Midterm project

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Contents

```r
library(ISLR)
library(caret)
library(tidymodels)
library(pls)
library(earth)
library(ggplot2)
library(patchwork)
library(corrplot)
library(gtsummary)
```

```r
load("./recovery.RData")
data <- subset(dat, select = -id)
data$study <- ifelse(data$study == "A", 0, 1)

data <- data |>
  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)
    )
```

Data Partition

Divide data into training data (80%) and testing data (20%)

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

# training data
training_data <- training(data_split)
training_data <- na.omit(training_data)


# testing data
testing_data <- testing(data_split)
testing_data <- na.omit(testing_data)

# matrix of predictors
x <- model.matrix(recovery_time ~ ., training_data) [ ,-1]
y <- training_data$recovery_time

x2 <- model.matrix(recovery_time ~ ., testing_data) [ ,-1]
y2 <- testing_data$recovery_time

# 10-fold cross validation
ctrl1 <- trainControl(method = "cv", number = 10)
```

EDA

Summary Statistics

```
summ_dat<-dat%>%
  select(-id)%>%
  mutate(
    gender = factor(case_when(
      gender == "1" ~ "male",
      gender == "0" ~ "female"),
      levels = c("female", "male")
    ),
    race= factor(case_when(
      race == "1" ~ "White",
      race == "2" ~ "Asian",
      race == "3" ~ "Black",
      race == "4" ~ "Hispanic"),
      levels = c("White", "Asian","Black","Hispanic")
    ),
    smoking=factor(case_when(
      smoking == "0" ~ "Never smoked",
      smoking == "1" ~ "Former smoker",
      smoking == "2" ~ "Current smoker"),
      levels = c("Never smoked", "Former smoker","Current smoker")
    ),
    hypertension=factor(case_when(
      hypertension == "0" ~ "No",
      hypertension == "1" ~ "Yes"),
      levels = c("No", "Yes")
    ),
    diabetes=factor(case_when(
      diabetes == "0" ~ "No",
      diabetes == "1" ~ "Yes"),
      levels = c("No", "Yes")
    ),
    vaccine=factor(case_when(
      vaccine == "0" ~ "Not vaccinated",
      vaccine == "1" ~ "Vaccinated"),
      levels = c("Not vaccinated", "Vaccinated")
    ),
    severity=factor(case_when(
      severity == "0" ~ "Not severe",
      severity == "1" ~ "Severe"),
      levels = c("Not severe", "Severe")
    )
    )

summ_dat %>%
  tbl_summary() %>%
  bold_labels()%>%
  as_gt(include = everything()) %>%
  gt::tab_header("Table 1: Summary of Dataset")
```

Table 1: Summary of Dataset

Characteristic	**N = 3,000**[1]
age	60.0 (57.0, 63.0)
gender	
female	1,544 (51%)
male	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)

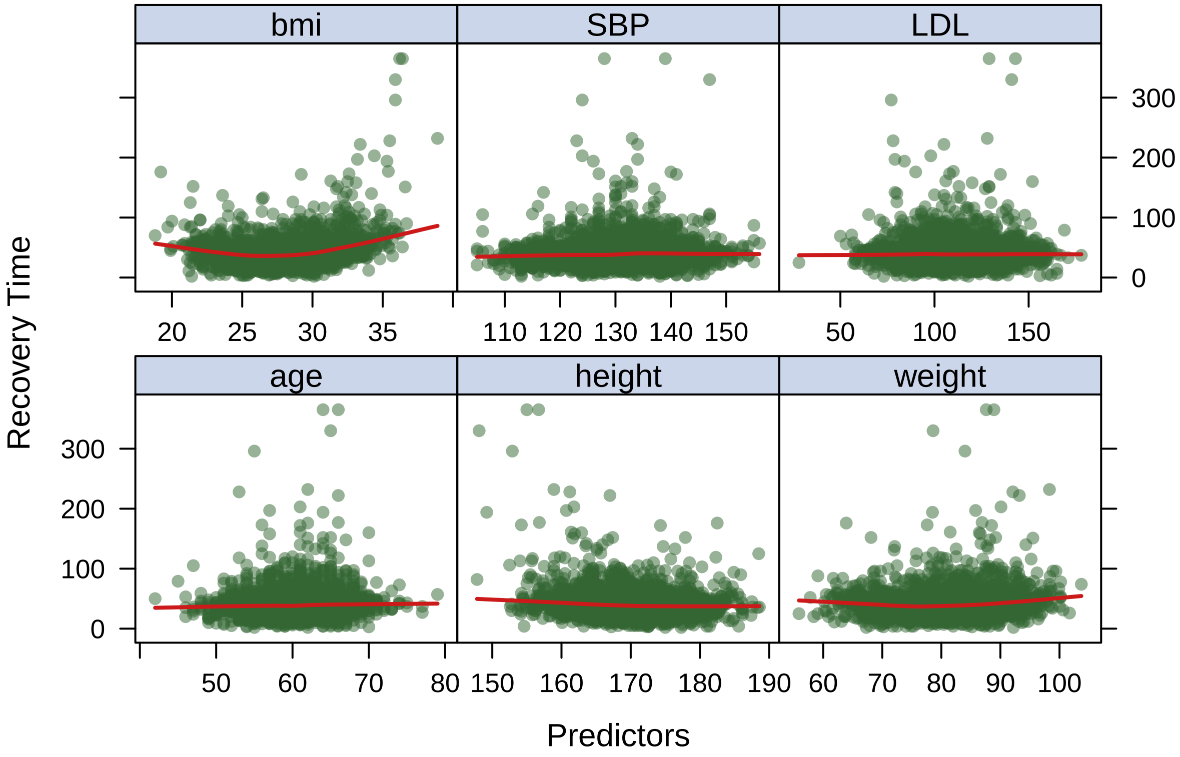
vaccine	
Not vaccinated	1,212 (40%)
Vaccinated	1,788 (60%)
severity	
Not severe	2,679 (89%)
Severe	321 (11%)
study	
A	2,000 (67%)
B	1,000 (33%)
recovery_time	39 (31, 49)

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

Feature plot for continuous variables

```r
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)

continuousData <- data|>
  dplyr::select('age', 'height', 'weight', 'bmi', 'SBP', 'LDL', 'recovery_time')
featurePlot(x = continuousData[ , 1:6],
            y = continuousData[ , 7],
            plot = "scatter",
            span = .5,
            labels = c("Predictors","Recovery Time"),
            main = "Figure 1:Relationship between Continuous Predictors and Recovery Time",
            type = c("p", "smooth"),
            layout = c(3, 2))
```

igure 1:Relationship between Continuous Predictors and Recovery Tim

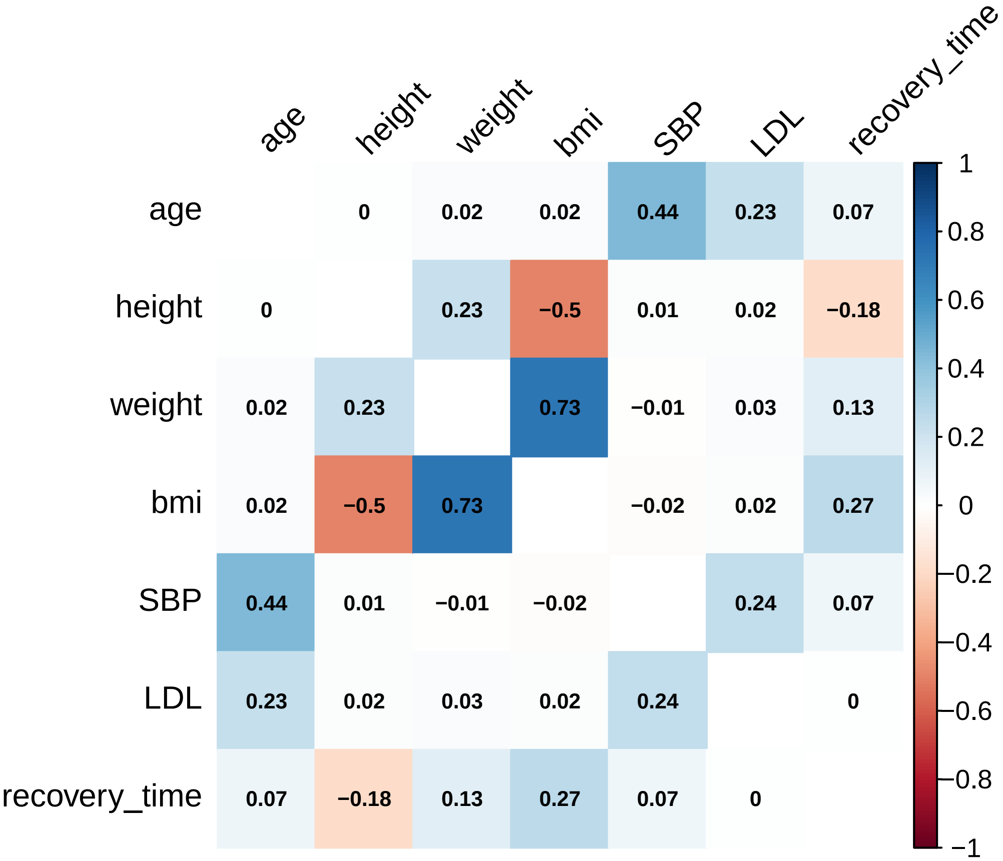


Correlation plot

```r
numerical_data <- summ_dat[, sapply(summ_dat, is.numeric)]
correlation_matrix <- cor(numerical_data)

# Set up the plotting device to save the output to a file
png(filename = "./result_files/cor_plot.png", width = 8, height = 8, units = 'in', res = 300)

# Create the correlation plot
corrplot::corrplot(correlation_matrix, method = "color", addCoef.col = "black",
                   tl.col = "black", tl.srt = 45, insig = "blank", number.cex = 0.7, diag = FALSE)

# Turn off the plotting device
dev.off()
```

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

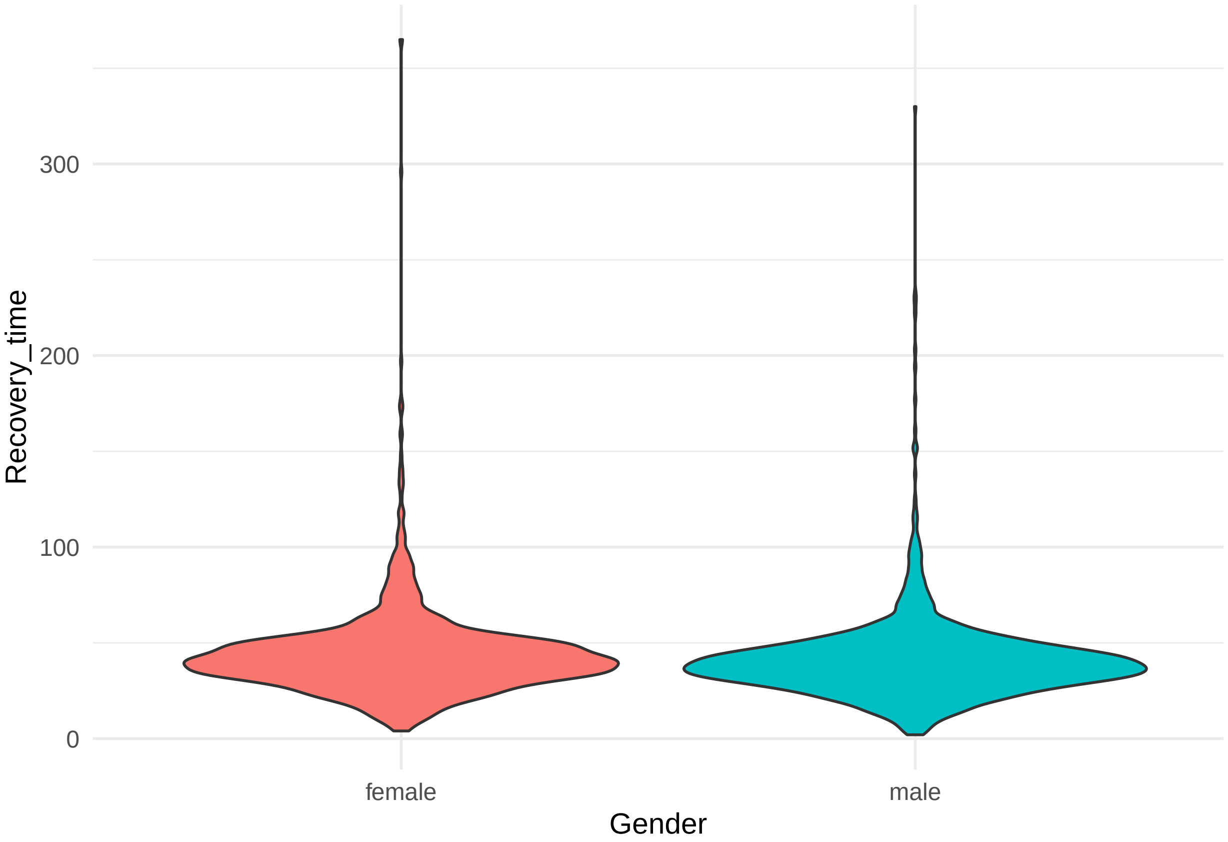
```r
corrplot::corrplot(correlation_matrix, method = "color", addCoef.col = "black",
                   tl.col = "black", tl.srt = 45, insig = "blank", number.cex = 0.7, diag = FALSE)
```



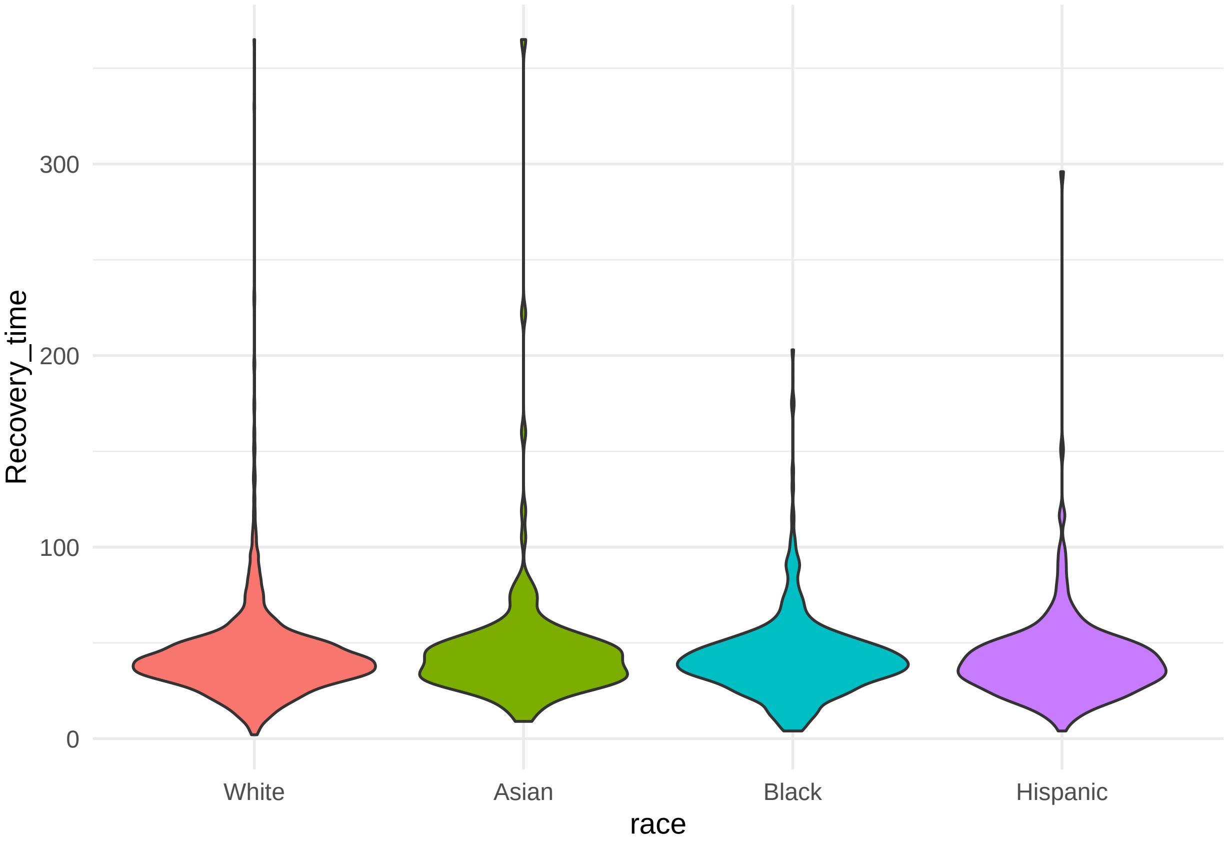
	age	height	weight	bmi	SBP	LDL	recovery_time
age		0	0.02	0.02	0.44	0.23	0.07
height	0		0.23	−0.5	0.01	0.02	−0.18
weight	0.02	0.23		0.73	−0.01	0.03	0.13
bmi	0.02	−0.5	0.73		−0.02	0.02	0.27
SBP	0.44	0.01	−0.01	−0.02		0.24	0.07
LDL	0.23	0.02	0.03	0.02	0.24		0
recovery_time	0.07	−0.18	0.13	0.27	0.07	0	

Violin plot for categorical variables

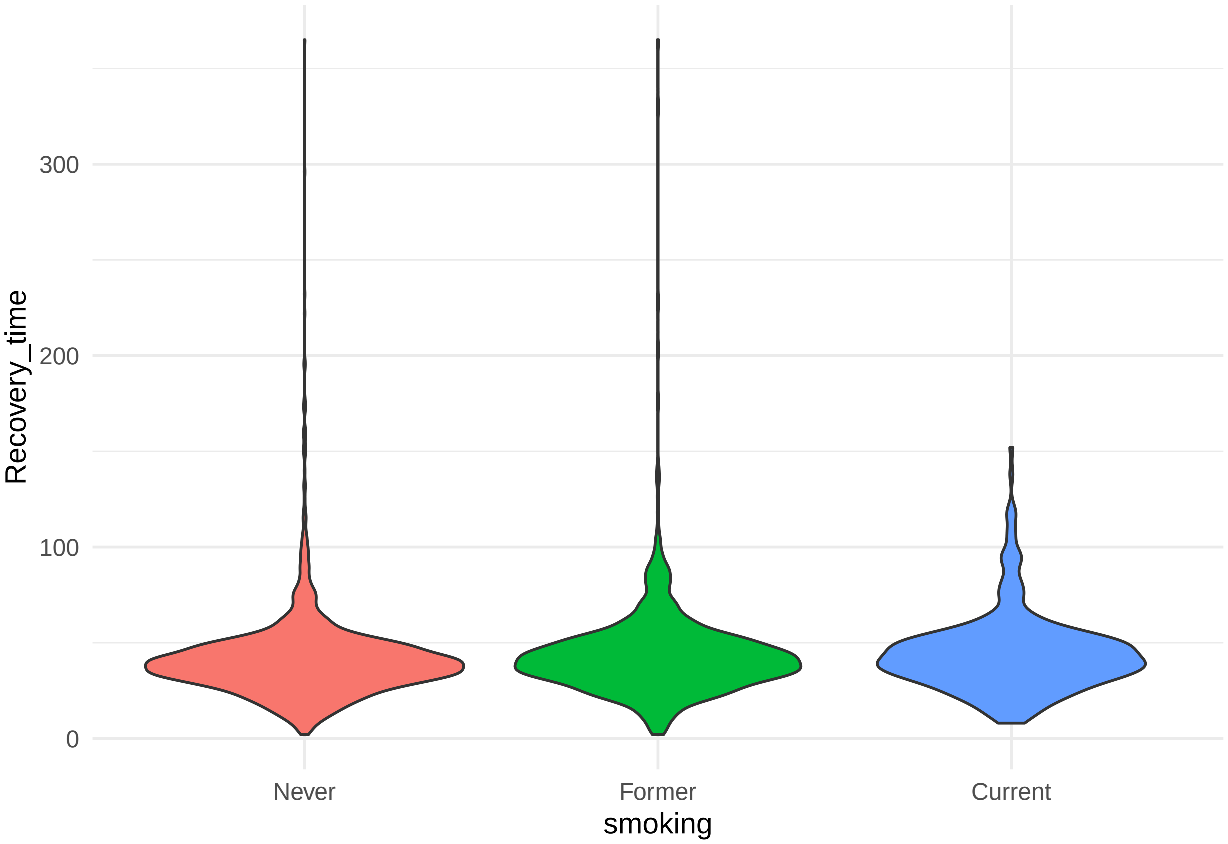
```
gender_plot <- data |>
  ggplot(aes(x = gender, y = recovery_time, fill = gender))+
  geom_violin() +
  scale_x_discrete(labels = c("female", "male")) +
  labs(
       x = "Gender",
       y = "Recovery_time") +
  theme_minimal() + theme(legend.position = "none")
gender_plot
```



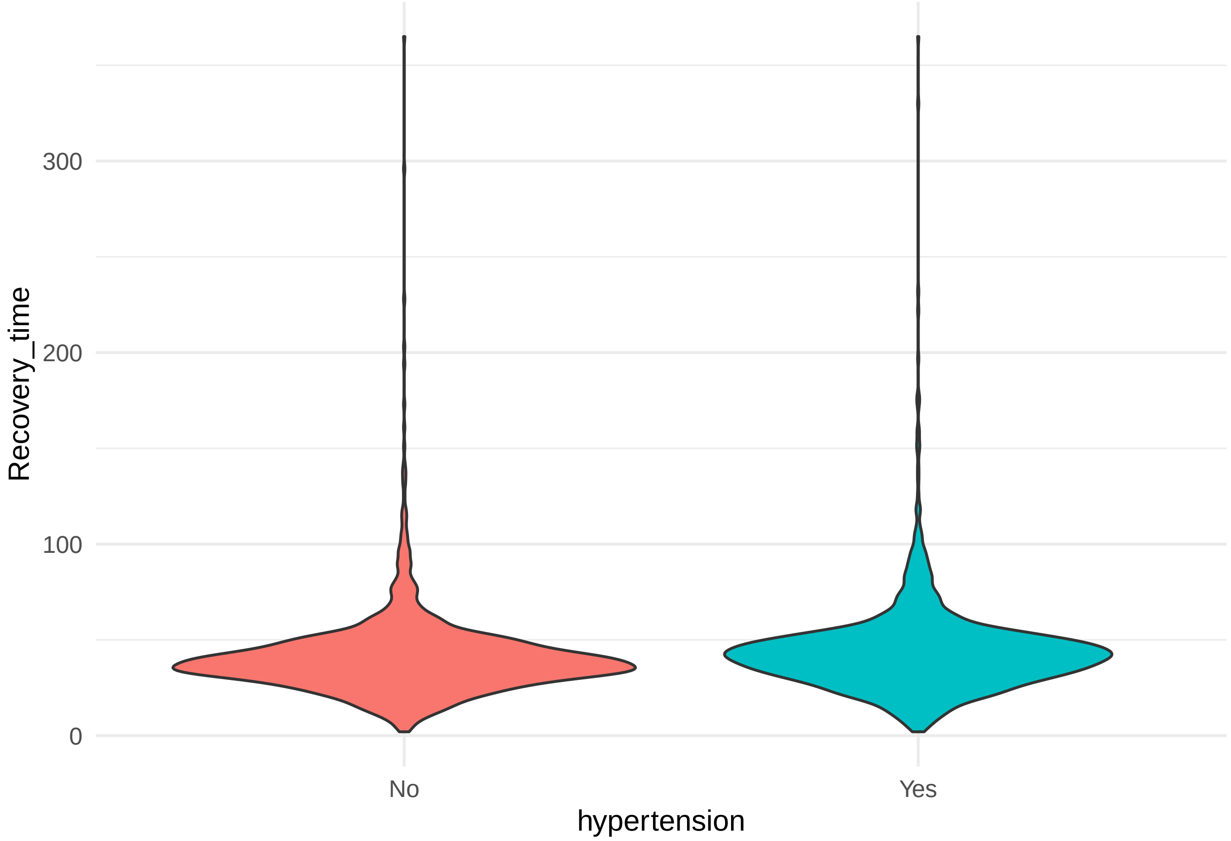
```r
race_plot <- data |>
  ggplot(aes(x = race, y = recovery_time, fill = race)) +
  geom_violin() +
  scale_x_discrete(labels = c("White", "Asian", "Black", "Hispanic")) +
  labs(
       x = "race",
       y = "Recovery_time") +
  theme_minimal() + theme(legend.position = "none")
race_plot
```



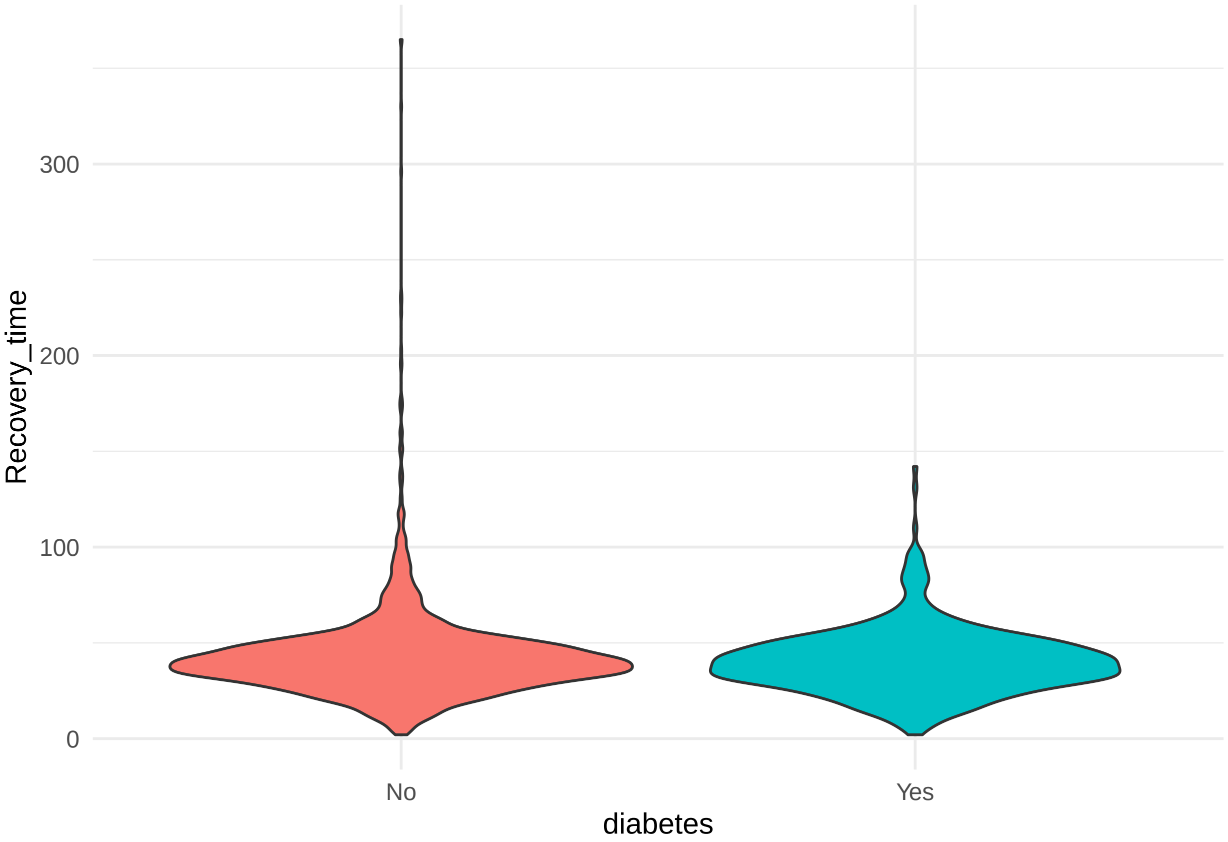
```
smoking_plot <- data |>
  ggplot(aes(x = smoking, y = recovery_time, fill = smoking)) +
  geom_violin() +
  scale_x_discrete(labels = c("Never", "Former", "Current")) +
  labs(
       x = "smoking",
       y = "Recovery_time") +
  theme_minimal() + theme(legend.position = "none")
smoking_plot
```



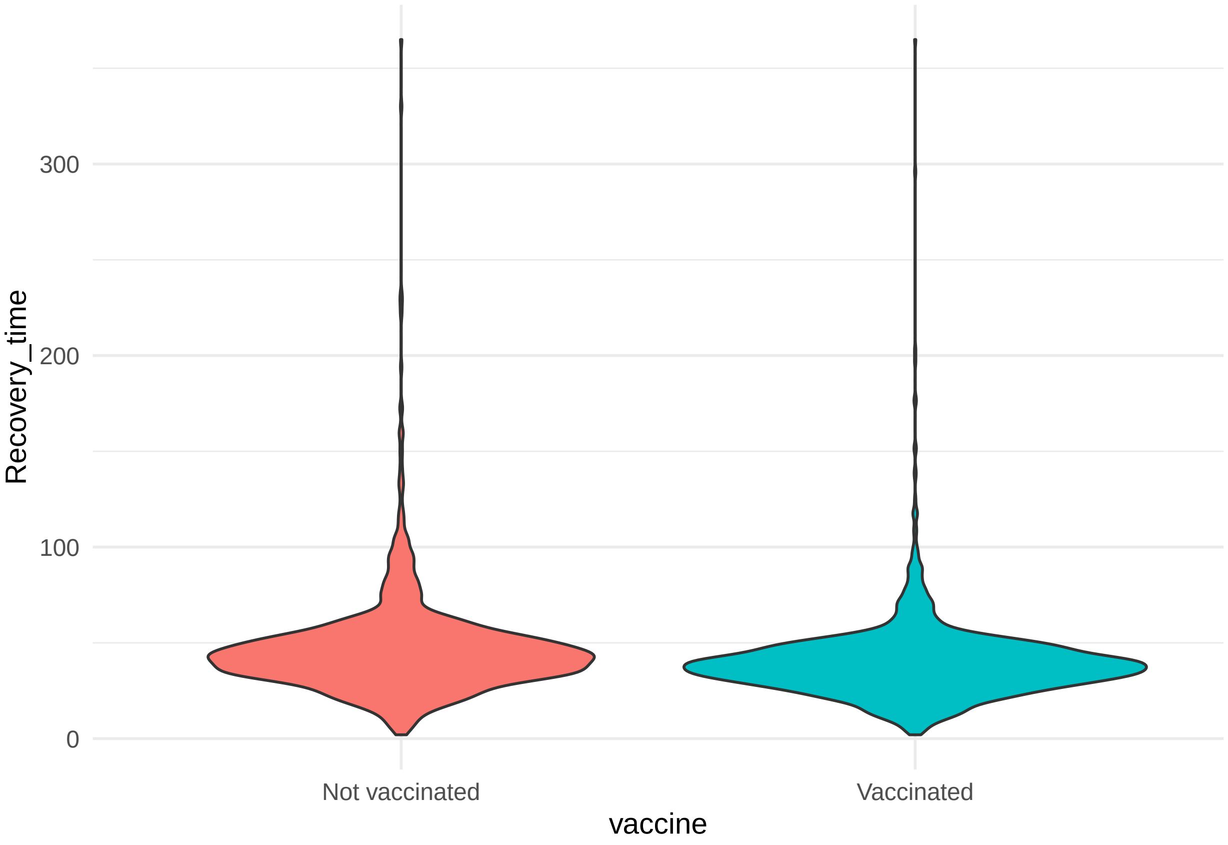
```
hypertension_plot <- data |>
  ggplot(aes(x = hypertension, y = recovery_time, fill = hypertension)) +
  geom_violin() +
  scale_x_discrete(labels = c("No", "Yes")) +
  labs(
       x = "hypertension",
       y = "Recovery_time") +
  theme_minimal() + theme(legend.position = "none")
hypertension_plot
```



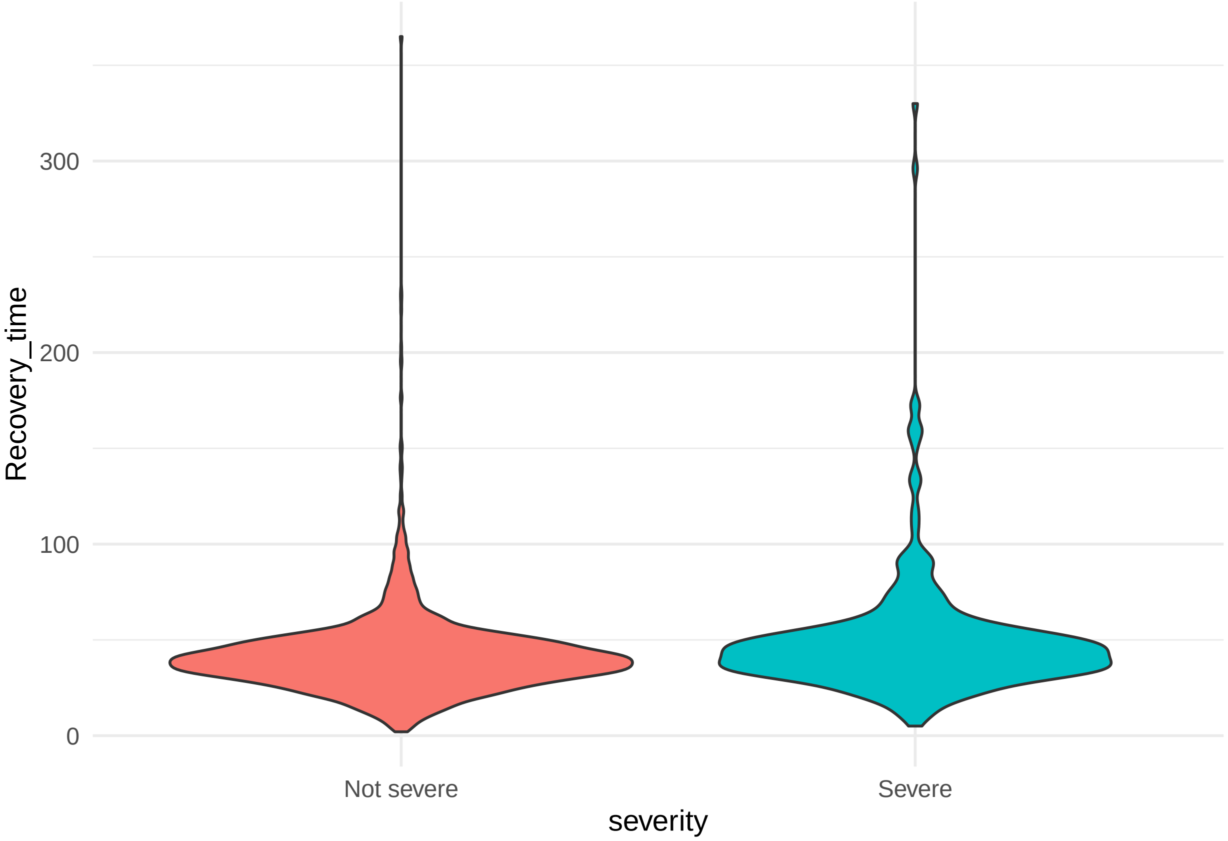
```
diabetes_plot <- data |>
  ggplot(aes(x = diabetes, y = recovery_time, fill = diabetes)) +
  geom_violin() +
  scale_x_discrete(labels = c("No", "Yes")) +
  labs(
       x = "diabetes",
       y = "Recovery_time") +
  theme_minimal() + theme(legend.position = "none")
diabetes_plot
```



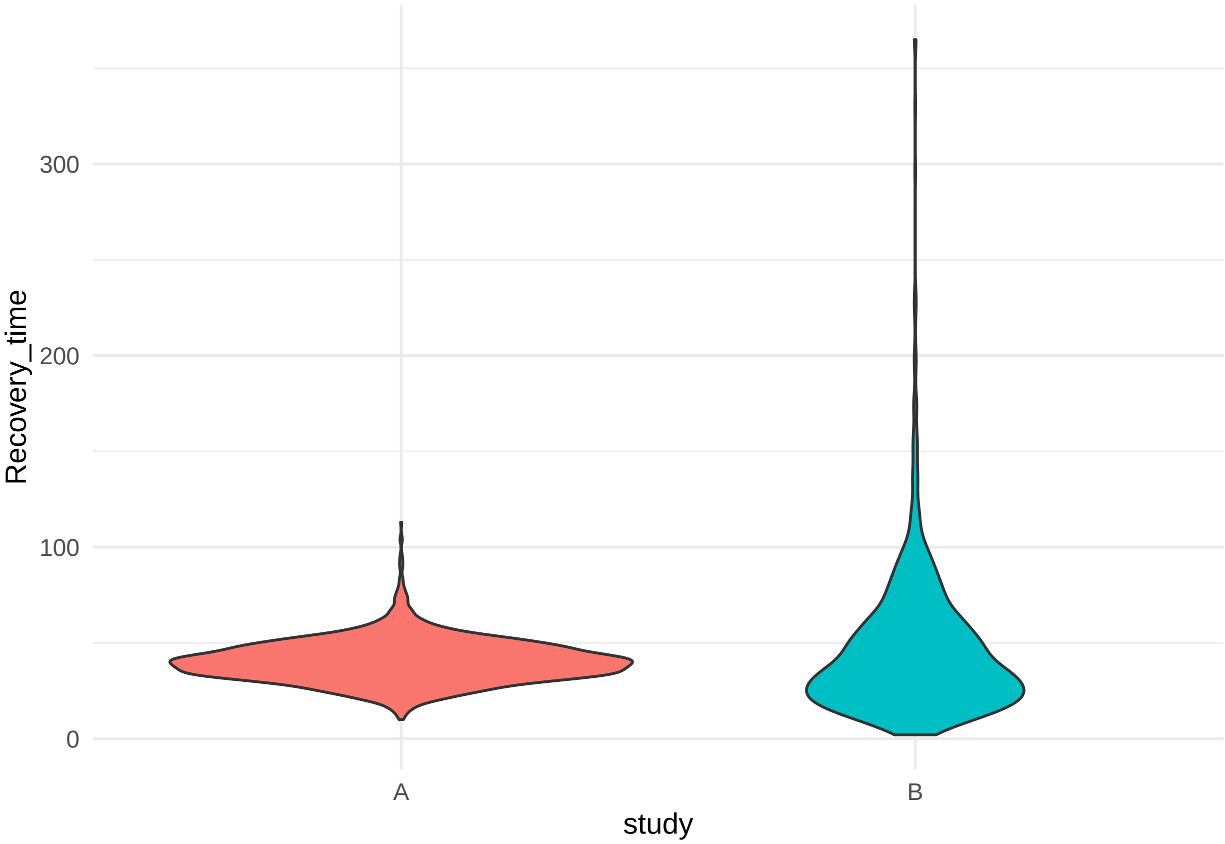
```r
vaccine_plot <- data |>
   ggplot(aes(x = vaccine, y = recovery_time, fill = vaccine)) +
   geom_violin() +
   scale_x_discrete(labels = c("Not vaccinated", "Vaccinated")) +
   labs(
        x = "vaccine",
        y = "Recovery_time") +
   theme_minimal() + theme(legend.position = "none")
vaccine_plot
```



```r
severity_plot <- data |>
  ggplot(aes(x = severity, y = recovery_time, fill = severity)) +
  geom_violin() +
  scale_x_discrete(labels = c("Not severe", "Severe")) +
  labs(
       x = "severity",
       y = "Recovery_time") +
  theme_minimal() + theme(legend.position = "none")
severity_plot
```

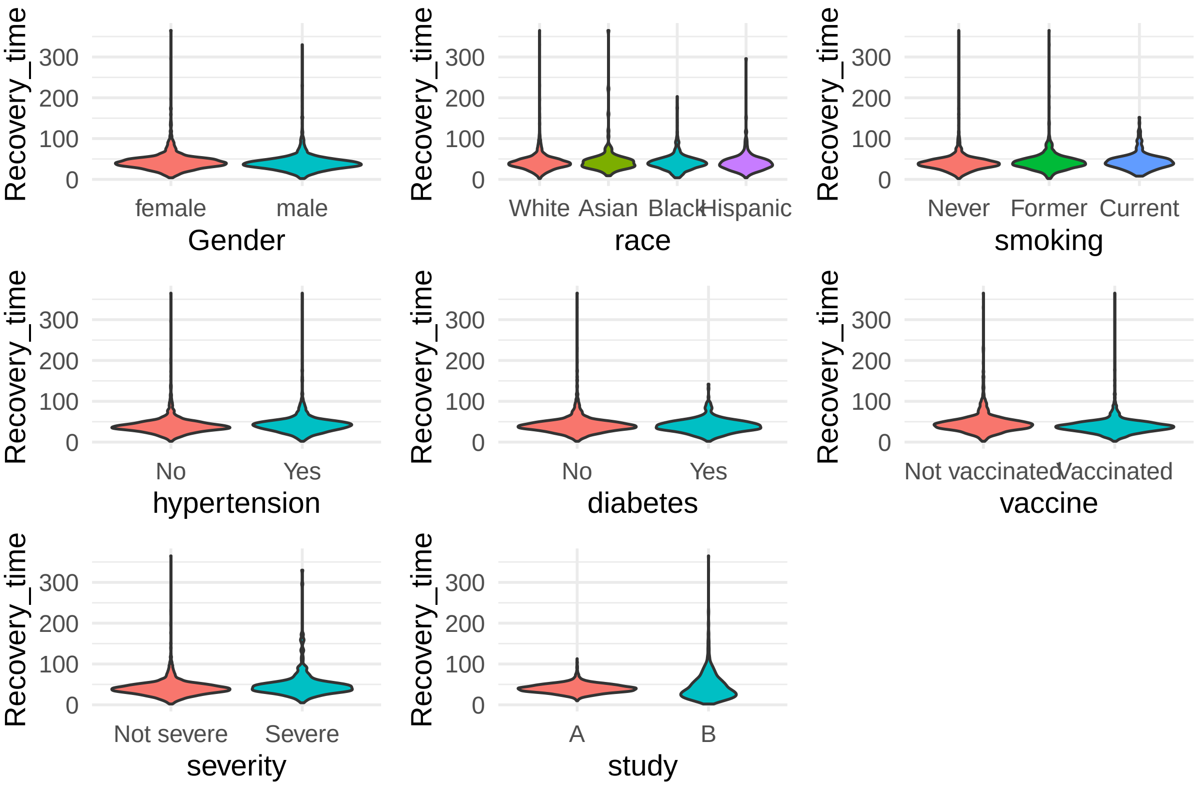


```
study_plot <- data |>
  ggplot(aes(x = study, y = recovery_time, fill = study)) +
  geom_violin() +
  scale_x_discrete(labels = c("A", "B")) +
  labs(
       x = "study",
       y = "Recovery_time") +
  theme_minimal() + theme(legend.position = "none")
study_plot
```



```
combined <- gender_plot + race_plot + smoking_plot + hypertension_plot + diabetes_plot + vaccine_plot +

combined + plot_annotation(title = "Figure 2: Relationship between Categorical Predictors and Recovery
```

Figure 2: Relationship between Categorical Predictors and Recovery Time



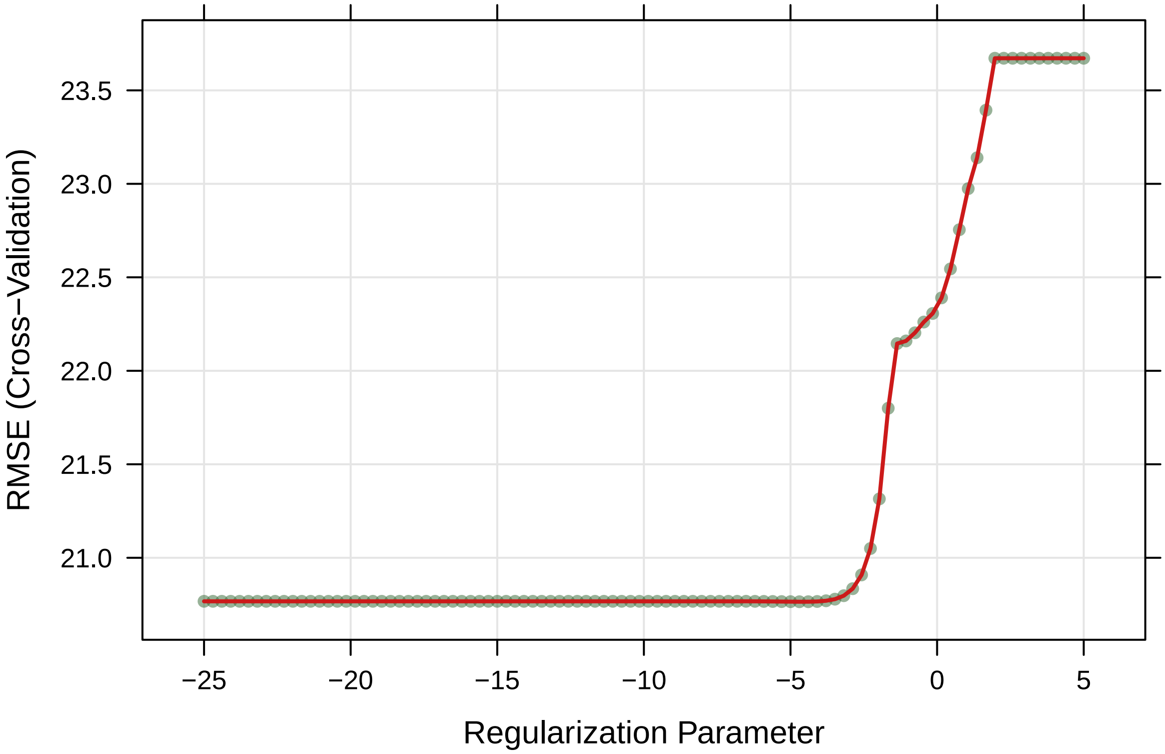
Linear models

Fit a 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 = ctrl1)
```

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

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



```
## Select the best tuning parameter
lasso.fit$bestTune
```

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

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

```
## 18 x 1 sparse Matrix of class "dgCMatrix"
##                          s1
## (Intercept)   -2.229189e+03
## age            2.736904e-01
## gender1       -3.698081e+00
## race2          1.629521e+00
## race3         -7.478838e-01
## race4         -8.493986e-01
## smoking1       2.764637e+00
## smoking2       3.624109e+00
## height         1.302739e+01
## weight        -1.414814e+01
## bmi            4.250183e+01
## hypertension1  3.023576e+00
## diabetes1     -1.066279e+00
## SBP           -1.899186e-02
## LDL           -3.709871e-02
## vaccine1      -6.014455e+00
## severity1      7.390563e+00
## study1         5.298800e+00
```

The selected tuning parameter is 0.00912288.

Test errors

```
set.seed(666)
lasso.pred <- predict(lasso.fit, newdata = testing_data)
mean((lasso.pred - testing_data[, "recovery_time"])^2)
```

```
## [1] 298.3016
```

The test error is 298.3016.

Fit an elastic net model

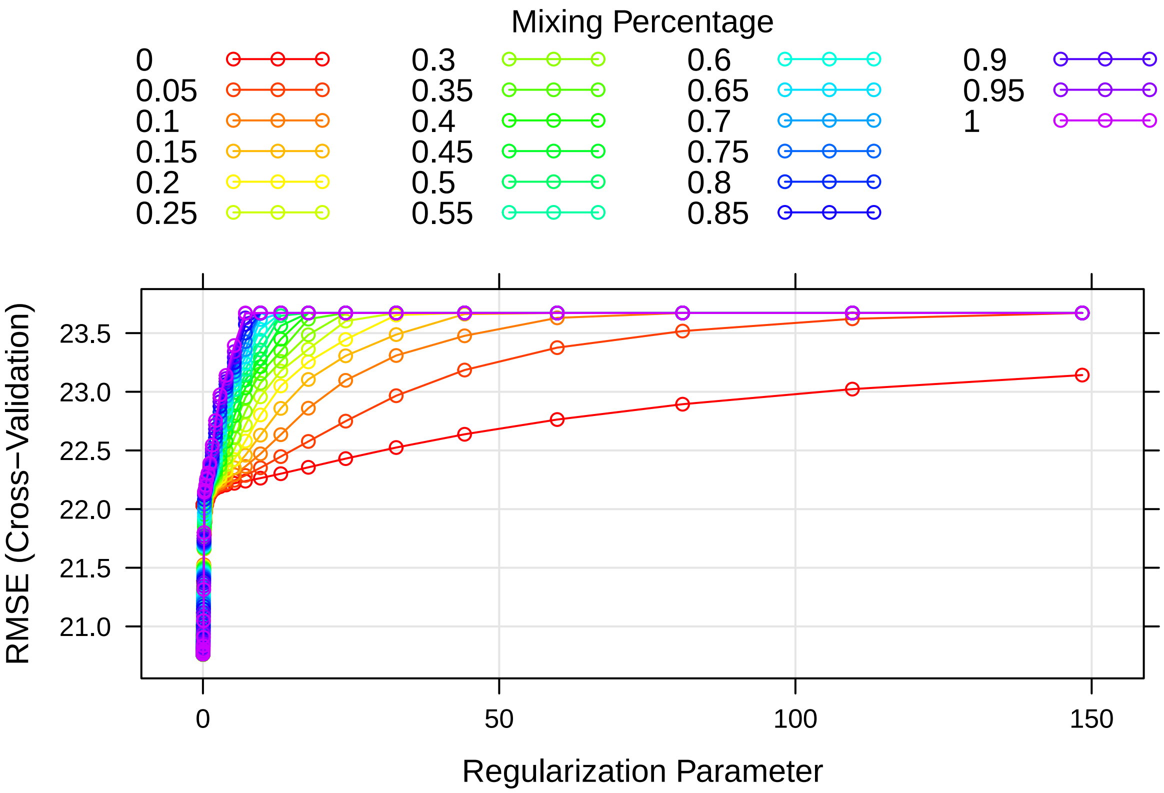
```
set.seed(666)
enet.fit <- train(recovery_time ~ .,
                  data = training_data,
                  method = "glmnet",
                  tuneGrid = expand.grid(alpha = seq(0, 1, length = 21),
                                         lambda = exp(seq(-25, 5, length = 100))),

                  trControl = ctrl1)
```

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

```
## Select the best tuning parameter
enet.fit$bestTune
```

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

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

plot(enet.fit, par.settings = myPar)
```



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

```
## 18 x 1 sparse Matrix of class "dgCMatrix"
##                          s1
## (Intercept)   -2.157409e+03
## age            2.786152e-01
## gender1       -3.708843e+00
## race2          1.666442e+00
## race3         -7.696907e-01
## race4         -9.113345e-01
## smoking1       2.780175e+00
## smoking2       3.645642e+00
## height         1.260703e+01
## weight        -1.370319e+01
## bmi            4.122283e+01
## hypertension1  3.105223e+00
## diabetes1     -1.101528e+00
## SBP           -2.443694e-02
## LDL           -3.746249e-02
## vaccine1      -6.040658e+00
## severity1      7.430536e+00
## study1         5.315665e+00
```

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

```
## [1] 297.1642
```

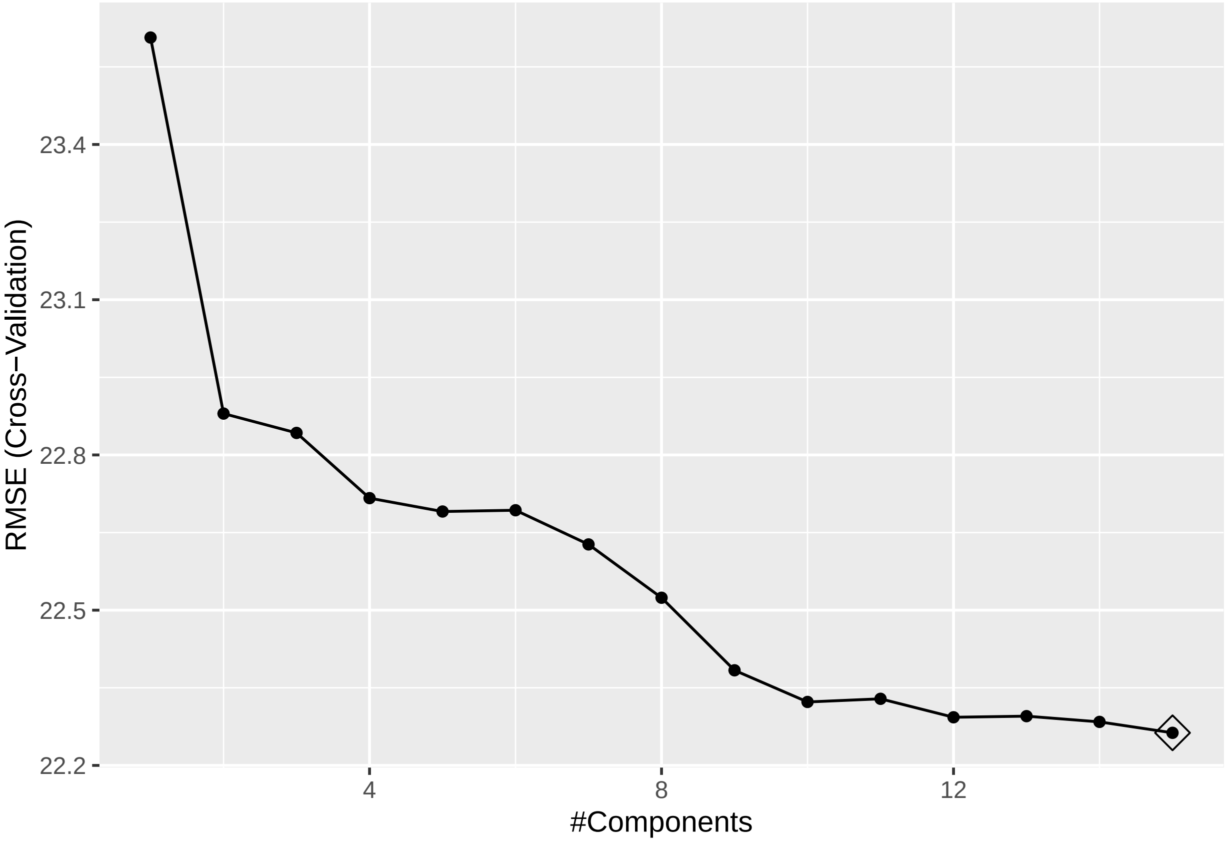
The selected tuning parameter is 0.00367552, and the test error is 297.1642.

Fit a PCR model

```
set.seed(666)
pcr.fit <- train(x, y,
                 method = "pcr",
                 tuneGrid = data.frame(ncomp = 1:15),
                 trControl = ctrl1,
                 scale = TRUE)
predy2.pcr2 <- predict(pcr.fit, newdata = x2)
mean((y2 - predy2.pcr2)^2)
```

```
## [1] 323.779
```

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



```
summary(pcr.fit)
```

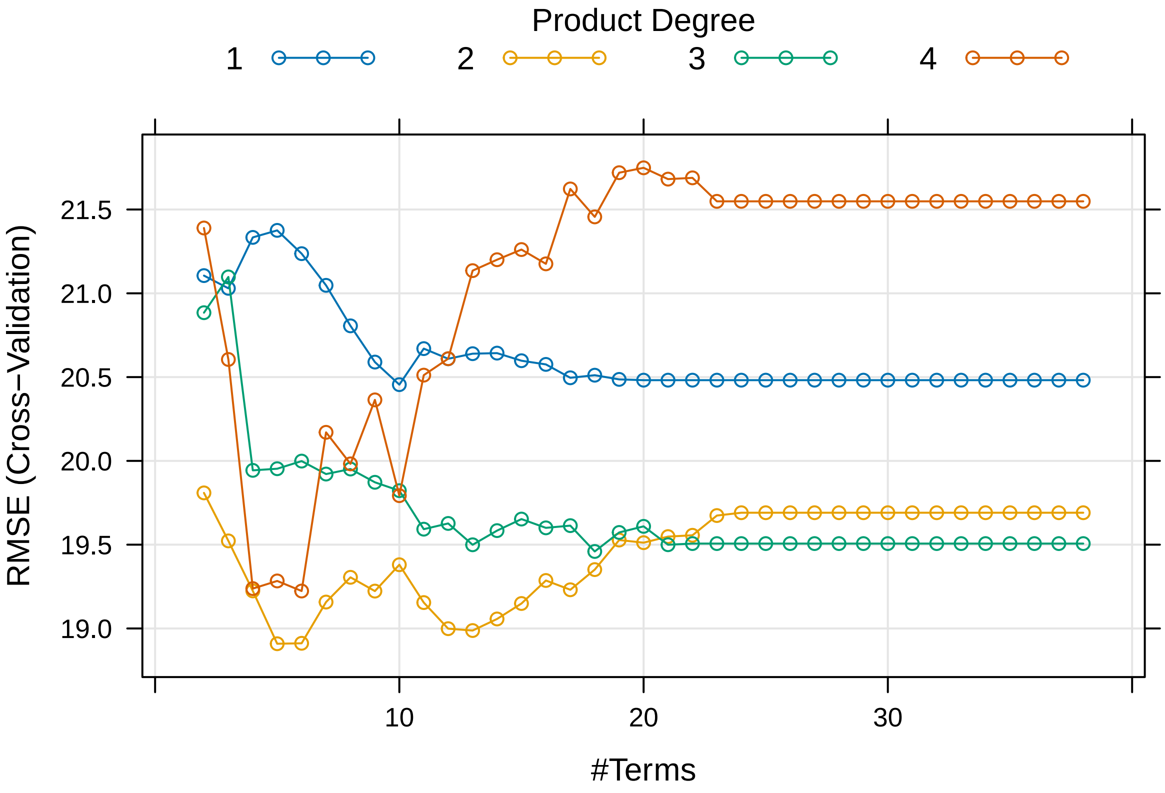
```
## Data:    X dimension: 2400 17
##  Y dimension: 2400 1
## Fit method: svdpc
## Number of components considered: 15
## TRAINING: % variance explained
##           1 comps  2 comps  3 comps  4 comps  5 comps  6 comps  7 comps
## X          13.117   23.728   31.171   38.302   45.266   51.762    57.87
## .outcome    0.602    7.376    7.832    9.341    9.353    9.575    10.59
##           8 comps  9 comps  10 comps  11 comps  12 comps  13 comps  14 comps
## X             63.91    69.84     75.59     81.01     85.98     90.51     94.88
## .outcome      11.16    12.02     12.51     12.51     12.88     12.98     13.16
##             15 comps
## X              98.82
## .outcome       13.32
```

There are 15 components in the model and the test error is 323.779.

Nonlinear models

Multivariate Adaptive Regression Spline (MARS)

```
set.seed(666)
mars.grid <- expand.grid(degree = 1:4,
                         nprune = 2:38)
mars.fit <- train(x, y,
                  method = "earth",
                  tuneGrid = mars.grid,
                  trControl = ctrl1)

plot(mars.fit)
```



```
# best tune
mars.fit$bestTune
```

```
##    nprune degree
## 41      5      2
```

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

```
##                (Intercept)                   h(31-bmi)
##                 -3.1983530                   6.3999877
##        h(bmi-31) * study1                 h(bmi-25.2)
##                 25.6820131                   7.9260754
## h(weight-86.4) * h(bmi-31)
##                 -0.6277843
```

Test error for MARS

```
mars.pred <- predict(mars.fit, newdata = x2)
mars.test.error <- mean((mars.pred - y2)^2)
mars.test.error
```

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

The regression function should be: -3.1983530 + 6.3999877 * h(31-bmi) + 25.6820131 * h(bmi-31) * study1 + 7.9260754 * h(bmi-25.2) - 0.6277843 * h(weight-86.4) * h(bmi-31)

The test error is 279.0367

GAM

```
set.seed(666)

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

```
## 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")'.
```

```
gam.fit$bestTune
```

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

```
gam.fit$finalModel
```

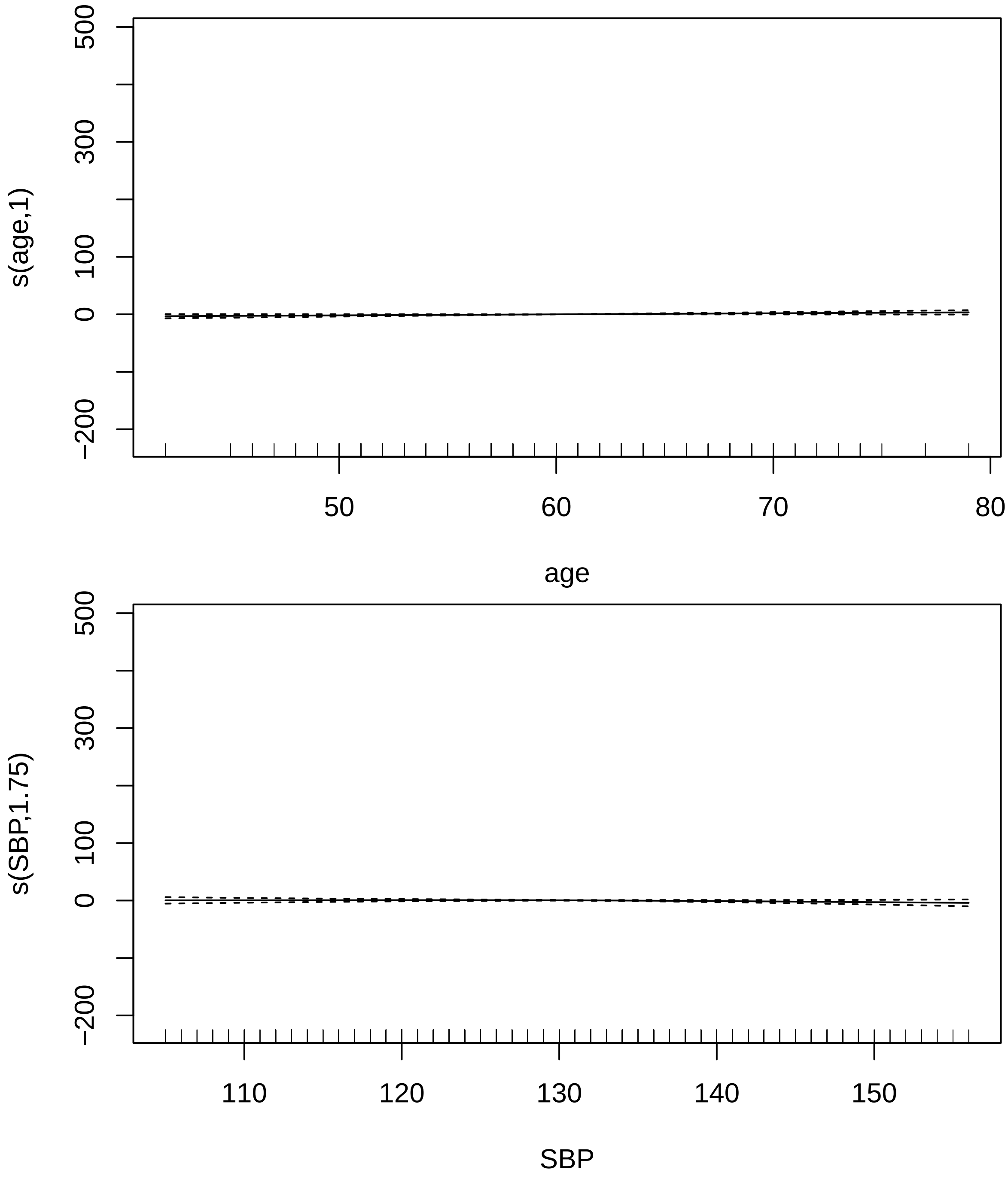
```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## .outcome ~ gender1 + race2 + race3 + race4 + smoking1 + smoking2 +
##     hypertension1 + diabetes1 + vaccine1 + severity1 + study1 +
##     s(age) + s(SBP) + s(LDL) + s(bmi) + s(height) + s(weight)
##
## Estimated degrees of freedom:
## 1.00 1.75 1.00 8.56 7.24 2.81  total = 34.36
```

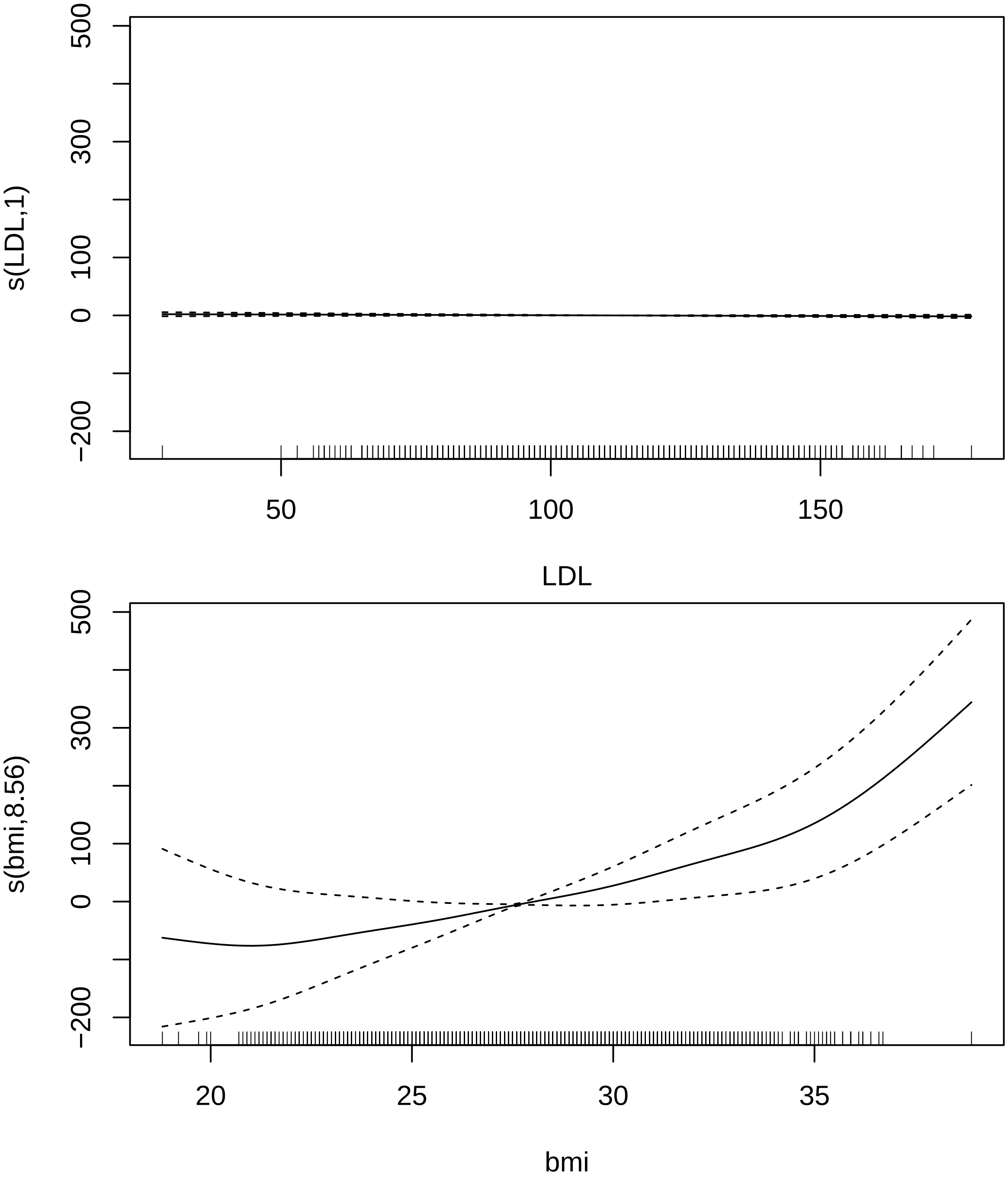
```
##
## GCV score: 384.8296
```

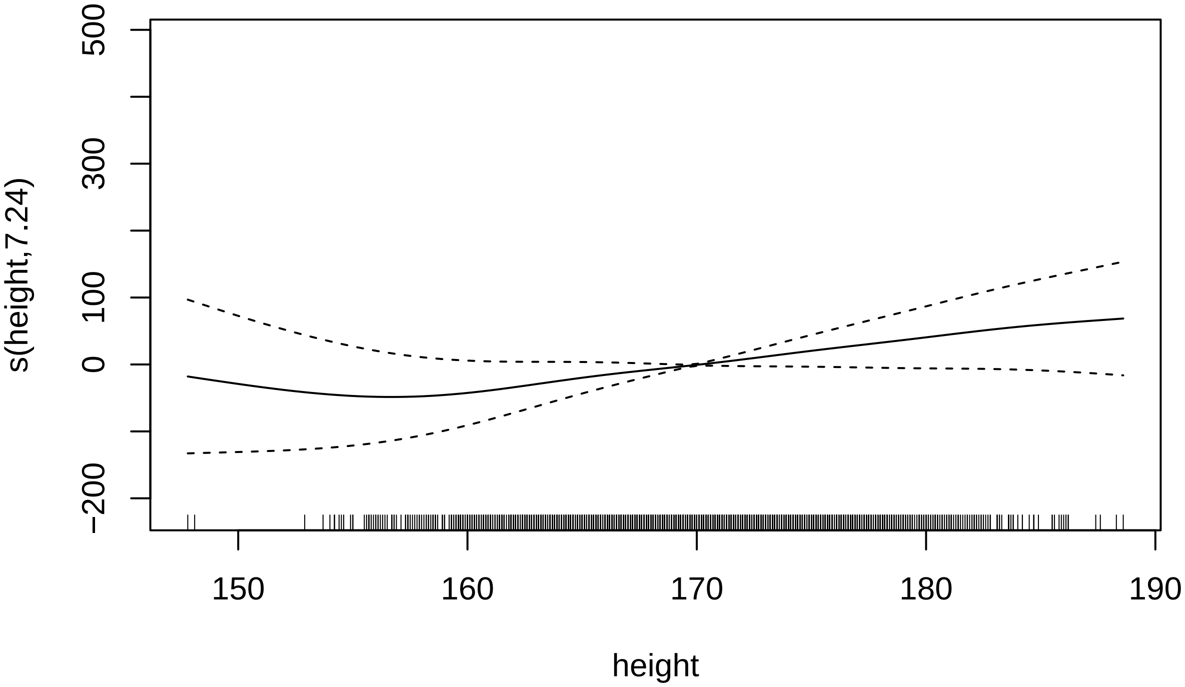
The GAM model includes all the predictors.

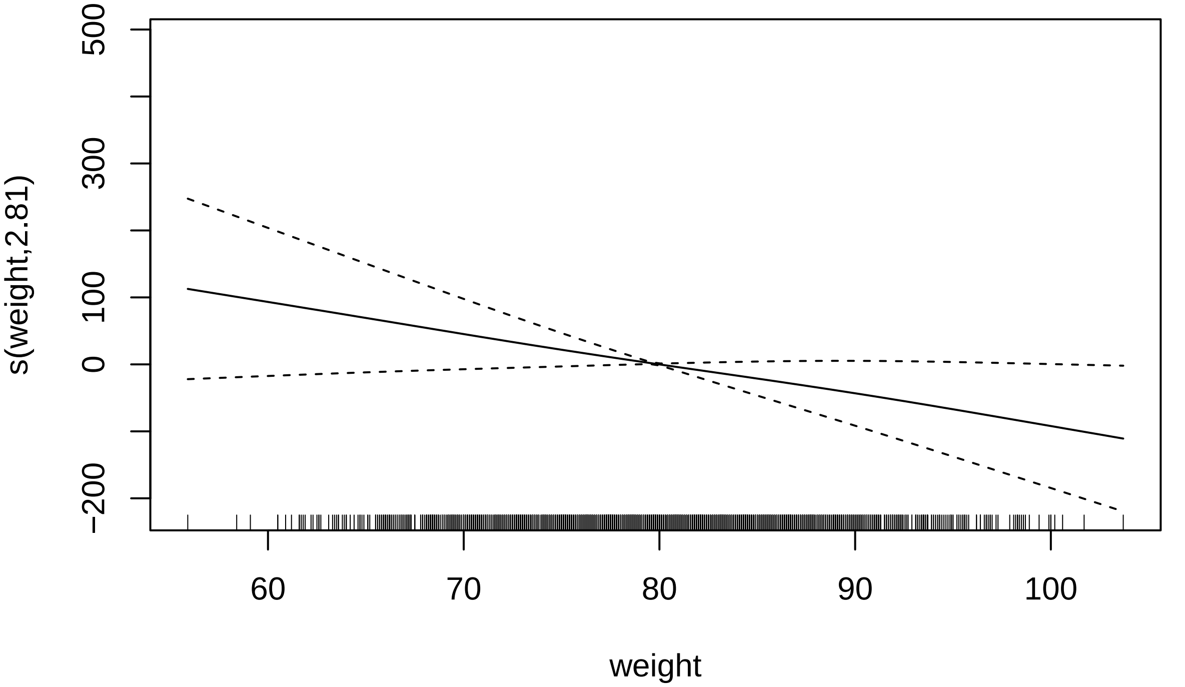
Generate plot for GAM

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




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





Test error for GAM

```
gam.pred <- predict(gam.fit, newdata = x2)
gam.test.error <- mean((gam.pred - y2)^2)
gam.test.error
```

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

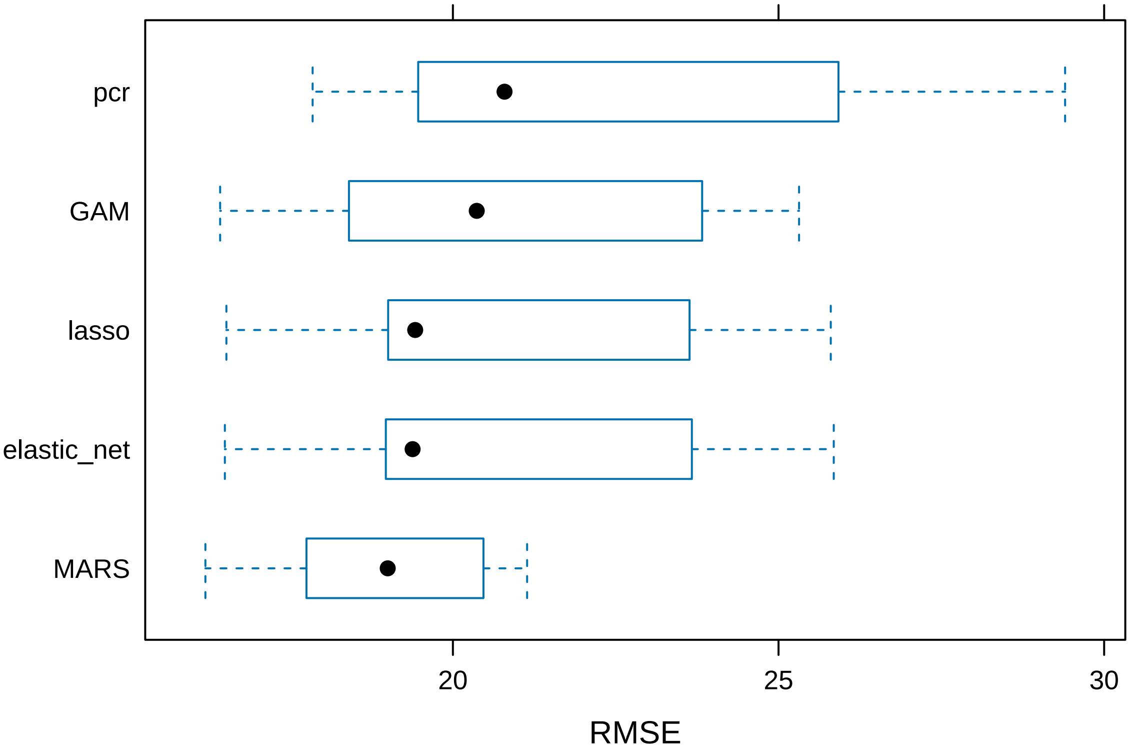
The test error for GAM is 272.0012.

Model comparison

```
resamp <- resamples(list(lasso = lasso.fit,
                         elastic_net = enet.fit,
                         pcr = pcr.fit,
                         MARS = mars.fit,
                         GAM = gam.fit))
summary(resamp)
```

```
##
## Call:
## summary.resamples(object = resamp)
##
## Models: lasso, elastic_net, pcr, MARS, GAM
## Number of resamples: 10
##
## MAE
##                 Min.  1st Qu.   Median     Mean  3rd Qu.     Max. NA's
## lasso       12.43437 13.34989 13.55760 13.60117 13.83628 14.80446    0
## elastic_net 12.39330 13.33858 13.50759 13.56655 13.79648 14.79199    0
## pcr         12.79843 13.31630 13.65714 13.79429 14.32701 15.26141    0
## 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
##
## RMSE
##                 Min.  1st Qu.   Median     Mean  3rd Qu.     Max. NA's
## lasso       16.52182 19.01349 19.42116 20.76489 22.92278 25.80217    0
## elastic_net 16.49848 18.99457 19.38126 20.76102 22.93865 25.84810    0
## pcr         17.84596 19.61842 20.79266 22.26300 24.74262 29.40059    0
## 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
##
## Rsquared
##                   Min.    1st Qu.    Median      Mean   3rd Qu.      Max. NA's
## lasso       0.12468127 0.17202217 0.2314610 0.2404963 0.2896872 0.3926191    0
## elastic_net 0.12572907 0.17252570 0.2295363 0.2401821 0.2906348 0.3898854    0
## pcr         0.05140385 0.09539054 0.1072900 0.1273979 0.1285069 0.2390132    0
## 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
```

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



Mars model should be selected as the final model since it has the lowest RMSE value.