midterm project

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```r
library(tidyverse)
```

```
## -- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
## v dplyr     1.1.3     v readr     2.1.4
## v forcats   1.0.0     v stringr   1.5.0
## v ggplot2   3.4.4     v tibble    3.2.1
## v lubridate 1.9.2     v tidyr     1.3.0
## v purrr     1.0.2
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become error
```

```r
library(summarytools)
```

```
##
## Attaching package: 'summarytools'
##
## The following object is masked from 'package:tibble':
##
##     view
```

```r
library(leaps)
library(corrplot)
```

```
## corrplot 0.92 loaded
```

```r
library(dplyr)
library(ggplot2)
library(ISLR)
library(glmnet)
```

```
## Loading required package: Matrix
##
## Attaching package: 'Matrix'
##
## The following objects are masked from 'package:tidyr':
##
##     expand, pack, unpack
##
## Loaded glmnet 4.1-8
```

```r
library(caret)
```

```
## Loading required package: lattice
##
## Attaching package: 'caret'
##
## The following object is masked from 'package:purrr':
##
##     lift
```

```r
library(tidymodels)
```

```
## -- Attaching packages -------------------------------------- tidymodels 1.1.1 --
## v broom        1.0.5     v rsample      1.2.0
## v dials        1.2.0     v tune         1.1.2
## v infer        1.0.5     v workflows    1.1.3
## v modeldata    1.2.0     v workflowsets 1.0.1
## v parsnip      1.1.1     v yardstick    1.2.0
## v recipes      1.0.8
## -- Conflicts ----------------------------------------- tidymodels_conflicts() --
## x scales::discard()        masks purrr::discard()
## x Matrix::expand()         masks tidyr::expand()
## x dplyr::filter()          masks stats::filter()
## x recipes::fixed()         masks stringr::fixed()
## x dplyr::lag()             masks stats::lag()
## x caret::lift()            masks purrr::lift()
## x Matrix::pack()           masks tidyr::pack()
## x yardstick::precision()   masks caret::precision()
## x yardstick::recall()      masks caret::recall()
## x yardstick::sensitivity() masks caret::sensitivity()
## x yardstick::spec()        masks readr::spec()
## x yardstick::specificity() masks caret::specificity()
## x recipes::step()          masks stats::step()
## x Matrix::unpack()         masks tidyr::unpack()
## x recipes::update()        masks Matrix::update(), stats::update()
## x summarytools::view()     masks tibble::view()
## * Dig deeper into tidy modeling with R at https://www.tmwr.org
```

```r
library(plotmo)
```

```
## Loading required package: Formula
## Loading required package: plotrix
##
## Attaching package: 'plotrix'
##
## The following object is masked from 'package:scales':
##
##     rescale
##
## Loading required package: TeachingDemos
```

```r
library(caret)
library(tidymodels)
library(splines)
library(mgcv)
```

```
## Loading required package: nlme
##
## Attaching package: 'nlme'
##
## The following object is masked from 'package:dplyr':
##
##     collapse
##
## This is mgcv 1.9-0. For overview type 'help("mgcv-package")'.
```

```r
library(pdp)
```

```
##
## Attaching package: 'pdp'
##
## The following object is masked from 'package:purrr':
##
##     partial
```

```r
library(earth)
library(tidyverse)
library(ggplot2)
library(bayesQR)
```

Exploratory analysis and data visualization

```r
load("recovery.RData")
st_options(plain.ascii = TRUE,
           style = "rmarkdown",
           dfSummary.silent = TRUE,
           footnote = NA,
           subtitle.emphasis = FALSE)
dfSummary(dat[,-1])
```

```
## Data Frame Summary
## dat
## Dimensions: 3000 x 15
## Duplicates: 0
##
## -----------------------------------------------------------------------------------------------------
## No   Variable        Stats / Values             Freqs (% of Valid)    Graph                 Valid
## ---- --------------- -------------------------- --------------------- --------------------- ---------
## 1    age             Mean (sd) : 60.2 (4.5)     34 distinct values          : .             3000
##      [numeric]       min < med < max:                                       : :             (100.0%)
##                      42 < 60 < 79                                           : :
##                      IQR (CV) : 6 (0.1)                                   . : : .
##                                                                           : : : :
##
## 2    gender          Min  : 0                   0 : 1544 (51.5%)      IIIIIIIIII            3000
##      [integer]       Mean : 0.5                 1 : 1456 (48.5%)      IIIIIIIII             (100.0%)
##                      Max  : 1
##
## 3    race            1. 1                       1967 (65.6%)          IIIIIIIIIIIII         3000
##      [factor]        2. 2                        158 ( 5.3%)          I                     (100.0%)
##                      3. 3                        604 (20.1%)          IIII
##                      4. 4                        271 ( 9.0%)          I
##
## 4    smoking         1. 0                       1822 (60.7%)          IIIIIIIIIIII          3000
##      [factor]        2. 1                        859 (28.6%)          IIIII                 (100.0%)
##                      3. 2                        319 (10.6%)          II
##
## 5    height          Mean (sd) : 169.9 (6)      313 distinct values           : :           3000
##      [numeric]       min < med < max:                                         : :           (100.0%)
##                      147.8 < 169.9 < 188.6                                  . : : : .
##                      IQR (CV) : 7.9 (0)                                     : : : :
##                                                                           . : : : : : .
##
## 6    weight          Mean (sd) : 80 (7.1)       364 distinct values           : .           3000
##      [numeric]       min < med < max:                                         : :           (100.0%)
##                      55.9 < 79.8 < 103.7                                    : : : :
##                      IQR (CV) : 9.6 (0.1)                                 . : : : : : .
##                                                                         . : : : : : : : .
##
## 7    bmi             Mean (sd) : 27.8 (2.8)     163 distinct values         . :             3000
##      [numeric]       min < med < max:                                       : : :           (100.0%)
##                      18.8 < 27.6 < 38.9                                     : : :
##                      IQR (CV) : 3.7 (0.1)                                 : : : : :
##                                                                         . : : : : : : .
##
## 8    hypertension    Min  : 0                   0 : 1508 (50.3%)      IIIIIIIIII            3000
##      [numeric]       Mean : 0.5                 1 : 1492 (49.7%)      IIIIIIIII             (100.0%)
##                      Max  : 1
##
## 9    diabetes        Min  : 0                   0 : 2537 (84.6%)      IIIIIIIIIIIIIIII      3000
##      [integer]       Mean : 0.2                 1 :  463 (15.4%)      III                   (100.0%)
##                      Max  : 1
##
## 10   SBP             Mean (sd) : 130.5 (8)      52 distinct values            : .           3000
##      [numeric]       min < med < max:                                         : : .         (100.0%)
##                      105 < 130 < 156                                        : : : :
##                      IQR (CV) : 11 (0.1)                                  . : : : : : .
##                                                                         . : : : : : : : .
##
## 11   LDL             Mean (sd) : 110.5 (19.8)   114 distinct values             :           3000
##      [numeric]       min < med < max:                                         : : .         (100.0%)
##                      28 < 110 < 178                                           : : :
##                      IQR (CV) : 27 (0.2)                                    . : : : .
##                                                                           . : : : : : : .
##
## 12   vaccine         Min  : 0                   0 : 1212 (40.4%)      IIIIIIII              3000
##      [integer]       Mean : 0.6                1 : 1788 (59.6%)      IIIIIIIIIII           (100.0%)
##                      Max  : 1
##
## 13   severity        Min  : 0                  0 : 2679 (89.3%)      IIIIIIIIIIIIIIIII     3000
##      [integer]       Mean : 0.1                1 :  321 (10.7%)      II                    (100.0%)
##                      Max  : 1
##
## 14   study           1. A                      2000 (66.7%)          IIIIIIIIIIIII         3000
##      [character]     2. B                      1000 (33.3%)          IIIIII                (100.0%)
##
## 15   recovery_time   Mean (sd) : 42.2 (23.2)   140 distinct values   : :                   3000
##      [numeric]       min < med < max:                                : :                   (100.0%)
##                      2 < 39 < 365                                    : :
##                      IQR (CV) : 18 (0.5)                             : :
##                                                                      : : .
## ----------------------------------------------------------------------------------------------------
```

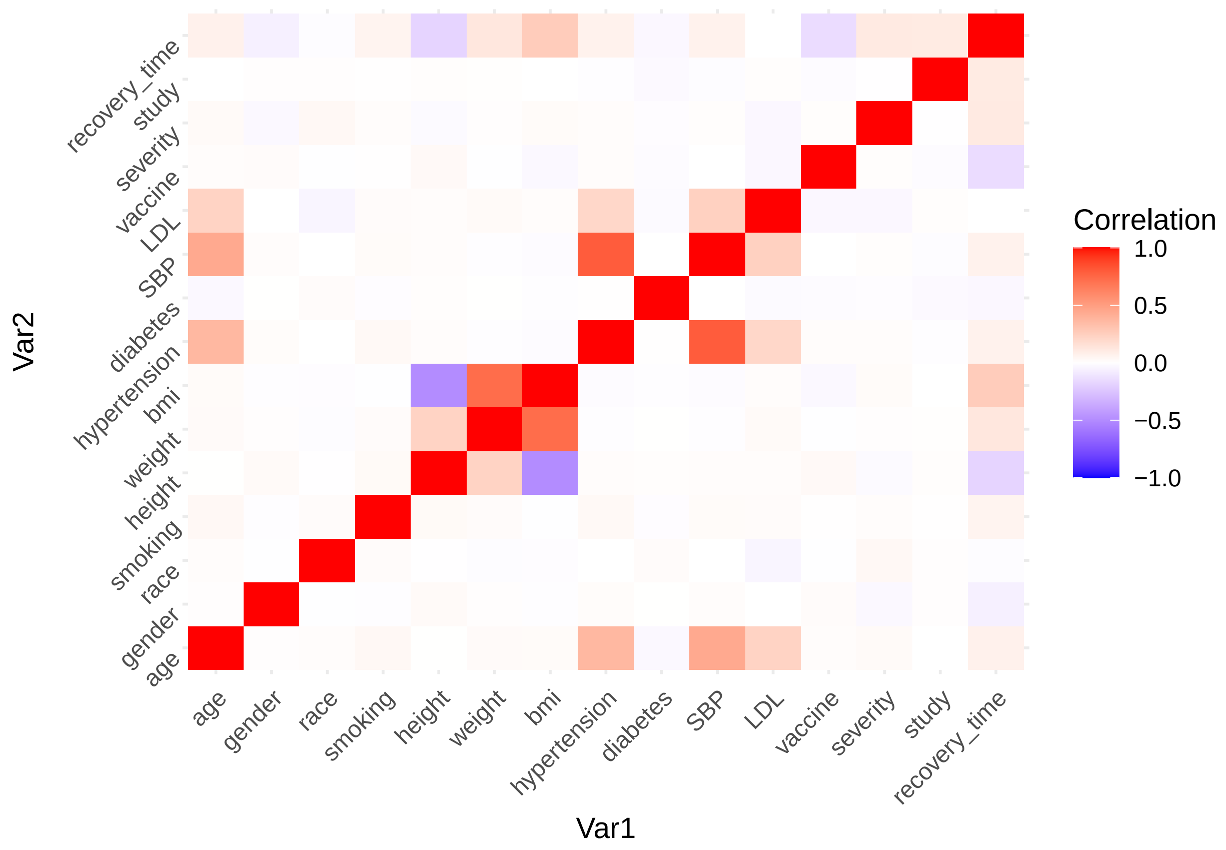
```r
summary(dat)
```

```
##        id              age            gender          race     smoking
##  Min.   :   1.0   Min.   :42.0   Min.   :0.0000   1:1967   0:1822
##  1st Qu.: 750.8   1st Qu.:57.0   1st Qu.:0.0000   2: 158   1: 859
##  Median :1500.5   Median :60.0   Median :0.0000   3: 604   2: 319
##  Mean   :1500.5   Mean   :60.2   Mean   :0.4853   4: 271
##  3rd Qu.:2250.2   3rd Qu.:63.0   3rd Qu.:1.0000
##  Max.   :3000.0   Max.   :79.0   Max.   :1.0000
##      height          weight            bmi         hypertension
##  Min.   :147.8   Min.   : 55.90   Min.   :18.80   Min.   :0.0000
##  1st Qu.:166.0   1st Qu.: 75.20   1st Qu.:25.80   1st Qu.:0.0000
##  Median :169.9   Median : 79.80   Median :27.65   Median :0.0000
##  Mean   :169.9   Mean   : 79.96   Mean   :27.76   Mean   :0.4973
##  3rd Qu.:173.9   3rd Qu.: 84.80   3rd Qu.:29.50   3rd Qu.:1.0000
##  Max.   :188.6   Max.   :103.70   Max.   :38.90   Max.   :1.0000
##     diabetes           SBP             LDL            vaccine
##  Min.   :0.0000   Min.   :105.0   Min.   : 28.0   Min.   :0.000
##  1st Qu.:0.0000   1st Qu.:125.0   1st Qu.: 97.0   1st Qu.:0.000
##  Median :0.0000   Median :130.0   Median :110.0   Median :1.000
##  Mean   :0.1543   Mean   :130.5   Mean   :110.5   Mean   :0.596
##  3rd Qu.:0.0000   3rd Qu.:136.0   3rd Qu.:124.0   3rd Qu.:1.000
##  Max.   :1.0000   Max.   :156.0   Max.   :178.0   Max.   :1.000
##     severity        study           recovery_time
##  Min.   :0.000   Length:3000        Min.   :  2.00
##  1st Qu.:0.000   Class :character   1st Qu.: 31.00
##  Median :0.000   Mode  :character   Median : 39.00
##  Mean   :0.107                      Mean   : 42.17
##  3rd Qu.:0.000                      3rd Qu.: 49.00
##  Max.   :1.000                      Max.   :365.00
```

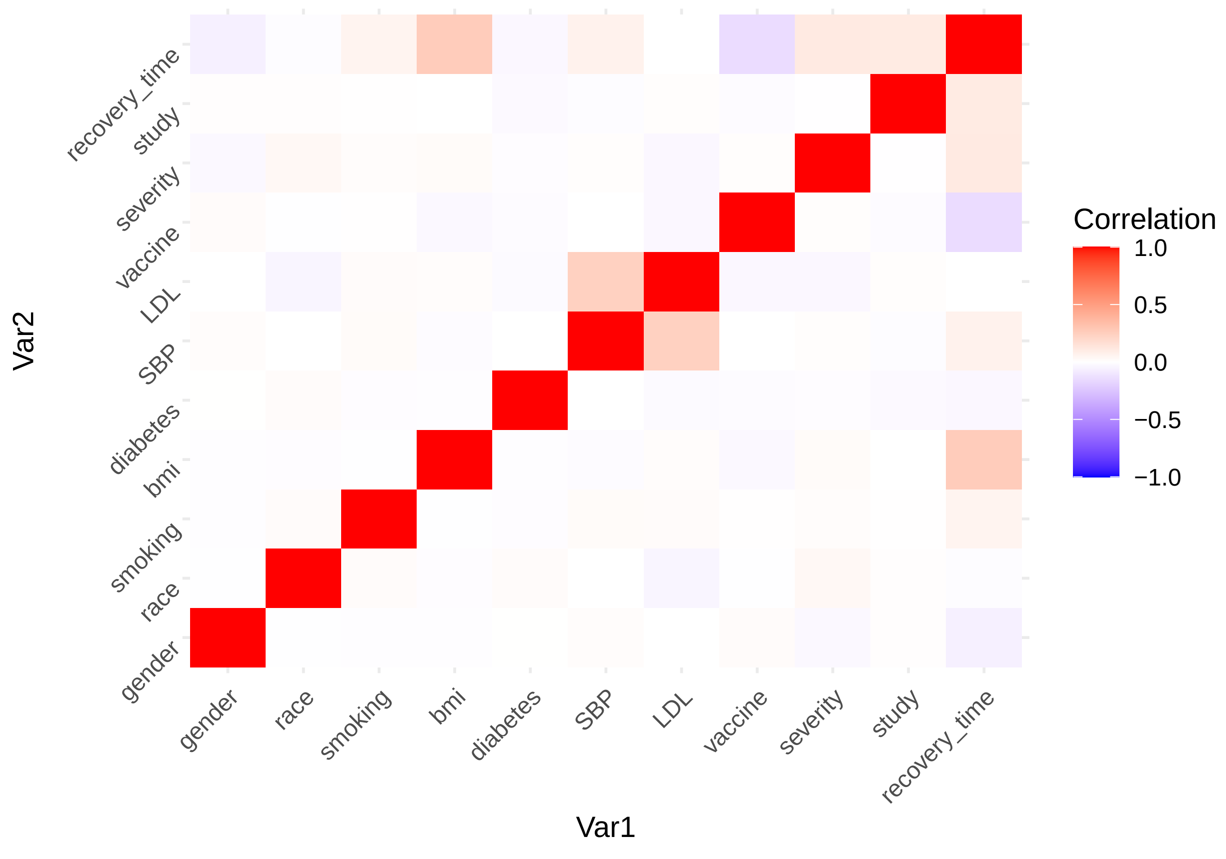
```r
columns_to_convert <- c("gender", "race", "smoking", "hypertension", "diabetes", "vaccine", "severity")

dat$study <- as.character(dat$study)
unique(dat$study)
```

```
## [1] "A" "B"
```

```r
# Convert selected factor variables to numeric using mutate
dat <- dat %>%
  mutate(across(all_of(columns_to_convert), as.numeric)) %>%
  mutate(study = case_when(
    study == "A" ~ 1,
    study == "B" ~ 2
  ))

numeric_data <- dat[, c("age", "gender", "race", "smoking", "height", "weight", "bmi", "hypertension",

# Compute correlation matrix
correlation_matrix <- cor(numeric_data)
correlation_df <- as.data.frame(as.table(correlation_matrix))
names(correlation_df) <- c("Var1", "Var2", "Correlation")

ggplot(correlation_df, aes(x = Var1, y = Var2, fill = Correlation)) +
  geom_tile() +
  scale_fill_gradient2(low = "blue", mid = "white", high = "red",
                       midpoint = 0, limits = c(-1, 1),
                       name = "Correlation") +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 45, vjust = 1, hjust = 1),
        axis.text.y = element_text(angle = 45, vjust = 1, hjust = 1))
```

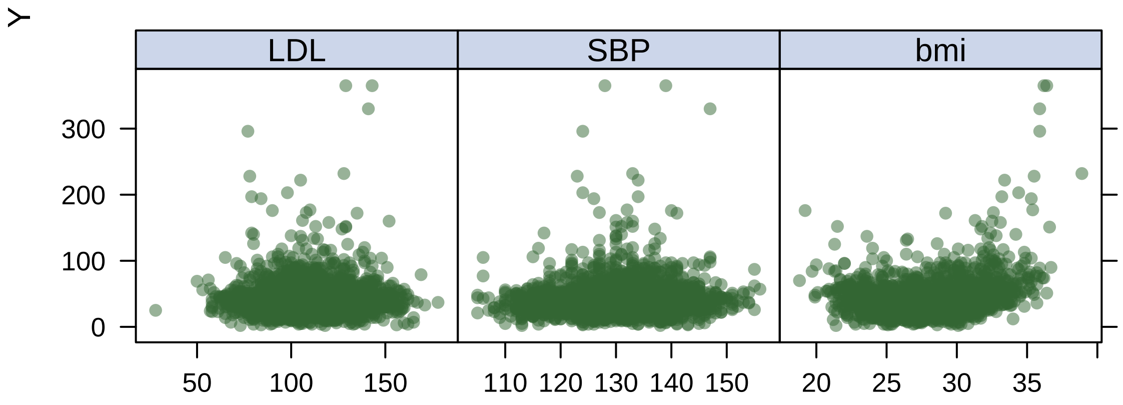


```r
dat_subset <- dat %>%
  select(-id, -height, -weight, -hypertension, -age)
numeric_data <- dat_subset[, c("gender", "race", "smoking", "bmi", "diabetes", "SBP", "LDL", "vaccine",

# Compute correlation matrix
correlation_matrix <- cor(numeric_data)
correlation_df <- as.data.frame(as.table(correlation_matrix))
names(correlation_df) <- c("Var1", "Var2", "Correlation")

ggplot(correlation_df, aes(x = Var1, y = Var2, fill = Correlation)) +
  geom_tile() +
  scale_fill_gradient2(low = "blue", mid = "white", high = "red",
                       midpoint = 0, limits = c(-1, 1),
                       name = "Correlation") +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 45, vjust = 1, hjust = 1),
        axis.text.y = element_text(angle = 45, vjust = 1, hjust = 1))
```



Model training

```r
ctrl1 <- trainControl(method = "cv", number = 10)
set.seed(1)
data <-
  dat_subset %>%
  mutate(gender = as.factor(gender),
         race = as.factor(race),
         smoking = as.factor(smoking),
         diabetes = as.factor(diabetes),
         vaccine = as.factor(vaccine),
         severity = as.factor(severity),
         study = as.factor(study))
data <- data %>% mutate(bmi2 = bmi^2,
                        bmi3 = bmi^3,
                        bmi4 = bmi^4)
data_split <- initial_split(data, prop = 0.8)
# Extract the training and test data
training_data <- training(data_split)
testing_data <- testing(data_split)

x<-model.matrix(recovery_time ~ ., data)[,-1]
y<-data$recovery_time

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)

featurePlot(x[, c('LDL','SBP','bmi')], y, plot = "scatter", labels = c("", "Y"), type = c("p"), layout
```



```r
fit1 <- lm(recovery_time ~ LDL, data = data)
fit2 <- lm(recovery_time ~ poly(LDL,2), data = data)
fit3 <- lm(recovery_time ~ poly(LDL,3), data = data)
fit4 <- lm(recovery_time ~ poly(LDL,4), data = data)
fit5 <- lm(recovery_time ~ poly(LDL,5), data = data)
anova(fit1, fit2, fit3, fit4, fit5)
```

```
## Analysis of Variance Table
##
## Model 1: recovery_time ~ LDL
## Model 2: recovery_time ~ poly(LDL, 2)
## Model 3: recovery_time ~ poly(LDL, 3)
## Model 4: recovery_time ~ poly(LDL, 4)
## Model 5: recovery_time ~ poly(LDL, 5)
##   Res.Df     RSS Df Sum of Sq      F Pr(>F)
## 1   2998 1607736
## 2   2997 1607696  1     39.47 0.0736 0.7862
## 3   2996 1607693  1      3.50 0.0065 0.9356
## 4   2995 1606441  1   1251.37 2.3326 0.1268
## 5   2994 1606218  1    222.94 0.4156 0.5192
```

```r
fit1 <- lm(recovery_time ~ bmi, data = data)
fit2 <- lm(recovery_time ~ poly(bmi,2), data = data)
fit3 <- lm(recovery_time ~ poly(bmi,3), data = data)
fit4 <- lm(recovery_time ~ poly(bmi,4), data = data)
fit5 <- lm(recovery_time ~ poly(bmi,5), data = data)
anova(fit1, fit2, fit3, fit4, fit5)
```

```
## Analysis of Variance Table
##
## Model 1: recovery_time ~ bmi
## Model 2: recovery_time ~ poly(bmi, 2)
## Model 3: recovery_time ~ poly(bmi, 3)
## Model 4: recovery_time ~ poly(bmi, 4)
## Model 5: recovery_time ~ poly(bmi, 5)
##   Res.Df     RSS Df Sum of Sq        F    Pr(>F)
## 1   2998 1493906
## 2   2997 1225737  1    268169 672.9018 < 2.2e-16 ***
## 3   2996 1209491  1     16246  40.7645 1.984e-10 ***
## 4   2995 1193212  1     16279  40.8479 1.902e-10 ***
## 5   2994 1193186  1        26   0.0654    0.7981
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
fit1 <- lm(recovery_time ~ SBP, data = data)
fit2 <- lm(recovery_time ~ poly(SBP,2), data = data)
fit3 <- lm(recovery_time ~ poly(SBP,3), data = data)
fit4 <- lm(recovery_time ~ poly(SBP,4), data = data)
fit5 <- lm(recovery_time ~ poly(SBP,5), data = data)
anova(fit1, fit2, fit3, fit4, fit5)
```

```
## Analysis of Variance Table
```

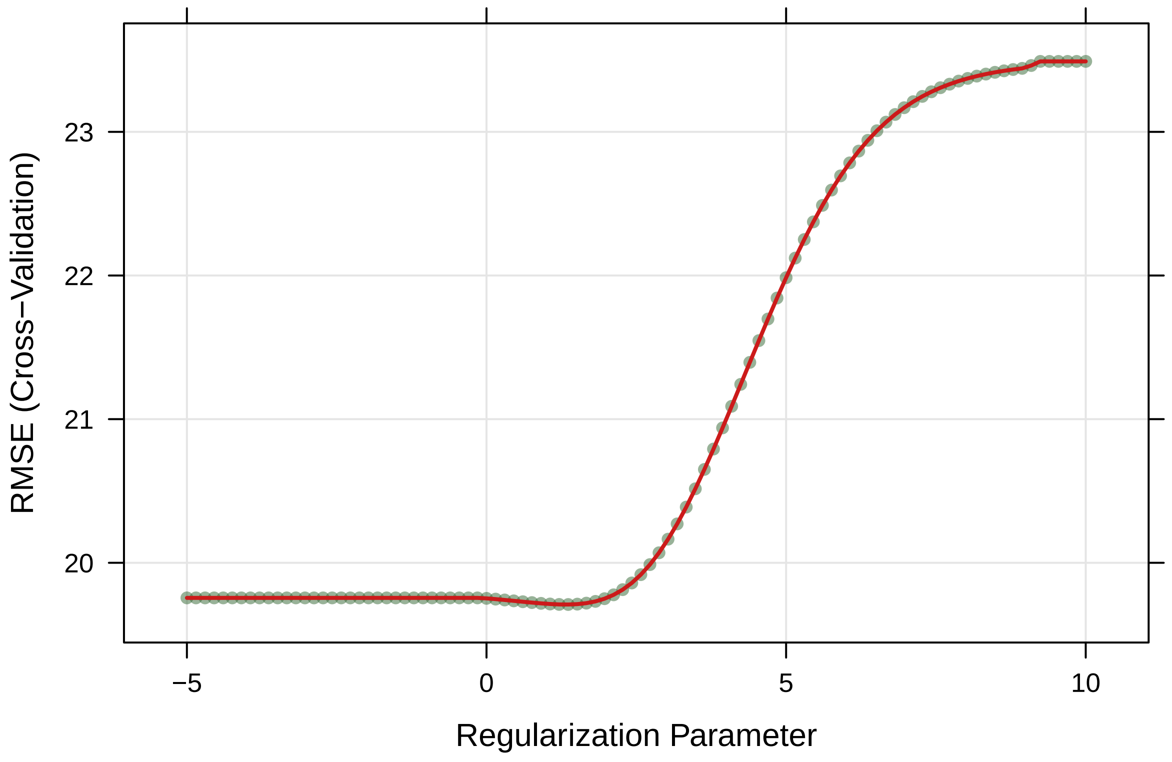
```
##
## Model 1: recovery_time ~ SBP
## Model 2: recovery_time ~ poly(SBP, 2)
## Model 3: recovery_time ~ poly(SBP, 3)
## Model 4: recovery_time ~ poly(SBP, 4)
## Model 5: recovery_time ~ poly(SBP, 5)
##   Res.Df     RSS Df Sum of Sq      F Pr(>F)
## 1   2998 1600160
## 2   2997 1599272  1    888.48 1.6649 0.1970
## 3   2996 1599086  1    185.73 0.3480 0.5553
## 4   2995 1597839  1   1247.49 2.3376 0.1264
## 5   2994 1597780  1     58.28 0.1092 0.7411
```

Ridge regression

```
set.seed(1)
ridge.fit <- train(recovery_time ~ . -bmi +poly(bmi,4),
                   data = training_data,
                   method = "glmnet",
                   tuneGrid = expand.grid(alpha = 0,
                       lambda = exp(seq(10, -5, length=100))),
                   trControl = ctrl1)
```

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

```
plot(ridge.fit, xTrans = log)
```



```
ridge.fit$bestTune
```

```
##    alpha   lambda
## 43     0 3.910387
```

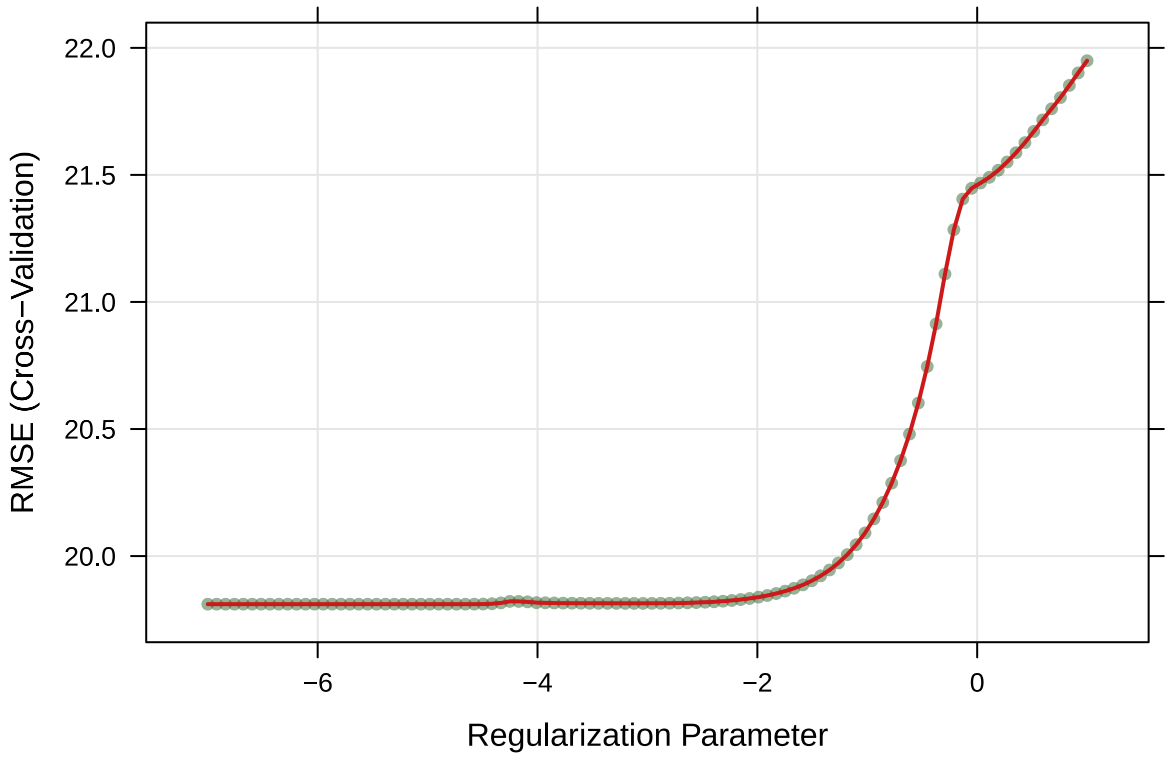
```
coef(ridge.fit$finalModel, s = ridge.fit$bestTune$lambda)
```

```
## 20 x 1 sparse Matrix of class "dgCMatrix"
##                          s1
## (Intercept)    5.333793e+00
## gender1       -2.955573e+00
## race2          4.828105e-01
## race3         -3.095463e-01
## race4         -6.370540e-01
## smoking2       2.628569e+00
## smoking3       3.282424e+00
## diabetes1     -1.012184e+00
## SBP            1.693015e-01
## LDL           -2.634208e-02
## vaccine1      -5.555976e+00
## severity1      6.860505e+00
## study2         3.995434e+00
## bmi2           9.172307e-03
## bmi3           2.915556e-04
## bmi4           9.487007e-06
## poly(bmi, 4)1  4.434198e+01
## poly(bmi, 4)2  3.667694e+02
## poly(bmi, 4)3  1.285576e+02
## poly(bmi, 4)4  8.337111e+01
```

```
ridge.pred <- predict(ridge.fit, newdata = testing_data)
# test error
mean((ridge.pred - testing_data[, "recovery_time"])^2)
```

```
## [1] 305.0968
```

```
set.seed(1)
lasso.fit <- train(recovery_time ~ .,
                   data = training_data,
                   method = "glmnet",
                   tuneGrid = expand.grid(alpha = 1,
                                          lambda = exp(seq(1, -7, length = 100))),
                   trControl = ctrl1)
plot(lasso.fit, xTrans = log)
```



```
lasso.fit$bestTune
```

```
##    alpha      lambda
## 30     1 0.009499029
```

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

```
## 17 x 1 sparse Matrix of class "dgCMatrix"
##                        s1
## (Intercept) 169.155809970
## gender1      -3.574149920
## race2         0.156095718
## race3        -0.323448879
## race4        -0.675742585
## smoking2      3.274206336
## smoking3      4.098609493
## bmi          -1.753584488
## diabetes1    -1.217219485
## SBP           0.198048448
## LDL          -0.030632238
## vaccine1     -6.472767874
## severity1     7.713670120
## study2        4.593372747
## bmi2         -0.325460260
## bmi3          .
## bmi4          0.000245325
```

```r
lasso.pred <- predict(lasso.fit, newdata = testing_data)
# test error
mean((lasso.pred - testing_data[, "recovery_time"])^2)
```

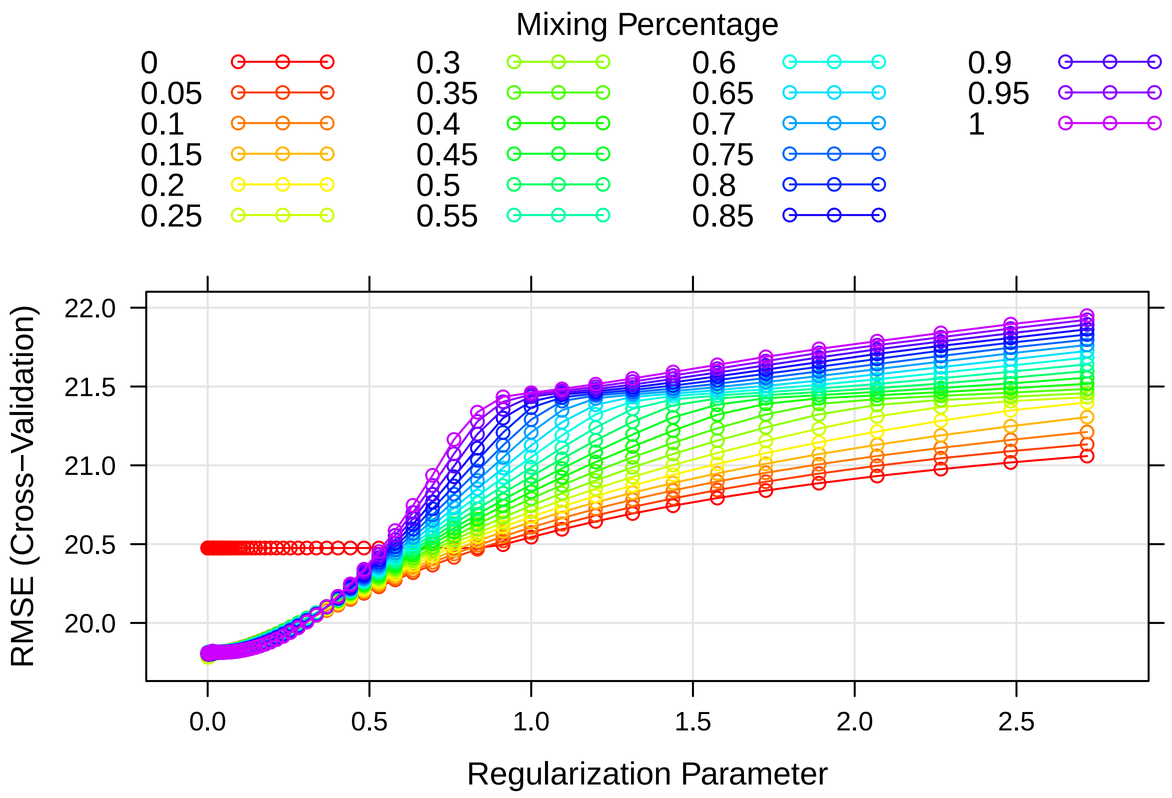
```
## [1] 304.8401
```

Elastic Net

```r
set.seed(1)
enet.fit <- train(recovery_time ~ .,
                  data = training_data,
                  method = "glmnet",
                  tuneGrid = expand.grid(alpha = seq(0, 1, length = 21),
                                         lambda = exp(seq(1, -8, length = 100))),
                  trControl = ctrl1)
enet.fit$bestTune
```

```
##     alpha      lambda
## 526  0.25 0.003255945
```

```r
myCol <- rainbow(25)
myPar <- list(superpose.symbol = list(col = myCol),
              superpose.line = list(col = myCol))
plot(enet.fit, par.settings = myPar)
```



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

```
## 17 x 1 sparse Matrix of class "dgCMatrix"
##                         s1
## (Intercept) 193.901653987
## gender1      -3.592612004
## race2         0.183024786
## race3        -0.348096094
## race4        -0.712789065
## smoking2      3.304545993
## smoking3      4.135463922
## bmi          -4.469201129
## diabetes1    -1.242388991
## SBP           0.199417123
## LDL          -0.031210770
## vaccine1     -6.491738379
## severity1     7.736171655
## study2        4.611309984
## bmi2         -0.222775216
## bmi3         -0.001498305
## bmi4          0.000251091
```

```r
enet.pred <- predict(enet.fit, newdata = testing_data)
# test error
mean((enet.pred - testing_data[, "recovery_time"])^2)
```

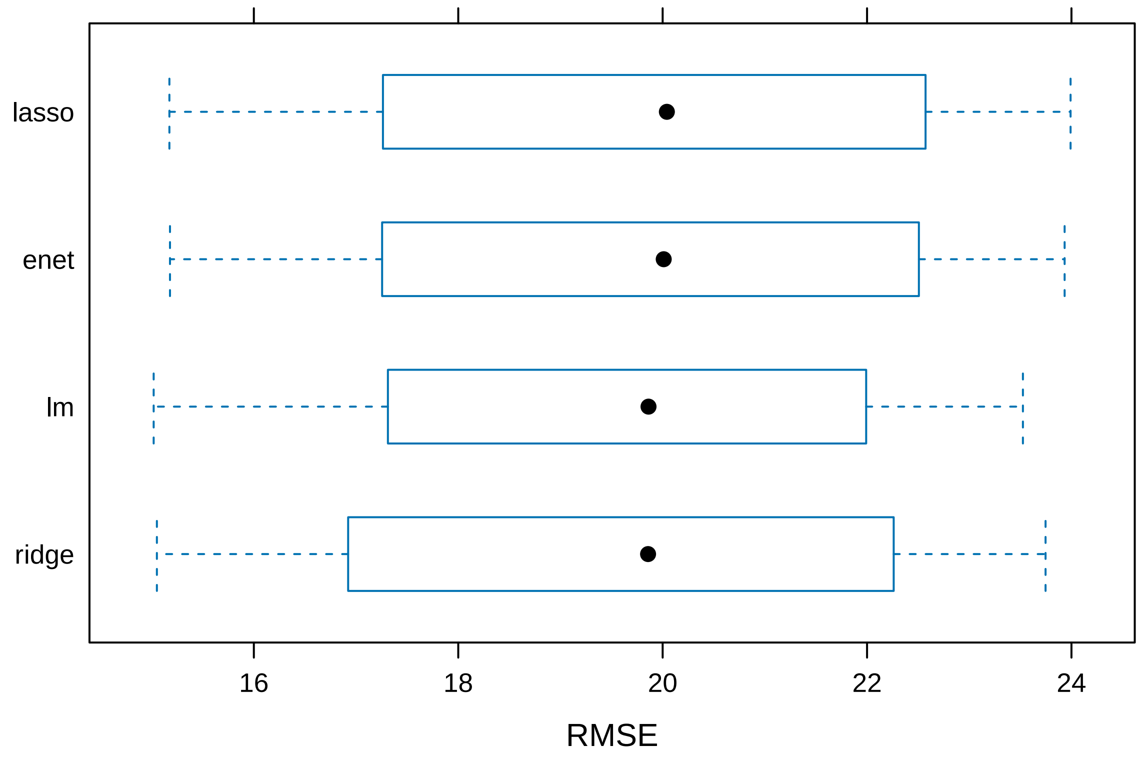
```
## [1] 304.6396
```

Comparison

```
set.seed(1)
lm.fit <- train(recovery_time ~ .,
                data = training_data,
                method = "lm",
                trControl = ctrl1)
resamp <- resamples(list(enet = enet.fit, lasso = lasso.fit, ridge = ridge.fit, lm = lm.fit))
summary(resamp)
```

```
##
## Call:
## summary.resamples(object = resamp)
##
## Models: enet, lasso, ridge, lm
## Number of resamples: 10
##
## MAE
##           Min.  1st Qu.   Median     Mean  3rd Qu.     Max. NA's
## enet  11.19243 12.28303 12.87973 12.82832 13.28650 14.37349    0
## lasso 11.18210 12.28336 12.88231 12.83247 13.31513 14.37639    0
## ridge 10.95950 11.98726 12.51584 12.55722 13.02833 14.28922    0
## lm    11.03198 12.32874 12.67890 12.74138 13.13532 14.46433    0
##
## RMSE
##           Min.  1st Qu.   Median     Mean  3rd Qu.     Max. NA's
## enet  15.17942 17.28326 20.01063 19.78329 22.43991 23.93315    0
## lasso 15.17382 17.28987 20.04142 19.81051 22.50011 23.99149    0
## ridge 15.05136 17.05601 19.85728 19.70967 22.25151 23.74660    0
## lm    15.01978 17.52849 19.86189 19.79750 21.96821 23.52521    0
##
## Rsquared
##            Min.   1st Qu.    Median      Mean   3rd Qu.      Max. NA's
## enet  0.1574160 0.2137419 0.3165027 0.2951554 0.3364036 0.5131303    0
## lasso 0.1571902 0.2135190 0.3140797 0.2930746 0.3314665 0.5126260    0
## ridge 0.1593233 0.2095450 0.3081263 0.3052204 0.3768813 0.5149272    0
## lm    0.1527942 0.2141530 0.3067285 0.3054667 0.3788317 0.5158586    0
```

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



PCR

```
# show information about the model
modelLookup("pcr")
```

```
##   model parameter       label forReg forClass probModel
## 1   pcr     ncomp #Components   TRUE    FALSE     FALSE
```

```
modelLookup("pls")
```

```
##   model parameter       label forReg forClass probModel
## 1   pls     ncomp #Components   TRUE     TRUE      TRUE
```

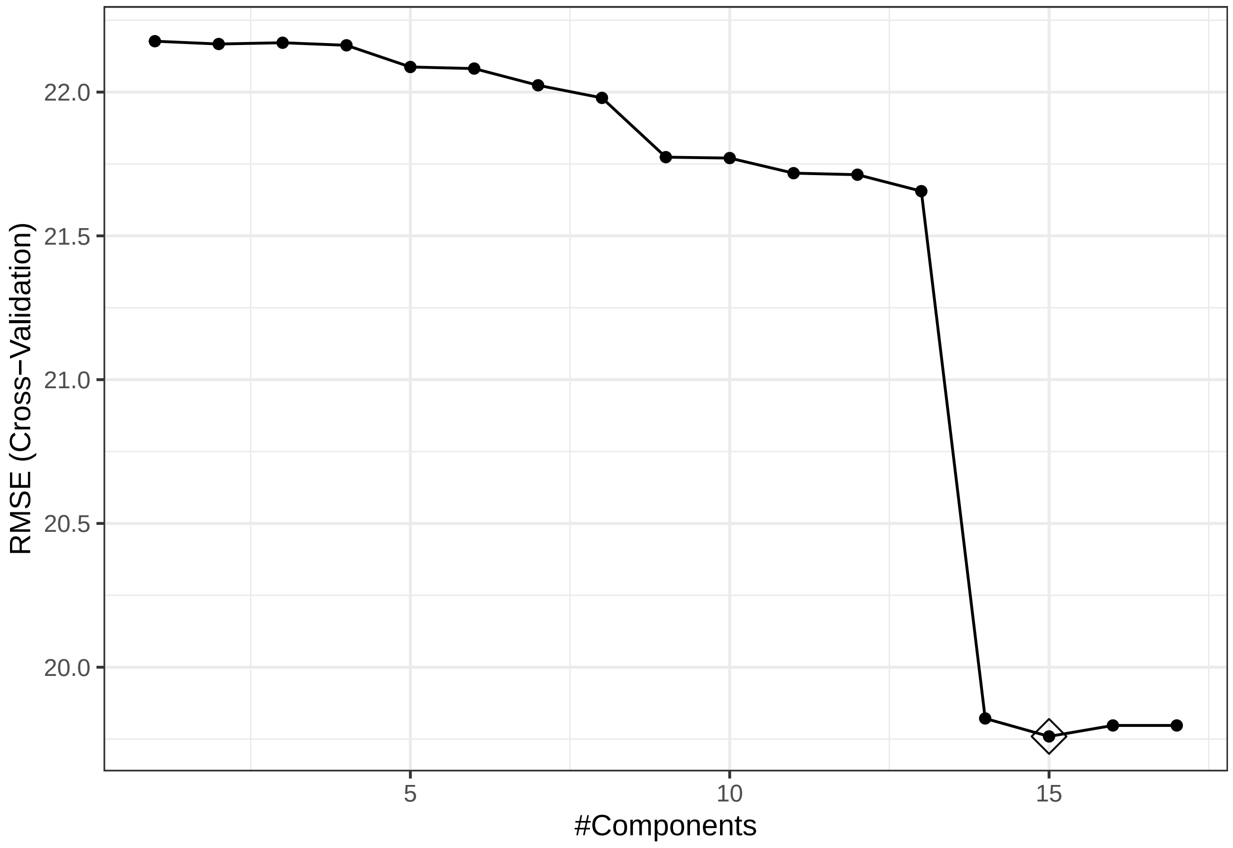
```
#x <- model.matrix(recovery_time ~ ., training_data)[, -1]
#y <- training_data$recovery_time
# test data
#x2 <- model.matrix(recovery_time ~ .,testing_data)[, -1]
#y2 <- testing_data$recovery_time

set.seed(1)
pcr.fit <- train(recovery_time ~ .,
                 data = training_data,
                 method = "pcr",
                 tuneGrid = data.frame(ncomp = 1:17),
                 trControl = ctrl1,
                 preProcess = c("center", "scale"))
pcr.fit$bestTune
```

```
##    ncomp
## 15    15
```

```
predy2.pcr2 <- predict(pcr.fit, newdata = testing_data)
mean((y - predy2.pcr2)^2)
```

```
## [1] 662.9783
```

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



PLS

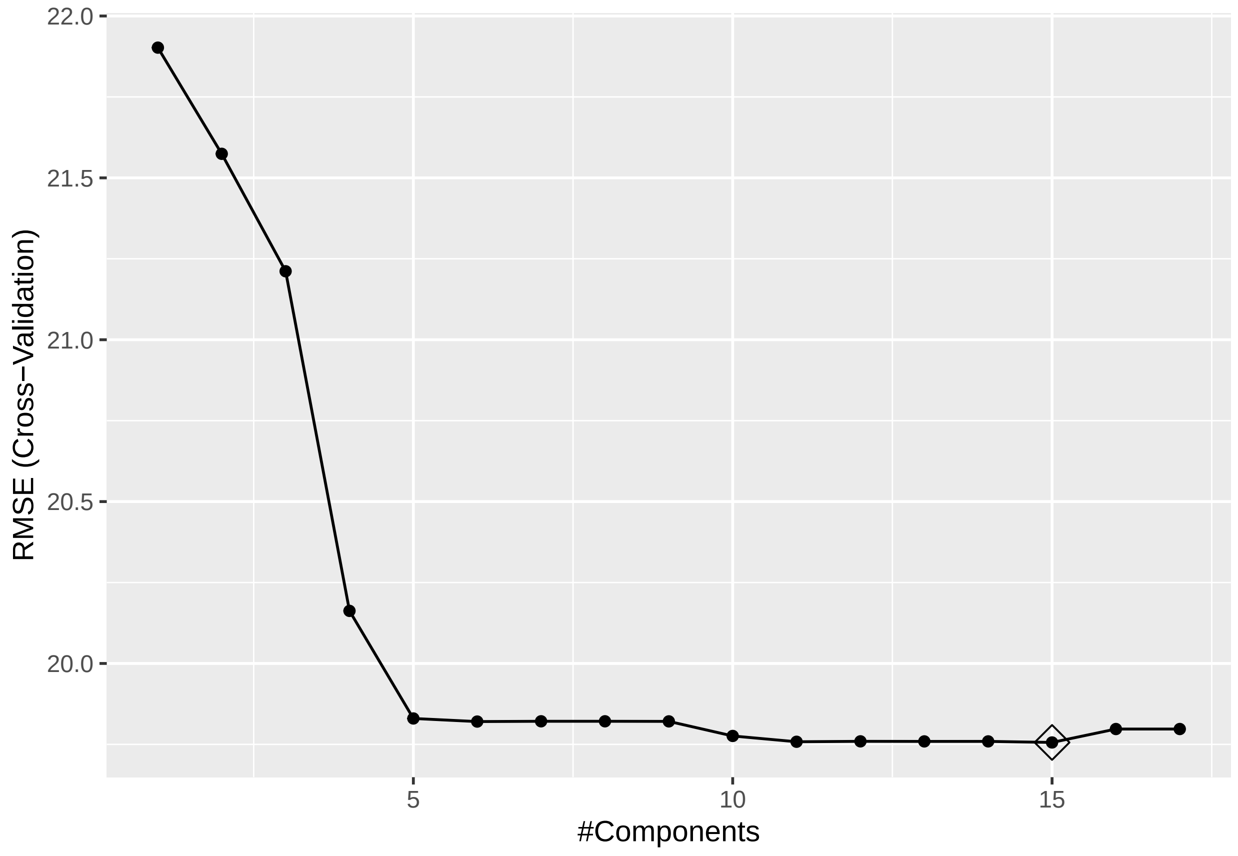
```
set.seed(1)
pls.fit <- train(recovery_time ~ .,
                 data = training_data,
                 method = "pls",
                 tuneGrid = data.frame(ncomp = 1:17),
                 trControl = ctrl1,
                 preProcess = c("center", "scale"))
predy2.pls2 <- predict(pls.fit, newdata = testing_data)
mean((y - predy2.pls2)^2)
```

```
## [1] 662.9475
```

```
pls.fit$bestTune
```

```
##    ncomp
## 15    15
```

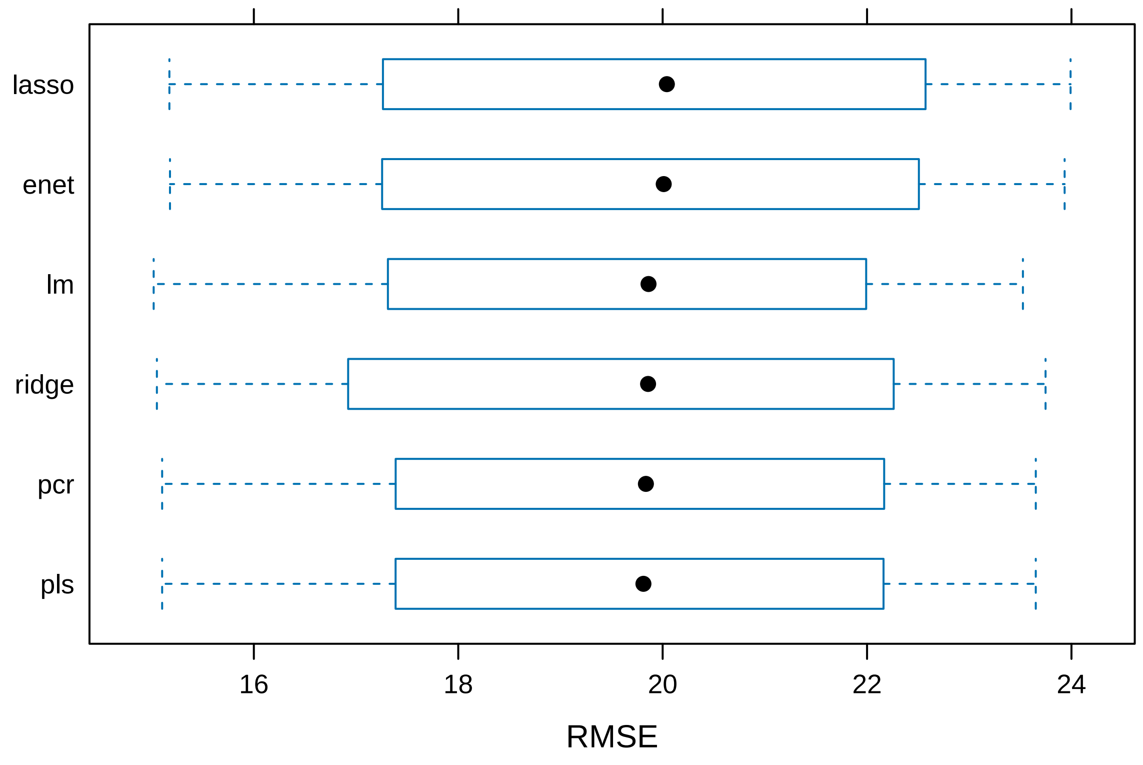
```
ggplot(pls.fit, highlight = TRUE)
```



```
resamp <- resamples(list(enet = enet.fit, lasso = lasso.fit, ridge = ridge.fit, lm = lm.fit,pls = pls.fi
summary(resamp)
```

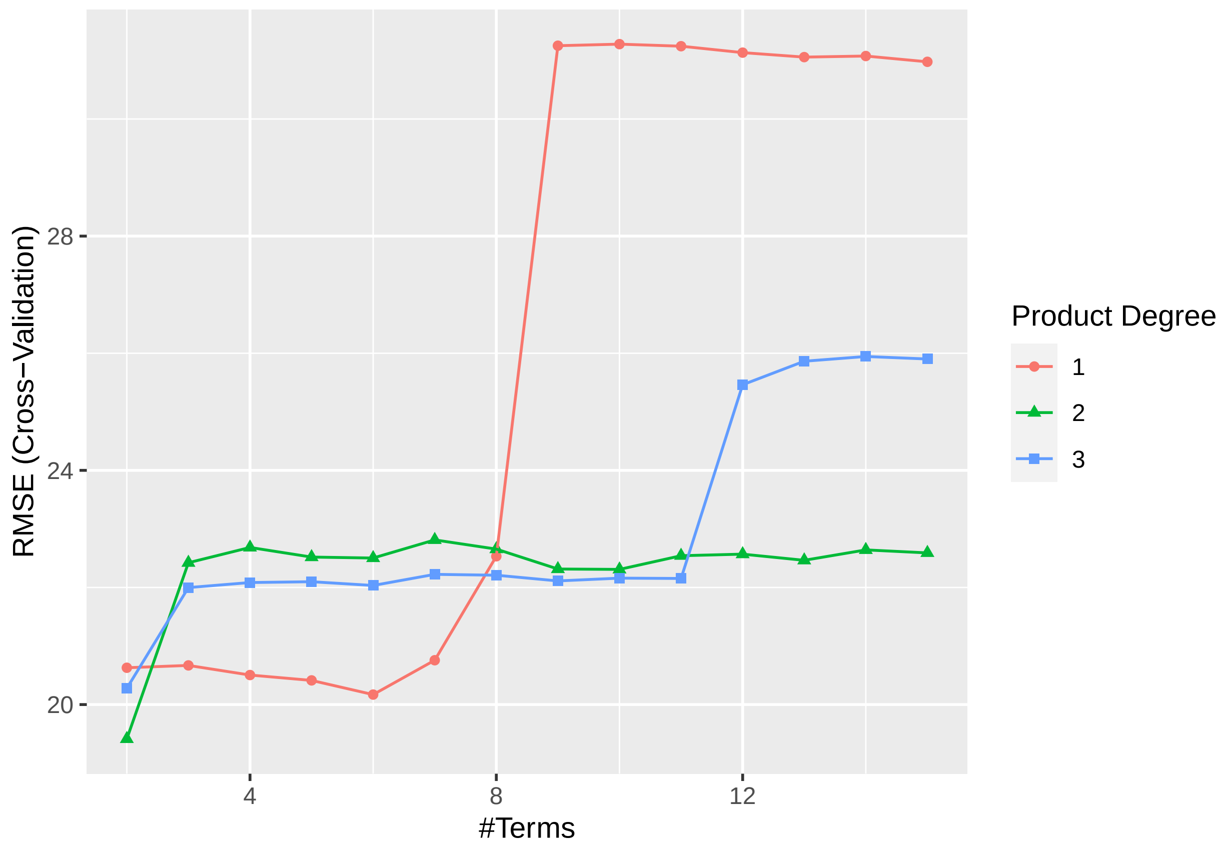
```
##
## Call:
## summary.resamples(object = resamp)
##
## Models: enet, lasso, ridge, lm, pls, pcr
## Number of resamples: 10
##
## MAE
##           Min.  1st Qu.   Median     Mean  3rd Qu.     Max. NA's
## enet  11.19243 12.28303 12.87973 12.82832 13.28650 14.37349    0
## lasso 11.18210 12.28336 12.88231 12.83247 13.31513 14.37639    0
## ridge 10.95950 11.98726 12.51584 12.55722 13.02833 14.28922    0
## lm    11.03198 12.32874 12.67890 12.74138 13.13532 14.46433    0
## pls   11.09836 12.30310 12.87270 12.79128 13.19942 14.42377    0
## pcr   11.09891 12.30337 12.85146 12.78847 13.19881 14.42453    0
##
## RMSE
##           Min.  1st Qu.   Median     Mean  3rd Qu.     Max. NA's
## enet  15.17942 17.28326 20.01063 19.78329 22.43991 23.93315    0
## lasso 15.17382 17.28987 20.04142 19.81051 22.50011 23.99149    0
## ridge 15.05136 17.05601 19.85728 19.70967 22.25151 23.74660    0
## lm    15.01978 17.52849 19.86189 19.79750 21.96821 23.52521    0
## pls   15.10279 17.43433 19.81192 19.75604 22.13012 23.65080    0
## pcr   15.10280 17.43486 19.83610 19.75938 22.14057 23.65119    0
##
## Rsquared
##            Min.   1st Qu.    Median      Mean   3rd Qu.      Max. NA's
## enet  0.1574160 0.2137419 0.3165027 0.2951554 0.3364036 0.5131303    0
## lasso 0.1571902 0.2135190 0.3140797 0.2930746 0.3314665 0.5126260    0
## ridge 0.1593233 0.2095450 0.3081263 0.3052204 0.3768813 0.5149272    0
## lm    0.1527942 0.2141530 0.3067285 0.3054667 0.3788317 0.5158586    0
## pls   0.1534147 0.2135833 0.3136269 0.3008433 0.3627103 0.5067731    0
## pcr   0.1533912 0.2114601 0.3137550 0.3005294 0.3625788 0.5067576    0
```

```r
bwplot(resamp, metric = "RMSE")
```



MARS

```
mars_grid <- expand.grid(degree = 1:3, nprune = 2:15)
set.seed(1)
mars.fit <- train(recovery_time ~ .,data = training_data,
                  method = "earth",
                  tuneGrid = mars_grid,
                  trControl = ctrl1)
ggplot(mars.fit)
```



```
mars.fit$bestTune
```

```
##    nprune degree
## 15      2      2
```

```
mars.pred <- predict(mars.fit, newdata = testing_data)
mean((mars.pred - testing_data[, "recovery_time"])^2)
```

```
## [1] 350.9301
```

```
set.seed(1)
gam.fit <- train(recovery_time ~ .,
```

```r
                  data = training_data,
                  method = "gam",
                  trControl = ctrl1)
gam.fit$bestTune
```

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

```r
gam.fit$finalModel
```

```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## .outcome ~ gender1 + race2 + race3 + race4 + smoking2 + smoking3 +
##     diabetes1 + vaccine1 + severity1 + study2 + s(SBP) + s(LDL) +
##     s(bmi) + s(bmi2) + s(bmi3) + s(bmi4)
##
## Estimated degrees of freedom:
## 0.9019 4.6205 0.5665 0.0619 8.0001 0.8229  total = 25.97
##
## GCV score: 382.9841
```

```r
gam_pred <- predict(gam.fit, newdata = testing_data)
mean((gam_pred - testing_data$recovery_time)^2)
```

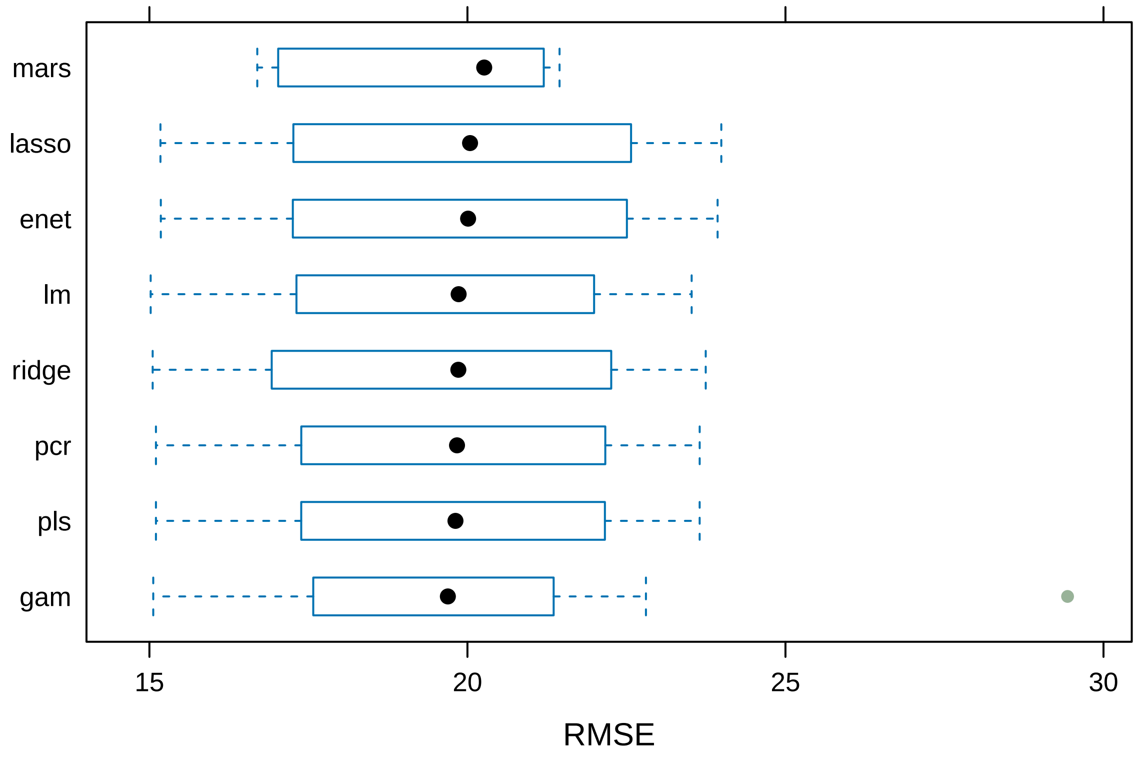
```
## [1] 307.2322
```

```r
set.seed(1)
resamp <- resamples(list(enet = enet.fit, lasso = lasso.fit, ridge = ridge.fit, lm = lm.fit,pls = pls.fi
summary(resamp)
```

```
##
## Call:
## summary.resamples(object = resamp)
##
## Models: enet, lasso, ridge, lm, pls, pcr, mars, gam
## Number of resamples: 10
##
## MAE
##           Min.  1st Qu.   Median     Mean  3rd Qu.     Max. NA's
## enet  11.19243 12.28303 12.87973 12.82832 13.28650 14.37349    0
## lasso 11.18210 12.28336 12.88231 12.83247 13.31513 14.37639    0
## ridge 10.95950 11.98726 12.51584 12.55722 13.02833 14.28922    0
## lm    11.03198 12.32874 12.67890 12.74138 13.13532 14.46433    0
## pls   11.09836 12.30310 12.87270 12.79128 13.19942 14.42377    0
## pcr   11.09891 12.30337 12.85146 12.78847 13.19881 14.42453    0
## mars  12.03188 12.39737 12.74942 12.84437 13.40388 13.69395    0
## gam   11.01263 12.33175 12.53916 12.81030 13.12889 15.67349    0
##
```

```
## RMSE
##            Min.  1st Qu.   Median     Mean  3rd Qu.     Max. NA's
## enet  15.17942 17.28326 20.01063 19.78329 22.43991 23.93315    0
## lasso 15.17382 17.28987 20.04142 19.81051 22.50011 23.99149    0
## ridge 15.05136 17.05601 19.85728 19.70967 22.25151 23.74660    0
## lm    15.01978 17.52849 19.86189 19.79750 21.96821 23.52521    0
## pls   15.10279 17.43433 19.81192 19.75604 22.13012 23.65080    0
## pcr   15.10280 17.43486 19.83610 19.75938 22.14057 23.65119    0
## mars  16.69585 17.22443 20.26374 19.41309 21.18100 21.44825    0
## gam   15.06042 17.64721 19.69238 20.15536 21.28434 29.43546    0
##
## Rsquared
##              Min.   1st Qu.    Median      Mean   3rd Qu.      Max. NA's
## enet  0.15741603 0.2137419 0.3165027 0.2951554 0.3364036 0.5131303    0
## lasso 0.15719022 0.2135190 0.3140797 0.2930746 0.3314665 0.5126260    0
## ridge 0.15932334 0.2095450 0.3081263 0.3052204 0.3768813 0.5149272    0
## lm    0.15279421 0.2141530 0.3067285 0.3054667 0.3788317 0.5158586    0
## pls   0.15341473 0.2135833 0.3136269 0.3008433 0.3627103 0.5067731    0
## pcr   0.15339123 0.2114601 0.3137550 0.3005294 0.3625788 0.5067576    0
## mars  0.02656562 0.1765903 0.3581283 0.3234134 0.4885344 0.5032351    0
## gam   0.14930906 0.1801864 0.3050085 0.3057842 0.4056275 0.5161894    0
```

```r
bwplot(resamp, metric = "RMSE")
```


mars
lasso
enet
lm
ridge
pcr
pls
gam
RMSE