Midterm Result

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Exploratory analysis and data visualization

In this section, use appropriate visualization techniques to explore the dataset and identify any patterns or relationships in the data.

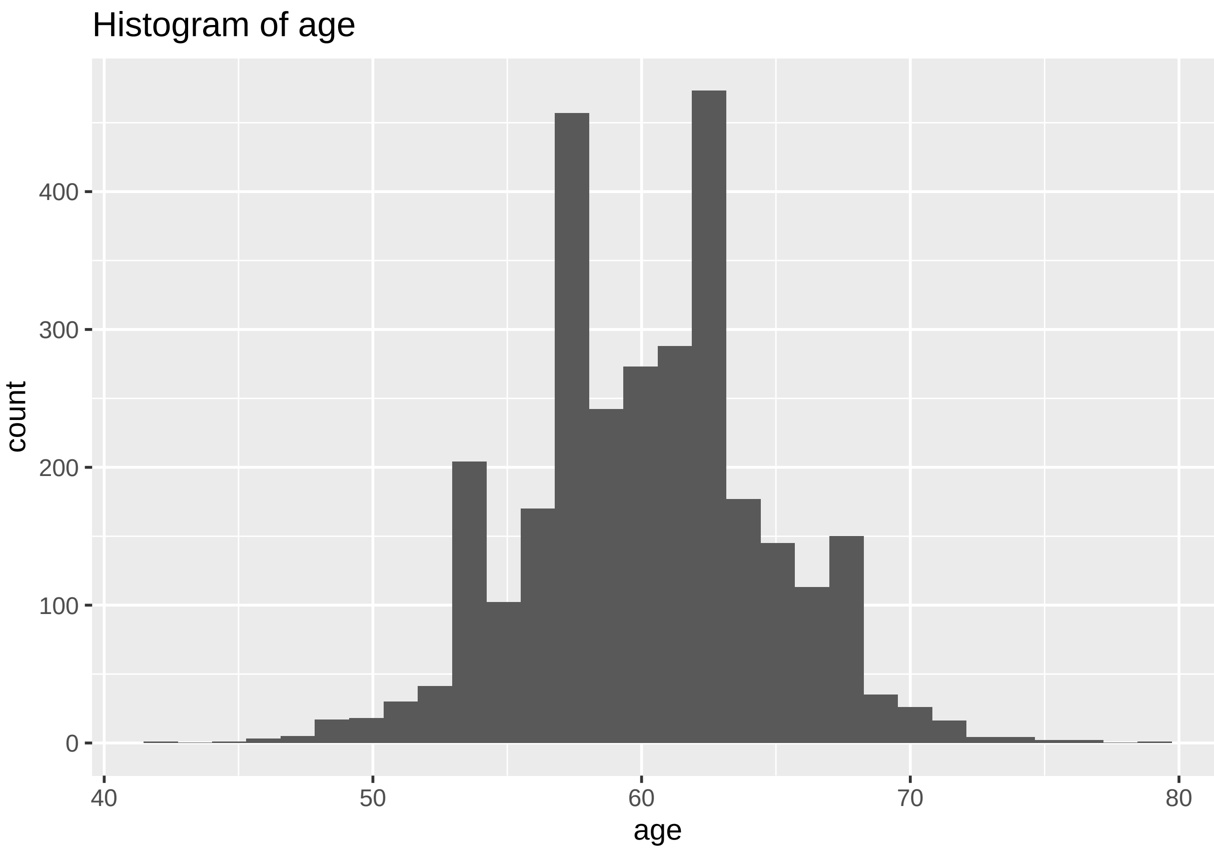
Summary statistics

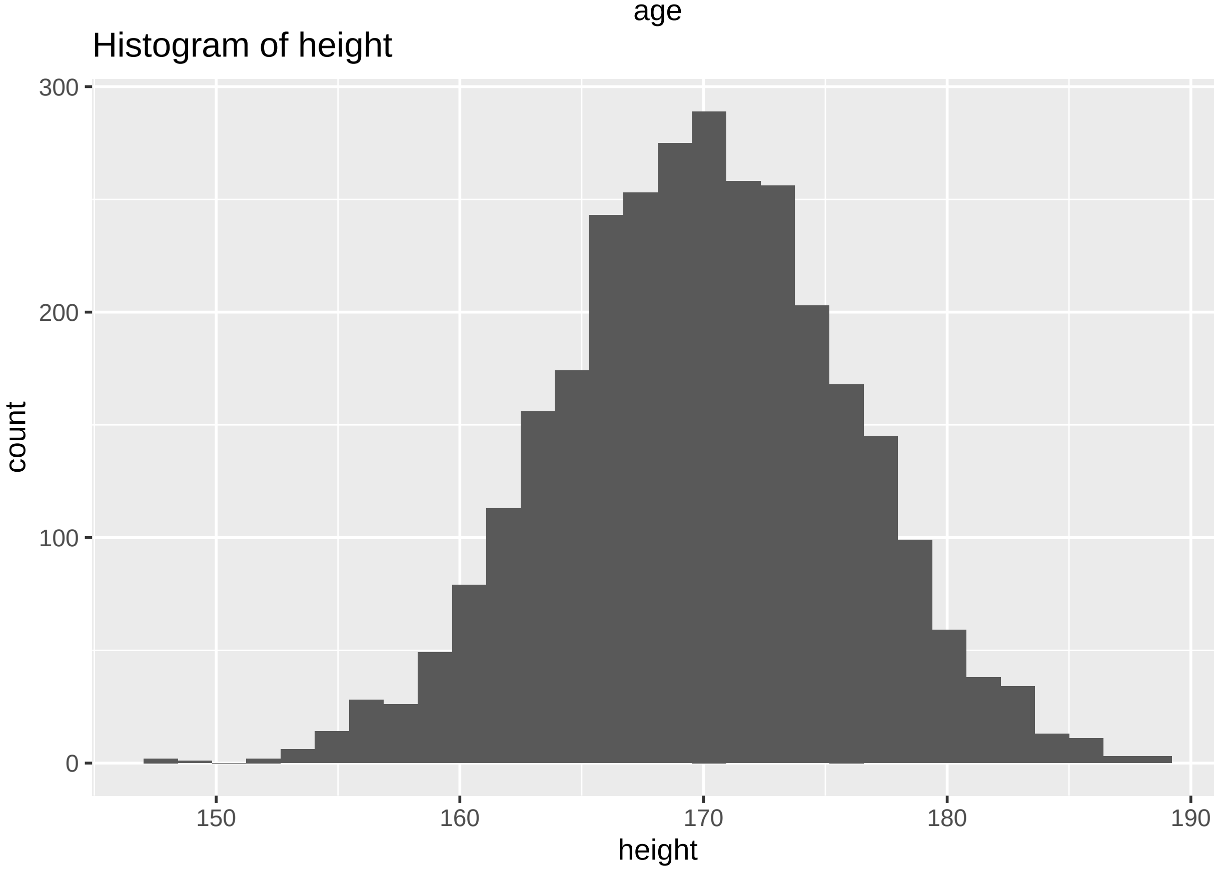
Table 1: Summary of Dataset

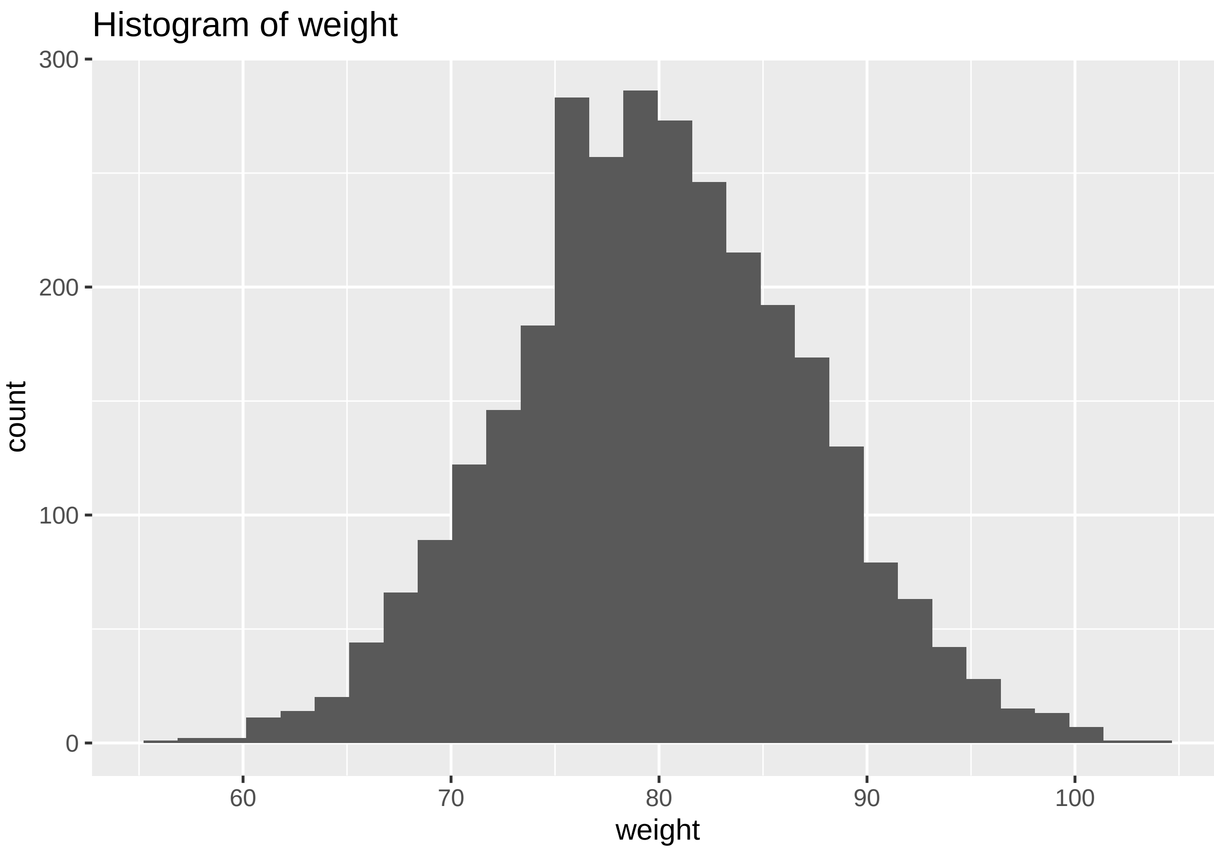
Characteristic	**N = 3,000**[1]
age	60.0 (57.0, 63.0)
gender	
male	1,544 (51%)
female	1,456 (49%)
race	
White	1,967 (66%)
Asian	158 (5.3%)
Black	604 (20%)
Hispanic	271 (9.0%)
smoking	
Never smoked	1,822 (61%)
Former smoker	859 (29%)
Current smoker	319 (11%)
height	169.9 (166.0, 173.9)
weight	80 (75, 85)
bmi	27.65 (25.80, 29.50)
hypertension	1,492 (50%)
diabetes	463 (15%)
SBP	130 (125, 136)
LDL	110 (97, 124)
vaccine	
Not vaccinated	1,212 (40%)
Vaccinated	1,788 (60%)
severity	
Not severe	2,679 (89%)
Severe	321 (11%)
study	
A	2,000 (67%)
B	1,000 (33%)
recovery_time	39 (31, 49)

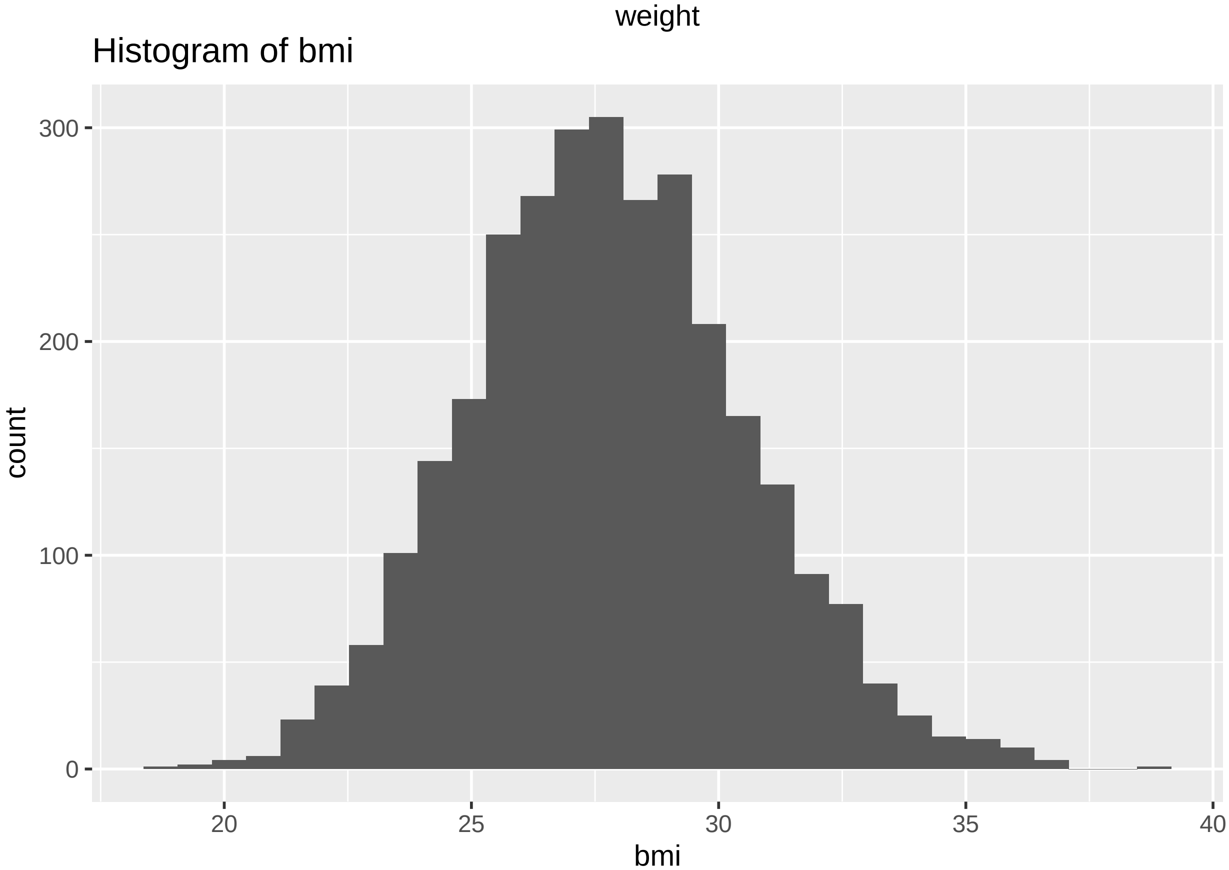
[1] Median (IQR); n (%)

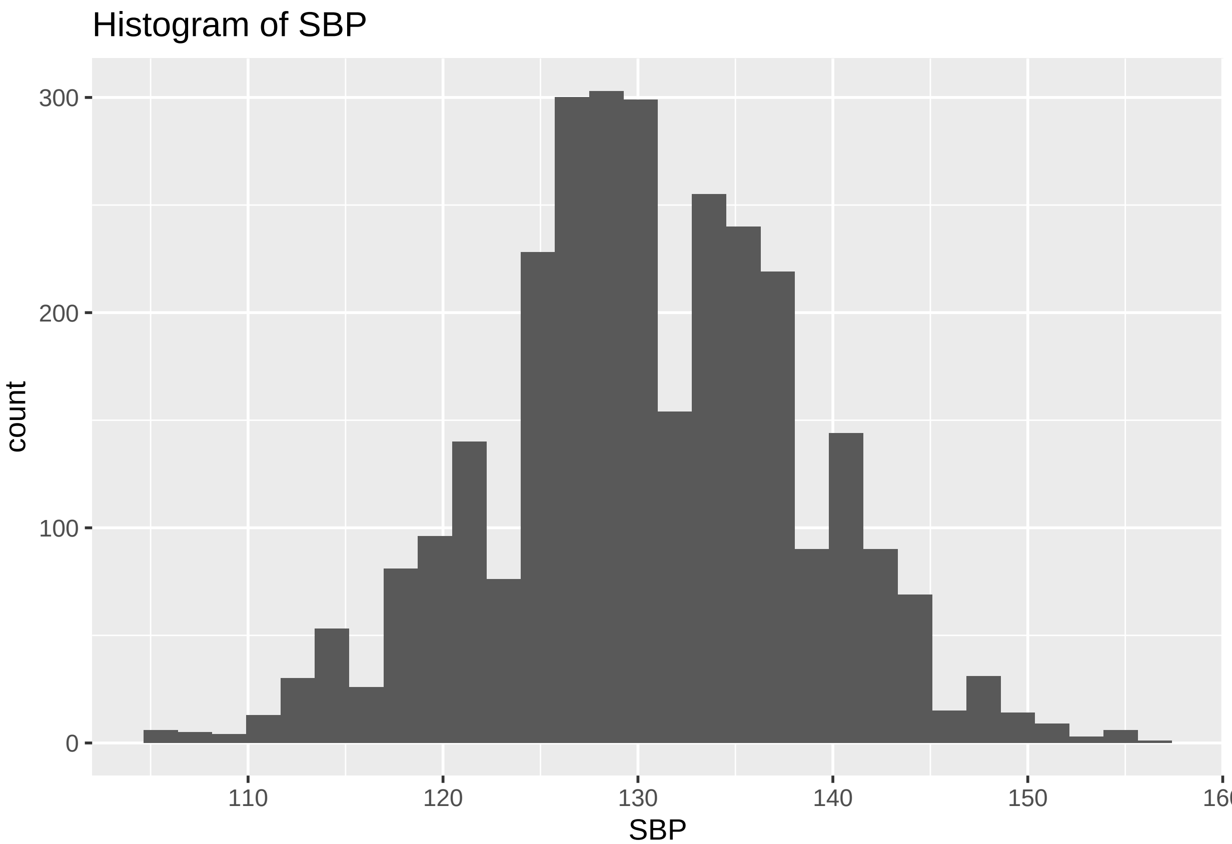
Visualizations for the numerical variables

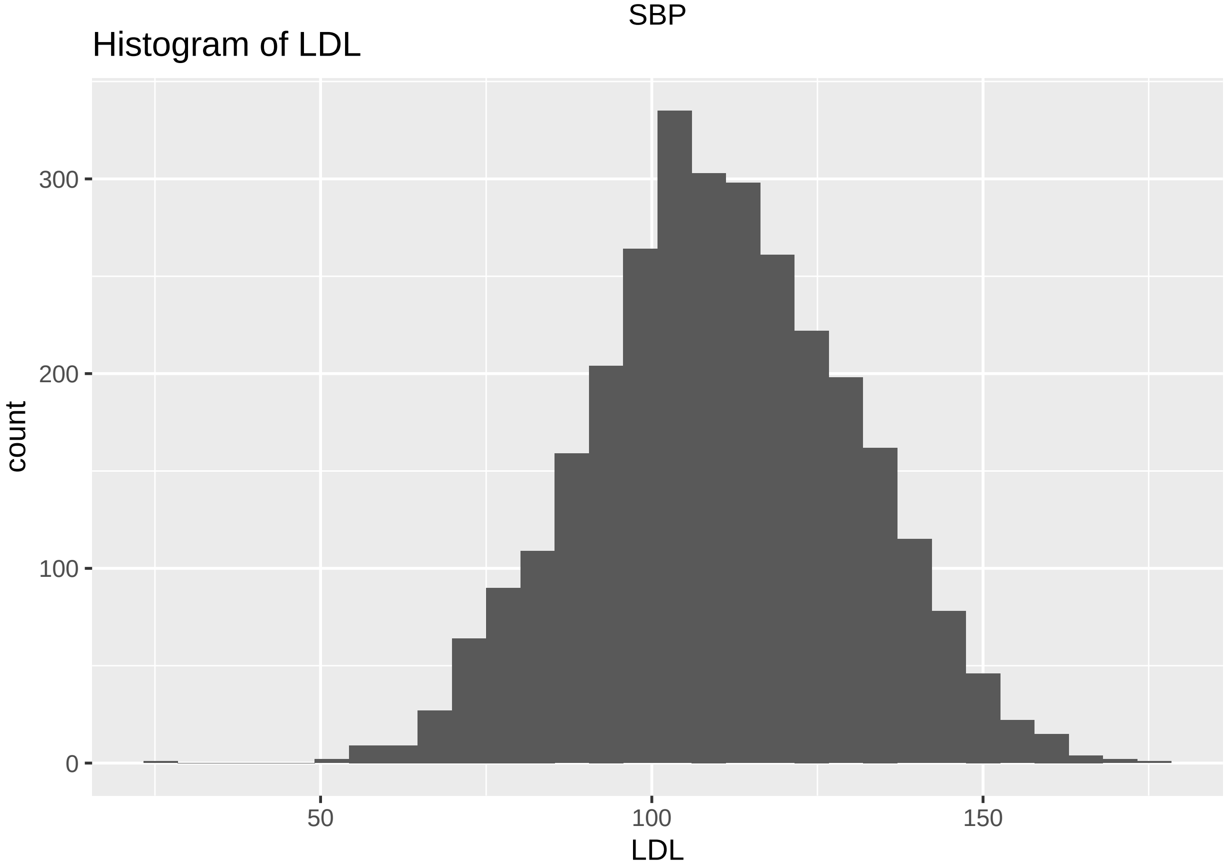

Histogram of age
count
0
100
200
300
400
40
50
60
70
80
age

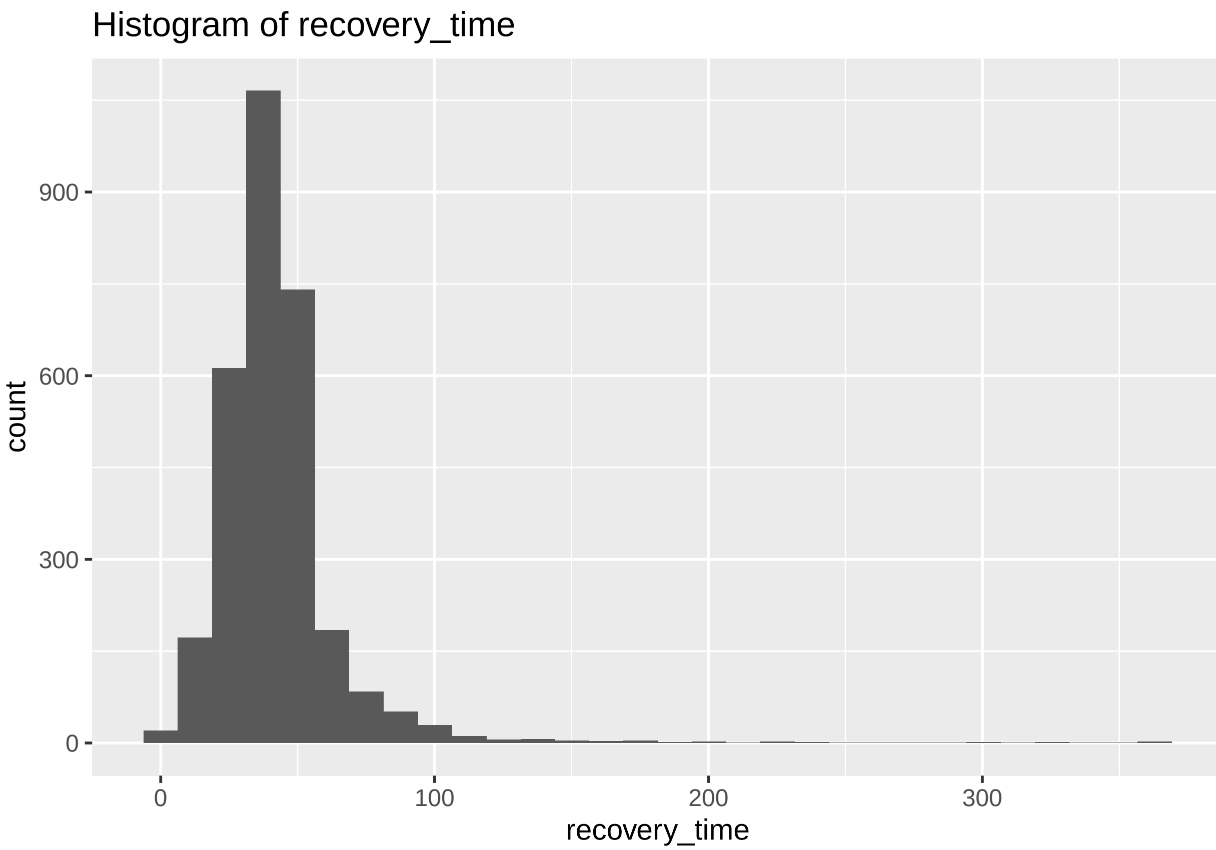

Histogram of height
count
0
100
200
300
150
160
170
180
190
height


Histogram of weight
300
200
100
0
count
60
70
80
90
100
weight

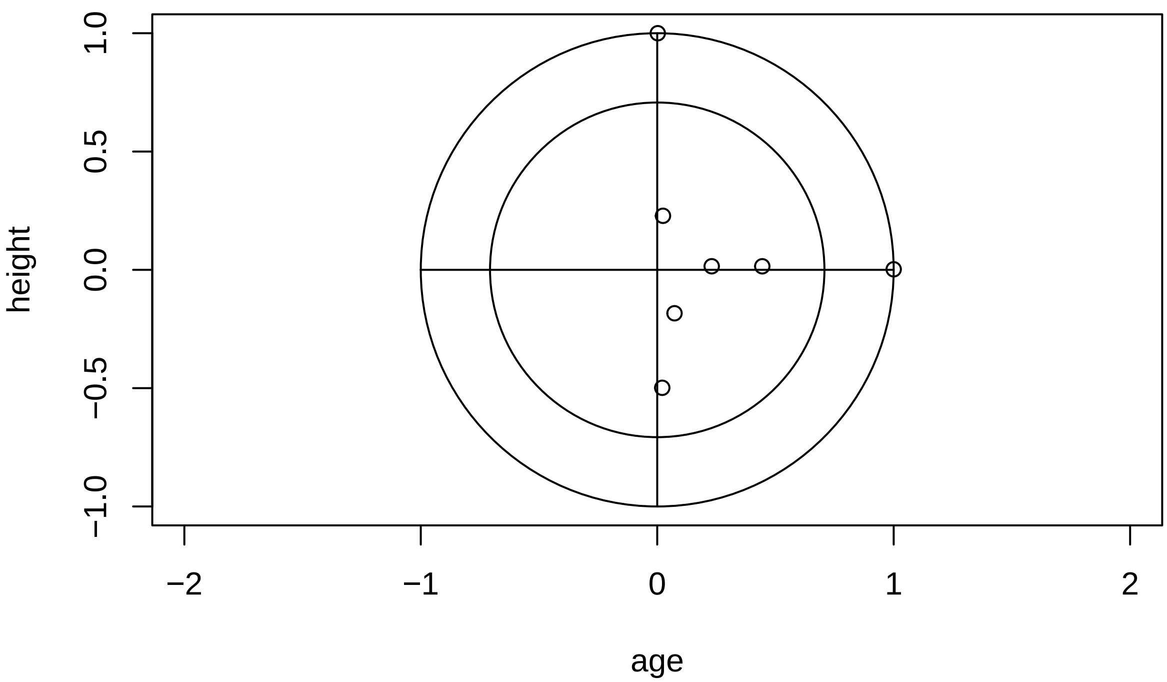

Histogram of bmi
300
200
100
0
count
20
25
30
35
40
bmi


Histogram of SBP
300
200
100
0
count
110
120
130
140
150
160
SBP


Histogram of LDL
300
200
100
0
count
50
100
150
LDL



correlation plot



Model training

In this section, describe the models you used to predict the time to recovery from COVID-19. Briefly state the assumptions made by using the models. Provide a detailed description of the model training procedure and how you obtained the final model.

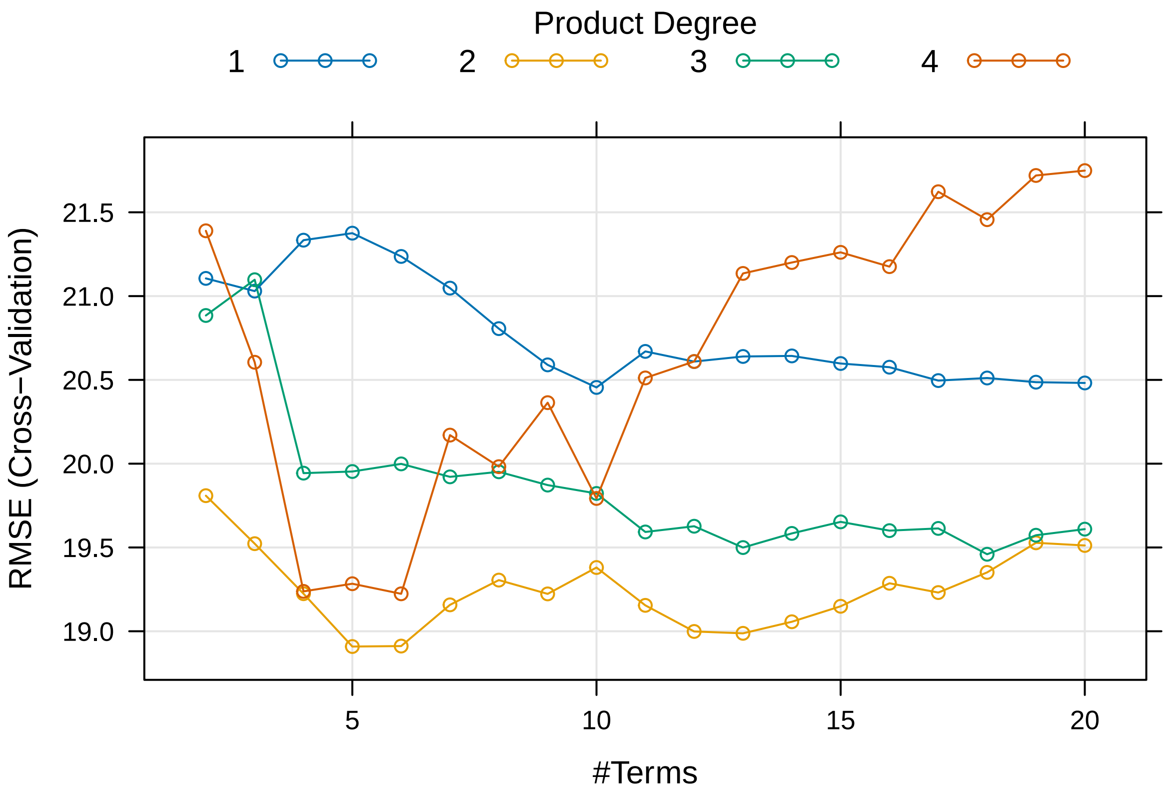
Outcome: recovery_time

Partition the dataset into two parts: training data (80%) and test data (20%).

```
set.seed(666)
data_split <- initial_split(dat, prop = 0.8)

# Extract the training and test data
training_data <- training(data_split)%>% select(-id,-gender)
x_train <- training_data %>% select(-recovery_time)
y_train <- training_data$recovery_time

testing_data <- testing(data_split)%>% select(-id,-gender)
x_test <- testing_data %>% select(-recovery_time)
y_test <- testing_data$recovery_time

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

Multivariate Adaptive Regression Spline (MARS) Model

```
set.seed(666)
model.mars <- train(x = x_train,
                    y = y_train,
                    method = "earth", # earth is for mars
                    tuneGrid = expand.grid(degree = 1:4,
                                           nprune = 2:20),
                    trControl = ctrl)

# degree from 1~4 is sufficient
# nprune can be larger than the number of predictors, make it as large as possible

plot(model.mars)
```




```
# both number of terms and product degree are upper bounds

# best tune
model.mars$bestTune
```

```
##    nprune degree
## 23      5      2
```

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

```
##                (Intercept)                  h(31-bmi)
##                 -3.1983530                  6.3999877
##           h(bmi-31) * studyB              h(bmi-25.2)
##                 25.6820131                  7.9260754
## h(weight-86.4) * h(bmi-31)
##                 -0.6277843
```

test error

```
mars.pred <- predict(model.mars, newdata = x_test)
test_error_mars <- mean((mars.pred - y_test)^2)
test_error_mars
```

```
## [1] 279.0367
```

```
RMSE_mars <- sqrt(test_error_mars)
RMSE_mars
```

```
## [1] 16.70439
```

The MSE of MARS model is 279.037.

Generalized Additive Model (GAM)

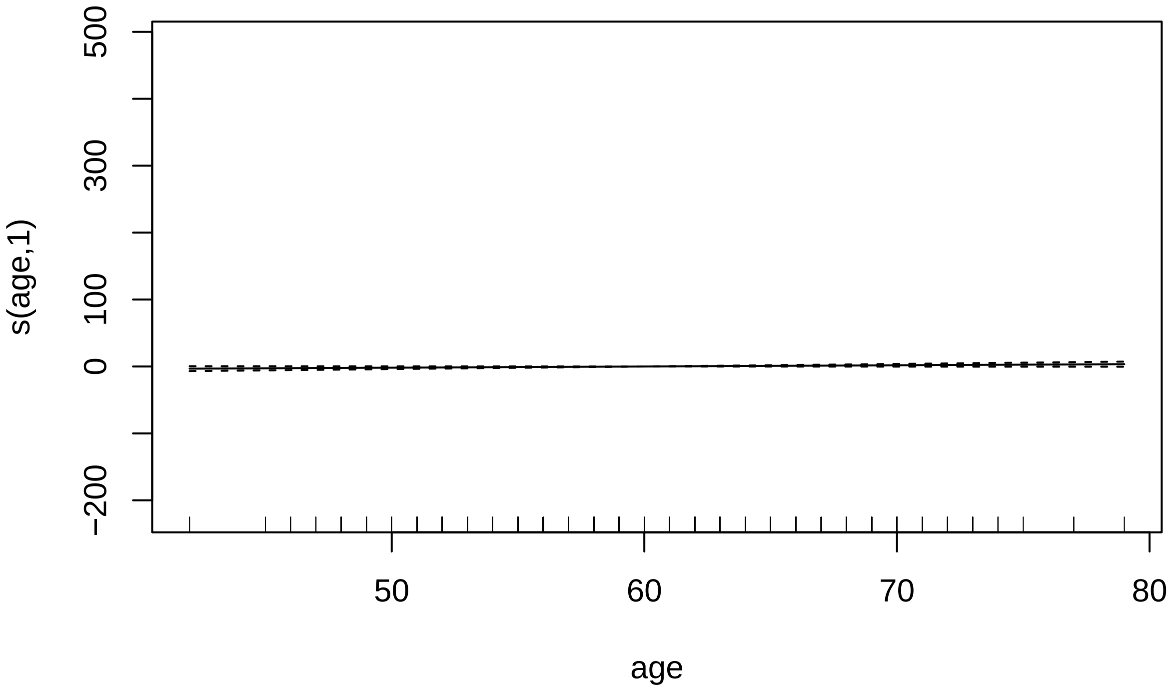
```
set.seed(666)
model.gam <- train(x = x_train,
                   y = y_train,
                   method = "gam",
                   trControl = ctrl)

model.gam$bestTune
```

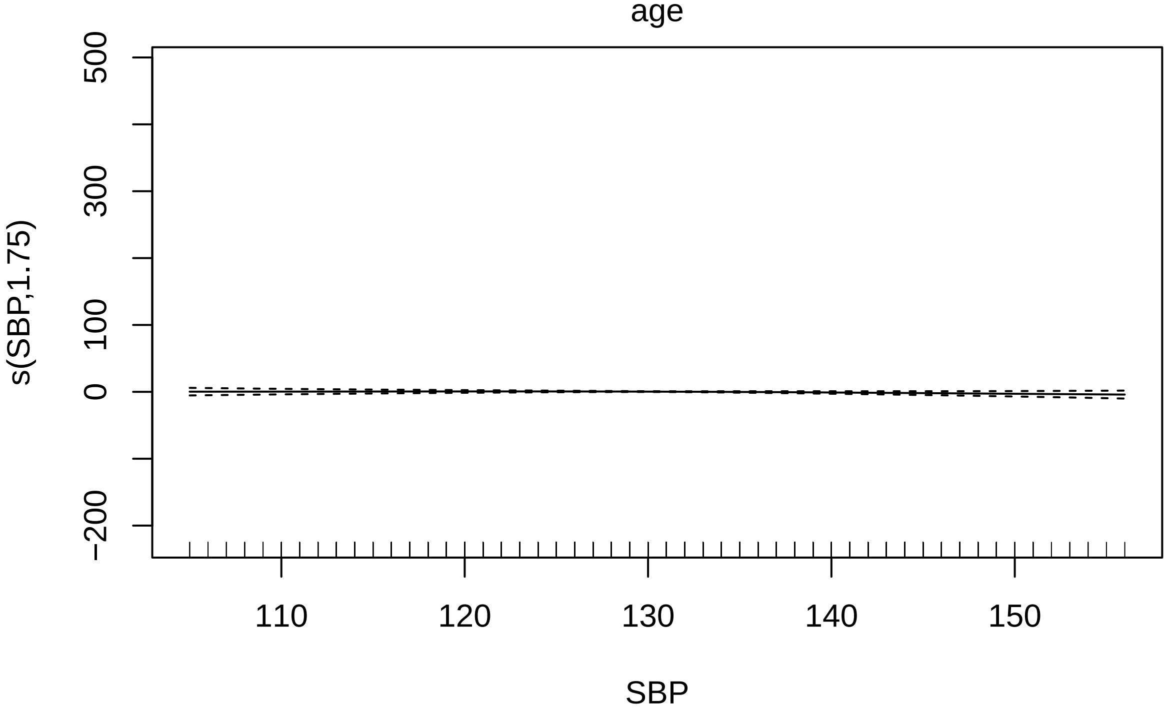
```
##   select method
## 1  FALSE GCV.Cp
```

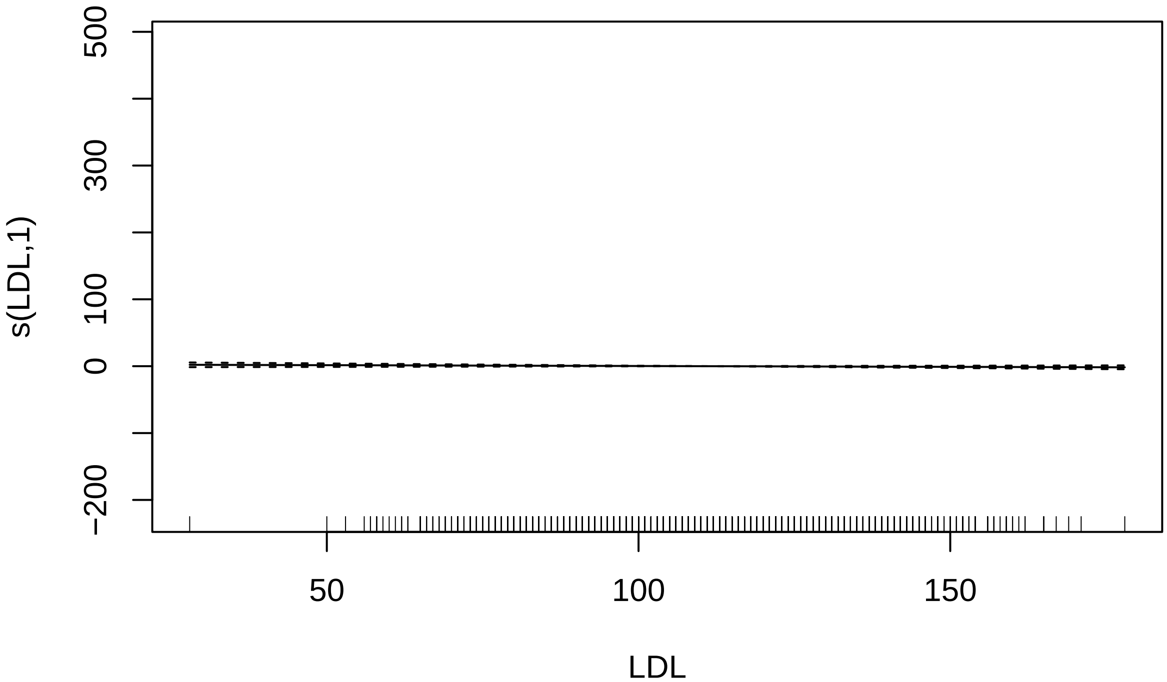
```
model.gam$finalModel
```

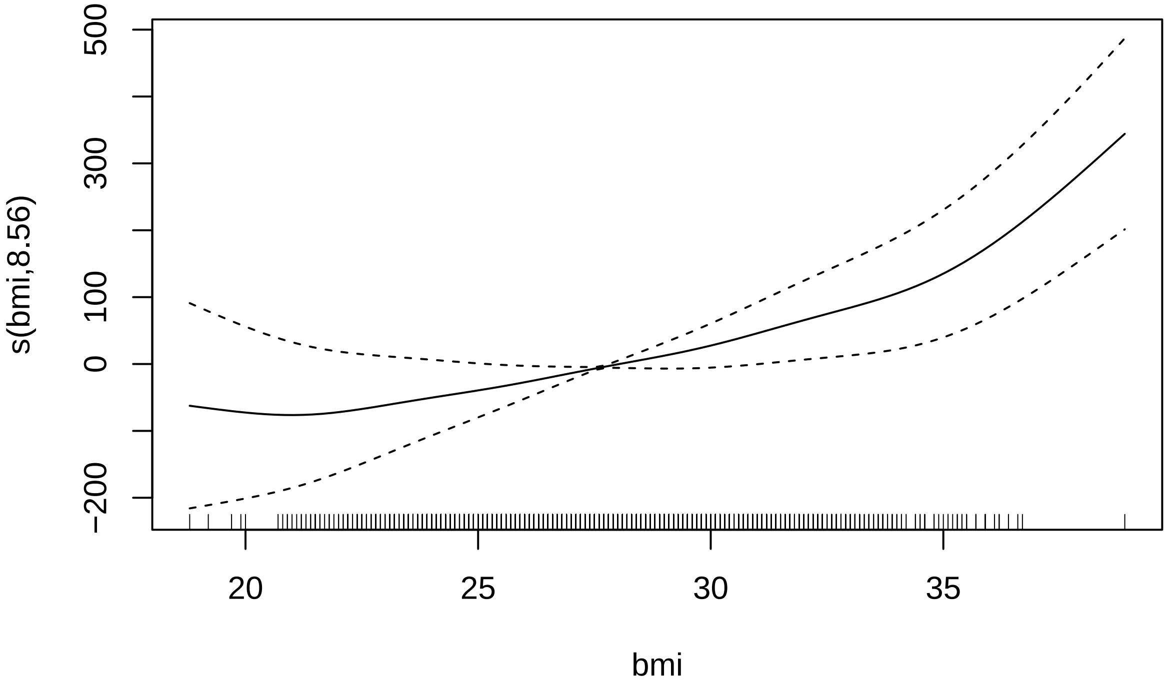
```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## .outcome ~ hypertension + diabetes + vaccine + severity + study +
##     male + smoking + race + s(age) + s(SBP) + s(LDL) + s(bmi) +
##     s(height) + s(weight)
##
## Estimated degrees of freedom:
## 1.00 1.75 1.00 8.56 7.24 2.81  total = 34.36
##
## GCV score: 384.8296
```

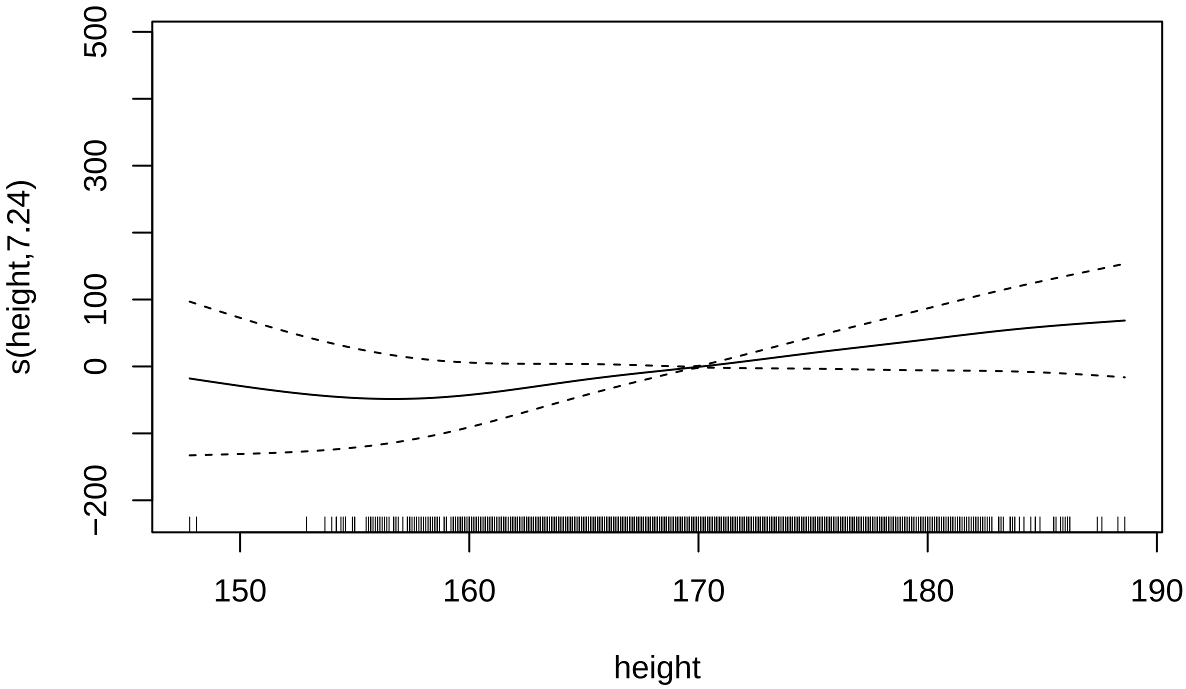
```
# degree of freedom=1 means linear

# Plotting
plot(model.gam$finalModel)
```

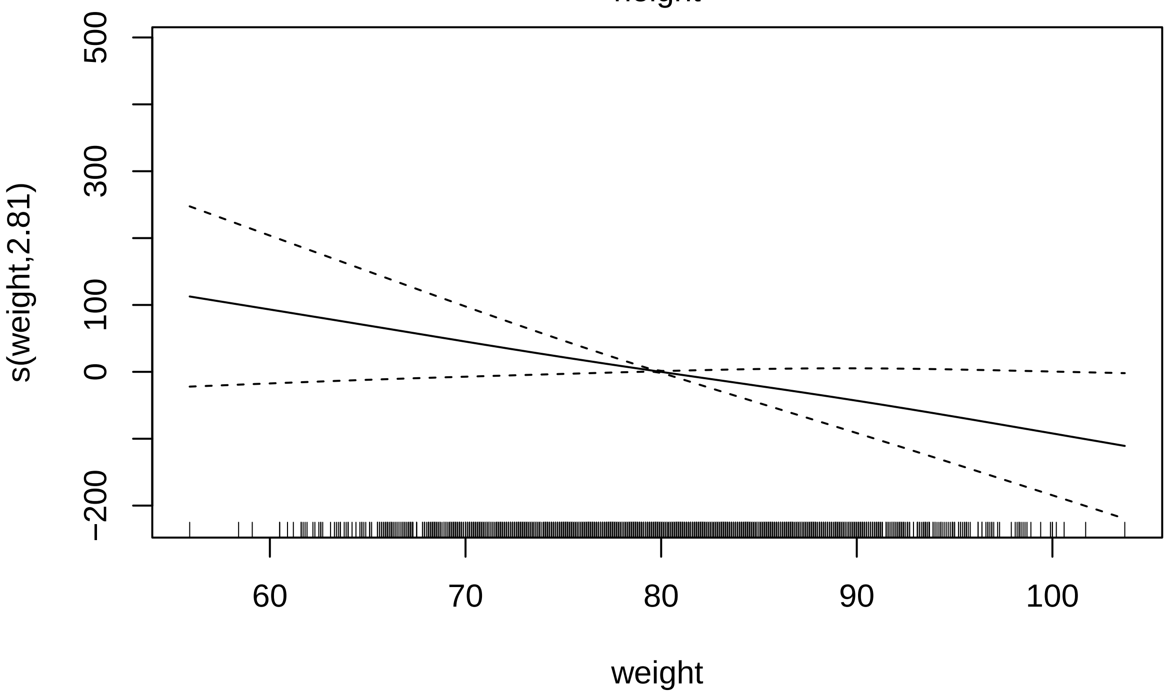

s(age,1)
500
300
100
0
−200
50
60
70
80
age


s(SBP,1.75)
500
300
100
0
−200
110
120
130
140
150
SBP


s(LDL,1)
−200
0
100
300
500
50
100
150
LDL


s(bmi,8.56)
−200
0
100
300
500
20
25
30
35
bmi






```
# compute and report the test error
predictions <- predict(model.gam, x_test)
test_error <- mean((predictions - y_test)^2) # Mean Squared Error (MSE)
test_error # Reporting the test error
```

```
## [1] 272.0012
```

The MSE of GAM model is 272.001

lasso model

```
set.seed(666)
lasso.fit <- train(recovery_time ~ .,
                   data = training_data,
                   method = "glmnet",
                   tuneGrid = expand.grid(alpha = 1,
                                          lambda = exp(seq(-25, 5, length = 100))),
                   trControl = ctrl)
```

Here's the selected tuning parameter when the minimal MSE rule is applied

```
lasso.fit$bestTune
```

```
##    alpha     lambda
## 68     1 0.00912288
```

The best tuning parameter is 0.009

And the test error is

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

```
## [1] 298.3018
```

The MSE of lasso model is 298.302

Elastic net model

```
set.seed(666)
enet.fit <- train(recovery_time ~ .,
                  data = training_data,
                  method = "glmnet",
                  tuneGrid = expand.grid(alpha = seq(0, 1, length = 21),
                                         lambda = exp(seq(-25, 5, length = 100))),
                  trControl = ctrl)
```

Here's the selected tuning parameter

```
enet.fit$bestTune
```

```
##     alpha     lambda
## 365  0.15 0.00367552
```

The best tuning parameter is 0.004

And the test error is

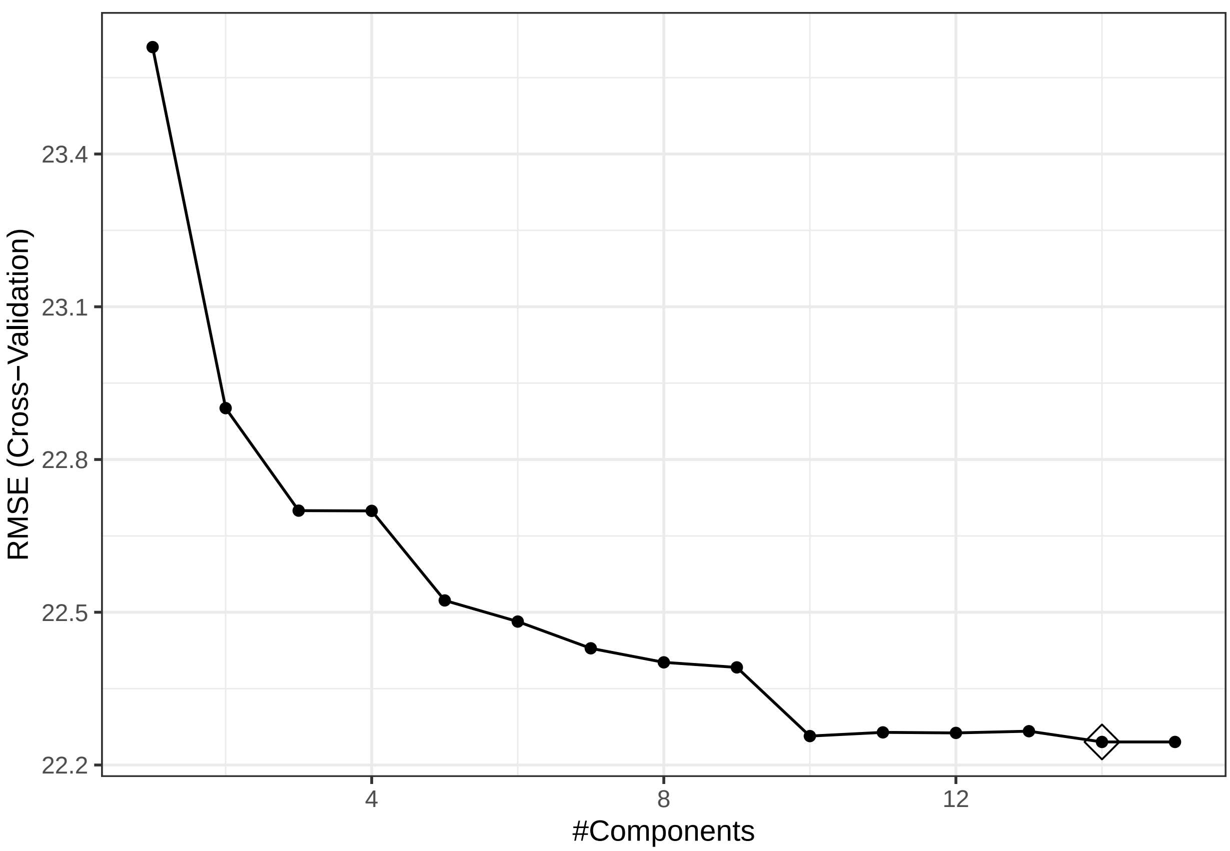
```
enet.pred <- predict(enet.fit, newdata = testing_data)
# test error
mean((enet.pred - testing_data$recovery_time)^2)
```

```
## [1] 297.1645
```

The MSE of elastic net model is 297.164

Principal components regression (PCR)

```
set.seed(666)

pcr.fit <- train(x = x_train,
                 y = y_train,
                 method = "pcr",
                 tuneGrid = data.frame(ncomp = 1:15),
                 trControl = ctrl,
                 preProcess = c("center", "scale"))
predy.pcr <- predict(pcr.fit, newdata = x_test)


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



```r
# test MSE
mean((y_test - predy.pcr)^2)
```

```
## [1] 326.7915
```

The MSE of pcr model is 326.792

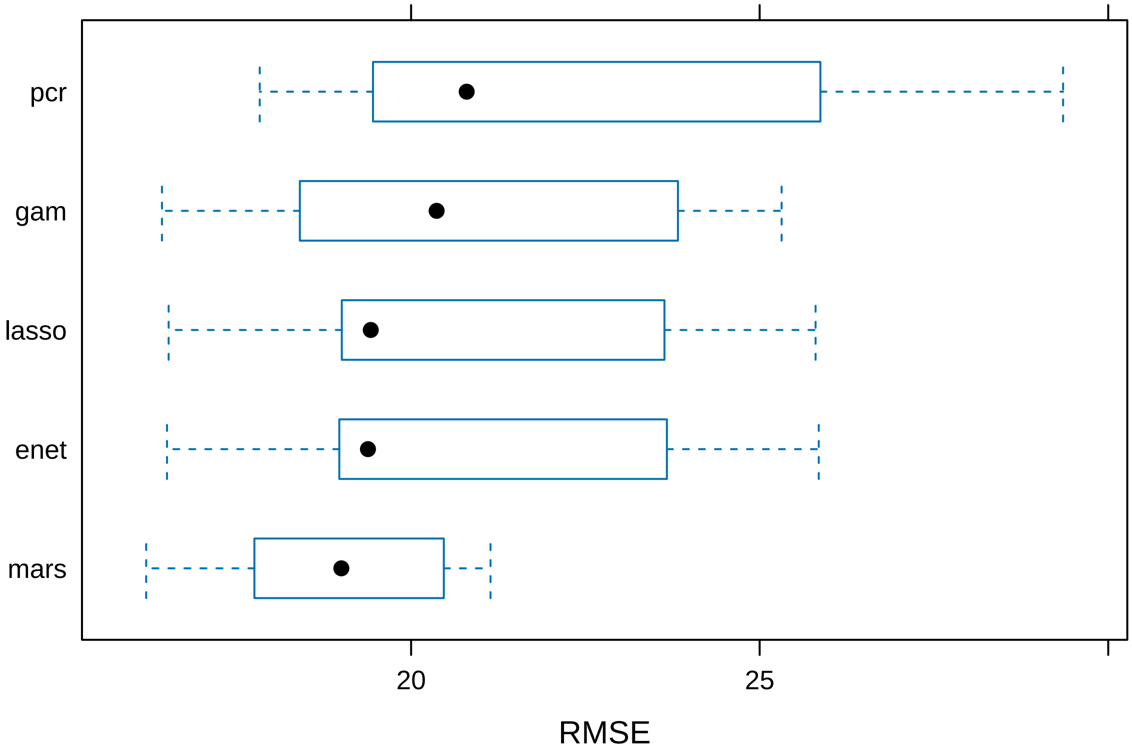
Model Comparison

compare the RMSE

```r
resamp <- resamples(list(mars=model.mars,
                         gam=model.gam,
                         lasso=lasso.fit,
                         enet=enet.fit,
                         pcr=pcr.fit))
summary(resamp)
```

```
##
## Call:
## summary.resamples(object = resamp)
##
## Models: mars, gam, lasso, enet, pcr
## Number of resamples: 10
##
## MAE
##           Min.  1st Qu.   Median     Mean  3rd Qu.     Max. NA's
## mars  11.10656 12.33992 12.52758 12.48434 12.95145 13.22857    0
## gam   11.95625 12.48434 12.90413 13.04720 13.67832 14.43838    0
## lasso 12.43438 13.34989 13.55761 13.60118 13.83628 14.80448    0
## enet  12.39331 13.33858 13.50760 13.56655 13.79648 14.79201    0
## pcr   12.72240 13.31222 13.55369 13.74933 14.24483 15.34219    0
##
## RMSE
##           Min.  1st Qu.   Median     Mean  3rd Qu.     Max. NA's
## mars  16.19940 17.79482 18.99934 18.90878 20.37825 21.13959    0
## gam   16.42592 18.51665 20.36608 20.61337 23.26164 25.31540    0
## lasso 16.52183 19.01349 19.42117 20.76489 22.92277 25.80218    0
## enet  16.49849 18.99457 19.38126 20.76102 22.93865 25.84811    0
## pcr   17.82883 19.58486 20.79741 22.24532 24.69032 29.35286    0
##
## Rsquared
##             Min.    1st Qu.    Median      Mean   3rd Qu.      Max. NA's
## mars  0.12610733 0.18362545 0.2804839 0.3515976 0.5442009 0.6258534    0
## gam   0.11451833 0.18716669 0.2610268 0.2888378 0.3891996 0.4926768    0
## lasso 0.12468177 0.17202246 0.2314607 0.2404962 0.2896867 0.3926191    0
## enet  0.12572956 0.17252601 0.2295363 0.2401820 0.2906342 0.3898855    0
## pcr   0.05353634 0.09951385 0.1073118 0.1279829 0.1298992 0.2421886    0
```

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



The MARS model is preferred since it has a lower mean value of RMSE compared to other models.