Linear Models

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To gain a better understanding of the factors that predict recovery time from COVID-19 illness, a study was designed to combine three existing cohort studies that have been tracking participants for several years. The study collects recovery information through questionnaires and medical records, and leverages existing data on personal characteristics prior to the pandemic.

In this project, we predict the recovery time based on important risk factors. The training data is in "training_df", and the test data is in "training_df". The response is in the column "Time to recovery (tt_recovery_time)", and other variables can be used as predictors. The variable definitions can be found in "dictionary.txt".

First, we import the data and adjust the variable type. As we want to compare different models afterwards, we use caret.

```
set.seed(2716)
# Load Data
load("./Data/recovery.RData")
dat <- dat |>
  mutate(gender = as_factor(gender),
         diabetes = as_factor(diabetes),
         hypertension = as_factor(hypertension),
         vaccine = as_factor(vaccine),
         severity = as_factor(severity)) |>
  select(-id)
```

```
# data splitting
data.split = initial_split(dat, prop = 0.8)
training_data = training(data.split)
testing_data = testing(data.split)

# check missing values
training_data |> is.na() |> sum()
```

```
## [1] 0
```

```
testing_data |> is.na() |> sum()
```

```
## [1] 0
```

```
# summary of training and testing data
training_data |> summary()
```

```
##       age        gender   race     smoking      height          weight
##  Min.   :42.00   0:1235   1:1569   0:1442   Min.   :147.8   Min.   : 57.80
##  1st Qu.:57.00   1:1165   2: 134   1: 700   1st Qu.:166.1   1st Qu.: 75.30
##  Median :60.00            3: 475   2: 258   Median :170.0   Median : 79.80
##  Mean   :60.13            4: 222            Mean   :170.0   Mean   : 80.01
##  3rd Qu.:63.00                              3rd Qu.:174.0   3rd Qu.: 84.83
##  Max.   :79.00                              Max.   :188.6   Max.   :103.70
##       bmi        hypertension diabetes      SBP             LDL        vaccine
##  Min.   :18.80   0:1223       0:2032   Min.   :105.0   Min.   : 28.0   0: 961
##  1st Qu.:25.80   1:1177       1: 368   1st Qu.:125.0   1st Qu.: 98.0   1:1439
##  Median :27.60                         Median :130.0   Median :111.0
##  Mean   :27.76                         Mean   :130.3   Mean   :110.8
##  3rd Qu.:29.52                         3rd Qu.:136.0   3rd Qu.:125.0
##  Max.   :36.70                         Max.   :156.0   Max.   :171.0
##  severity    study           recovery_time
##  0:2145   Length:2400        Min.   :  2.00
##  1: 255   Class :character   1st Qu.: 30.00
##           Mode  :character   Median : 39.00
##                              Mean   : 42.03
##                              3rd Qu.: 49.00
##                              Max.   :365.00
```

```
testing_data |> summary()
```

```
##       age        gender  race    smoking     height          weight
##  Min.   :47.00   0:309   1:398   0:380   Min.   :148.1   Min.   : 55.90
##  1st Qu.:57.00   1:291   2: 24   1:159   1st Qu.:165.8   1st Qu.: 75.10
##  Median :60.00           3:129   2: 61   Median :169.7   Median : 79.55
##  Mean   :60.47           4: 49           Mean   :169.6   Mean   : 79.75
##  3rd Qu.:64.00                           3rd Qu.:173.7   3rd Qu.: 84.50
##  Max.   :74.00                           Max.   :186.1   Max.   :100.00
##       bmi        hypertension diabetes      SBP           LDL        vaccine
##  Min.   :19.20   0:285        0:505    Min.   :105   Min.   : 57.0   0:251
##  1st Qu.:25.90   1:315        1: 95    1st Qu.:126   1st Qu.: 95.0   1:349
##  Median :27.80                         Median :131   Median :108.0
##  Mean   :27.78                         Mean   :131   Mean   :108.9
##  3rd Qu.:29.50                         3rd Qu.:136   3rd Qu.:123.0
##  Max.   :38.90                         Max.   :154   Max.   :178.0
##  severity    study           recovery_time
##  0:534    Length:600         Min.   :  2.00
##  1: 66    Class :character   1st Qu.: 31.00
##           Mode  :character   Median : 39.00
##                              Mean   : 42.73
##                              3rd Qu.: 49.00
##                              Max.   :330.00
```

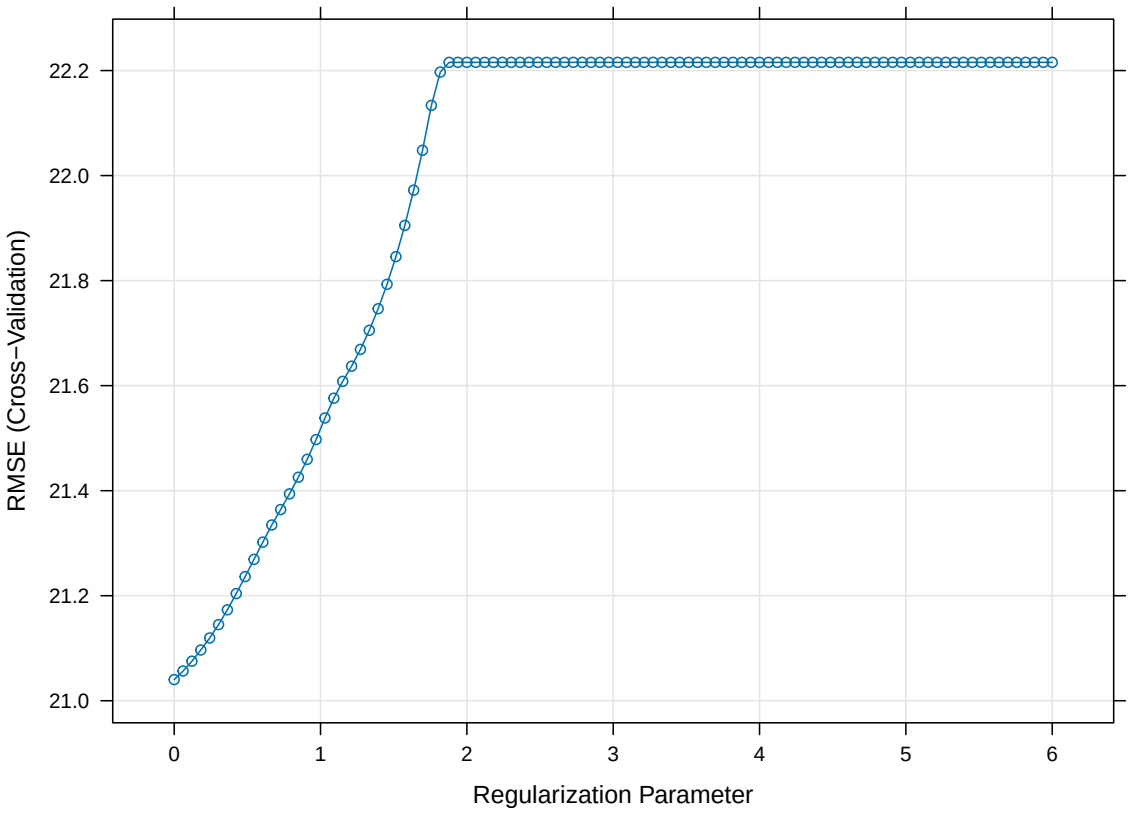
```
# training data
train.x = model.matrix(recovery_time ~ ., training_data)[, -1]
train.y = training_data$recovery_time

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

```r
# cross validation
ctrl = trainControl(method = "cv", number = 10)
```

There is no missing data in both datasets. The training dataset has 2400 observation and 16 variables, and the test dataset has 600 samples and 17 variables.

Lasso Regression Model

```r
set.seed(2716)
lasso.fit = training_data |>
  train(recovery_time ~ ., data = _, method = "glmnet",
        tuneGrid = expand.grid(
          alpha = 1,
          lambda = exp(seq(6, 0, length = 100))),
        trControl = ctrl,
        preProcess = c("center", "scale"))
plot(lasso.fit, xTrans = log)
```



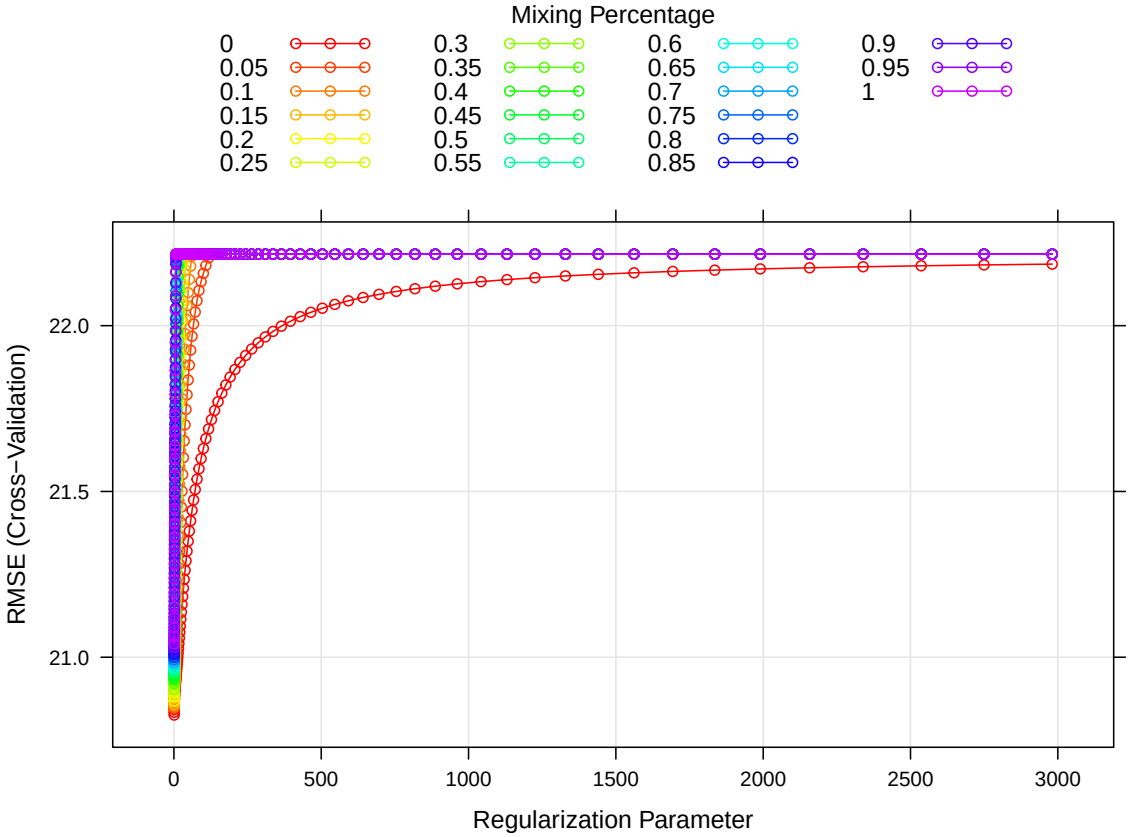
The flattening in the curve occurs because the lasso regression model has reached a stable solution where no more coefficients become zero as the regularization parameter increases. At this point, further increasing the regularization parameter does not change the set of non-zero coefficients or their values, resulting in a flat region where the model's performance remains constant. This behavior indicates that the model has achieved the optimal level of sparsity, with the regularization parameter value at the start of the flat region corresponding to the desired sparse solution.

```
lasso.pred = predict(lasso.fit, newdata = testing_data)
mse.lasso = mean((test.y - lasso.pred) ^ 2)
```

The selected best tuning parameter is $\lambda = 1$ $\alpha = 1$, and the test error (MSE) is 562.263383.

Elastic Net Model

```
set.seed(2716)
enet.fit = training_data |>
  train(recovery_time ~ ., data = _, method = "glmnet",
        tuneGrid = expand.grid(
          alpha = seq(0, 1, length = 21),
          lambda = exp(seq(8, 0, length = 100))),
        preProcess = c("center", "scale"),
        trControl = ctrl)
myCol = rainbow(25)
myPar =
  list(superpose.symbol = list(col = myCol),
       superpose.line = list(col = myCol))
plot(enet.fit, par.settings = myPar)
```



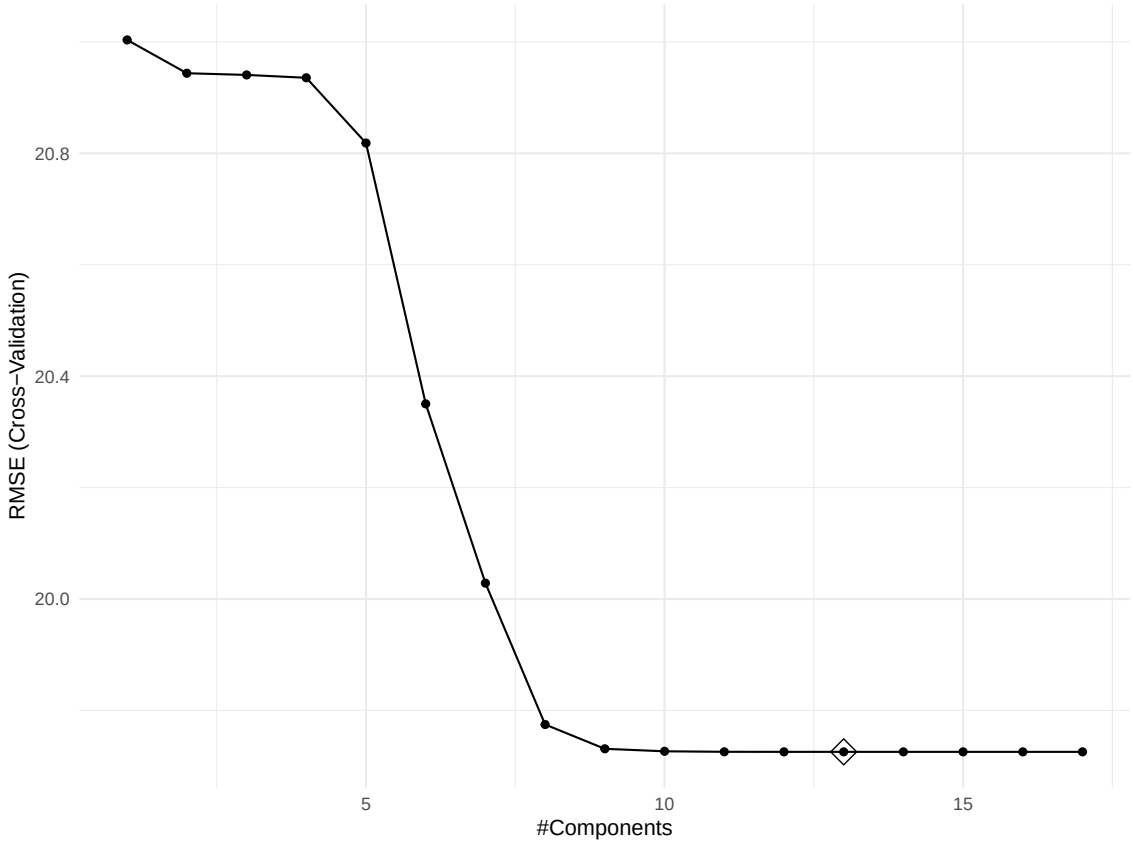
The vertical line pattern in the graph is a characteristic behavior of the elastic net model. It occurs because the elastic net combines lasso and ridge regularization, which can lead to sparse solutions with some coefficients becoming exactly zero. As the regularization parameter increases, the model transitions between different sparse solutions, causing sudden drops or jumps in the cross-validation error curve.

```
enet.pred = predict(enet.fit, newdata = testing_data)
mse.enet = mean((test.y - enet.pred) ^ 2)
```

The selected tuning parameter is $\alpha = 0$, $\lambda = 1$, and the test error (MSE) is 536.2385884

Partial Least Square

```
set.seed(2716)

pls.fit = train(train.x, train.y, method = "pls",
  tuneGrid = data.frame(ncomp = 1:17),
  trControl = ctrl, preProcess = c("center", "scale"))
ggplot(pls.fit, highlight = T)
```




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

As illustrated in the plot, 13 components are included in my model, and the test error (MSE) is 464.8643889

The coefficients are as follows:

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

```
## , , 13 comps
##
##                    .outcome
## age              1.04306479
## gender1         -1.79478232
## race2            0.67651655
## race3            0.09607768
## race4           -0.14876310
## smoking1         0.98529363
## smoking2         1.02530399
## height          74.39909797
## weight         -96.19301259
## bmi            112.57056811
## hypertension1    0.68131672
## diabetes1       -0.28468608
## SBP              0.46391355
## LDL             -0.95602747
## vaccine1        -2.97123020
## severity1        1.62625094
## studyB           2.02187127
```

MARS

Now, train a multivariate adaptive regression spline (MARS) model to predict the response variable.

Since there are two tuning parameters associated with the MARS model: the degree of interactions and the number of retained terms, we need to perform a grid search to identify the optimal combination of these hyperparameters that minimize prediction error.

```
ctrl = trainControl(method = "cv", number = 10)
mars.grid = expand.grid(degree = 1 : 3, nprune = seq(2, 20, by = 2))
set.seed(2716)
mars.fit = train(train.x, train.y, method = "earth", tuneGrid = mars.grid, trControl = ctrl)
```

```
## Loading required package: earth
```

```
## Loading required package: Formula
```

```
## Loading required package: plotmo
```

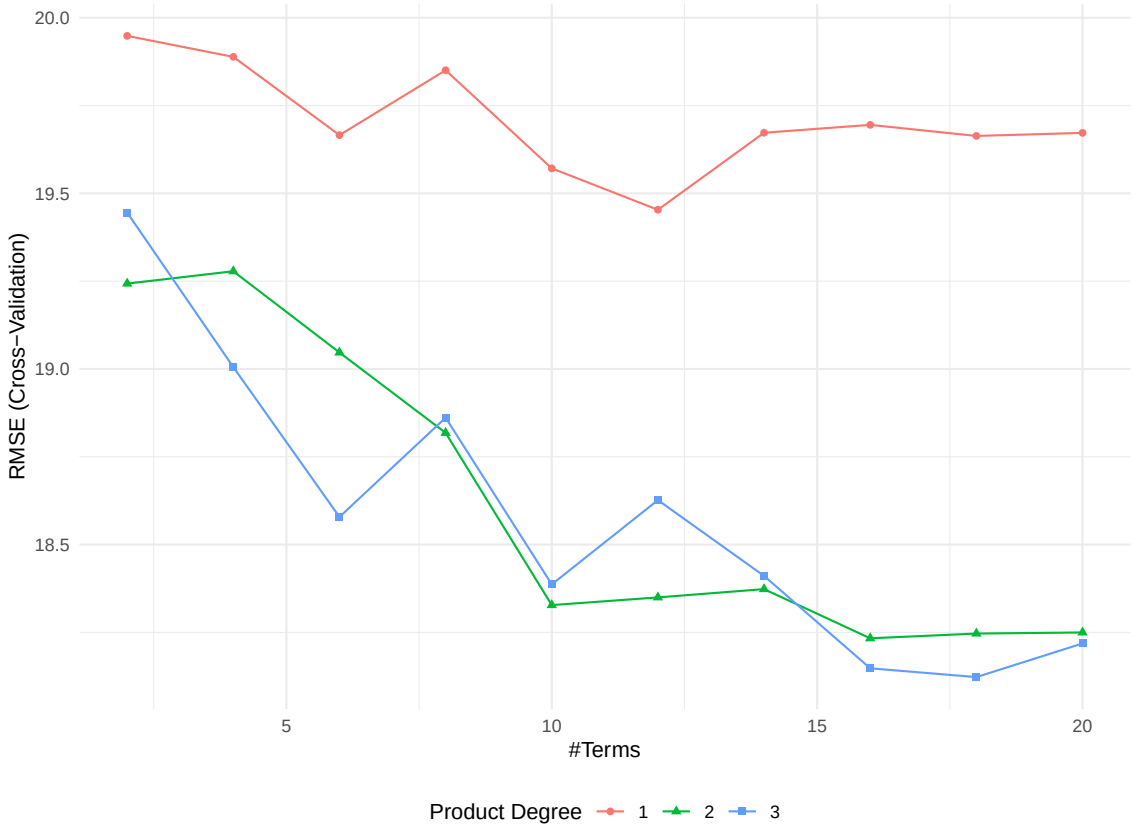
```
## Loading required package: plotrix
```

```
##
## Attaching package: 'plotrix'
```

```
## The following object is masked from 'package:scales':
##
##     rescale
```

```
## Loading required package: TeachingDemos
```

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




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

```
## Call: earth(x=matrix[2400,17], y=c(69,9,7,43,36,...), keepxy=TRUE, degree=3,
##             nprune=18)
##
##                                        coefficients
## (Intercept)                              17.425888
## gender1                                  -3.838226
## vaccine1                                 -5.523433
## severity1                                 5.146386
## h(bmi-25.7)                               6.207509
## h(31.1-bmi)                               4.065175
## h(bmi-35.4)                              27.540176
## h(bmi-31.1) * studyB                   -305.070403
## h(bmi-25.7) * h(140-SBP)                 -0.064119
## smoking1 * h(bmi-31.1) * studyB          15.366973
## smoking2 * h(bmi-31.1) * studyB          28.176098
## h(age-61) * h(bmi-31.1) * studyB          5.249927
## h(weight-78.7) * h(bmi-31.1) * studyB    23.765436
## h(89.3-weight) * h(bmi-31.1) * studyB    24.335697
## h(weight-89.3) * h(bmi-31.1) * studyB   -25.433893
## h(bmi-31.1) * h(LDL-94) * studyB         -5.448260
## h(bmi-31.1) * h(94-LDL) * studyB          5.533714
## h(bmi-31.1) * h(LDL-84) * studyB          5.716112
```

```
##
## Selected 18 of 25 terms, and 11 of 17 predictors (nprune=18)
## Termination condition: Reached nk 35
## Importance: bmi, studyB, LDL, age, vaccine1, weight, smoking1, gender1, ...
## Number of terms at each degree of interaction: 1 6 2 9
## GCV 261.8665    RSS 605903.8    GRSq 0.4893553    RSq 0.5072879
```

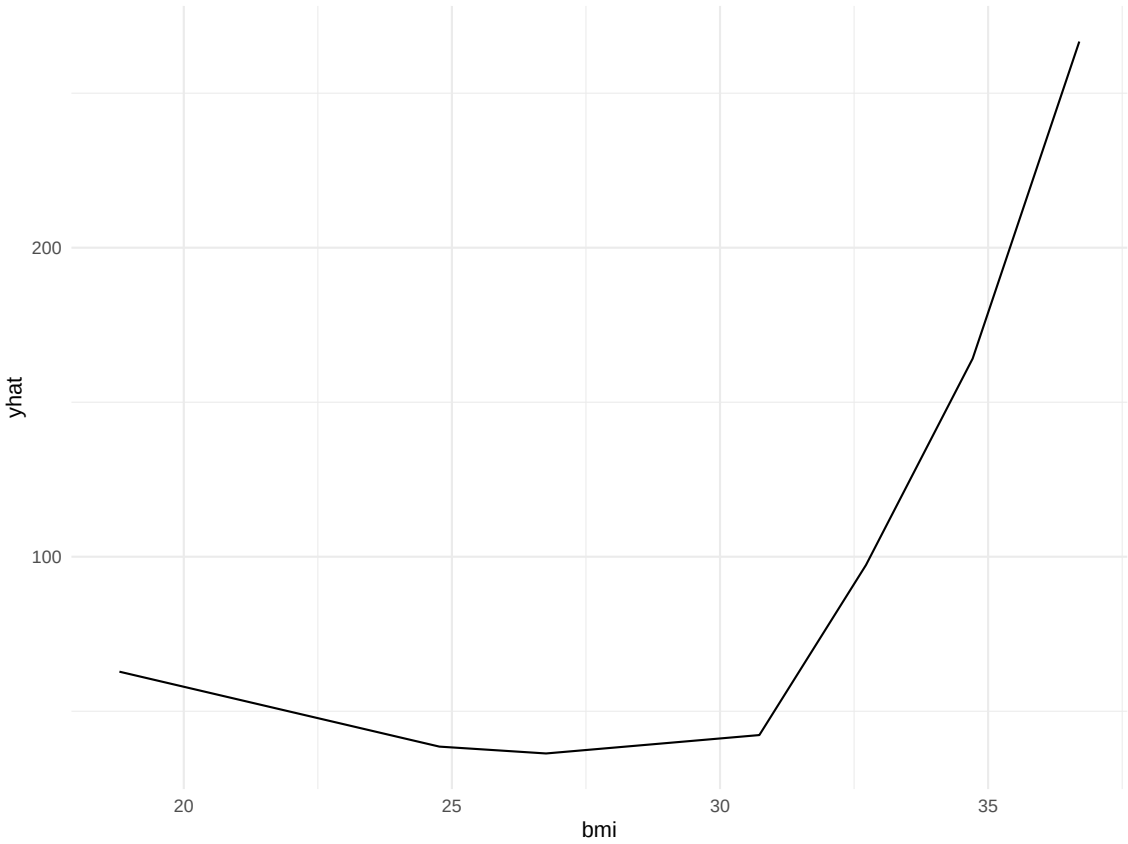
```
## Coefficient of the MARS model
coef(mars.fit$finalModel)
```

```
##                           (Intercept)                           h(31.1-bmi)
##                           17.42588791                            4.06517510
##                  h(bmi-31.1) * studyB      h(age-61) * h(bmi-31.1) * studyB
##                         -305.07040296                            5.24992718
##                           h(bmi-25.7)                              vaccine1
##                            6.20750882                           -5.52343301
##      h(bmi-31.1) * h(LDL-94) * studyB      h(bmi-31.1) * h(94-LDL) * studyB
##                           -5.44825972                            5.53371358
## h(weight-89.3) * h(bmi-31.1) * studyB h(89.3-weight) * h(bmi-31.1) * studyB
##                          -25.43389302                           24.33569724
##      h(bmi-31.1) * h(LDL-84) * studyB       smoking1 * h(bmi-31.1) * studyB
##                            5.71611207                           15.36697296
##                               gender1                             severity1
##                           -3.83822562                            5.14638556
##       smoking2 * h(bmi-31.1) * studyB             h(bmi-25.7) * h(140-SBP)
##                           28.17609759                           -0.06411943
## h(weight-78.7) * h(bmi-31.1) * studyB                           h(bmi-35.4)
##                           23.76543599                           27.54017572
```

The MARS model selects 12 of 27 terms, and 8 of 17 predictors. The most important variables are *bmi* (Body Mass Index; BMI = weight (in kilograms) / height (in meters) squared) and *studyB*(The study (A/B) that the participant belongs to).

To better understand the relationship between these features and outstate, we can create partial dependence plots (PDPs) for each feature individually and also an interaction PDP. To simplify, here we only present the PDP for number of full-time undergraduates *sbp*.

```
pdp::partial(mars.fit, pred.var = c("bmi"), grid.resolution = 10) |> autoplot()
```



Using the final model, we can predict on the test data.

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

The test error measured by MSE using the final MARS model is 392.3426264

GAM

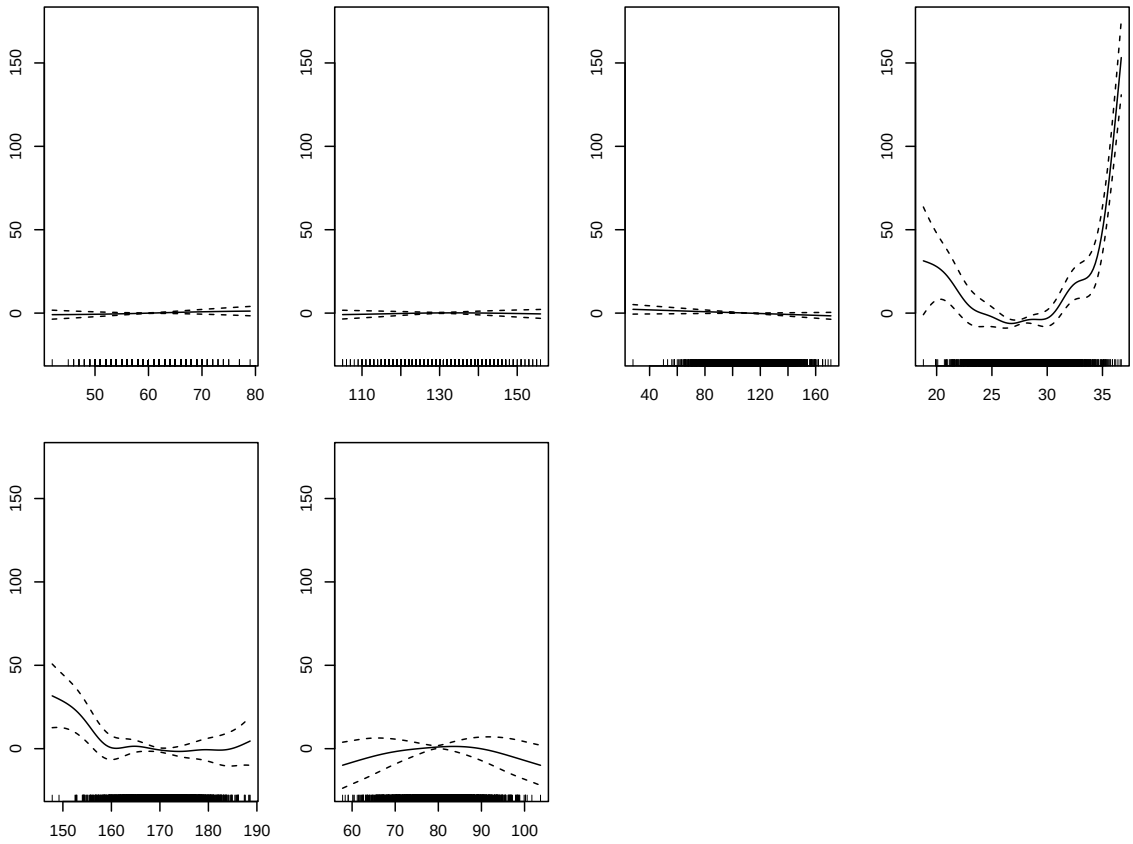
```
set.seed(2716)
gam.fit = train(train.x, train.y, method = "gam", trControl = ctrl)
```

```
## Loading required package: 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
summary(gam.fit$finalModel)
```

```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## .outcome ~ gender1 + race2 + race3 + race4 + smoking1 + smoking2 +
##     hypertension1 + diabetes1 + vaccine1 + severity1 + studyB +
##     s(age) + s(SBP) + s(LDL) + s(bmi) + s(height) + s(weight)
##
## Parametric coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)    43.5319     1.0022  43.437  < 2e-16 ***
## gender1        -3.9286     0.7579  -5.184 2.36e-07 ***
## race2           2.4897     1.6763   1.485  0.13761
## race3           0.2184     0.9730   0.224  0.82239
## race4          -1.0791     1.3330  -0.810  0.41831
## smoking1        2.4333     0.8578   2.837  0.00460 **
## smoking2        3.7986     1.2536   3.030  0.00247 **
## hypertension1   2.2691     1.0394   2.183  0.02913 *
## diabetes1      -0.9912     1.0520  -0.942  0.34617
## vaccine1       -6.2577     0.7773  -8.051 1.29e-15 ***
## severity1       5.6267     1.2306   4.572 5.07e-06 ***
## studyB          4.1707     0.8026   5.197 2.20e-07 ***
## ---
## 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)    0.6260      9  0.153 0.115489
## s(SBP)    0.5946      9  0.079 0.293041
## s(LDL)    0.7589      9  0.277 0.068772 .
## s(bmi)    8.8974      9 67.421  < 2e-16 ***
## s(height) 6.6451      9  3.220 2.26e-05 ***
## s(weight) 2.3895      9  1.614 0.000227 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.334   Deviance explained = 34.3%
## GCV = 345.74  Scale est. = 341.14    n = 2400
```

```r
par(mar = c(2, 2, 2, 2), mfrow = c(2, 4))
plot(gam.fit$finalModel)
```



It could be observed that certain variables (*age*, *sbp*, *ldl*) have no relationship with the *recovery_time*, *bmi*, and *height* both have a positive relationship with *recovery_time*.

Using the final model, we can predict on the test data.

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

Model Comparison

Here, we compare the CV results of different models and choose the model with the smallest median RMSE.

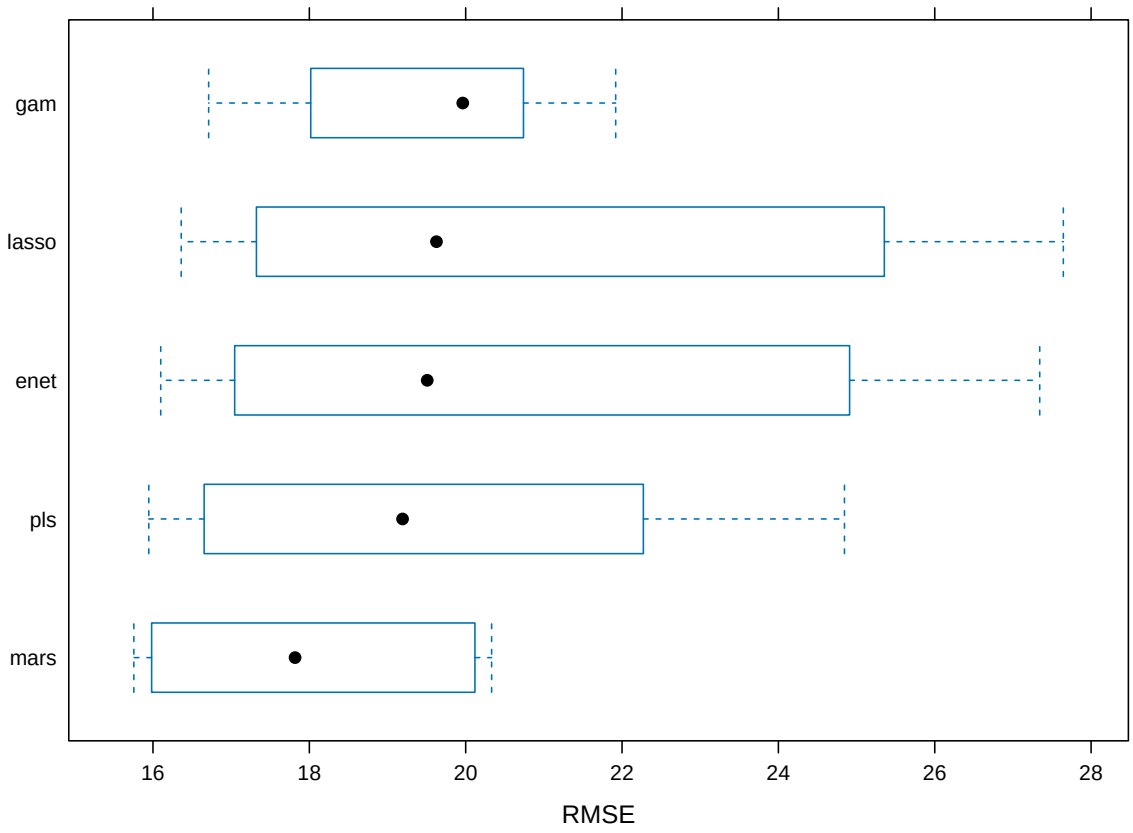
```
resamp =
  resamples(list(lasso = lasso.fit,
                 gam = gam.fit,
                 enet = enet.fit,
                 pls = pls.fit,
                 mars = mars.fit))
summary(resamp)
```

```
##
## Call:
## summary.resamples(object = resamp)
##
## Models: lasso, gam, enet, pls, mars
## Number of resamples: 10
```

```
##
## MAE
##           Min.  1st Qu.   Median     Mean  3rd Qu.     Max. NA's
## lasso 11.91749 12.22876 12.78822 13.10307 13.97511 14.75607    0
## gam   11.71387 12.30531 12.64584 12.60154 13.04721 13.17282    0
## enet  11.82640 12.24000 12.86273 13.14786 14.09859 14.70406    0
## pls   12.00552 12.42079 13.07887 13.06909 13.69203 14.12036    0
## mars  10.80694 11.46341 11.88141 11.87063 12.24314 12.74929    0
##
## RMSE
##           Min.  1st Qu.   Median     Mean  3rd Qu.     Max. NA's
## lasso 16.36102 17.35644 19.62606 21.04028 24.59723 27.64478    0
## gam   16.71229 18.02794 19.96280 19.42835 20.62654 21.91883    0
## enet  16.09922 17.14833 19.50831 20.82568 24.22164 27.34263    0
## pls   15.94665 16.77630 19.19268 19.72570 22.05070 24.84530    0
## mars  15.75520 16.33340 17.81756 18.12274 20.06809 20.33183    0
##
## Rsquared
##             Min.    1st Qu.    Median      Mean   3rd Qu.      Max. NA's
## lasso 0.07035909 0.08459142 0.1095733 0.1133160 0.1199068 0.1790213    0
## gam   0.12563865 0.16945853 0.2130396 0.2981010 0.4564618 0.5962197    0
## enet  0.08321485 0.10886399 0.1216388 0.1284815 0.1374788 0.1954873    0
## pls   0.10933283 0.16901995 0.2338977 0.2315719 0.2969252 0.3415088    0
## mars  0.07128380 0.22502531 0.2658819 0.3406511 0.4887175 0.7078823    0
```

Using bw-plot to compare their RMSE.

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



Hence, we selected MARS model as it has smallest RMSE.