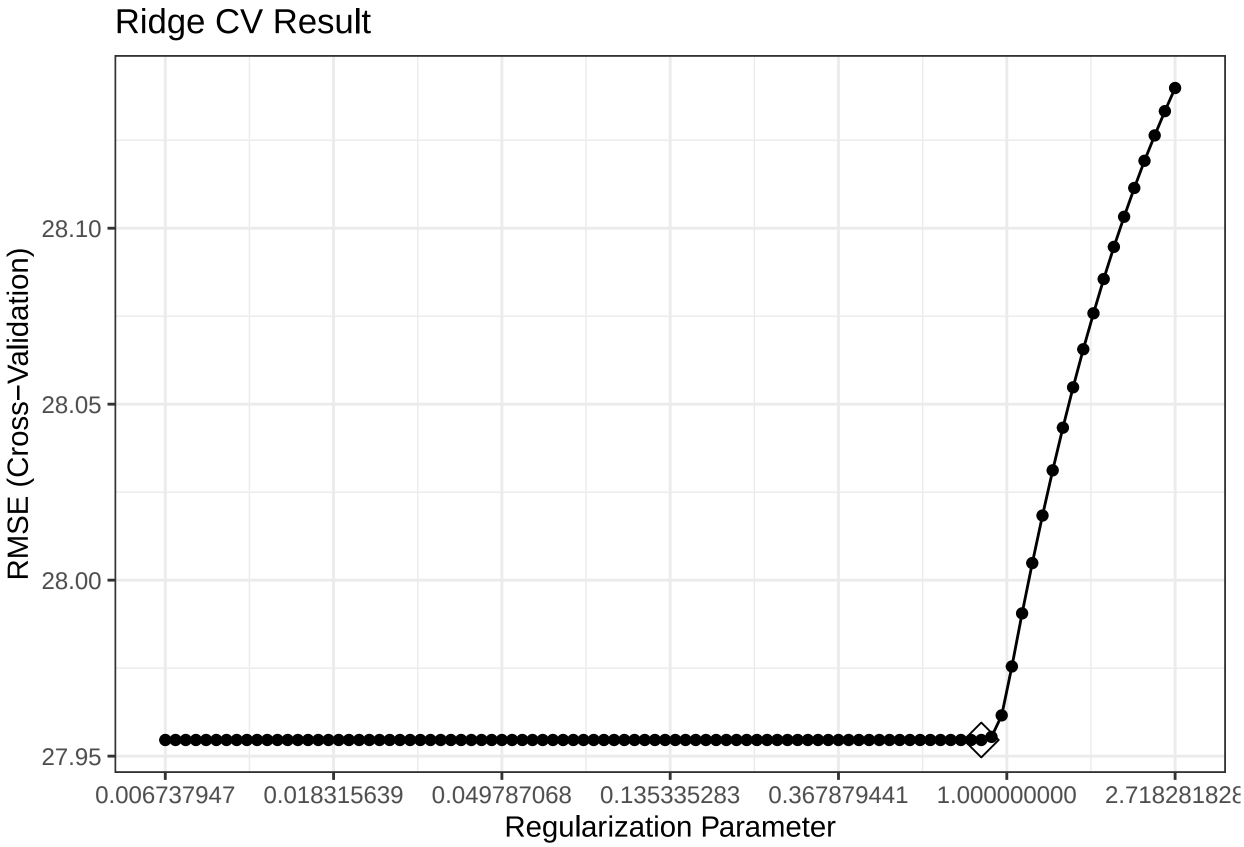
```
set.seed(2023)
ridge.fit <- train(train.x, train.y,
                   method = "glmnet",
                   tuneGrid = expand.grid(alpha = 0,
                                          lambda = exp(seq(1, -5, length=100))),
                   trControl = ctrl1)

ridge.fit$bestTune
```

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

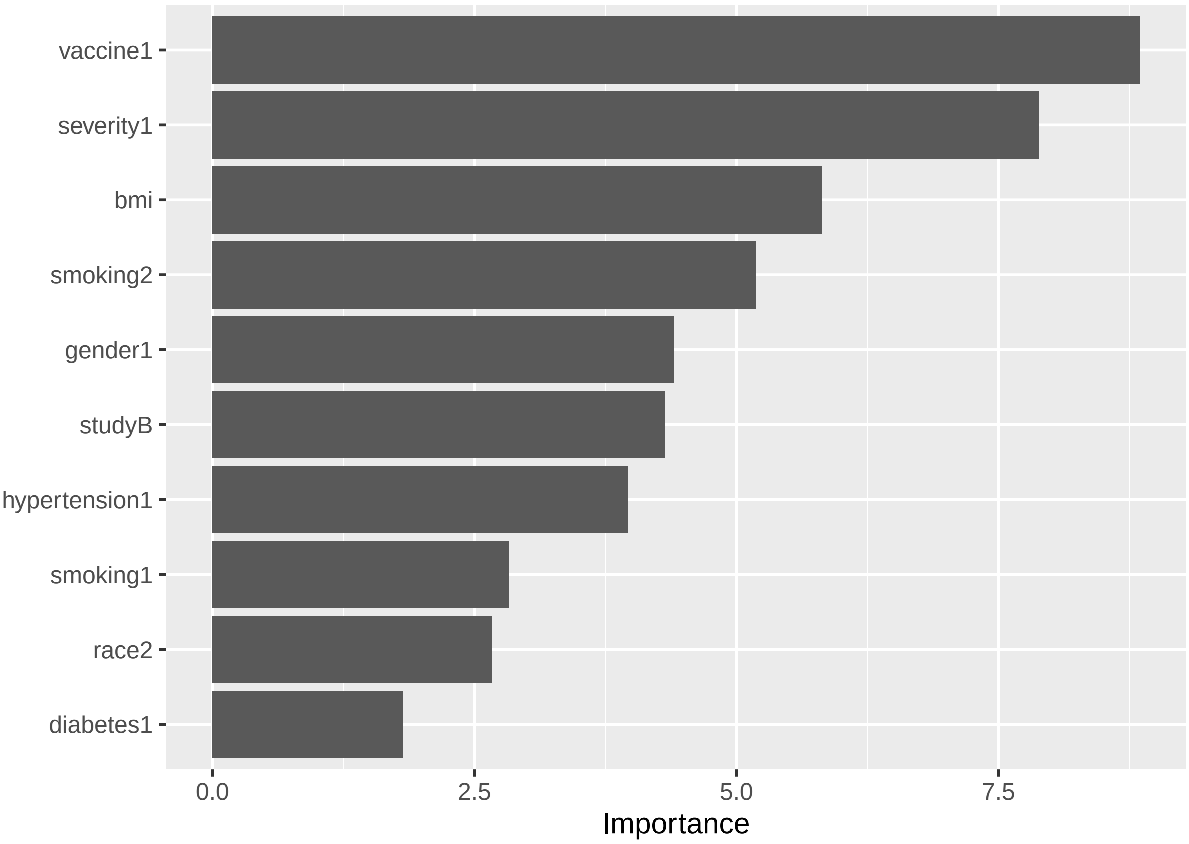
```
coef(ridge.fit$finalModel, s = ridge.fit$bestTune$lambda)
```

```
## 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)
```



### 3.2.4 Elastic Net

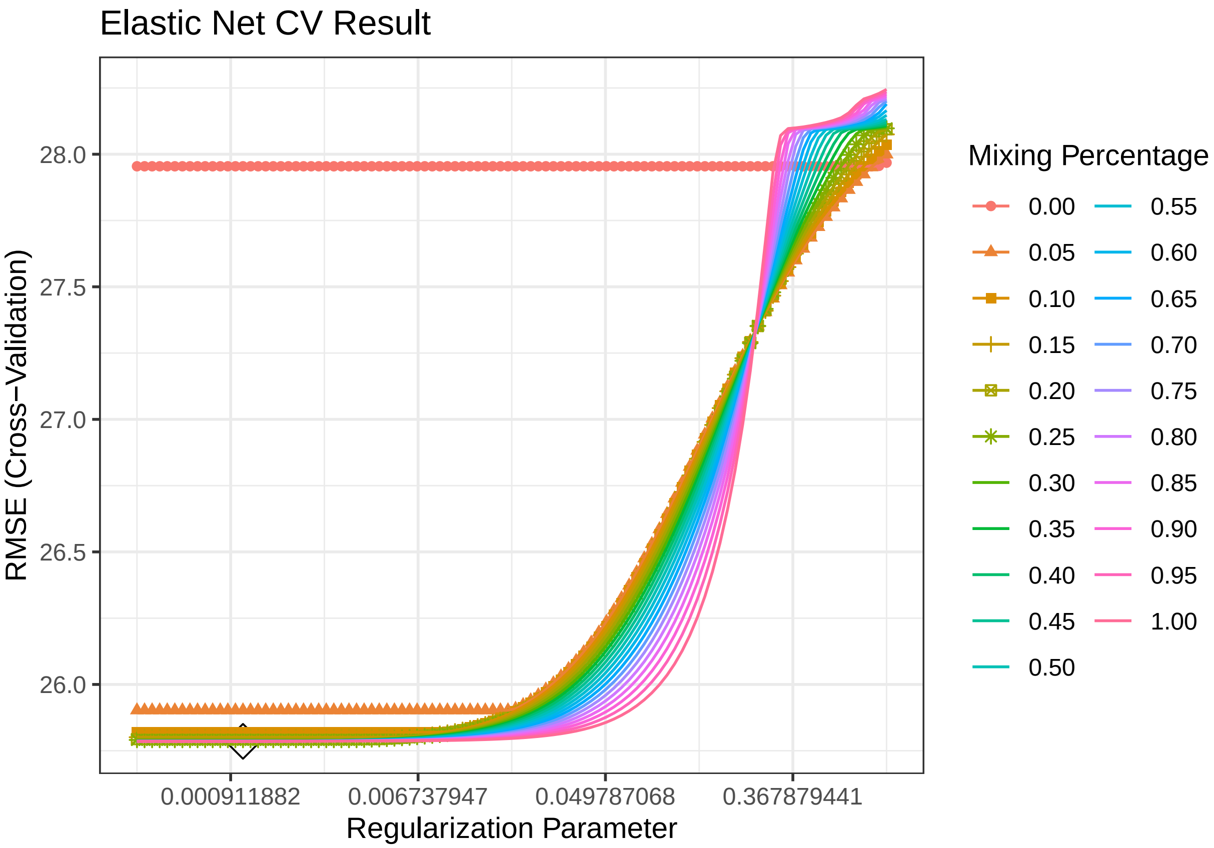
```
set.seed(2023)
enet.fit <- train(train.x, train.y,
                  method = "glmnet",
                  tuneGrid = expand.grid(
                    alpha = seq(0, 1, length = 21),
                    lambda = exp(seq(0, -8, length = 100))),
                  trControl = ctrl1)

enet.fit$bestTune
```

```
##      alpha      lambda
## 1815   0.9 0.001039842
```

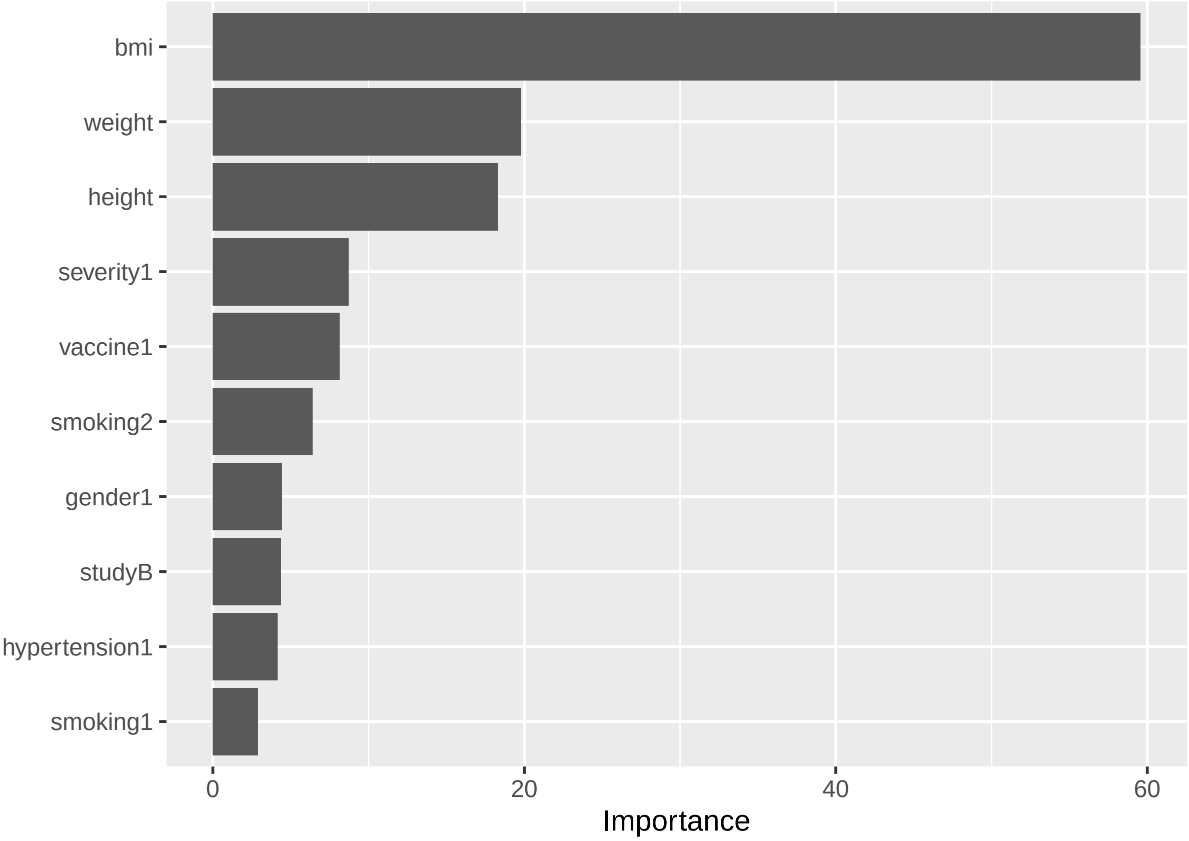
```
coef(enet.fit$finalModel, enet.fit$bestTune$lambda)
```

```
## 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()
```

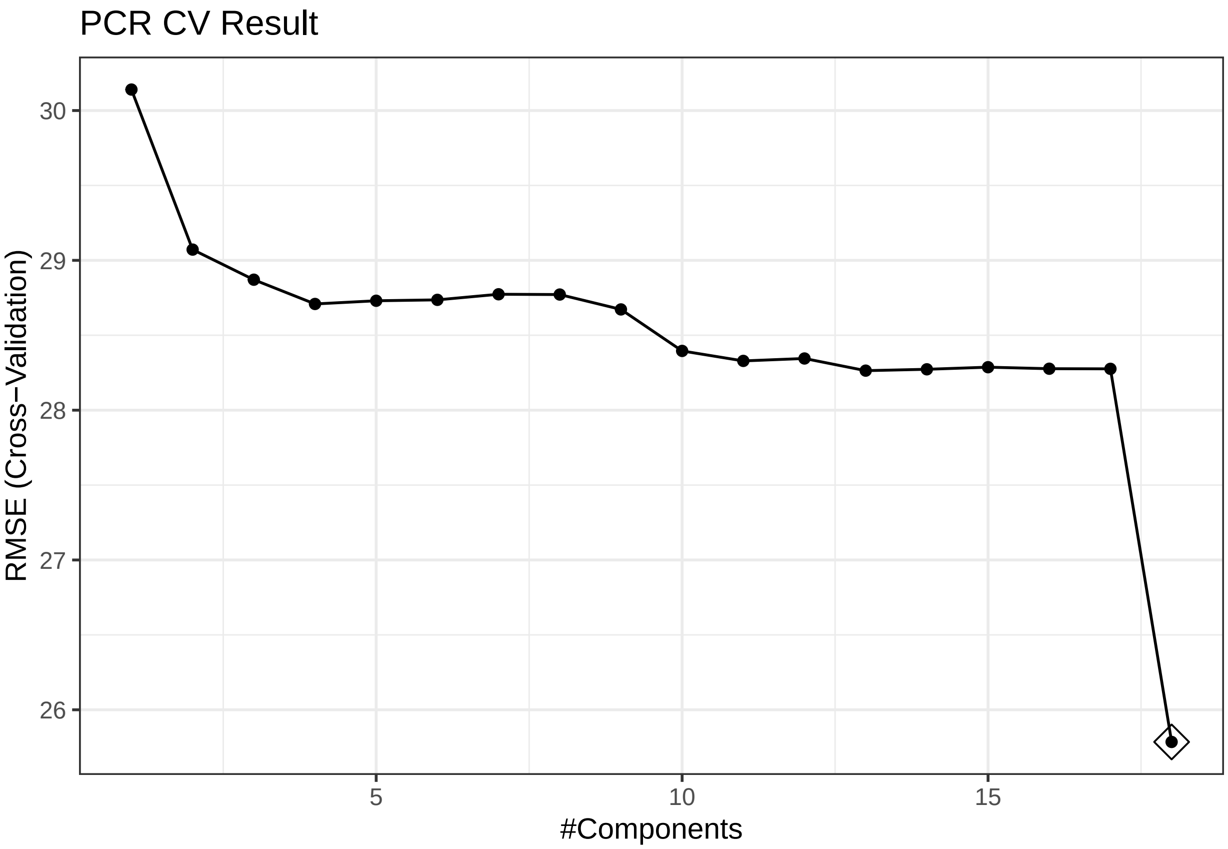


```
ggsave("./figure/enet_cv.jpeg", dpi = 500)

vip(enet.fit$finalModel)
```



### 3.2.5 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()
```



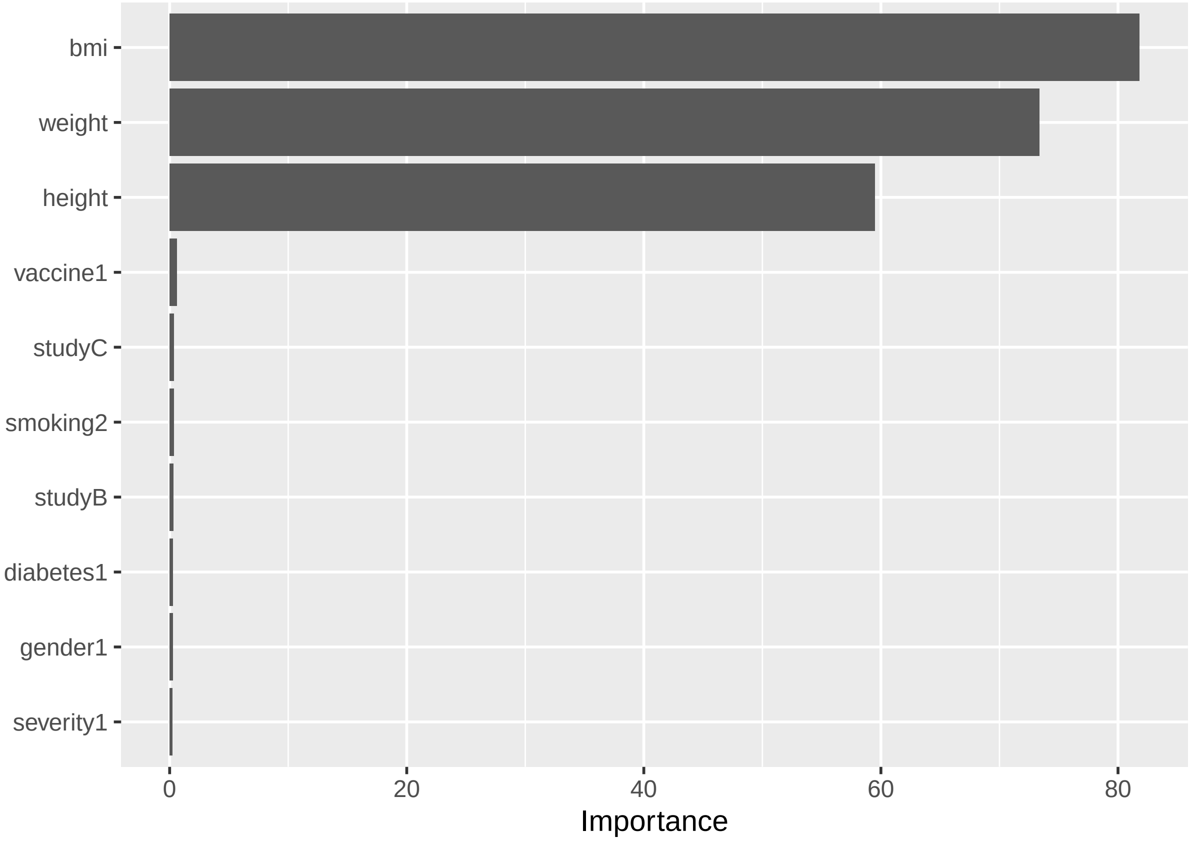
```
ggsave("./figure/pcr_cv.jpeg", dpi = 500)

pcr.fit$bestTune
```

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

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

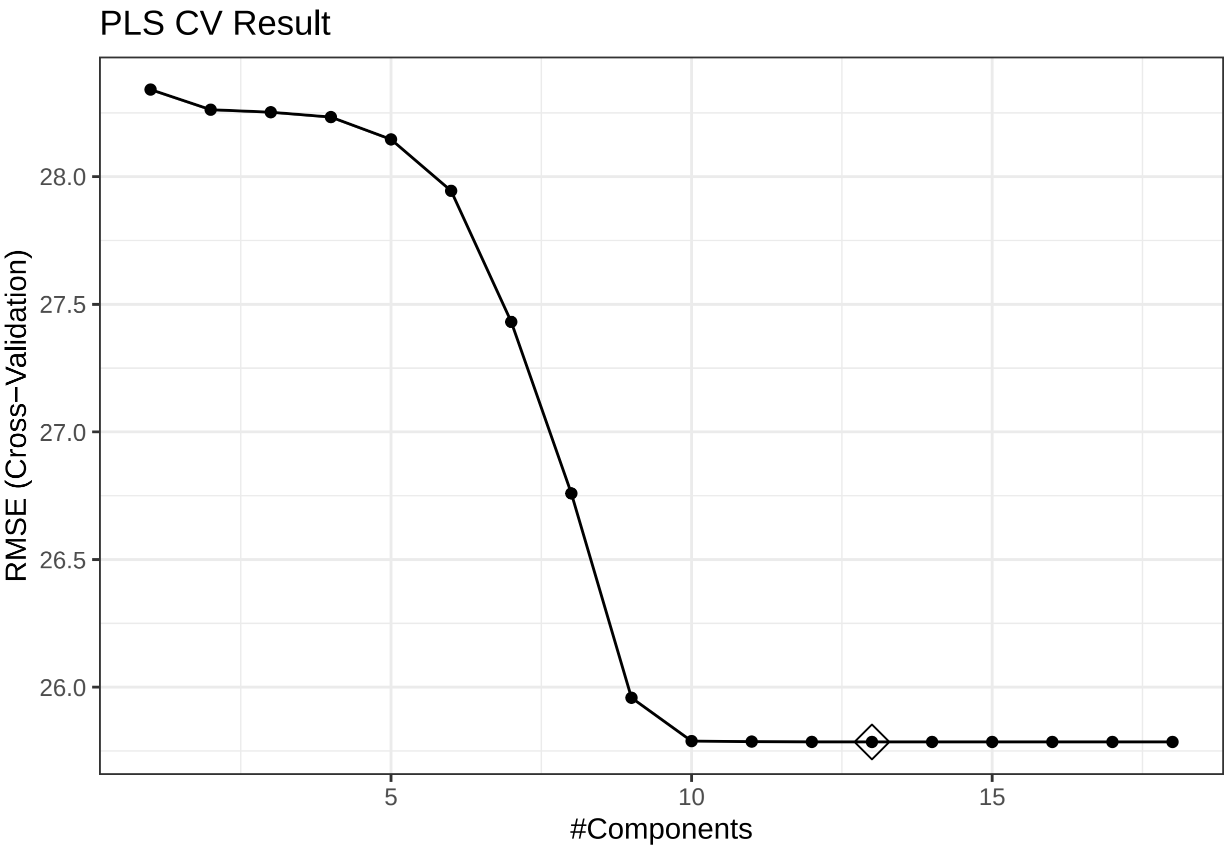
```
## , , 18 comps
##
##                     .outcome
## age                0.5252538
## gender1           -2.2221586
## race2              0.4563464
## race3             -0.2619635
## race4             -0.3476329
## smoking1           1.3205684
## smoking2           1.9344423
## height           112.6936931
## 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)
```



### 3.2.6 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()
```



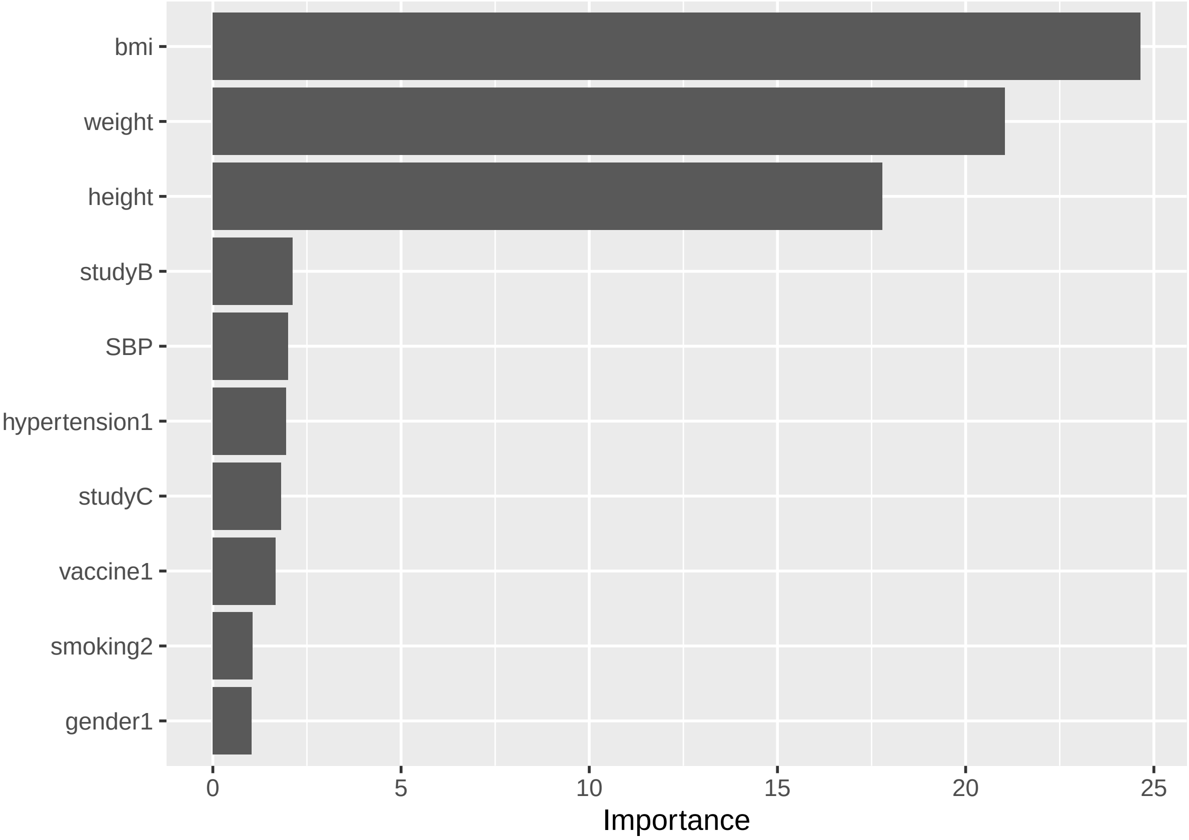
```
ggsave("./figure/pls_cv.jpeg", dpi = 500)

pls.fit$bestTune
```

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

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

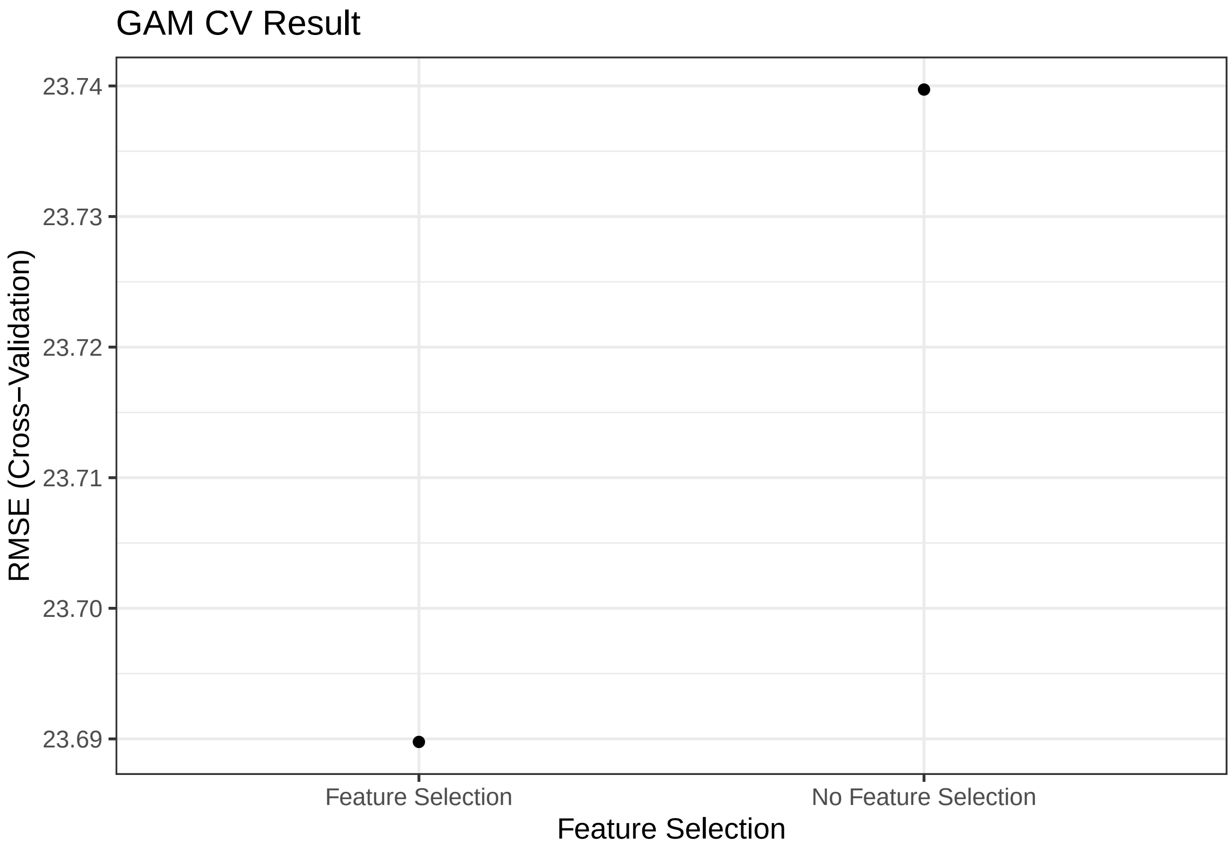
```
## , , 13 comps
##
##                    .outcome
## age               0.5253162
## gender1          -2.2224171
## race2             0.4564699
## race3            -0.2616135
## race4            -0.3472528
## smoking1          1.3206873
## smoking2          1.9344789
## height          112.6936914
## 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)
```



### 3.2.7 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()
```



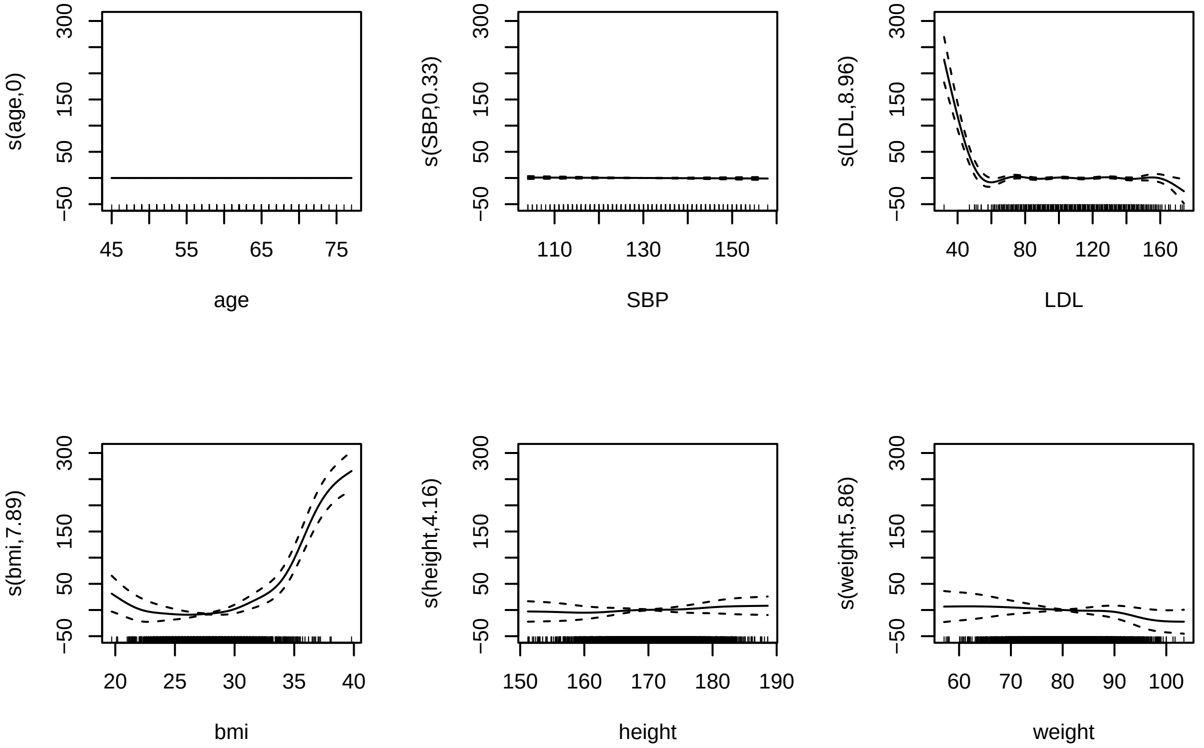
```
ggsave("./figure/gam_cv.jpeg", dpi = 500)

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
```

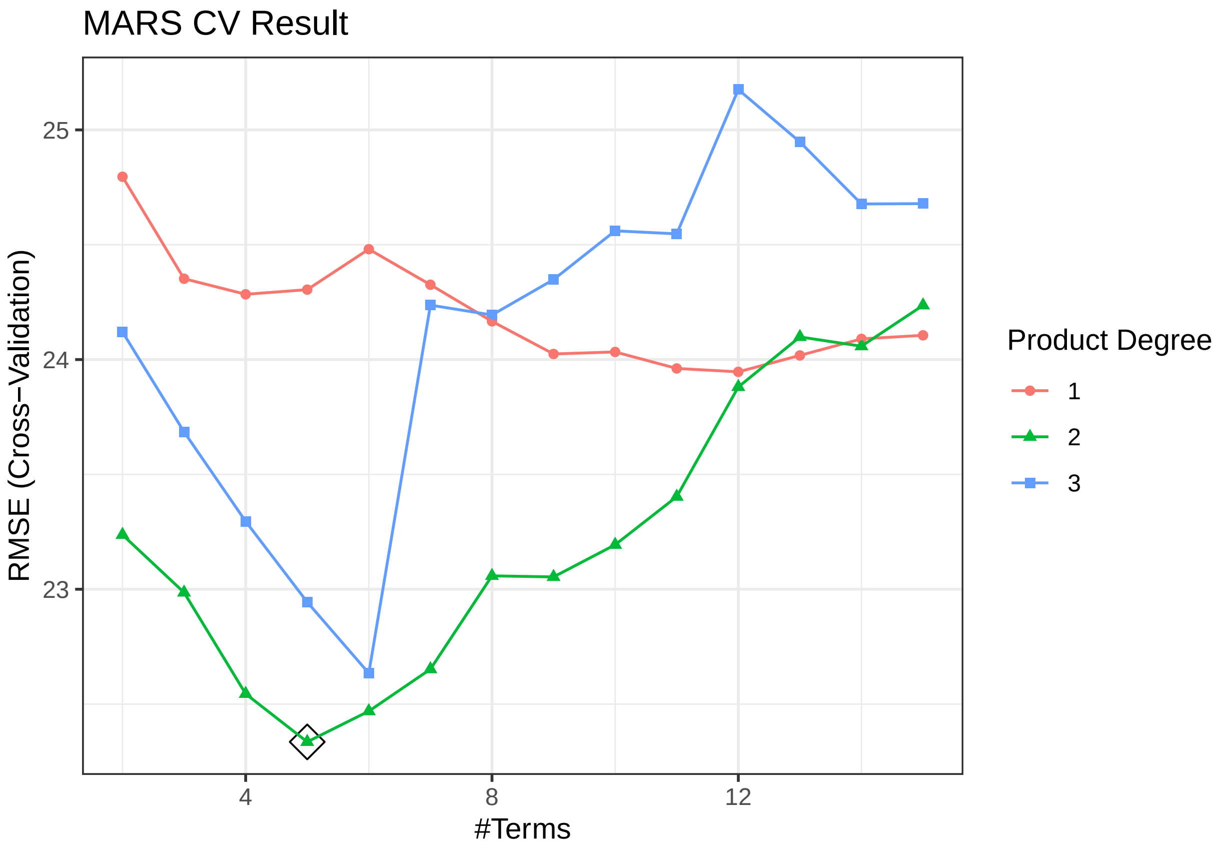
```
par(mfrow=c(2, 3))
plot(gam.fit$finalModel)
```



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

### 3.2.8 Multivariate Adaptive Regression Splines (MARS)

```
mars_grid <- expand.grid(degree = 1:3,
                         nprune = 2:15)
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
## 18      5      2
```

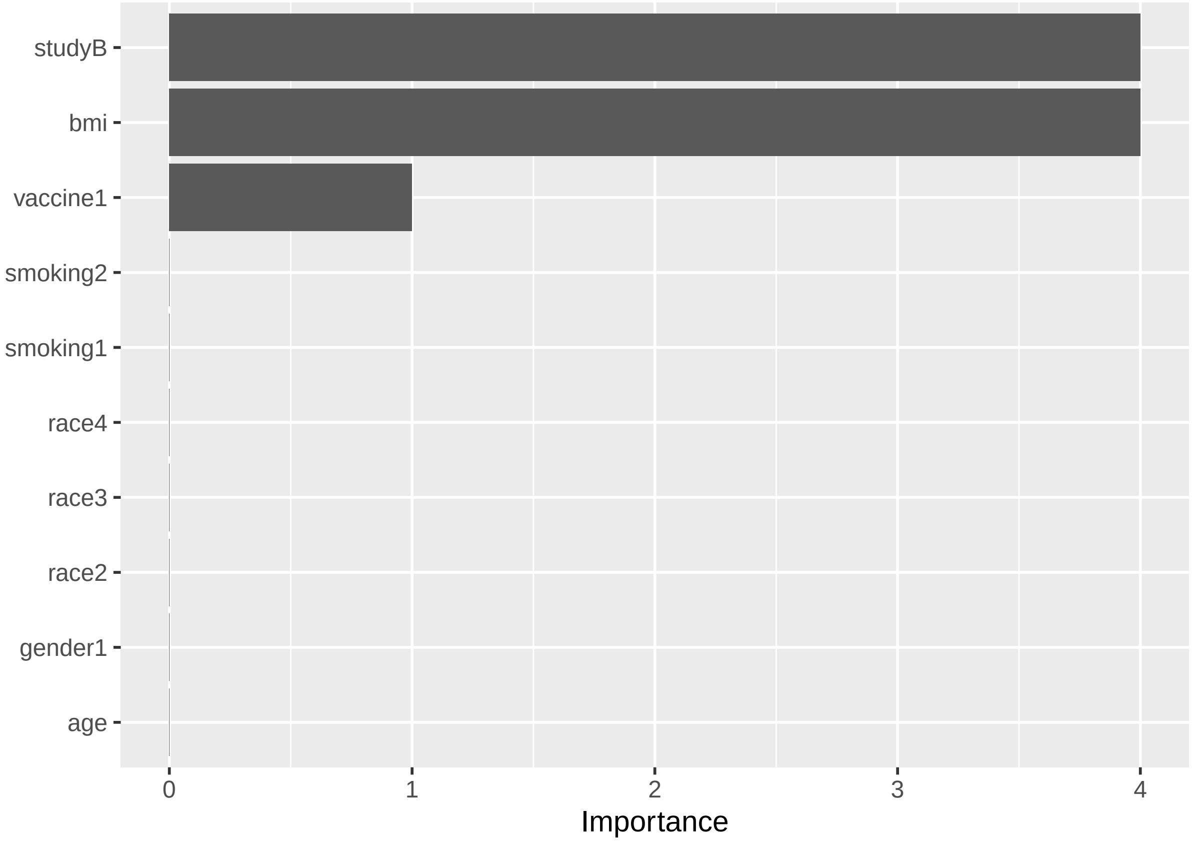
```
coef(mars.fit$finalModel)
```

```
##           (Intercept)          h(31.7-bmi) h(bmi-31.7) * studyB
##             19.366730             3.705371            34.383832
##           h(bmi-26.8)             vaccine1
##              6.695655            -7.788338
```

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

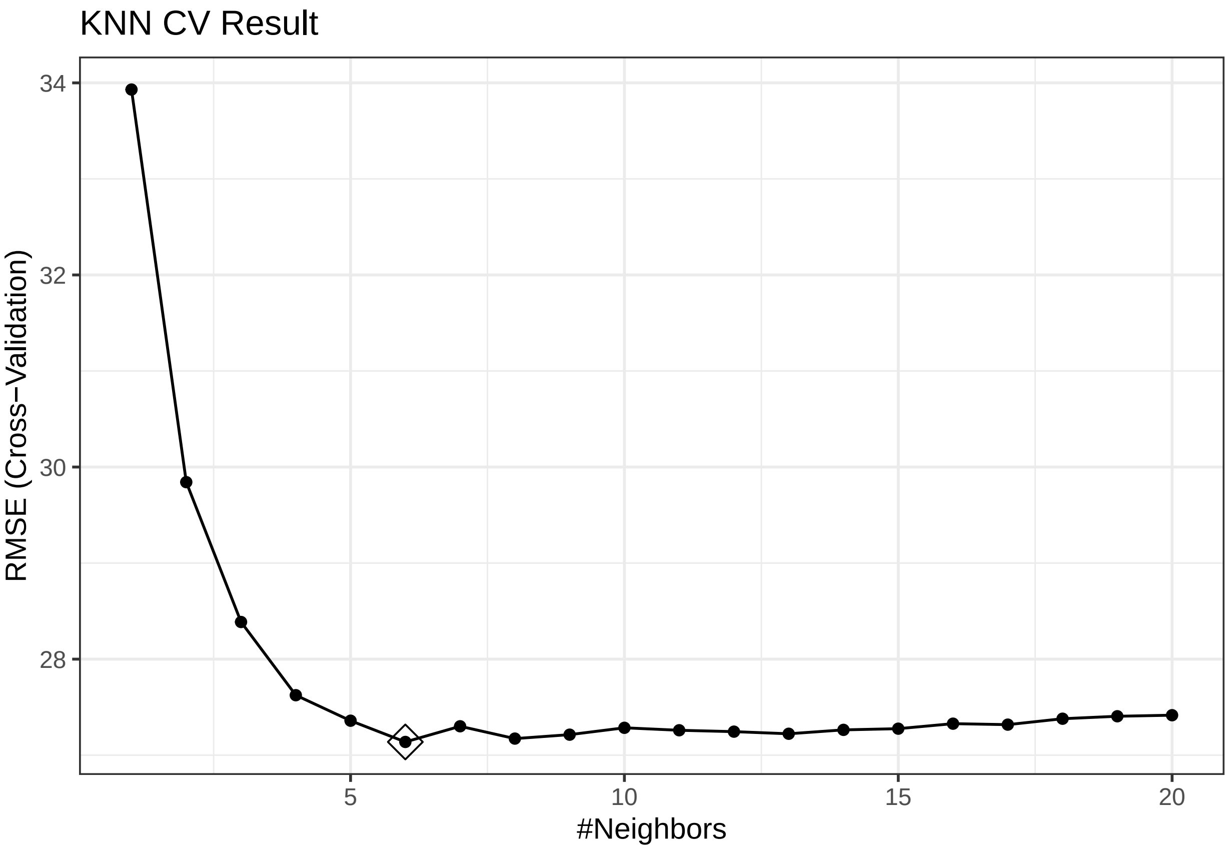
```
## Call: earth(x=matrix[2900,18], y=c(40,34,31,50,3...), keepxy=TRUE, degree=2,
##             nprune=5)
##
##                        coefficients
## (Intercept)               19.366730
## vaccine1                  -7.788338
## h(bmi-26.8)                6.695655
## h(31.7-bmi)                3.705371
## h(bmi-31.7) * studyB      34.383832
##
## Selected 5 of 25 terms, and 3 of 18 predictors (nprune=5)
## Termination condition: Reached nk 37
## Importance: bmi, studyB, vaccine1, age-unused, gender1-unused, ...
## Number of terms at each degree of interaction: 1 3 1
## GCV 491.1694    RSS 1413606    GRSq 0.4723714    RSq 0.4760052
```

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



### 3.2.9 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
```

#### 3.2.10 Bagging

#### 3.2.11 Random Forest

#### 3.2.12 Boosting

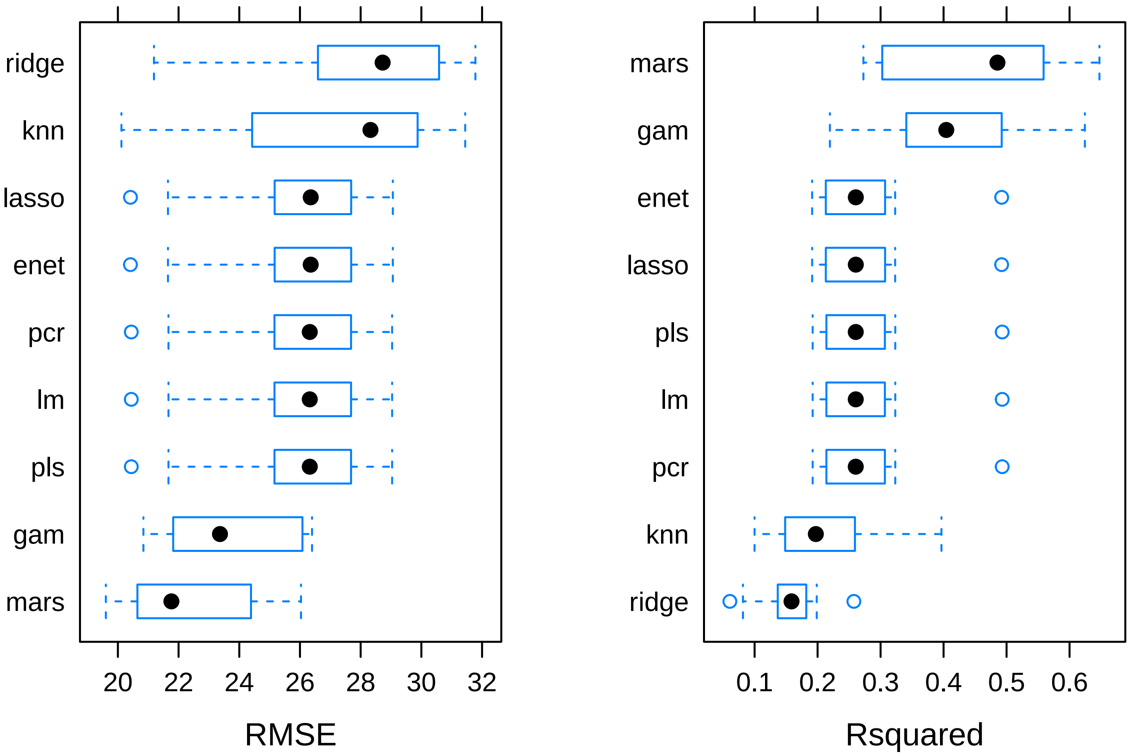
#### 3.2.13 Regression Trees

### 3.3 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))

summary(resamp)
```

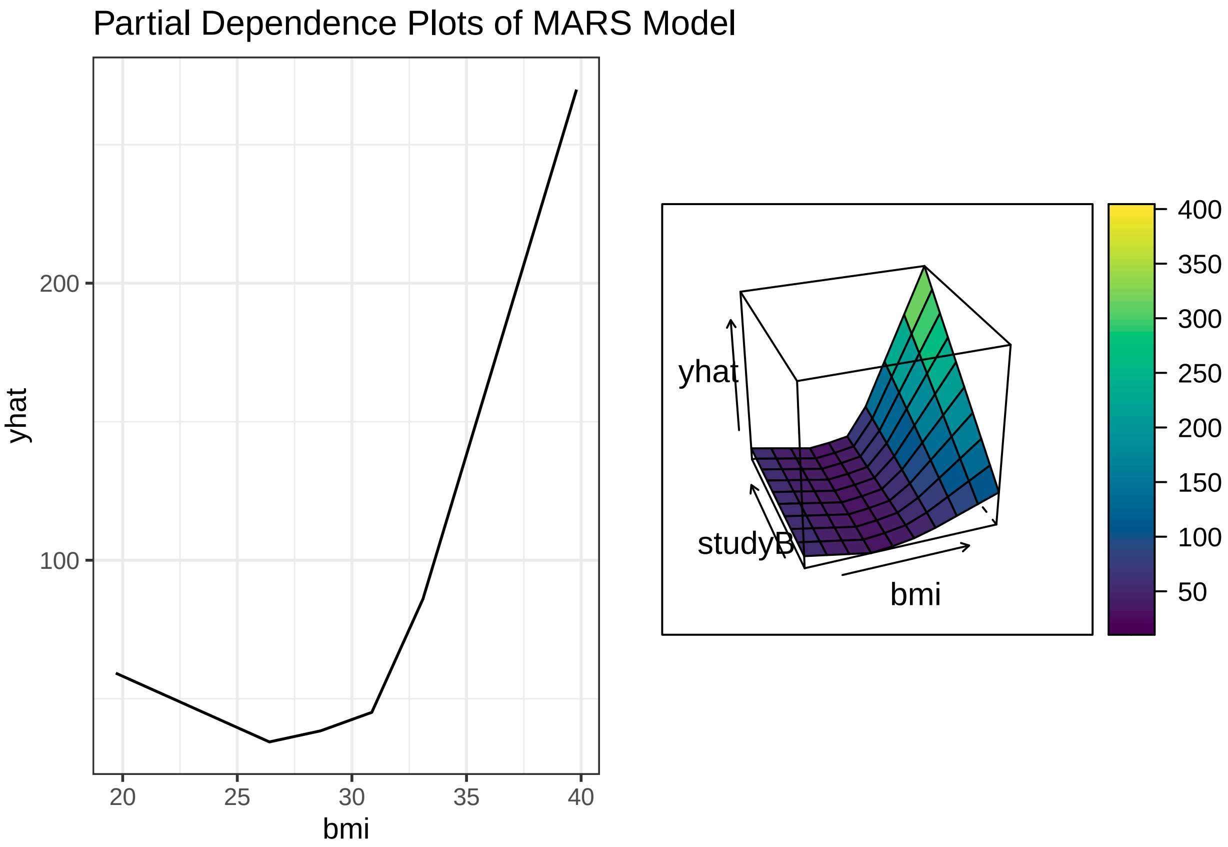
```
##
## Call:
## summary.resamples(object = resamp)
##
## Models: lm, lasso, ridge, enet, pcr, pls, gam, mars, knn
## Number of resamples: 10
##
## MAE
##           Min.  1st Qu.   Median     Mean  3rd Qu.     Max. NA's
## lm    15.54483 15.80758 16.63529 16.59842 17.13204 18.12333    0
## lasso 15.51069 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  14.06187 14.29497 14.88239 14.89479 15.31286 16.10880    0
## knn   14.43602 16.28400 16.79135 16.77166 17.45629 18.38966    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  19.60380 20.76550 21.76341 22.33527 23.91386 26.03407    0
## knn   20.11678 25.01933 28.32298 27.13762 29.65682 31.44427    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  0.27268902 0.3335869 0.4855151 0.4599541 0.5506146 0.6474131    0
## knn   0.09988269 0.1495740 0.1971881 0.2119237 0.2570144 0.3966191    0
```

```
# jpeg("./figure/resample.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()
```

```
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)
```



```
# dev.off()

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

```
##              Overall
## bmi        100.00000
## studyB     100.00000
## vaccine1    17.78457
```

## 3.4 Training / Testing Error

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

```
## [1] 22.07828
```

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

```
## [1] 22.1712
```

# 4 Secondary Analysis

## 4.1 Exploratory analysis and data visualization

```
# data summary
st_options(plain.ascii = FALSE,
           style = "rmarkdown",
           dfSummary.silent = TRUE,
           footnote = NA,
           subtitle.emphasis = FALSE)
dfSummary(train.bin.dat)
```

### 4.1.1 Data Frame Summary

**train.bin.dat**
**Dimensions:** 2900 x 15
**Duplicates:** 0

| No | Variable | Stats / Values | Freqs (% of Valid) | Graph | Valid | Missing |
|---|---|---|---|---|---|---|
| 1 | age [numeric] | Mean (sd) : 60.1 (4.5)<br>min < med < max:<br>45 < 60 < 77<br>IQR (CV) : 6 (0.1) | 33 distinct values | :<br>:<br>. : :<br>: : : .<br>. : : : : : . | 2900 (100.0%) | 0 (0.0%) |
| 2 | gender [factor] | 1. 0<br>2. 1 | 1468 (50.6%)<br>1432 (49.4%) | IIIIIIIIII<br>IIIIIIIII | 2900 (100.0%) | 0 (0.0%) |
| 3 | race [factor] | 1. 1<br>2. 2<br>3. 3<br>4. 4 | 1909 (65.8%)<br>132 ( 4.6%)<br>568 (19.6%)<br>291 (10.0%) | IIIIIIIIIIIII<br><br>III<br>II | 2900 (100.0%) | 0 (0.0%) |
| 4 | smoking [factor] | 1. 0<br>2. 1<br>3. 2 | 1763 (60.8%)<br>845 (29.1%)<br>292 (10.1%) | IIIIIIIIIIII<br>IIIII<br>II | 2900 (100.0%) | 0 (0.0%) |
| 5 | height [numeric] | Mean (sd) : 170.2 (6)<br>min < med < max:<br>151.2 < 170.1 < 188.6<br>IQR (CV) : 8 (0) | 312 distinct values | : :<br>: :<br>. : : .<br>: : : :<br>. : : : : . | 2900 (100.0%) | 0 (0.0%) |
| 6 | weight [numeric] | Mean (sd) : 80.2 (7)<br>min < med < max:<br>57.1 < 80.3 < 103.4<br>IQR (CV) : 9.5 (0.1) | 361 distinct values | . :<br>. : :<br>: : : :<br>. : : : : .<br>. : : : : : : . | 2900 (100.0%) | 0 (0.0%) |
| 7 | bmi [numeric] | Mean (sd) : 27.8 (2.7)<br>min < med < max:<br>19.7 < 27.7 < 39.8<br>IQR (CV) : 3.6 (0.1) | 160 distinct values | : .<br>: :<br>: : : .<br>: : : :<br>: : : : : : . | 2900 (100.0%) | 0 (0.0%) |
| 8 | hypertension [factor] | 1. 0<br>2. 1 | 1514 (52.2%)<br>1386 (47.8%) | IIIIIIIIII<br>IIIIIIIII | 2900 (100.0%) | 0 (0.0%) |
| 9 | diabetes [factor] | 1. 0<br>2. 1 | 2446 (84.3%)<br>454 (15.7%) | IIIIIIIIIIIIIIII<br>III | 2900 (100.0%) | 0 (0.0%) |

| No | Variable | Stats / Values | Freqs (% of Valid) | Graph | Valid | Missing |
|---|---|---|---|---|---|---|
| 10 | SBP<br>[numeric] | Mean (sd) : 130.2 (8.1)<br>min < med < max:<br>104 < 130 < 158<br>IQR (CV) : 11 (0.1) | 54 distinct values | :<br>: .<br>: : : .<br>. : : : :<br>. : : : : : : | 2900<br>(100.0%) | 0<br>(0.0%) |
| 11 | LDL<br>[numeric] | Mean (sd) : 110.3 (19.9)<br>min < med < max:<br>32 < 110 < 174<br>IQR (CV) : 27 (0.2) | 116 distinct values | . :<br>: : :<br>: : : .<br>: : : : :<br>. : : : : : . | 2900<br>(100.0%) | 0<br>(0.0%) |
| 12 | vaccine<br>[factor] | 1. 0<br>2. 1 | 1192 (41.1%)<br>1708 (58.9%) | IIIIIIII<br>IIIIIIIIIII | 2900<br>(100.0%) | 0<br>(0.0%) |
| 13 | severity<br>[factor] | 1. 0<br>2. 1 | 2619 (90.3%)<br>281 ( 9.7%) | IIIIIIIIIIIIIIIIII<br>I | 2900<br>(100.0%) | 0<br>(0.0%) |
| 14 | study<br>[factor] | 1. A<br>2. B<br>3. C | 580 (20.0%)<br>1750 (60.3%)<br>570 (19.7%) | IIII<br>IIIIIIIIIIII<br>III | 2900<br>(100.0%) | 0<br>(0.0%) |
| 15 | recovery_time<br>[numeric] | Min : 0<br>Mean : 0.7<br>Max : 1 | 0 : 887 (30.6%)<br>1 : 2013 (69.4%) | IIIIII<br>IIIIIIIIIIIII | 2900<br>(100.0%) | 0<br>(0.0%) |

```
skimr::skim_without_charts(train.bin.dat)
```

Table 6: Data summary

| | |
|---|---|
| Name | train.bin.dat |
| Number of rows | 2900 |
| Number of columns | 15 |
| Column type frequency: | |
| factor | 8 |
| numeric | 7 |
| Group variables | None |

**Variable type: factor**

| skim_variable | n_missing | complete_rate | ordered | n_unique | top_counts |
|---|---|---|---|---|---|
| gender | 0 | 1 | FALSE | 2 | 0: 1468, 1: 1432 |
| race | 0 | 1 | FALSE | 4 | 1: 1909, 3: 568, 4: 291, 2: 132 |
| smoking | 0 | 1 | FALSE | 3 | 0: 1763, 1: 845, 2: 292 |
| hypertension | 0 | 1 | FALSE | 2 | 0: 1514, 1: 1386 |
| diabetes | 0 | 1 | FALSE | 2 | 0: 2446, 1: 454 |
| vaccine | 0 | 1 | FALSE | 2 | 1: 1708, 0: 1192 |
| severity | 0 | 1 | FALSE | 2 | 0: 2619, 1: 281 |
| study | 0 | 1 | FALSE | 3 | B: 1750, A: 580, C: 570 |

**Variable type: numeric**

| skim_variable | n_missing | complete_rate | mean | sd | p0 | p25 | p50 | p75 | p100 |
|---|---|---|---|---|---|---|---|---|---|
| age | 0 | 1 | 60.07 | 4.51 | 45.0 | 57.0 | 60.00 | 63.0 | 77.0 |
| height | 0 | 1 | 170.17 | 6.04 | 151.2 | 166.1 | 170.15 | 174.1 | 188.6 |
| weight | 0 | 1 | 80.20 | 7.00 | 57.1 | 75.4 | 80.30 | 84.9 | 103.4 |
| bmi | 0 | 1 | 27.76 | 2.73 | 19.7 | 25.9 | 27.70 | 29.5 | 39.8 |
| SBP | 0 | 1 | 130.19 | 8.08 | 104.0 | 125.0 | 130.00 | 136.0 | 158.0 |
| LDL | 0 | 1 | 110.27 | 19.87 | 32.0 | 97.0 | 110.00 | 124.0 | 174.0 |
| recovery_time | 0 | 1 | 0.69 | 0.46 | 0.0 | 0.0 | 1.00 | 1.0 | 1.0 |

```
######################################################################
## Remember to edit the next chunk if you do any modification here:)
######################################################################
```

## 4.2 Model Training

### 4.2.1 Logistic Regression

### 4.2.2 Penalized Logistic Regression

### 4.2.3 Generalized Additive Model (GAM) for classification

### 4.2.4 Multivariate Adaptive Regression Splines (MARS) for classification

### 4.2.5 Linear Discriminant Analysis (LDA)

### 4.2.6 Quadratic Discriminant Analysis (QDA)

### 4.2.7 Naive Bayes (NB)

### 4.2.8 Bagging

### 4.2.9 Random Forest

### 4.2.10 Boosting

### 4.2.11 Classification Trees

### 4.2.12 Support Vector Machine (SVM)

### 4.2.13 Hierarchical Clustering

### 4.2.14 Principal Component Analysis (PCA)

## 4.3 Model Selection

## 4.4 Training / Testing Error