model_result_008

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Create and Save data

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

#get data from 2 team members uni
set.seed(3554)
dat1 <- dat[sample(1:10000, 2000),]
set.seed(4437)
dat2 <- dat[sample(1:10000, 2000),]

#combine the data and discard duplicates
dat_temp <- rbind(dat1, dat2)
dat <- dat_temp[!duplicated(dat_temp$id),]

#dat is now the final data and it has the length as following:
length(dat$id)
```

```
## [1] 3593
```

```
data =
  dat %>%
  mutate(study = factor(dat$study),
         gender = factor(dat$gender),
         hypertension = factor(dat$hypertension),
         diabetes = factor(dat$diabetes),
         vaccine = factor(dat$vaccine),
         severity = factor(dat$severity)) %>%
  dplyr::select(-id)

#save data
save(data, file = "data/covid_recovery.RData")
head(data)
```

```
##      age gender race smoking height weight  bmi hypertension diabetes SBP LDL
## 2989  63      1    1       0  174.8   83.6 27.4            1        0 137 108
## 620   60      1    1       0  170.0   80.7 27.9            0        0 128  80
## 9226  64      0    1       0  167.5   89.1 31.7            1        0 137 126
## 4098  69      0    1       2  173.0   72.5 24.2            1        0 135 149
## 8349  62      0    1       0  172.6   82.4 27.7            1        0 138 136
## 184   60      1    1       0  166.5   82.9 29.9            0        0 128 118
##      vaccine severity study recovery_time
## 2989       1        0     B            14
## 620        1        0     A            36
## 9226       0        0     C            50
## 4098       0        0     B            65
## 8349       1        0     C            34
## 184        1        0     A            32
```

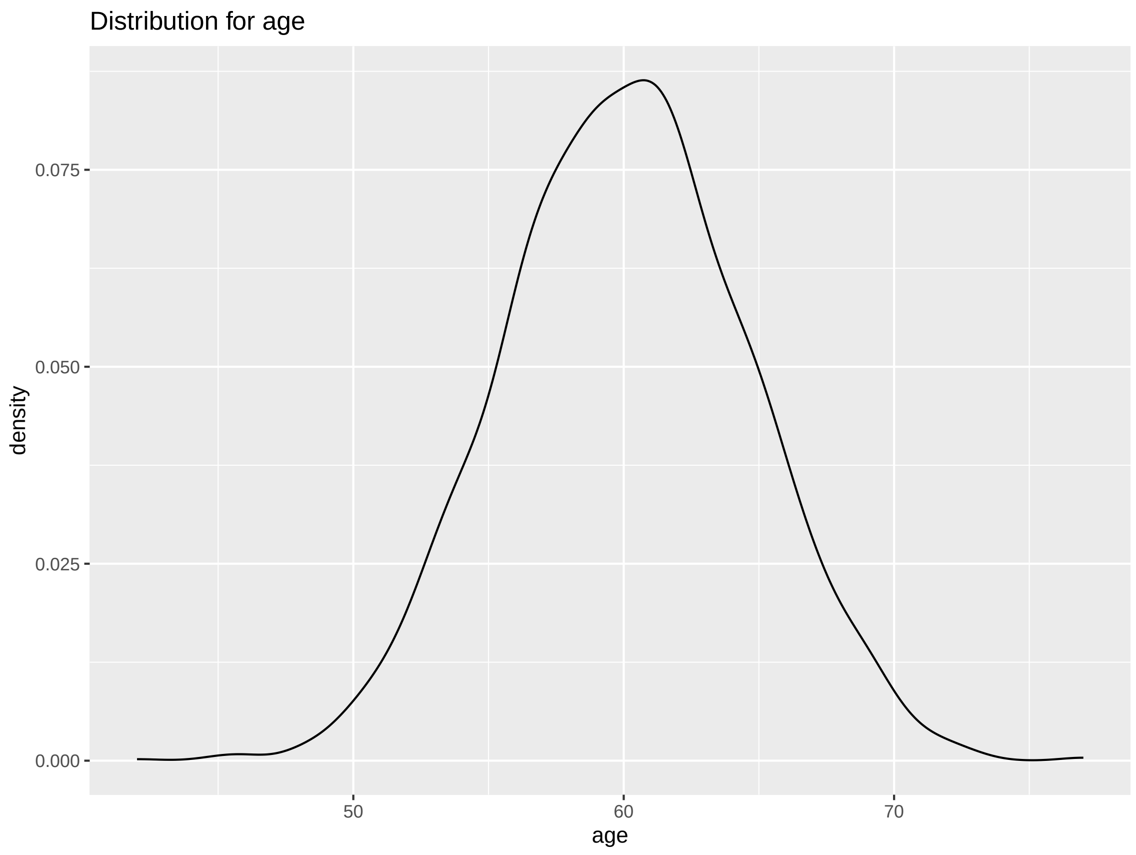
Load data, data partition

```
# load data
load("data/covid_recovery.Rdata")

#Split data into 70-300, using the third member's uni
```

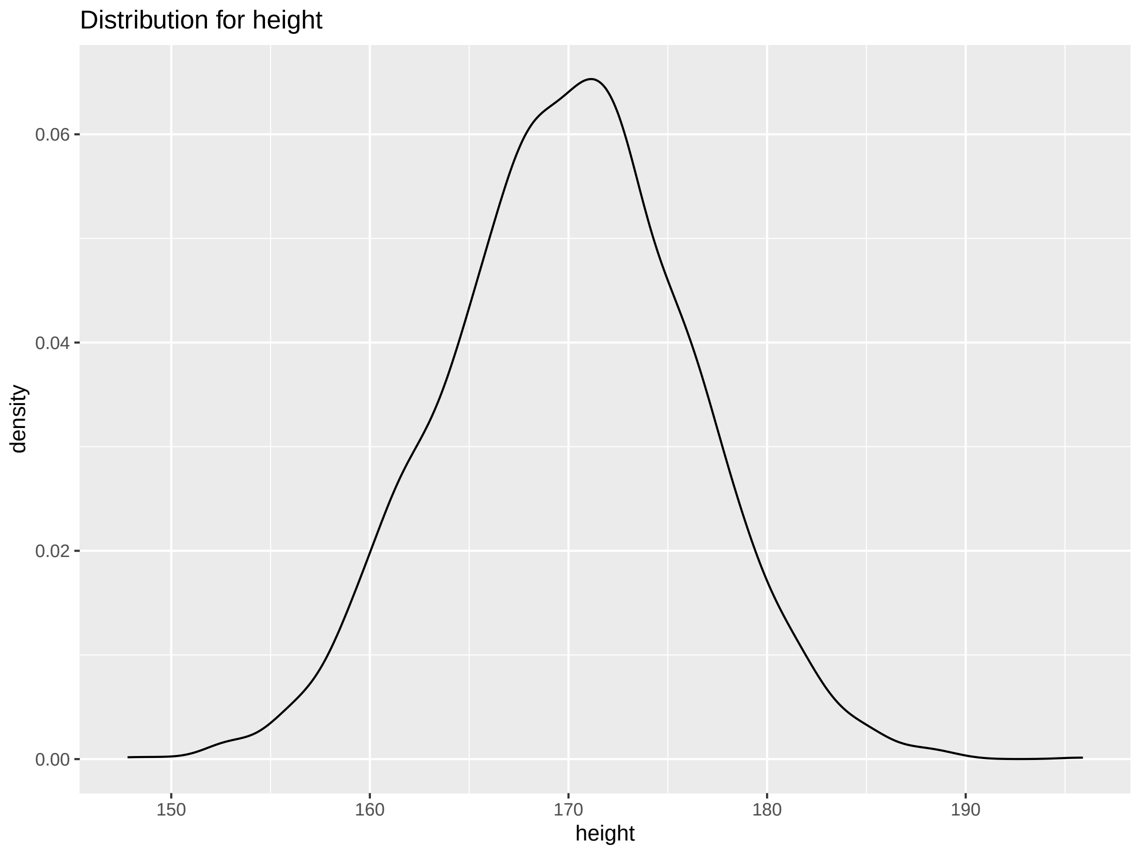
```r
set.seed(2337)
indexTrain <- createDataPartition(y = data$recovery_time, p = 0.7, list = FALSE)

# training data
train_data <- data[indexTrain,]
# matrix of predictors
train_x <- model.matrix(recovery_time~.,train_data)[,-1]
# vector of response
train_y <- train_data$recovery_time

# test data
test_data <- data[-indexTrain,]
# matrix of predictors
test_x <- model.matrix(recovery_time~.,test_data)[,-1]
# vector of response
test_y <- test_data$recovery_time

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

EDA on training data

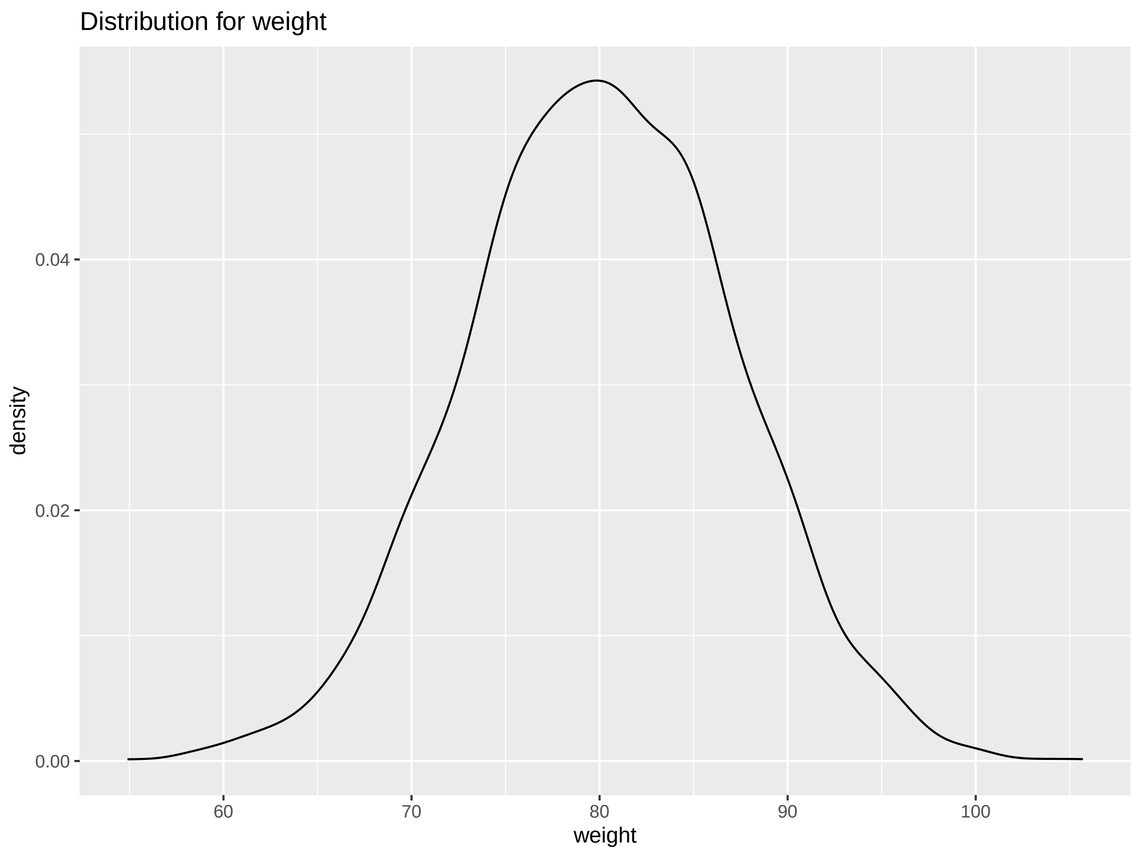
```r
#continuous
ggplot(train_data, aes(x = age))+geom_density()+labs(title="Distribution for age")
```



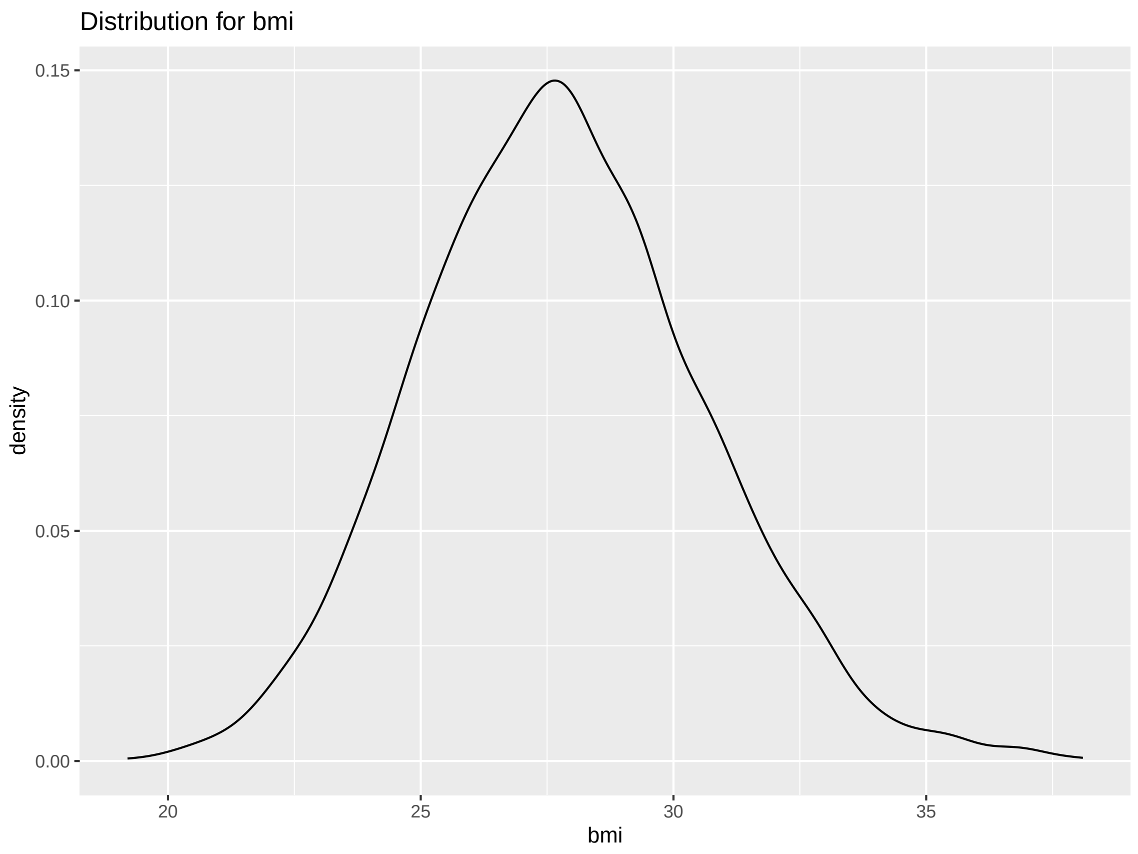
```
ggplot(train_data, aes(x = height))+geom_density()+labs(title="Distribution for height")
```



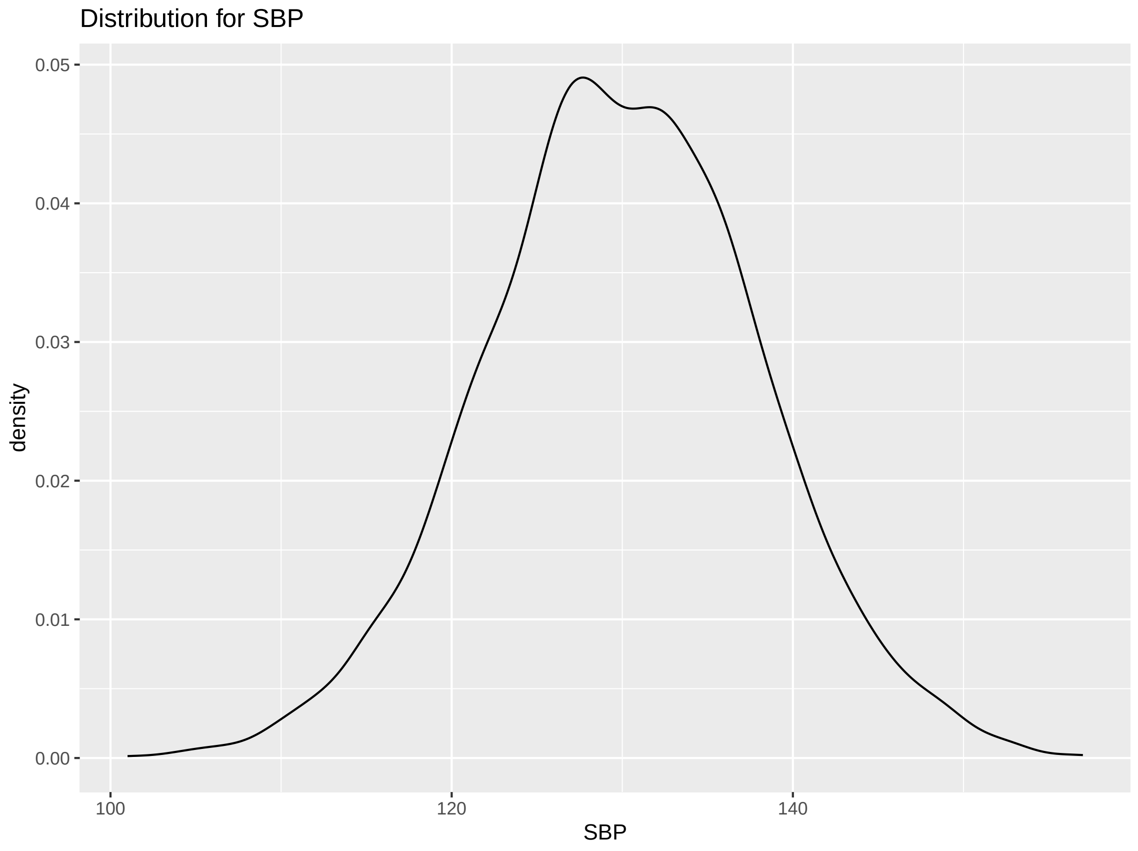
```
ggplot(train_data, aes(x = weight))+geom_density()+labs(title="Distribution for weight")
```



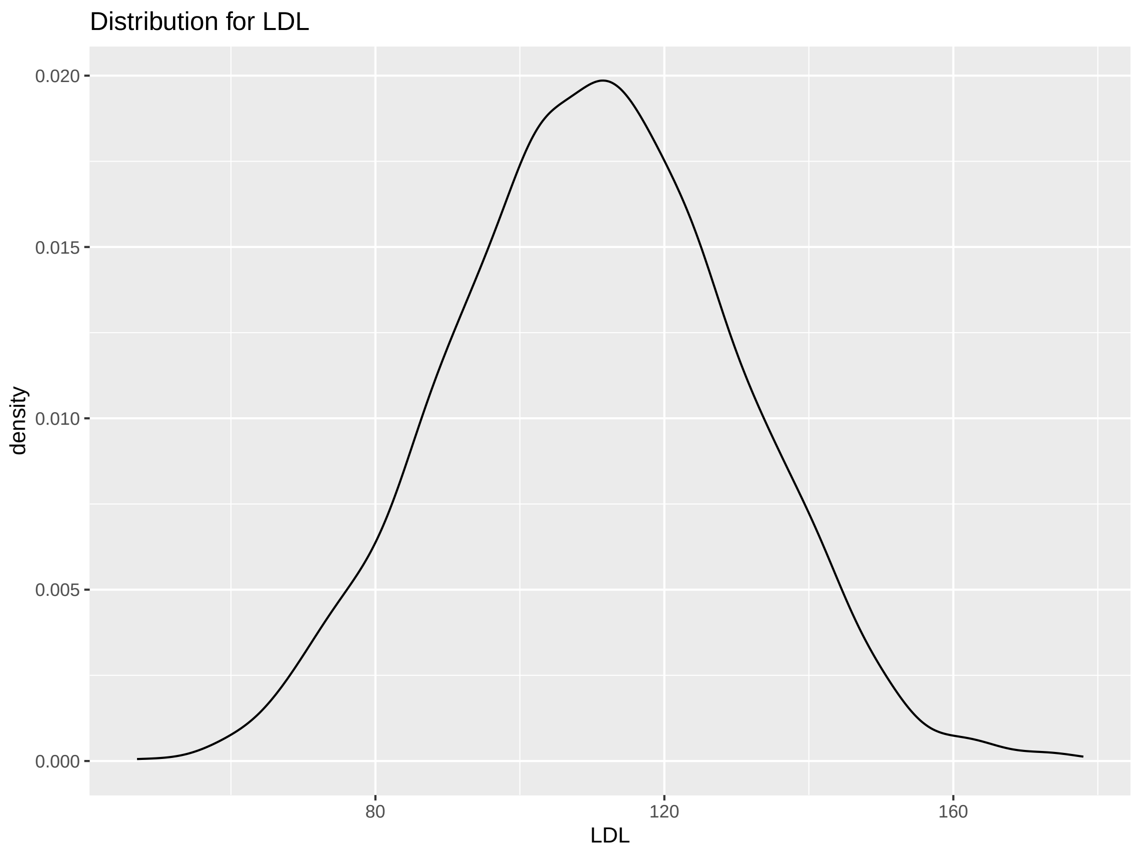
```
ggplot(train_data, aes(x = bmi))+geom_density()+labs(title="Distribution for bmi")
```



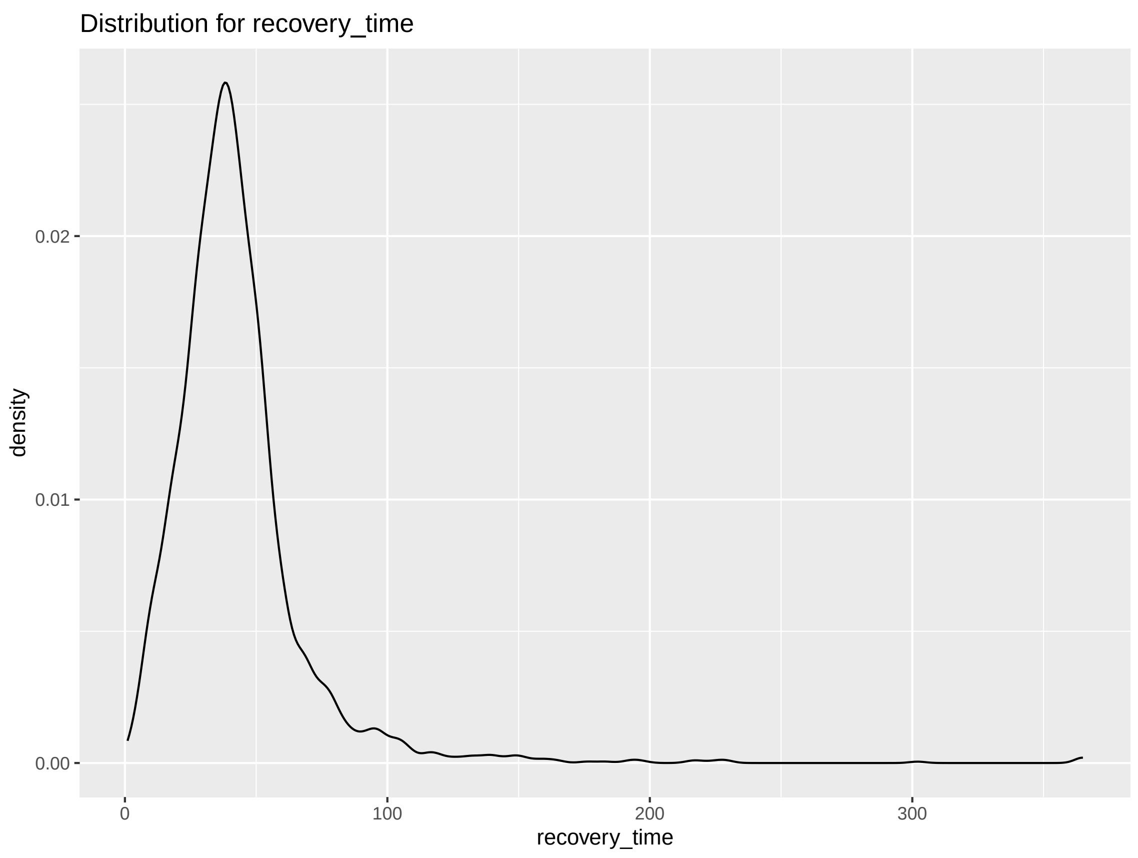
```
ggplot(train_data, aes(x = SBP))+geom_density()+labs(title="Distribution for SBP")
```



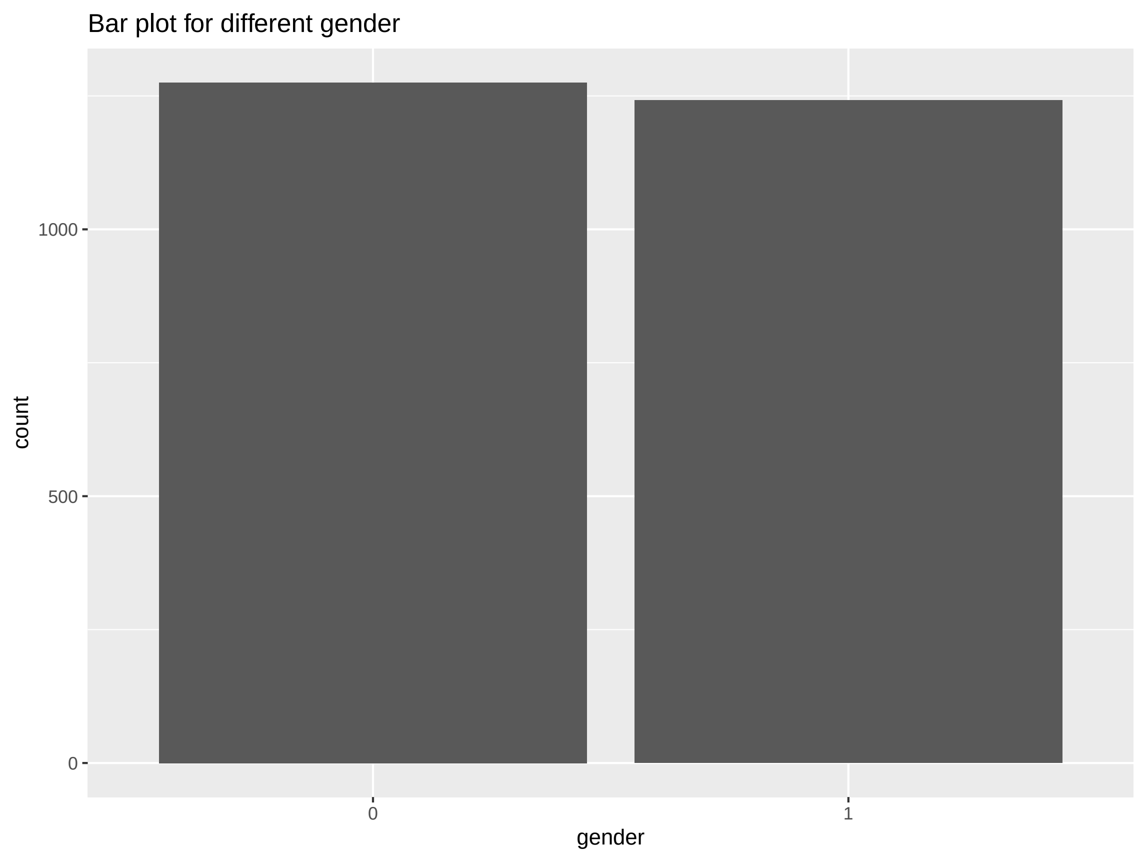
```r
ggplot(train_data, aes(x = LDL))+geom_density()+labs(title="Distribution for LDL")
```



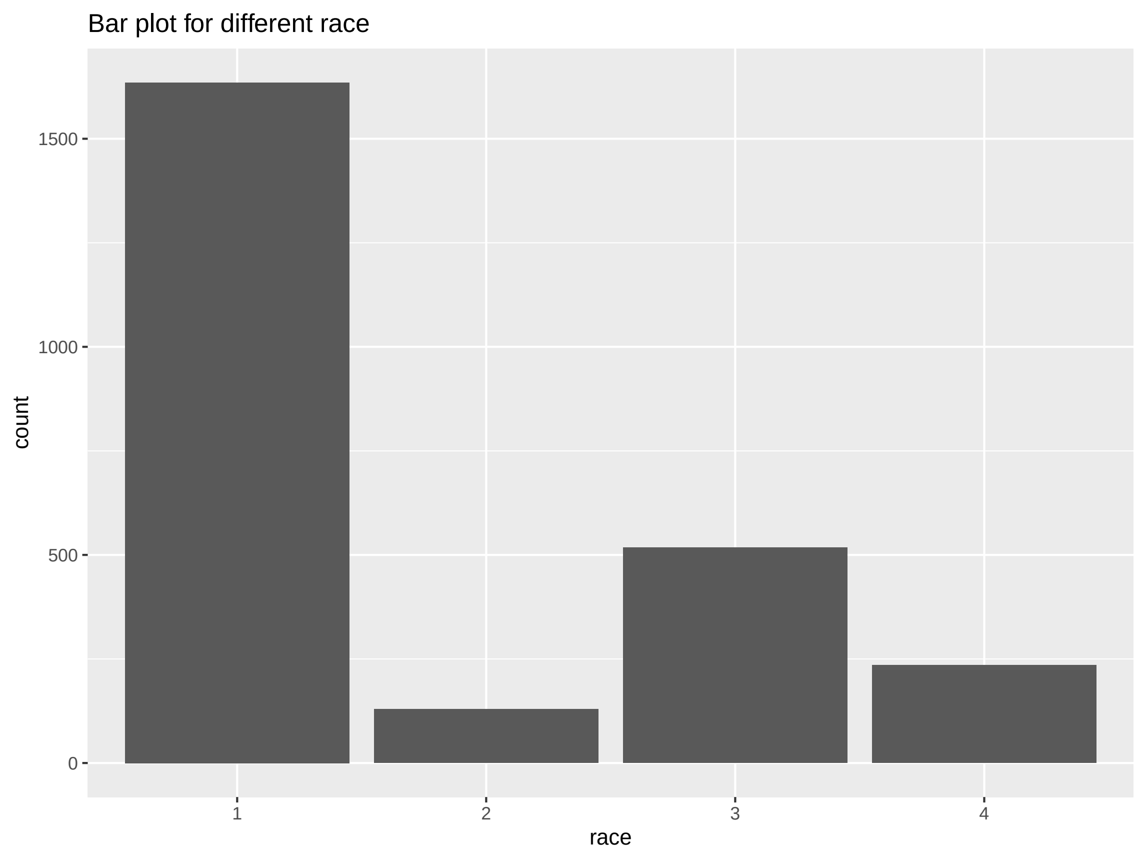
```
ggplot(train_data, aes(x = recovery_time))+geom_density()+labs(title="Distribution for recovery_time")
```



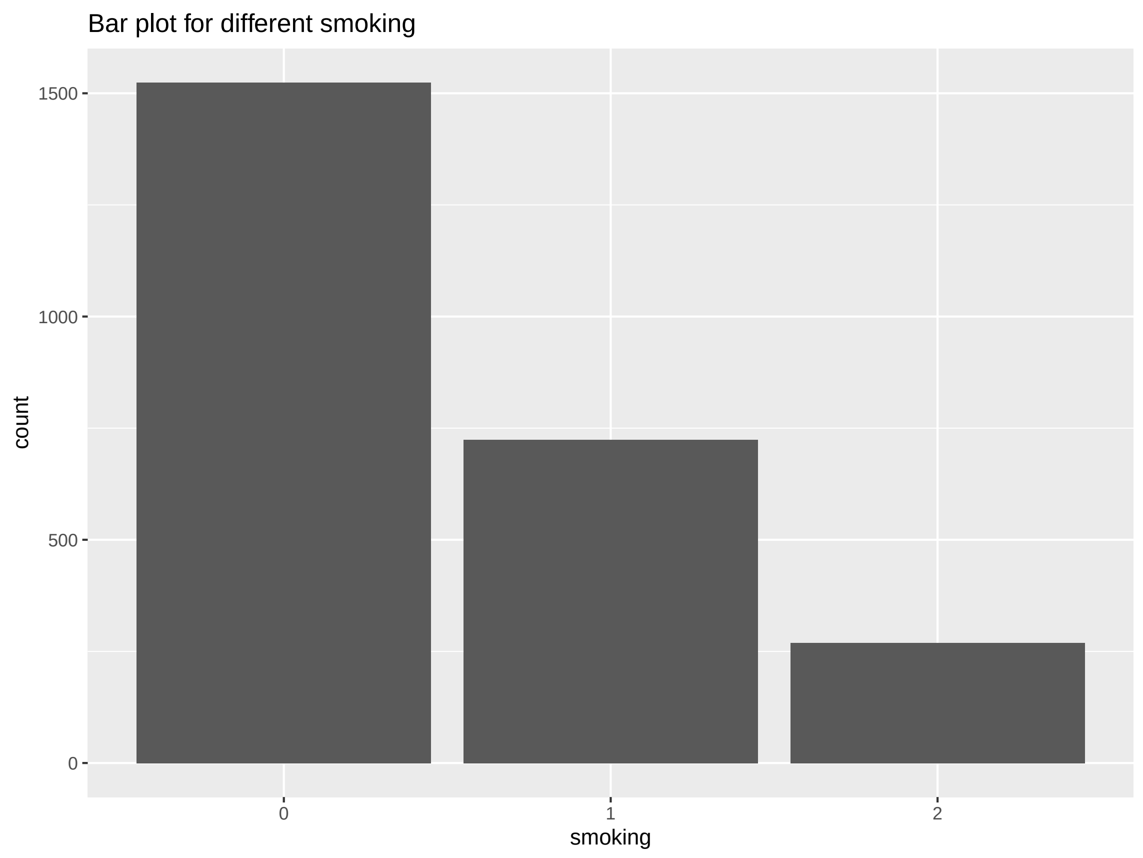
```
#discrete
ggplot(train_data) + geom_bar(aes(x=gender))+labs(title="Bar plot for different gender")
```



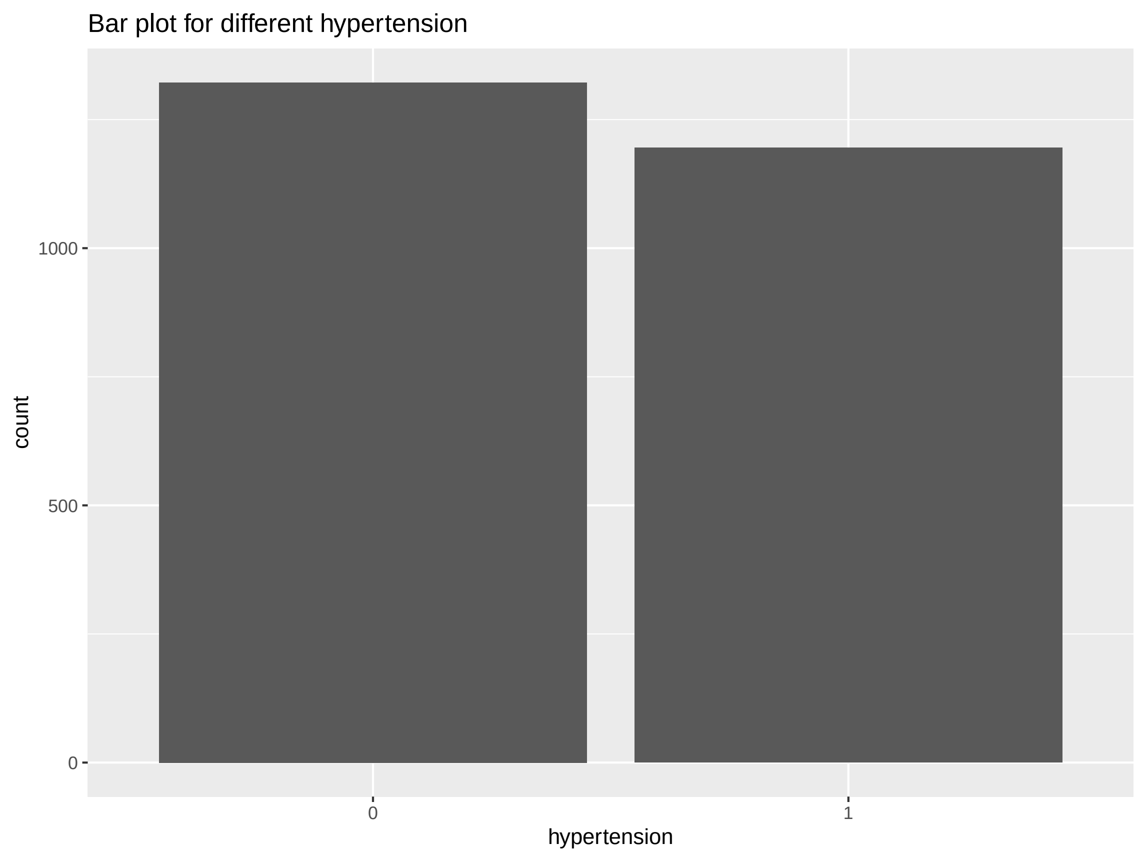
```r
ggplot(train_data) + geom_bar(aes(x=race))+labs(title="Bar plot for different race")
```



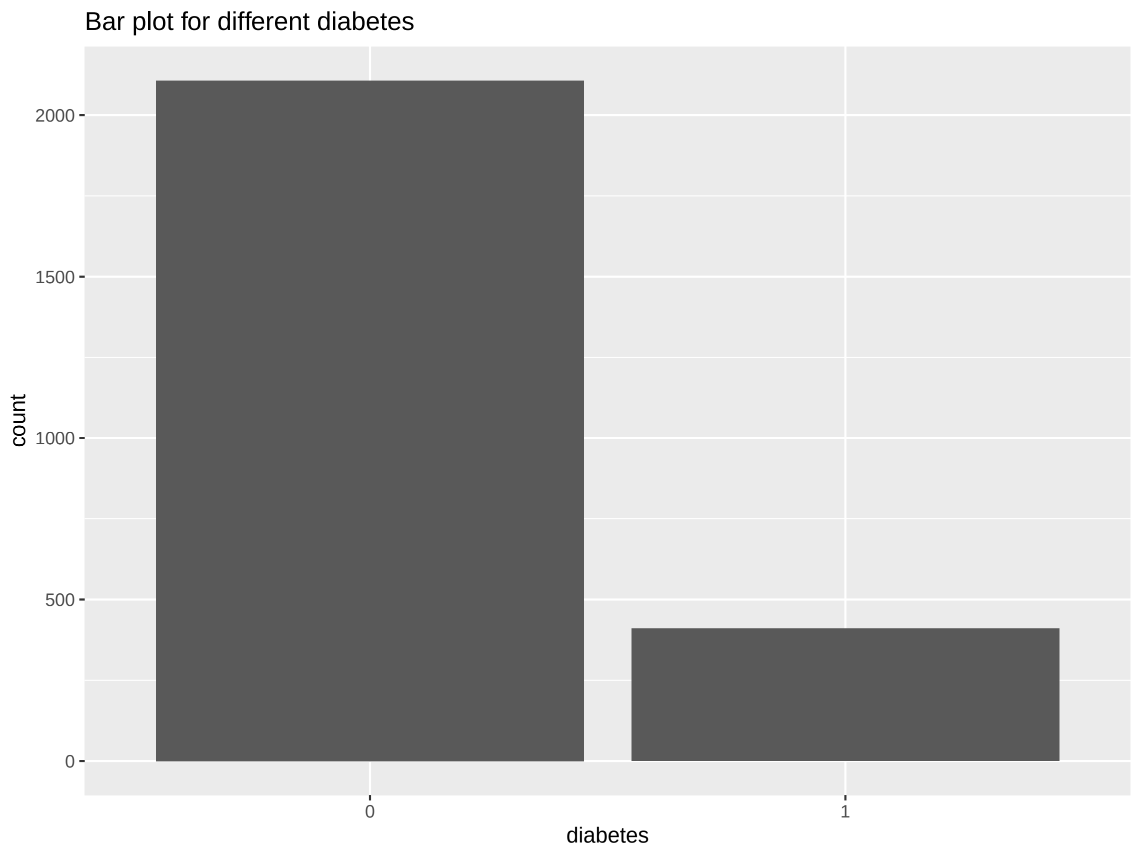
```
ggplot(train_data) + geom_bar(aes(x=smoking))+labs(title="Bar plot for different smoking")
```



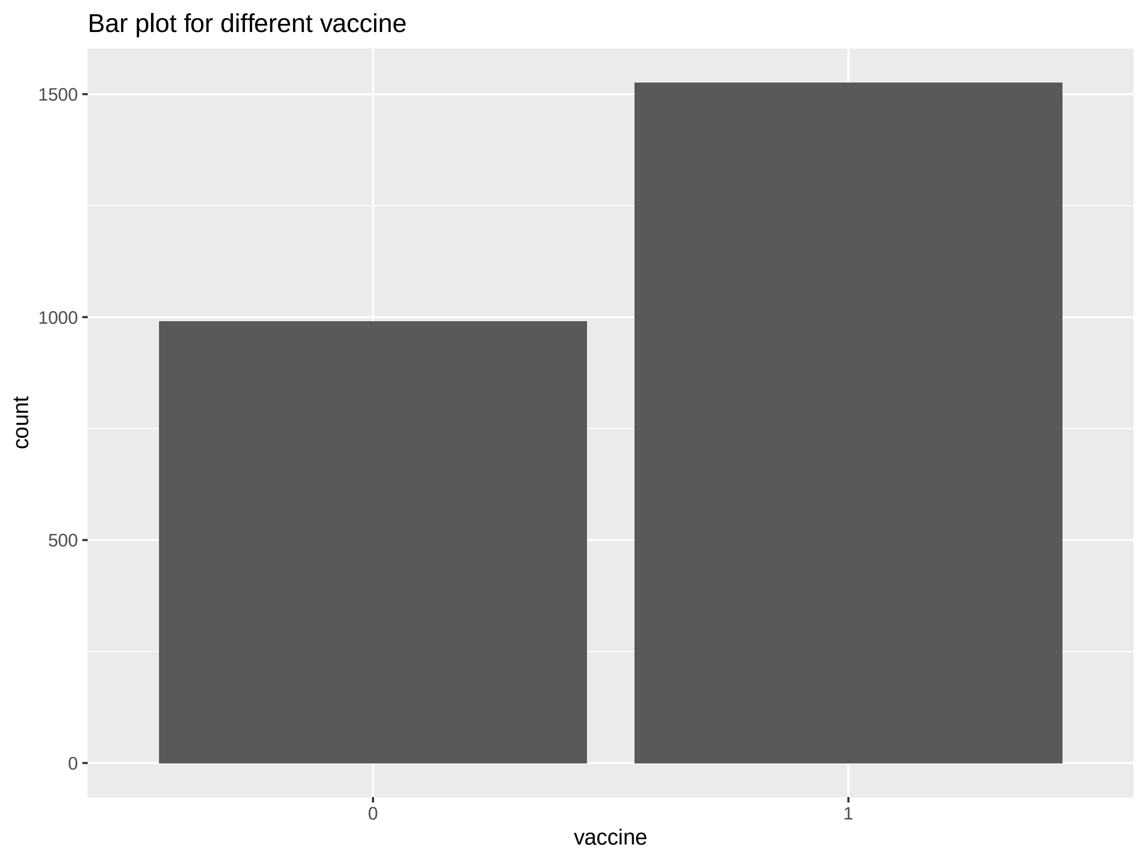
```r
ggplot(train_data) + geom_bar(aes(x=hypertension))+labs(title="Bar plot for different hypertension")
```



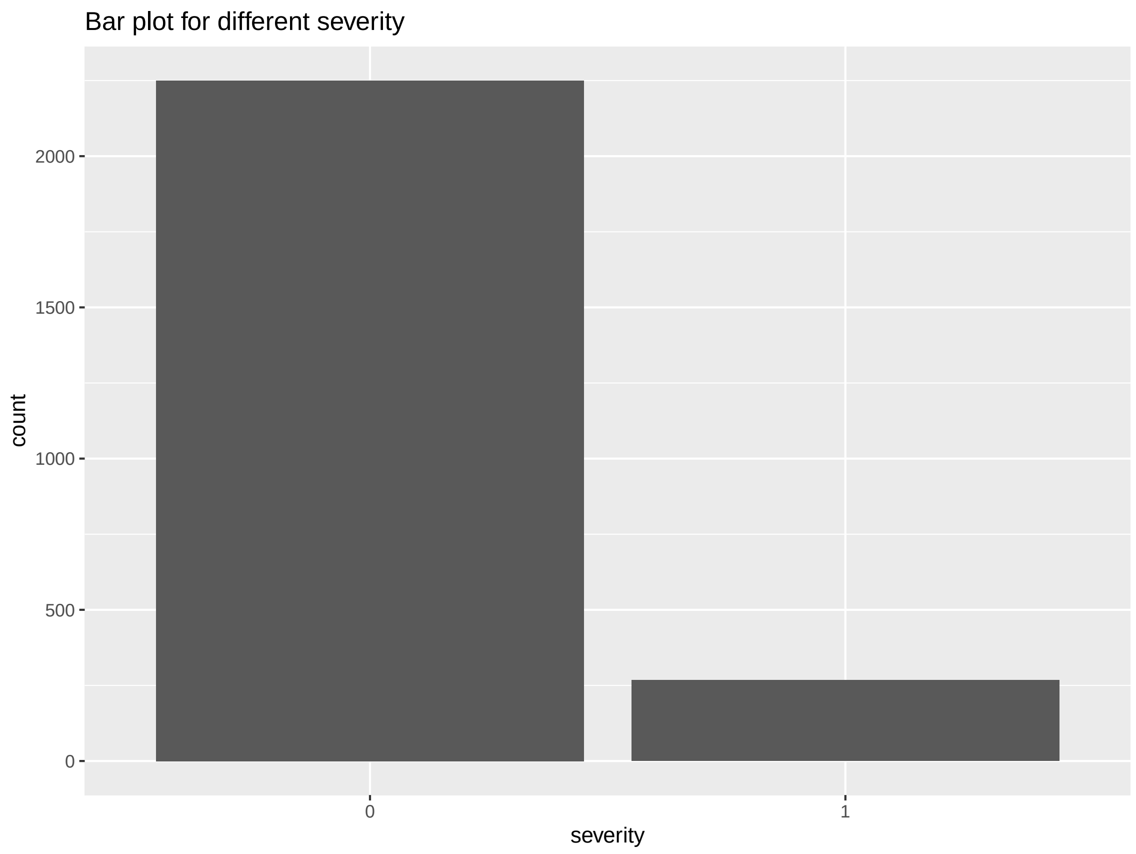
```
ggplot(train_data) + geom_bar(aes(x=diabetes))+labs(title="Bar plot for different diabetes")
```



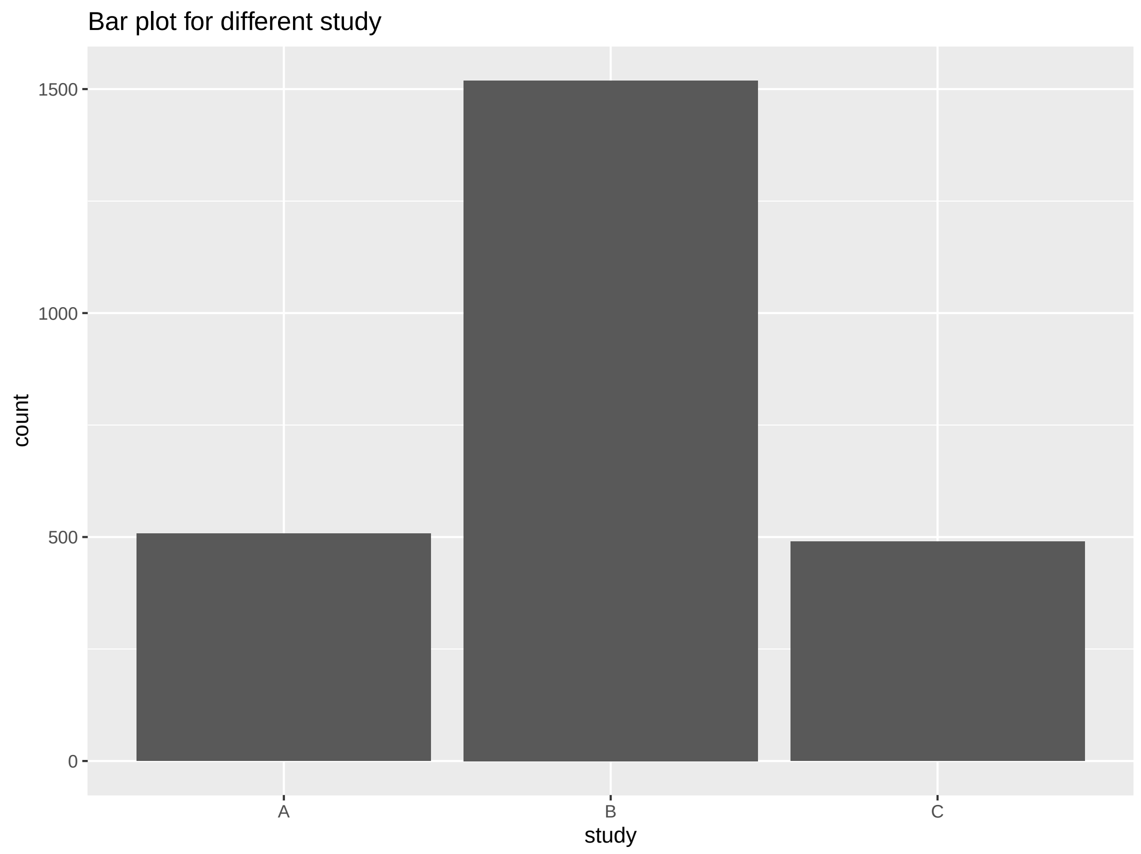
```
ggplot(train_data) + geom_bar(aes(x=vaccine))+labs(title="Bar plot for different vaccine")
```



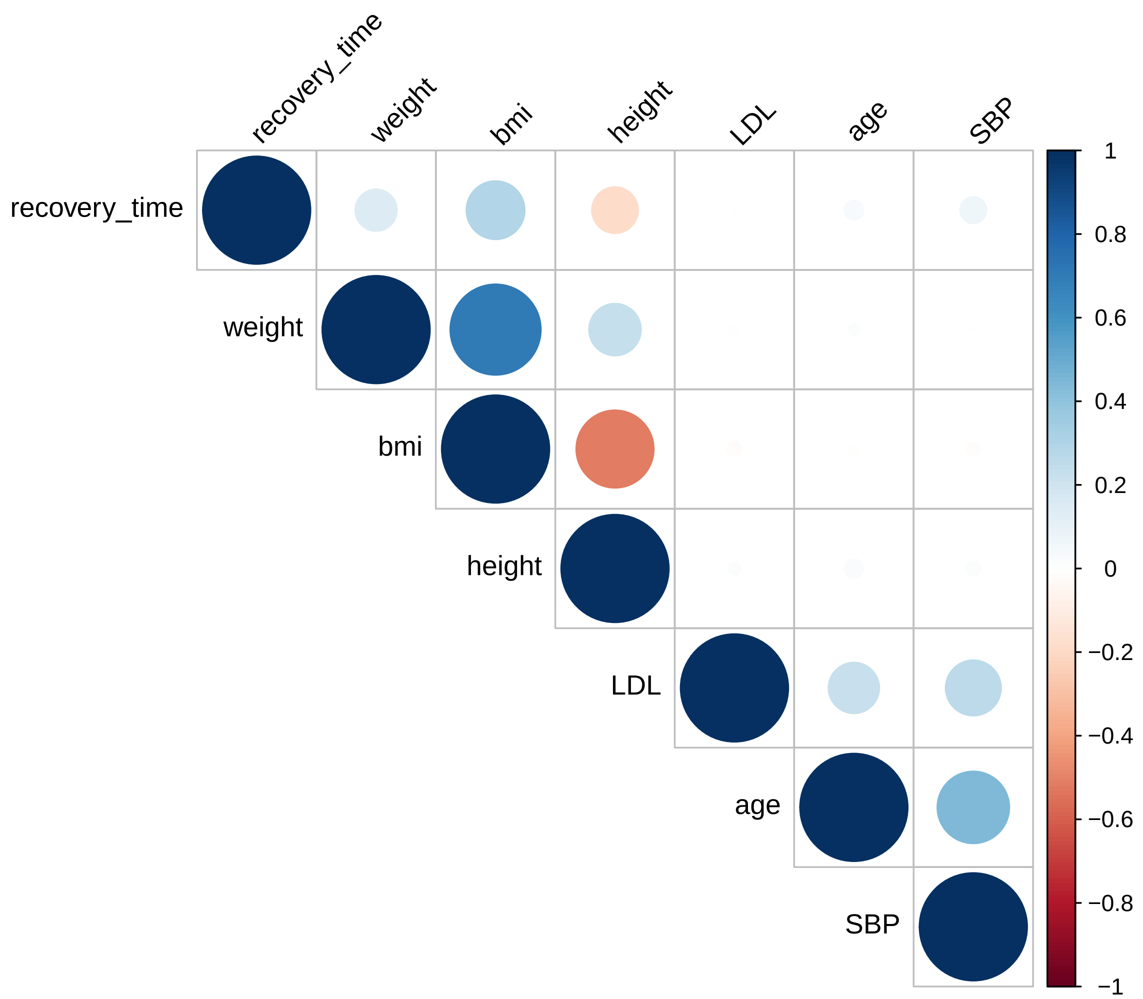
```
ggplot(train_data) + geom_bar(aes(x=severity))+labs(title="Bar plot for different severity")
```



```
ggplot(train_data) + geom_bar(aes(x=study))+labs(title="Bar plot for different study")
```

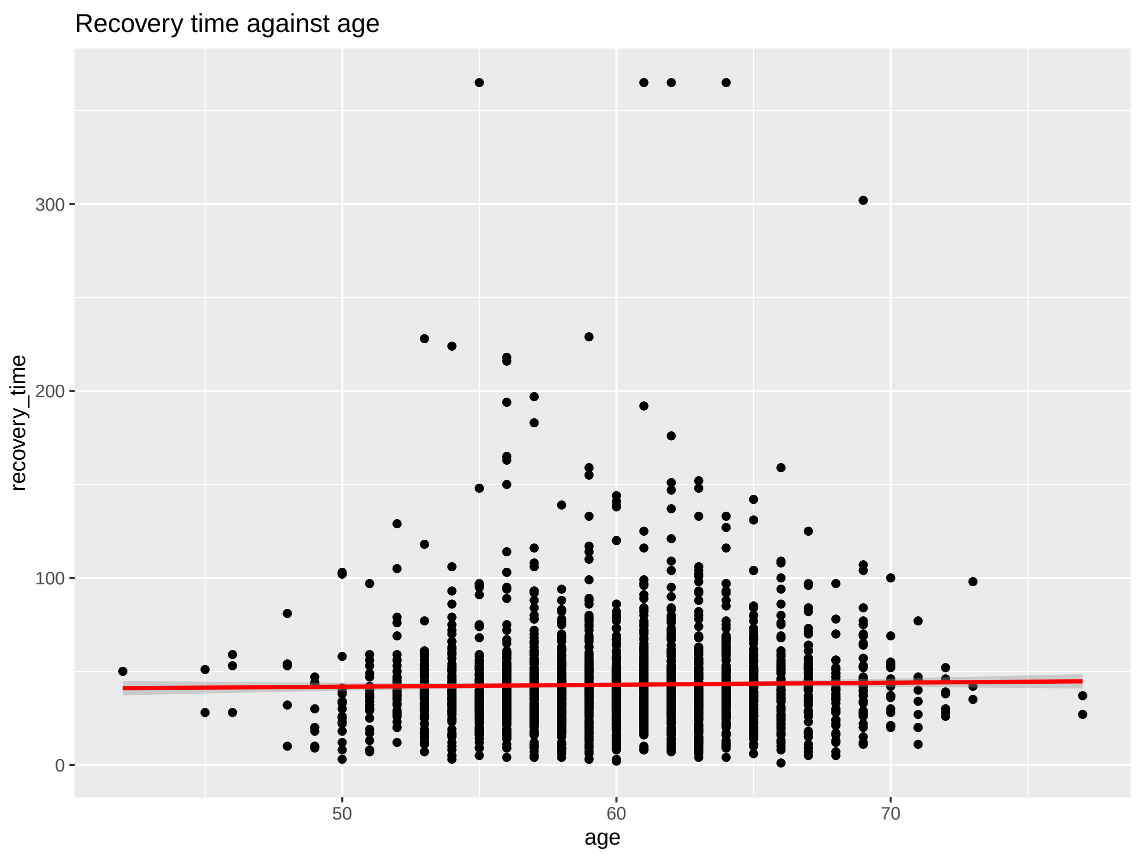


```
num_df <-
  train_data %>%
  dplyr::select(age, height, weight, bmi, SBP, LDL, recovery_time)


# calulate the correlations
res <- cor(num_df, use="complete.obs")

corrplot(res, type = "upper", order = "hclust",
         tl.col = "black", tl.srt = 45)
```



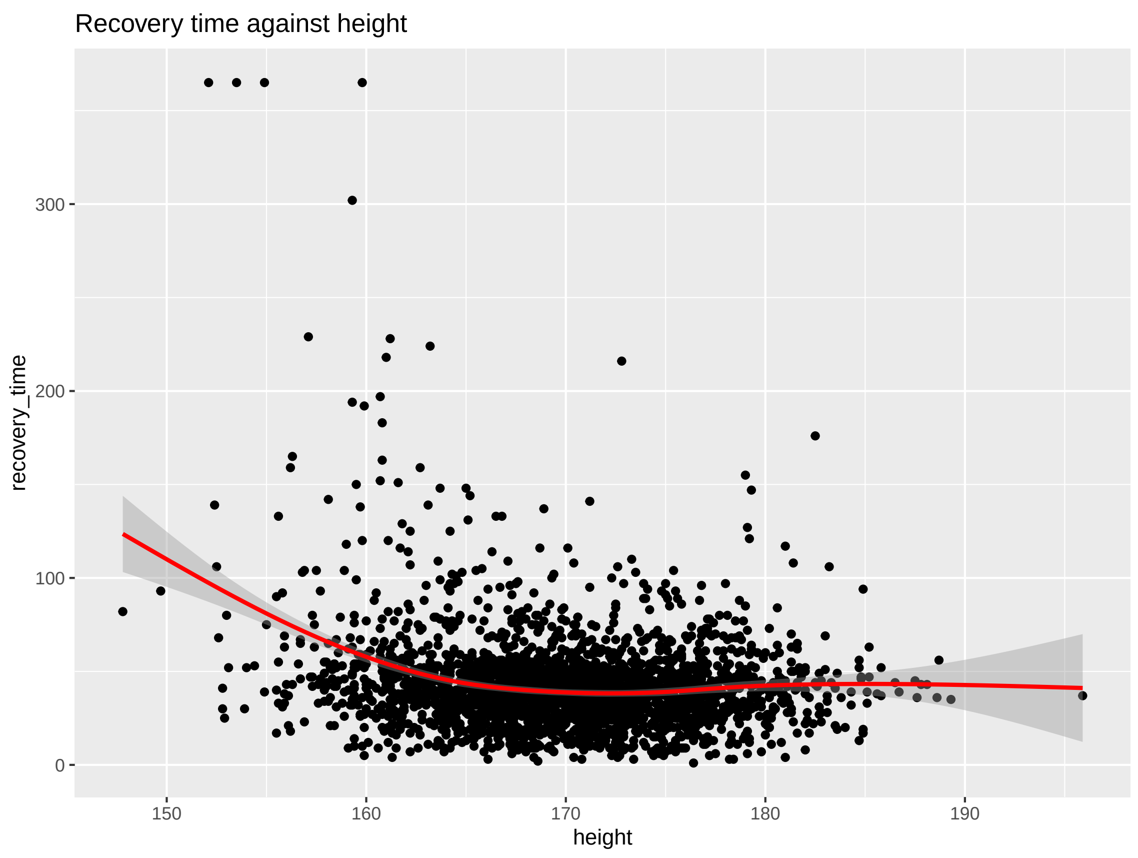
```
ggplot(train_data, aes(x = age, y = recovery_time))+geom_point()+geom_smooth(method = 'gam', se = TRUE,
```

```
## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'
```



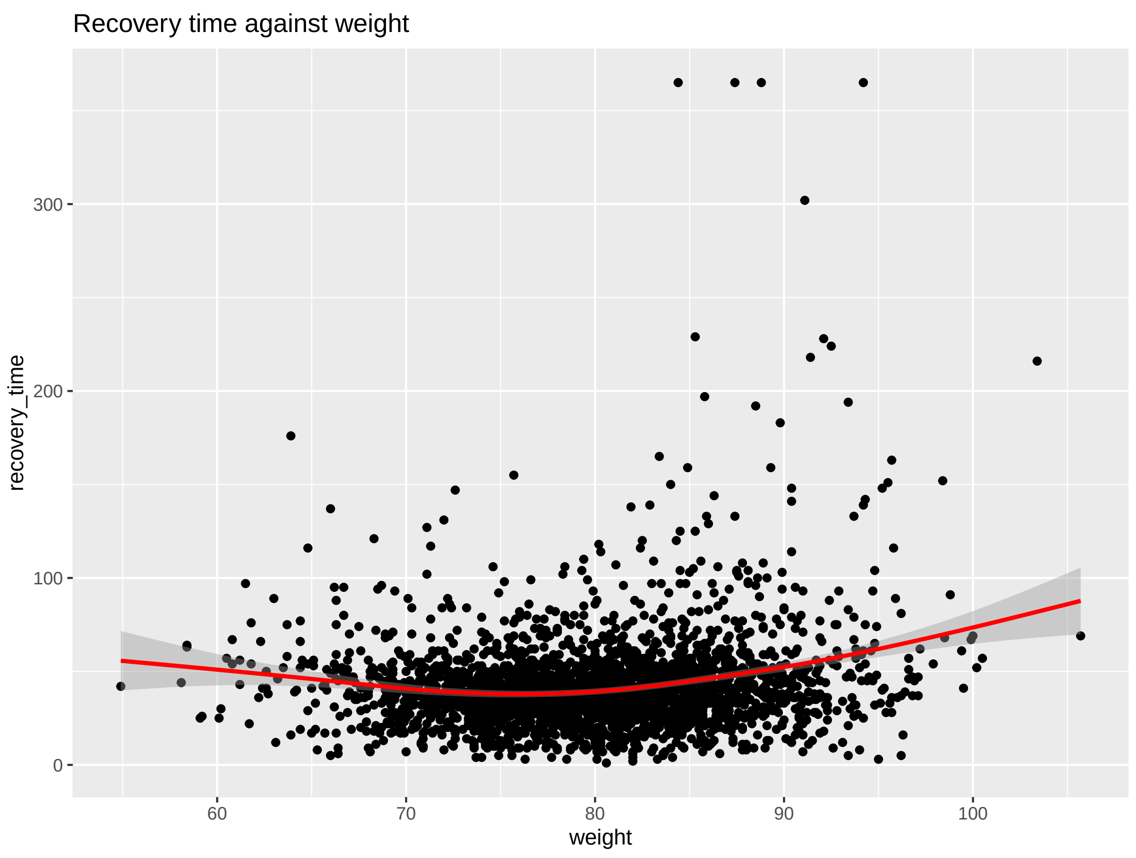
```
ggplot(train_data, aes(x = height, y = recovery_time))+geom_point()+geom_smooth(method = 'gam', se = TRU
```

```
## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'
```



```
ggplot(train_data, aes(x = weight, y = recovery_time))+geom_point()+geom_smooth(method = 'gam', se = TRU
```

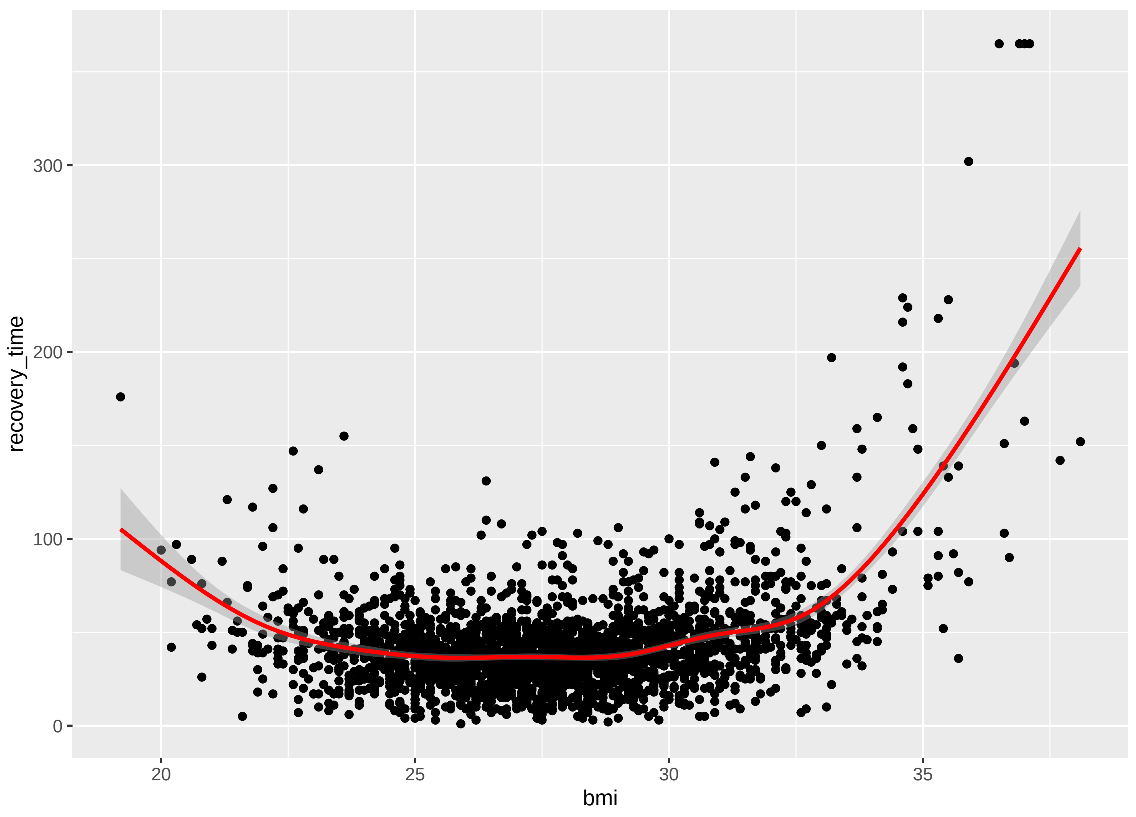
```
## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'
```



```
ggplot(train_data, aes(x = bmi, y = recovery_time))+geom_point()+geom_smooth(method = 'gam', se = TRUE,
```

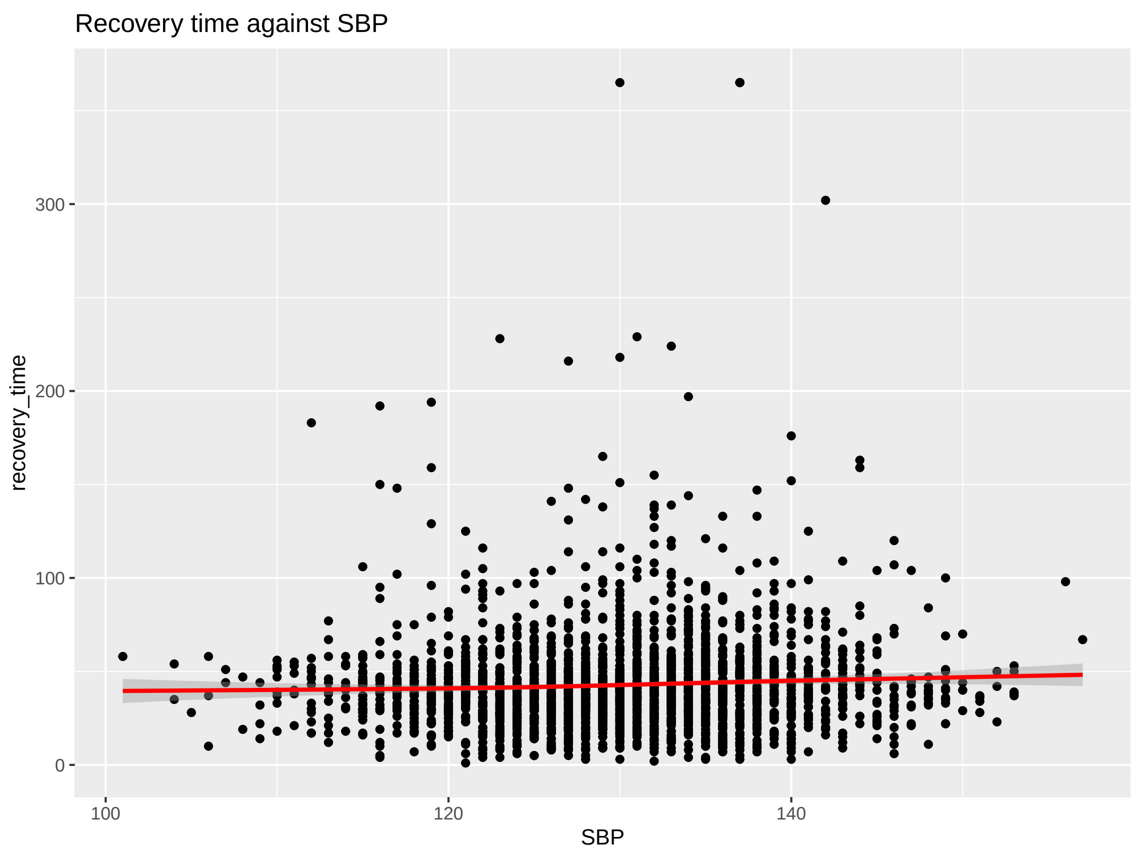
```
## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'
```

Recovery time against bmi



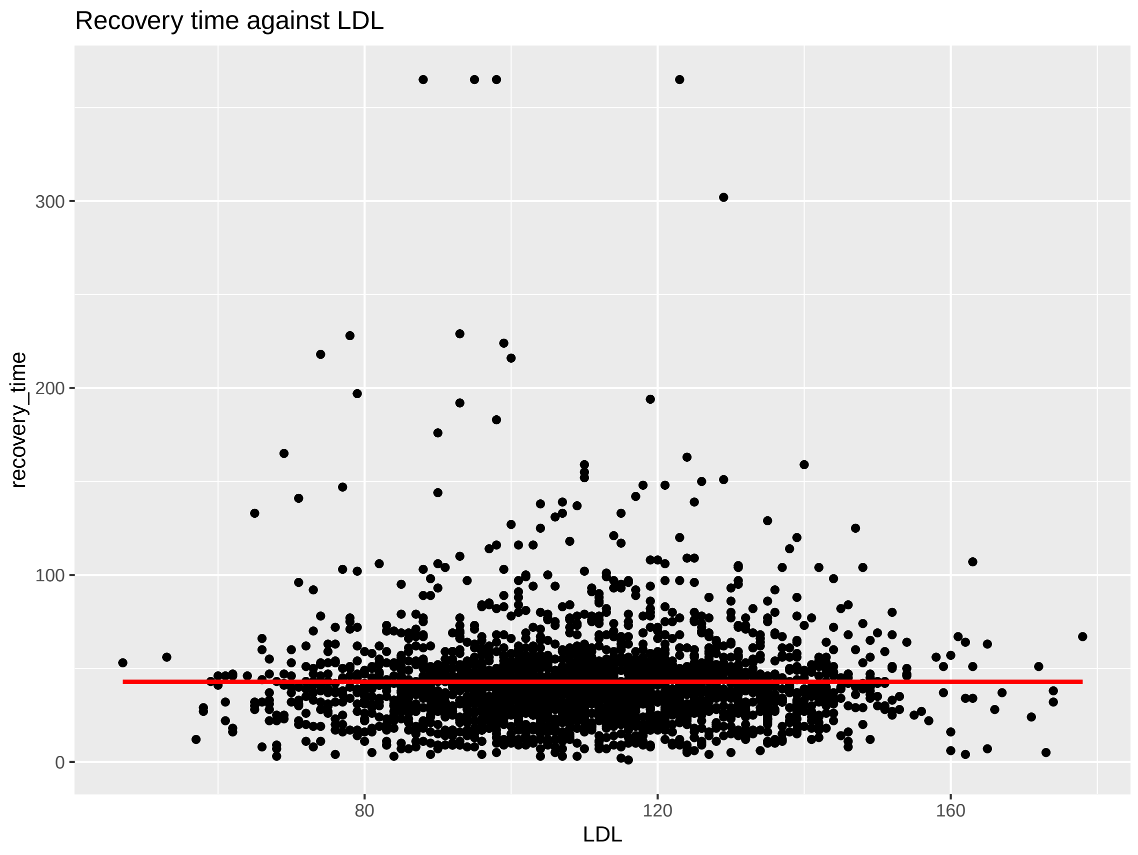
```
ggplot(train_data, aes(x = SBP, y = recovery_time))+geom_point()+geom_smooth(method = 'gam', se = TRUE,
```

```
## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'
```

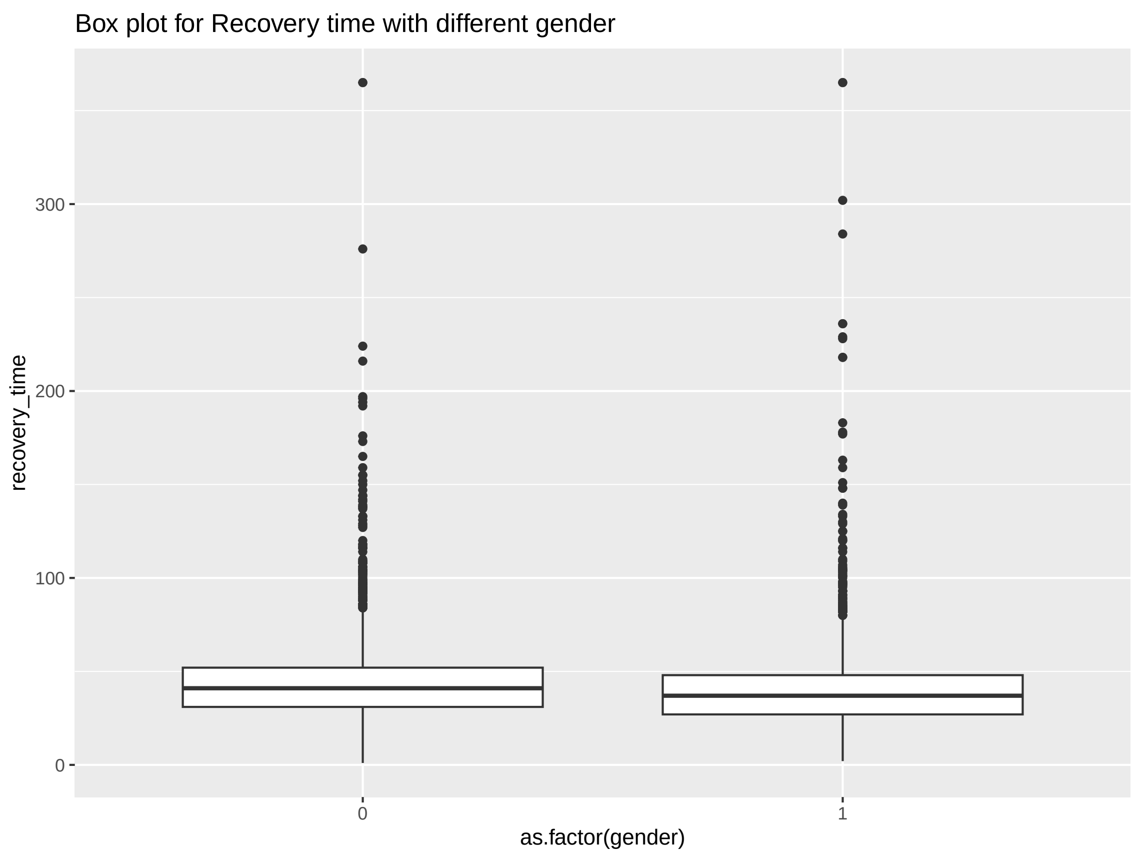


```
ggplot(train_data, aes(x = LDL, y = recovery_time))+geom_point()+geom_smooth(method = 'gam', se = TRUE,
```

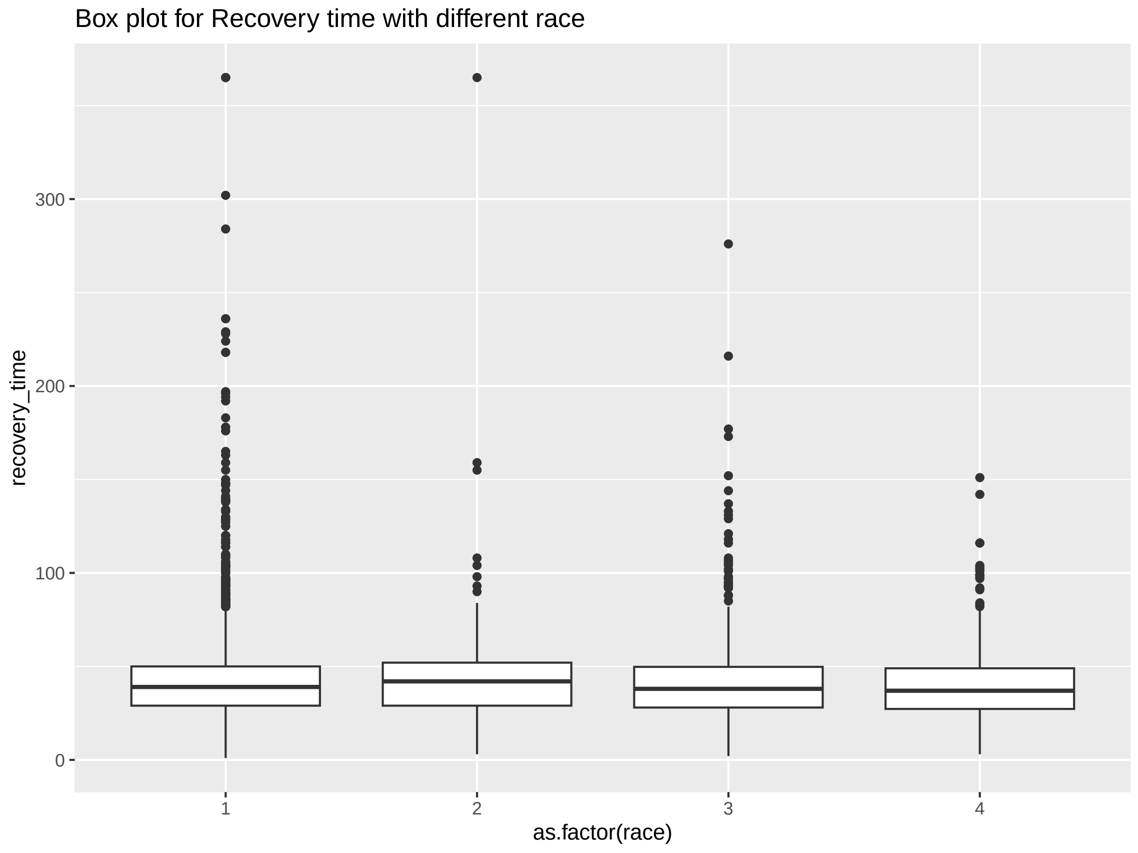
```
## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'
```



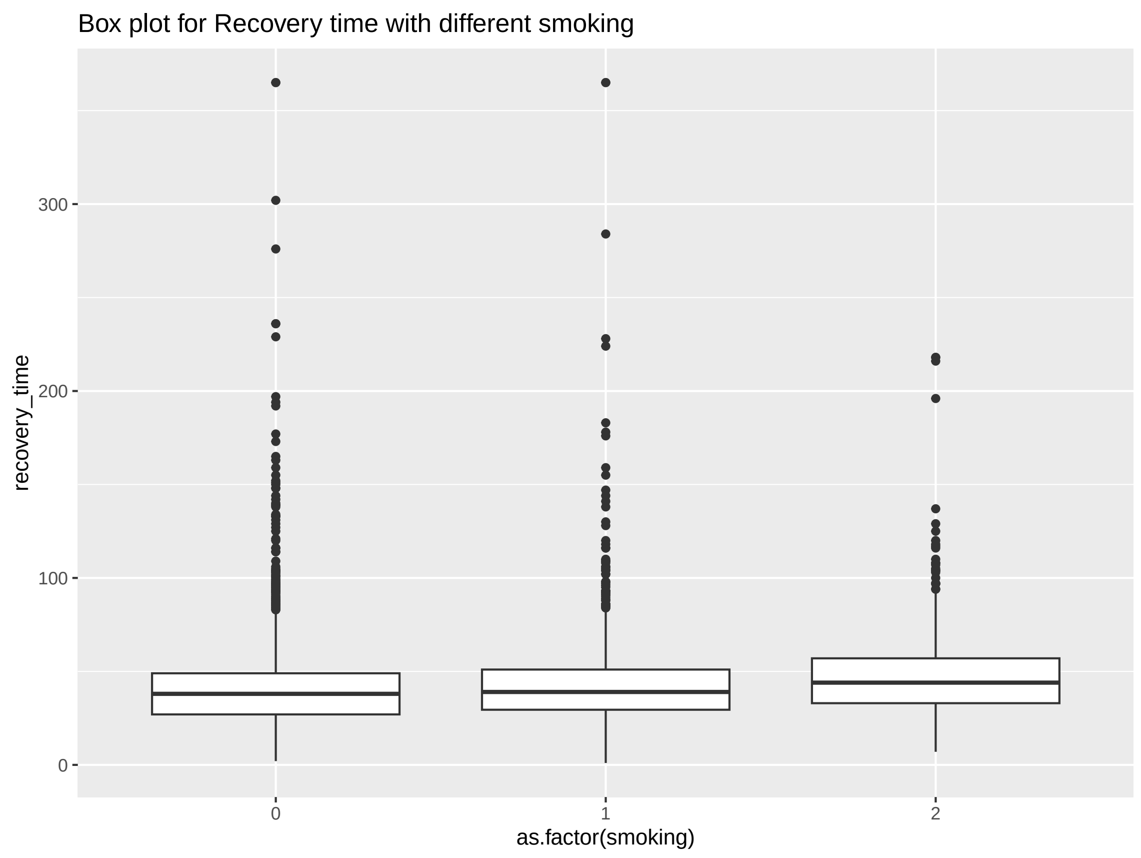
```
ggplot(data, aes(x = as.factor(gender), y = recovery_time))+geom_boxplot()+labs(title="Box plot for Rec
```



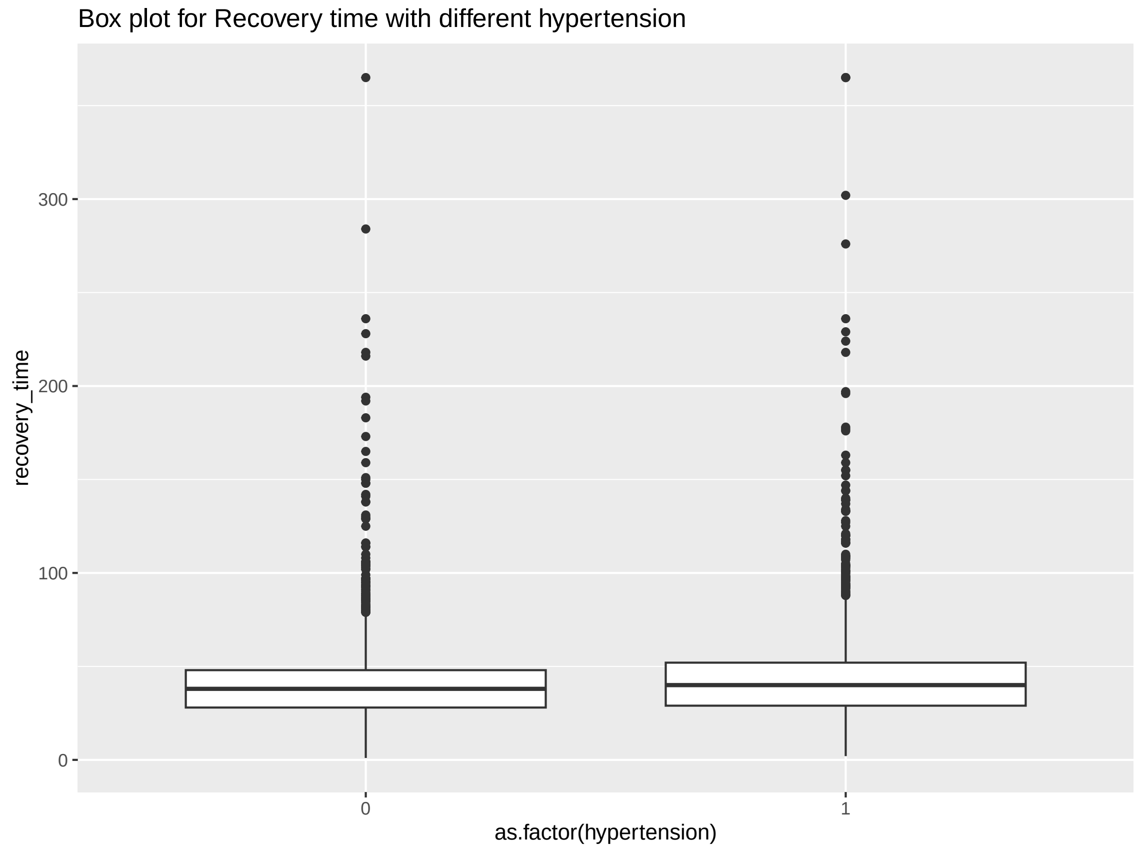
```
ggplot(data, aes(x = as.factor(race), y = recovery_time))+geom_boxplot()+labs(title="Box plot for Recove
```



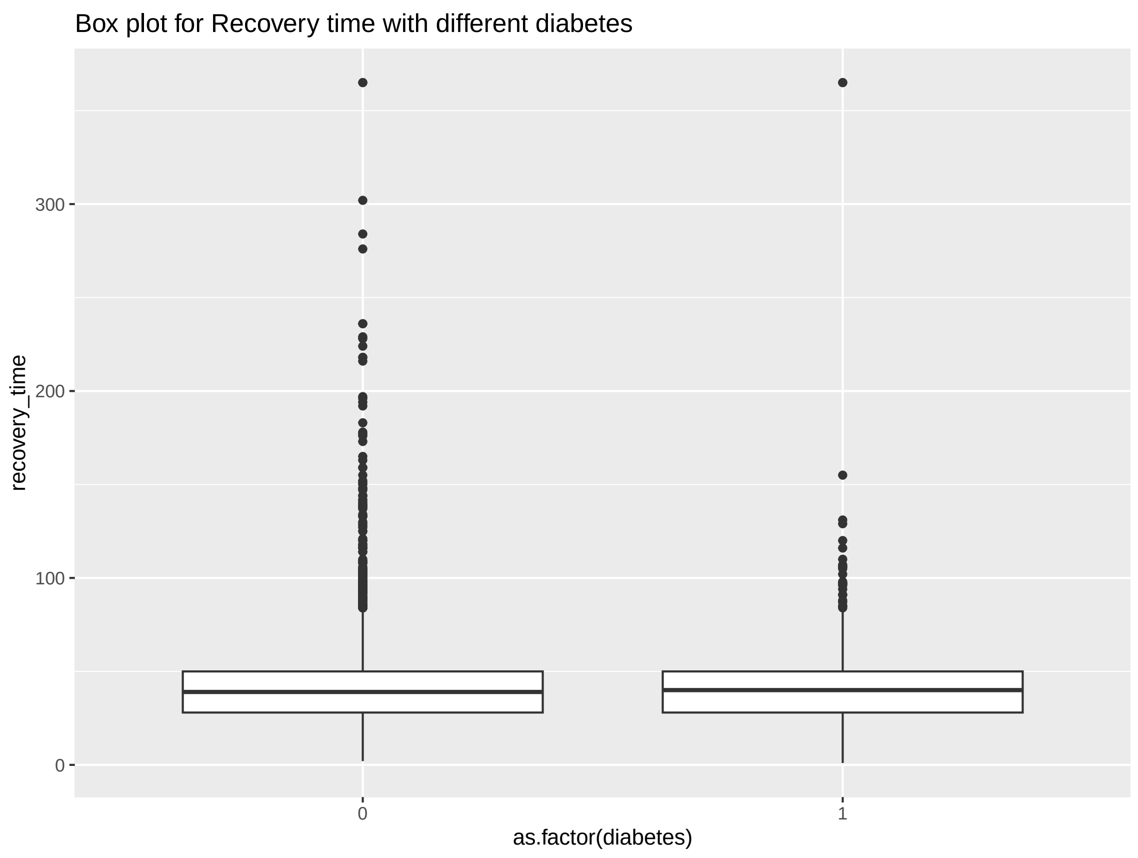
```
ggplot(data, aes(x = as.factor(smoking), y = recovery_time))+geom_boxplot()+labs(title="Box plot for Rec
```



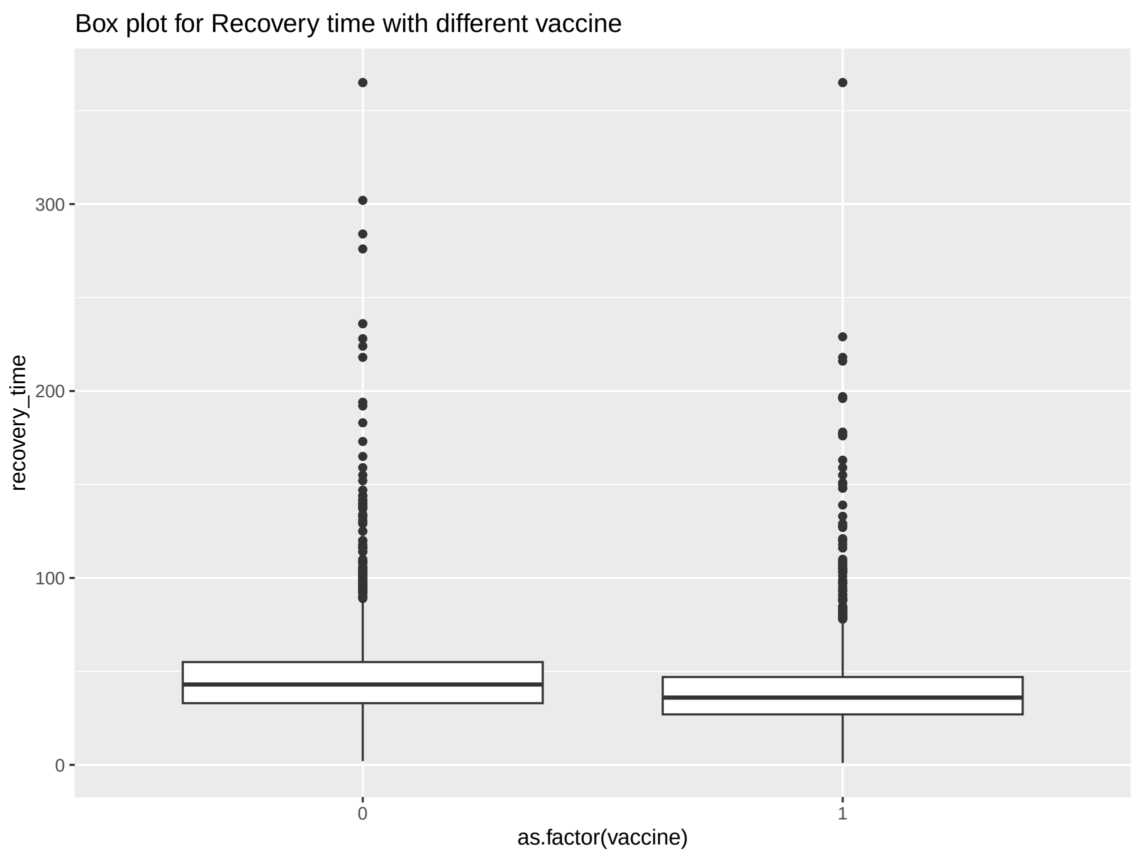
```
ggplot(data, aes(x = as.factor(hypertension), y = recovery_time))+geom_boxplot()+labs(title="Box plot fo
```



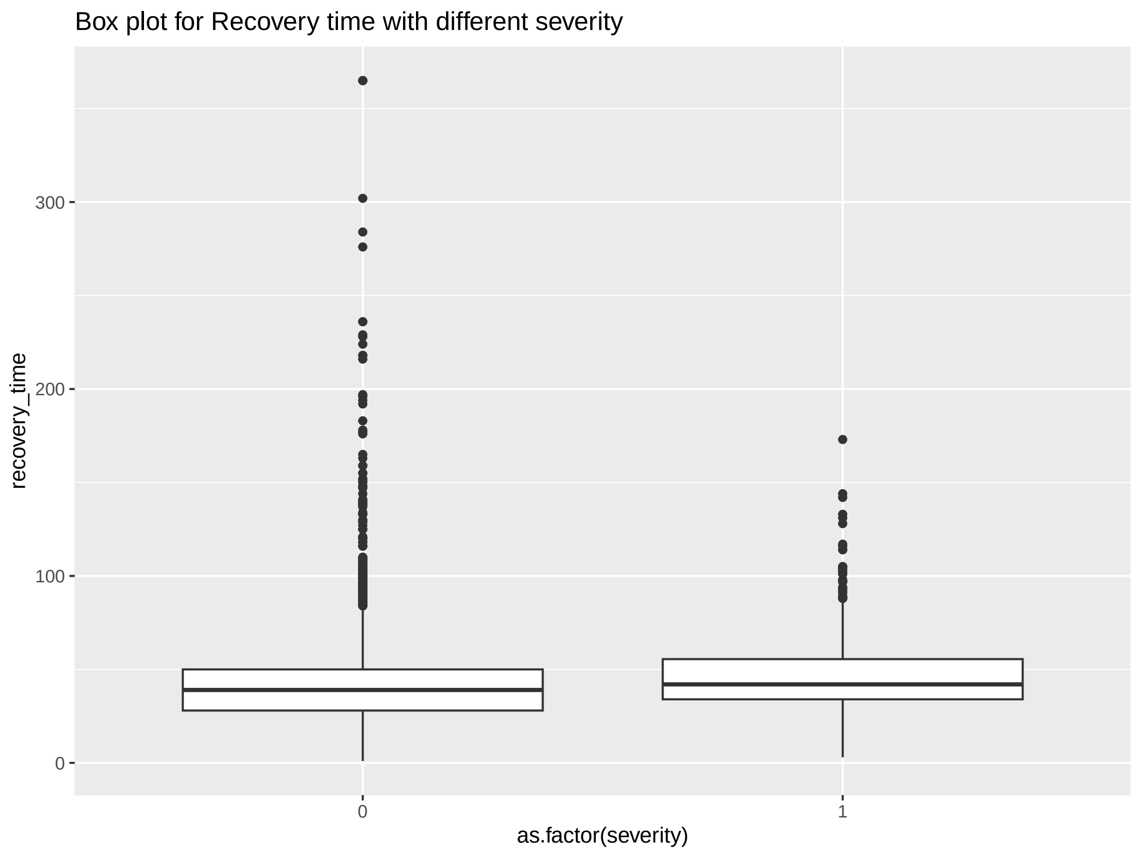
```
ggplot(data, aes(x = as.factor(diabetes), y = recovery_time))+geom_boxplot()+labs(title="Box plot for Re
```



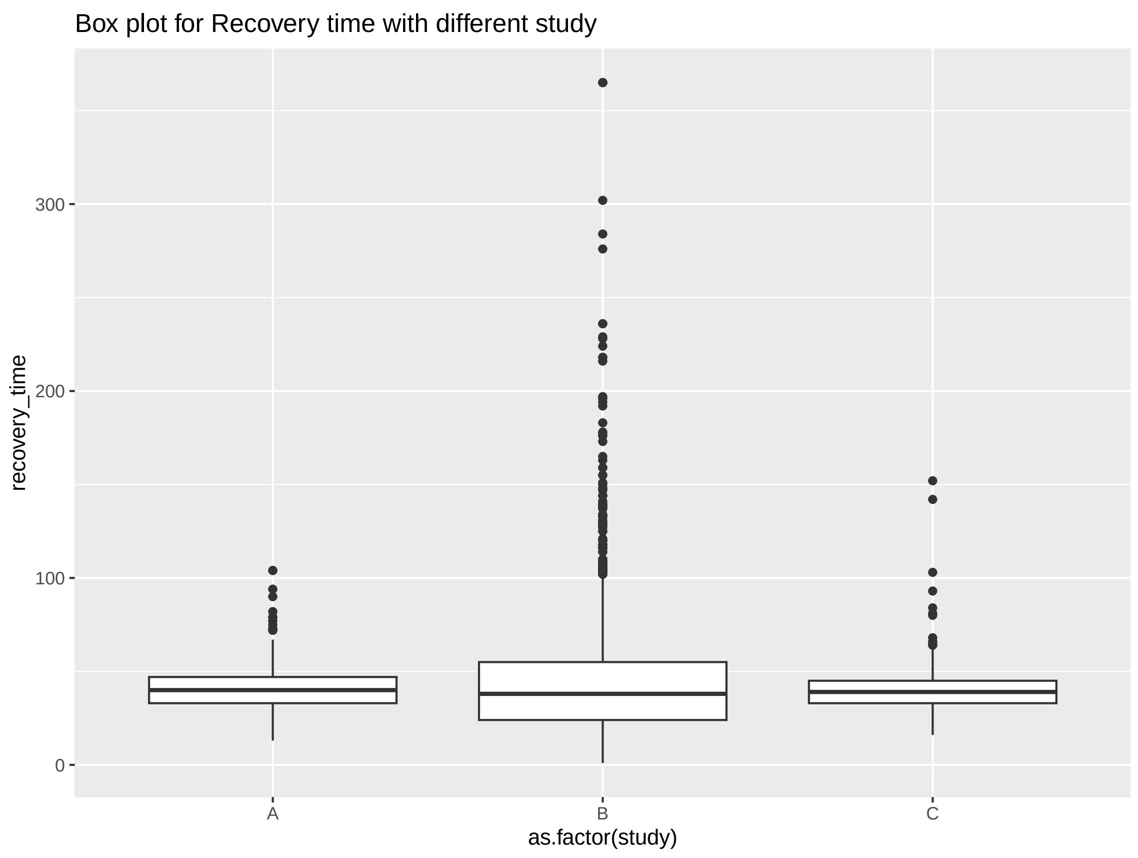
```
ggplot(data, aes(x = as.factor(vaccine), y = recovery_time))+geom_boxplot()+labs(title="Box plot for Rec
```



```
ggplot(data, aes(x = as.factor(severity), y = recovery_time))+geom_boxplot()+labs(title="Box plot for R
```



```
ggplot(data, aes(x = as.factor(study), y = recovery_time))+geom_boxplot()+labs(title="Box plot for Reco
```



Regression

primary analysis (Regression)

- Linear regression
- K-Nearest Neighbors (KNN)
- Elastic net
- Partial least squares (PLS)
- Generalized Additive Model (GAM)
- Multivariate Adaptive Regression Splines (MARS)
- Boosting
- Random forest

Linear regression

```
## fit linear model on train data
set.seed(8)
linear_model <- train(train_x,
                      train_y,
                      method = "lm",
                      trControl = ctrl)
summary(linear_model)
```

```
##
## Call:
## lm(formula = .outcome ~ ., data = dat)
##
```

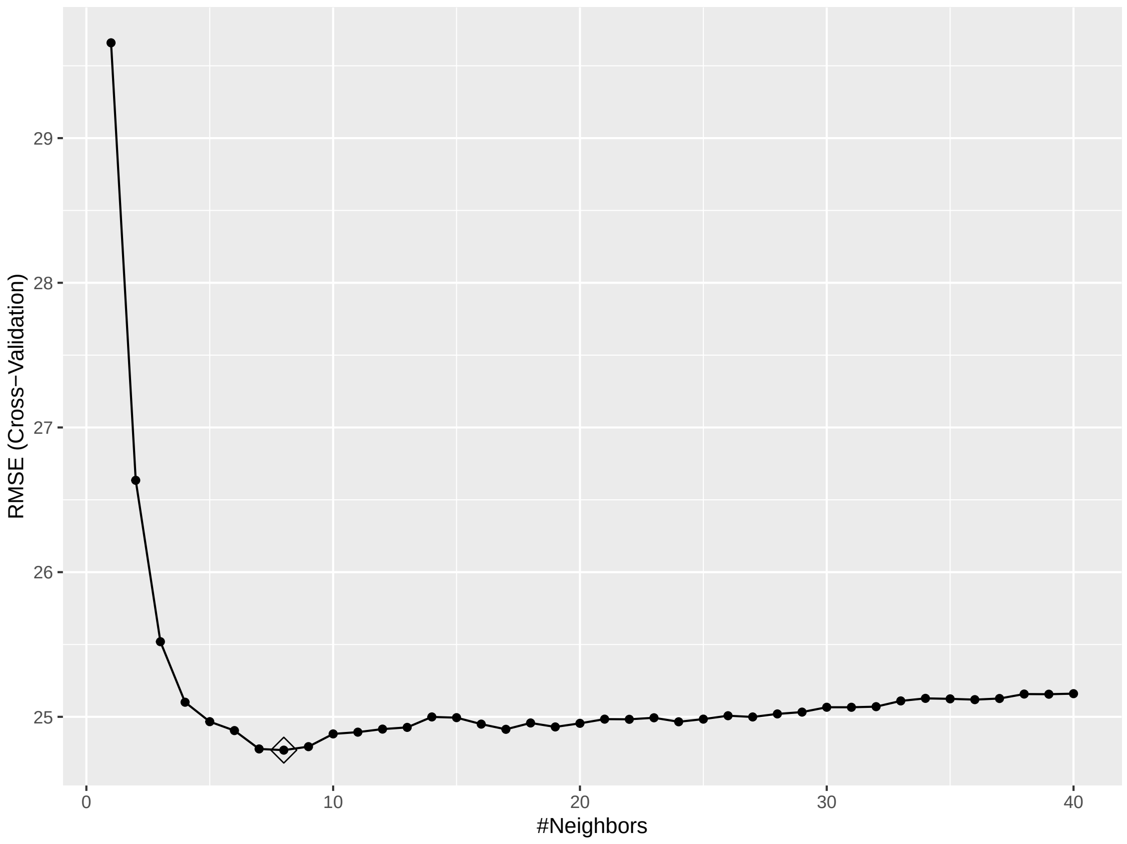
```
## Residuals:
##     Min      1Q  Median      3Q     Max 
## -73.848 -13.472  -1.414   9.399 257.759 
## 
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)    
## (Intercept)   -2.743e+03  1.295e+02 -21.171  < 2e-16 ***
## age           -1.353e-02  1.177e-01  -0.115 0.908505    
## gender1       -4.538e+00  9.432e-01  -4.812 1.59e-06 ***
## race2          5.460e-01  2.166e+00   0.252 0.800997    
## race3         -1.639e+00  1.193e+00  -1.374 0.169550    
## race4         -9.671e-01  1.653e+00  -0.585 0.558518    
## smoking1       3.052e+00  1.066e+00   2.863 0.004236 ** 
## smoking2       7.843e+00  1.563e+00   5.018 5.58e-07 ***
## height         1.608e+01  7.612e-01  21.120  < 2e-16 ***
## weight        -1.733e+01  8.043e-01 -21.541  < 2e-16 ***
## bmi            5.195e+01  2.300e+00  22.587  < 2e-16 ***
## hypertension1  3.229e+00  1.560e+00   2.070 0.038547 *  
## diabetes1     -2.210e-01  1.277e+00  -0.173 0.862608    
## SBP            3.232e-04  1.012e-01   0.003 0.997453    
## LDL           -1.013e-02  2.499e-02  -0.405 0.685287    
## vaccine1      -8.167e+00  9.684e-01  -8.434  < 2e-16 ***
## severity1      5.717e+00  1.534e+00   3.726 0.000199 ***
## studyB         4.315e+00  1.215e+00   3.552 0.000389 ***
## studyC        -3.479e-01  1.500e+00  -0.232 0.816566    
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 23.58 on 2498 degrees of freedom
## Multiple R-squared:  0.2754, Adjusted R-squared:  0.2702 
## F-statistic: 52.75 on 18 and 2498 DF,  p-value: < 2.2e-16
```

```r
# view performance on the test set (RMSE)
lm_test_pred <- predict(linear_model, newdata = test_x) # test dataset
lm_test_rmse <- sqrt(mean((lm_test_pred - test_y)^2))
sprintf("test error for lm is: %.3f",lm_test_rmse)
```

```
## [1] "test error for lm is: 23.569"
```

K-Nearest Neighbors (KNN)

```r
set.seed(8)
# fit knn on train data use caret
kGrid <- expand.grid(k = seq(1, to = 40, by = 1))
knn_model <- train(train_x,
                   train_y,
                   method = "knn",
                   trControl = ctrl,
                   tuneGrid = kGrid)
ggplot(knn_model, highlight = TRUE)
```



```
# knn with K = 18 was selected as the final model

# view performance on the test set (RMSE)
knn_test_pred <- predict(knn_model, newdata = test_x) # test dataset
knn_test_rmse <- sqrt(mean((knn_test_pred - test_y)^2))
sprintf("test error for K-Nearest Neighbors is: %.3f", knn_test_rmse)
```

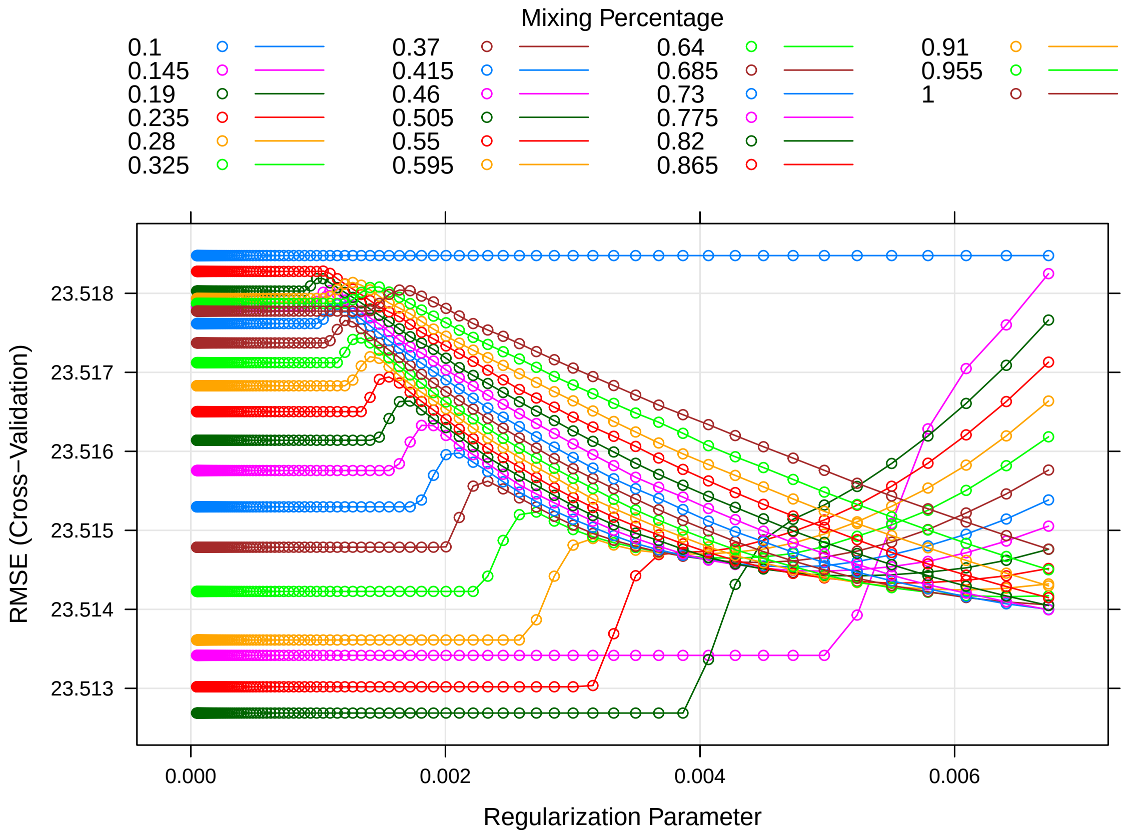
```
## [1] "test error for K-Nearest Neighbors is: 25.181"
```

Enet

```
#tuning glmnet alpha 0 and 0.05 have large RMSE. So alpha start from 0.1
set.seed(8)
enet.fit.min <- train(train_x, train_y,
                  method = "glmnet",
                  tuneGrid = expand.grid(alpha = seq(0.1, 1, length = 21),
                                         lambda = exp(seq(-10, -5, length = 100))),
                  trControl = ctrl)
enet.fit.min$bestTune
```

```
##     alpha     lambda
## 289  0.19 0.00386592
```

```
plot(enet.fit.min)
```

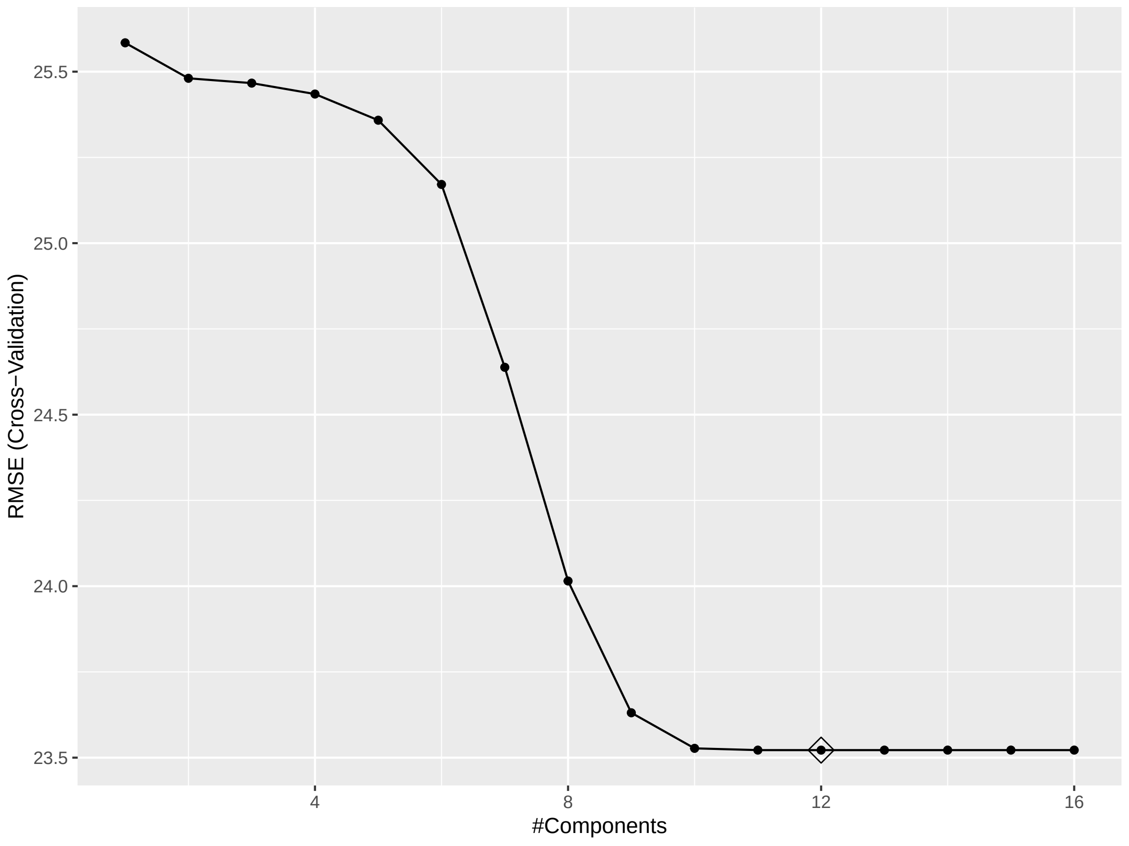


```
# view performance on the test set (RMSE)
enet_test_pred <- predict(enet.fit.min, newdata = test_x) # test dataset
enet_test_rmse <- sqrt(mean((enet_test_pred - test_y)^2))
sprintf("test error for enet is: %.3f",enet_test_rmse)
```

```
## [1] "test error for enet is: 23.523"
```

PLS

```
set.seed(8)
pls_model <- train(train_x,
                   train_y,
                   method = "pls",
                   tuneGrid = data.frame(ncomp = 1:16),
                   trControl = ctrl,
                   preProcess = c("center", "scale"))
ggplot(pls_model, highlight = TRUE)
```



```
ggsave(file = "image/pls_number_of_component.png", width = 10, height = 7)

# view performance on the test set (RMSE)
pls_test_pred <- predict(pls_model, newdata = test_x) # test dataset
pls_test_rmse <- sqrt(mean((pls_test_pred - test_y)^2))
sprintf("test error for pls is: %.3f",pls_test_rmse)
```

```
## [1] "test error for pls is: 23.569"
```

Generalised additive regression (GAM)

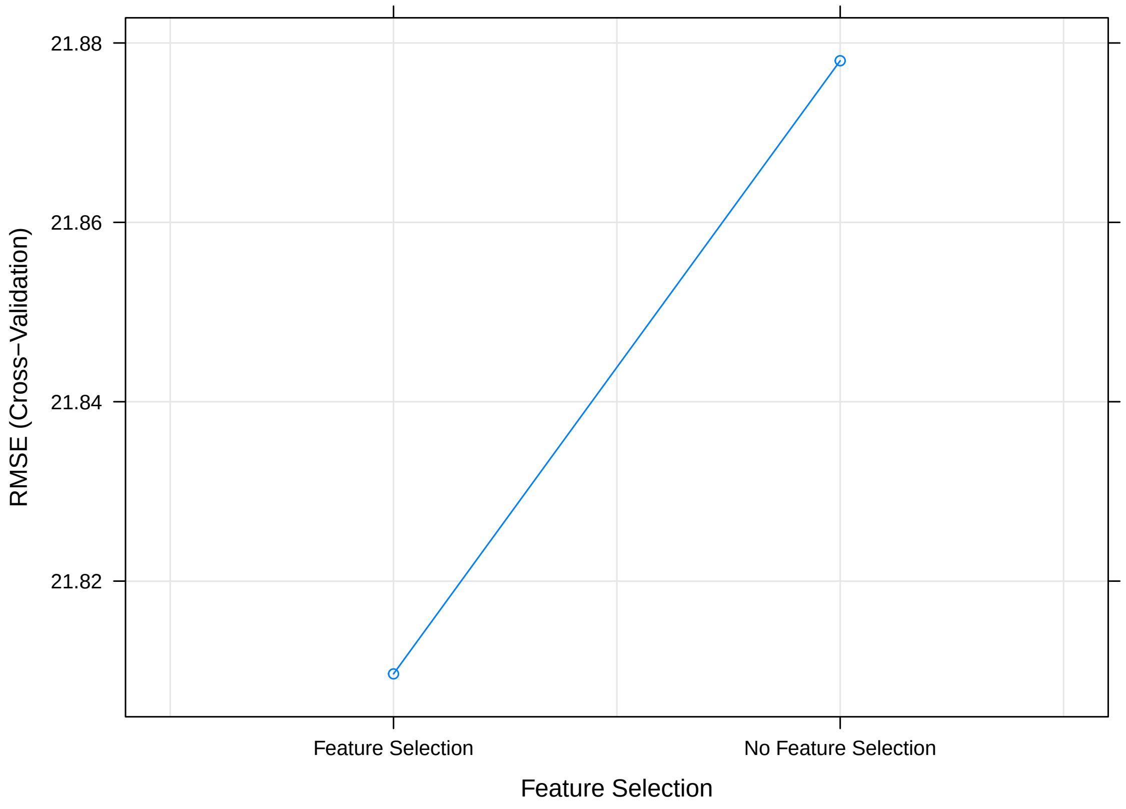
```
# gam use caret
# fit GAM model using all predictors
# parallel computing
no_cores <- detectCores() - 1
cl <- makePSOCKcluster(no_cores)
registerDoParallel(cl)
set.seed(8)
gam_model <- train(train_x, train_y, # training dataset
                   method = "gam",
                   trControl = ctrl,
                   control = gam.control(maxit = 200))
stopCluster(cl)
registerDoSEQ()

gam_model$bestTune
```

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

```
gam_model$finalModel
```

```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## .outcome ~ gender1 + race2 + 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:
## 0.00 0.00 0.00 7.78 2.65 4.50  total = 27.93
##
## GCV score: 448.2538
```

```
plot(gam_model)
```



```
summary(gam_model$finalModel)
```

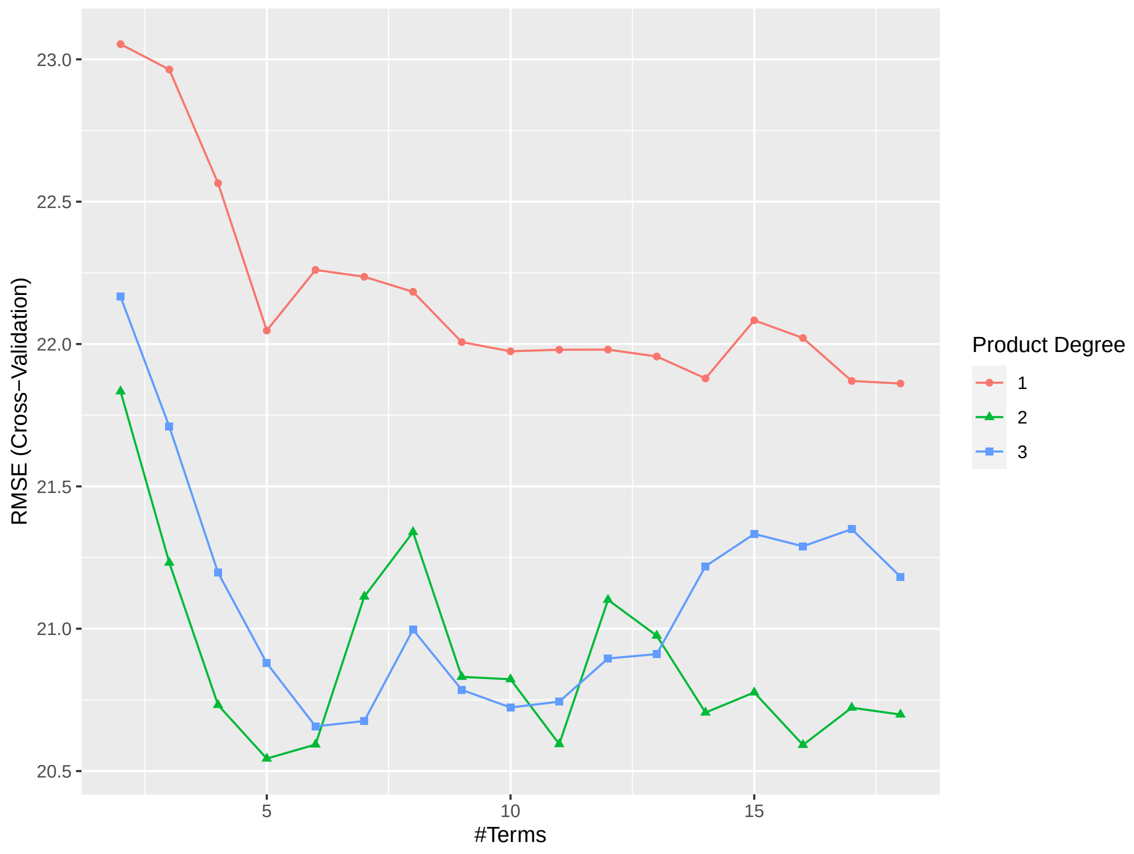
```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## .outcome ~ gender1 + race2 + race3 + race4 + smoking1 + smoking2 +
##     hypertension1 + diabetes1 + vaccine1 + severity1 + studyB +
##     studyC + s(age) + s(SBP) + s(LDL) + s(bmi) + s(height) +
##     s(weight)
##
## Parametric coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)    43.7183     1.3232  33.040  < 2e-16 ***
## gender1        -4.6981     0.8434  -5.570 2.82e-08 ***
## race2           0.5405     1.9332   0.280 0.779829
## race3          -1.5605     1.0659  -1.464 0.143332
## race4          -2.6252     1.4791  -1.775 0.076054 .
## smoking1        4.3355     0.9556   4.537 5.98e-06 ***
## smoking2        8.0325     1.3975   5.748 1.01e-08 ***
## hypertension1   3.0143     0.8471   3.558 0.000380 ***
## diabetes1       0.6857     1.1425   0.600 0.548453
## vaccine1       -7.7120     0.8649  -8.916  < 2e-16 ***
## severity1       5.9722     1.3716   4.354 1.39e-05 ***
## studyB          4.1736     1.0846   3.848 0.000122 ***
## studyC         -0.6406     1.3400  -0.478 0.632678
## ---
## 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)    1.123e-06      9   0.000 0.55847
## s(SBP)    8.397e-07      9   0.000 0.68712
## s(LDL)    1.176e-06      9   0.000 0.51661
## s(bmi)    7.775e+00      9 111.700 < 2e-16 ***
## s(height) 2.649e+00      9   1.019 0.00269 **
## s(weight) 4.501e+00      9   1.049 0.04744 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.418   Deviance explained = 42.5%
## GCV = 448.25  Scale est. = 443.28    n = 2517
```

```
# view performance on the test set (RMSE)
gam_test_pred <- predict(gam_model, newdata = test_x) # test dataset
gam_test_rmse <- sqrt(mean((gam_test_pred - test_y)^2))
sprintf("test error for Generalised additive regression is: %.3f", knn_test_rmse)
```

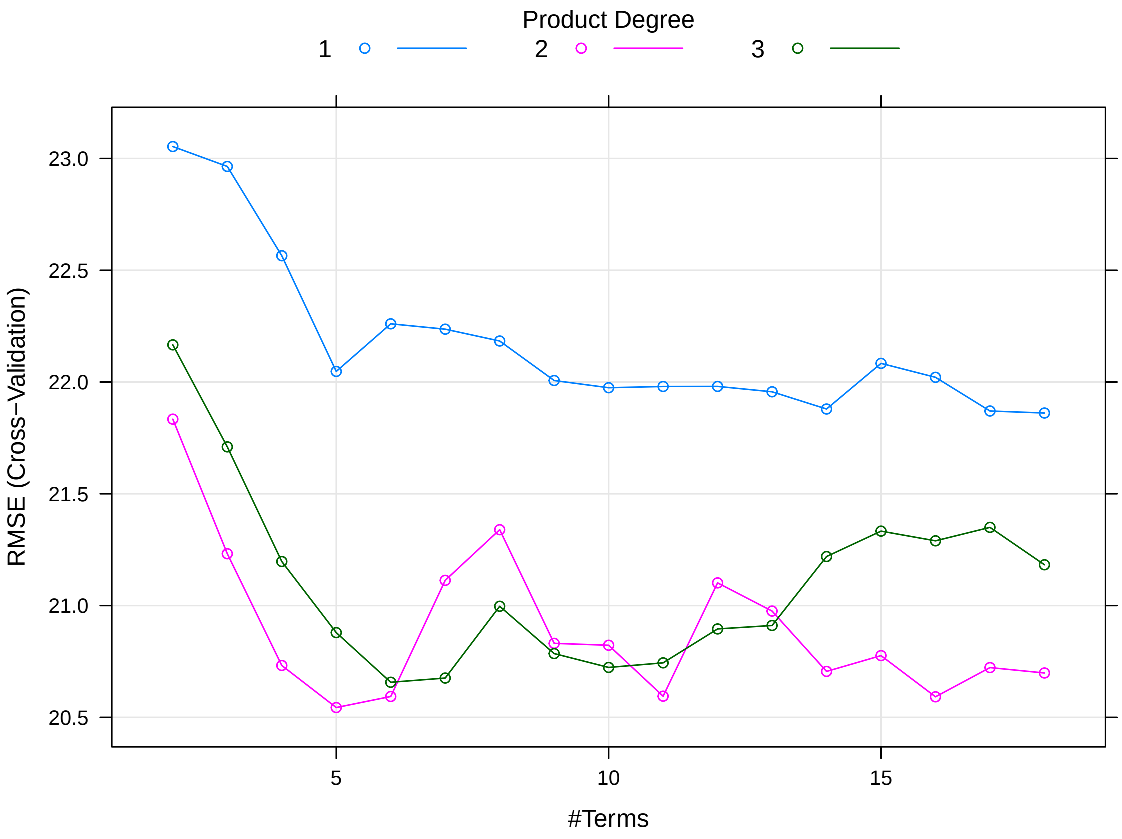
```
## [1] "test error for Generalised additive regression is: 25.181"
```

Multivariate adaptive regression

```
set.seed(8)

# create dummy variables for categorical variables
df_dummies <- data.frame(model.matrix(~ . - 1,
                                      # exclude ID and continuous variables
                                      data = data[, c("gender", "race", "smoking", "hypertension", "dia
                                                      "vaccine", "severity", "study")]),
                         # add continuous variables back to the data frame
                         age = data$age,
                         height = data$height,
                         weight = data$weight,
                         bmi = data$bmi,
                         SBP = data$SBP,
                         LDL = data$LDL,
                         recovery_time = data$recovery_time)

# rename df_dummies dataset as dat
dat_mars <- df_dummies


# training data, using previous indexTrain so the same as x_train
dat_train_mars <- dat_mars[indexTrain, ]
x_mars <- model.matrix(recovery_time~.,dat_mars)[indexTrain,-1]
y_mars <- dat_mars$recovery_time[indexTrain]

# test data, using previous indexTrain so the same as x_test
dat_test_mars <- dat_mars[-indexTrain, ]
x2_mars <- model.matrix(recovery_time~.,dat_mars)[-indexTrain,-1]
y2_mars <- dat_mars$recovery_time[-indexTrain]


# create grid of all possible pairs that can take degree and nprune values
mars_grid <- expand.grid(degree = 1:3, # number of possible product hinge functions in 1 term
                         nprune = 2:18) # upper bound of number of terms in model
# parallel computing
cl <- makePSOCKcluster(no_cores)
registerDoParallel(cl)

set.seed(8)
mars_model <- train(x_mars, y_mars, # training dataset
                  method = "earth",
                  tuneGrid = mars_grid,
                  trControl = ctrl)

stopCluster(cl)
registerDoSEQ()

ggplot(mars_model)
```



```
print(plot(mars_model))
```



```
summary(mars_model$finalModel)
```

```
## Call: earth(x=matrix[2517,19], y=c(14,36,50,65,3...), keepxy=TRUE, degree=2,
##             nprune=5)
##
##                        coefficients
## (Intercept)               -1.264634
## vaccine1                  -7.897168
## h(bmi-25.9)                8.611315
## h(32.6-bmi)                5.699561
## studyB * h(bmi-32.6)      41.724058
##
## Selected 5 of 24 terms, and 3 of 19 predictors (nprune=5)
## Termination condition: Reached nk 39
## Importance: studyB, bmi, vaccine1, gender0-unused, gender1-unused, ...
## Number of terms at each degree of interaction: 1 3 1
## GCV 413.5903    RSS 1031928    GRSq 0.4574914    RSq 0.4617953
```

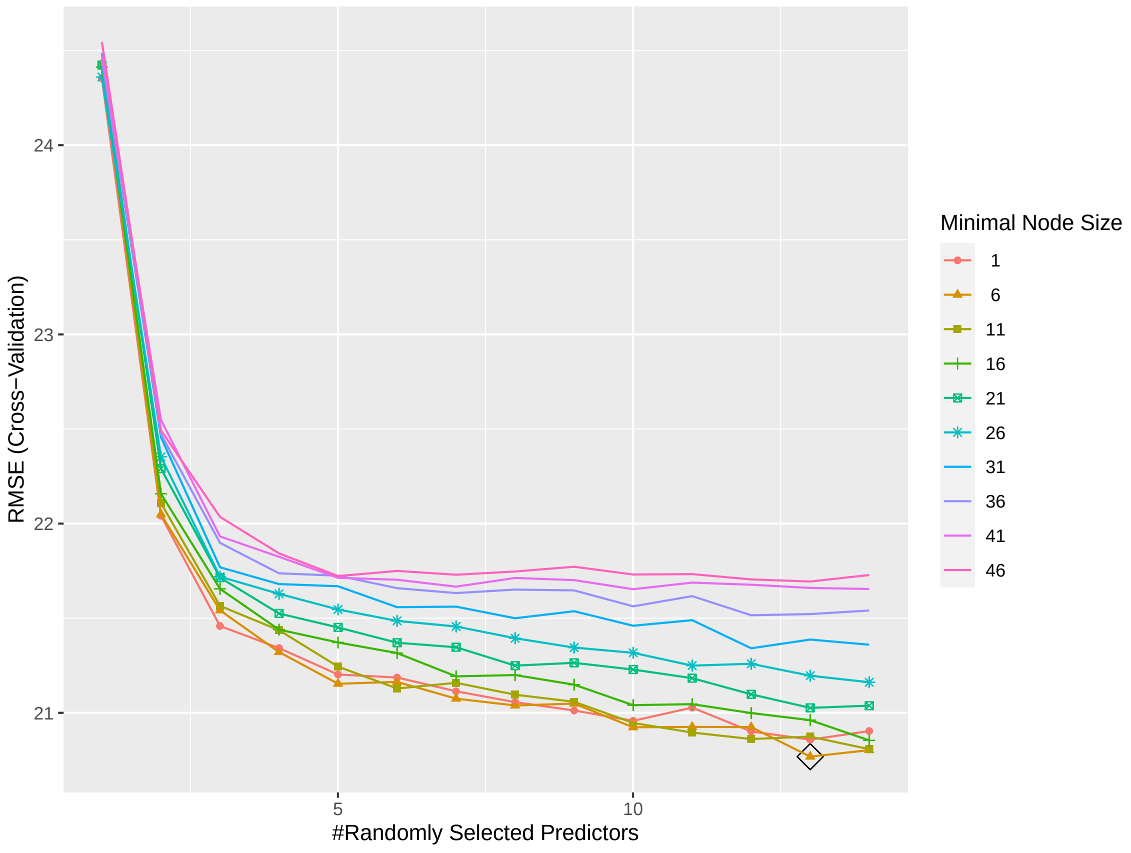
```
# view performance on the test set (RMSE)
mars_test_pred <- predict(mars_model, newdata = x2_mars) # test dataset
mars_test_rmse <- sqrt(mean((mars_test_pred - test_y)^2))
sprintf("test error for MARS is: %.3f", mars_test_rmse)
```

```
## [1] "test error for MARS is: 22.586"
```

Random Forest - Regression

```r
set.seed(8)
rf.grid <- expand.grid(mtry = 1:14,
                       splitrule = "variance",
                       min.node.size = seq(from = 1, to = 50, by = 5))

# parallel computing
no_cores <- detectCores() - 1
cl <- makePSOCKcluster(no_cores)
registerDoParallel(cl)

set.seed(8)
rf_model <- train(recovery_time ~ . ,
                  train_data,
                  method = "ranger",
                  tuneGrid = rf.grid,
                  trControl = ctrl)

stopCluster(cl)
registerDoSEQ()
ggplot(rf_model, highlight = TRUE)
```

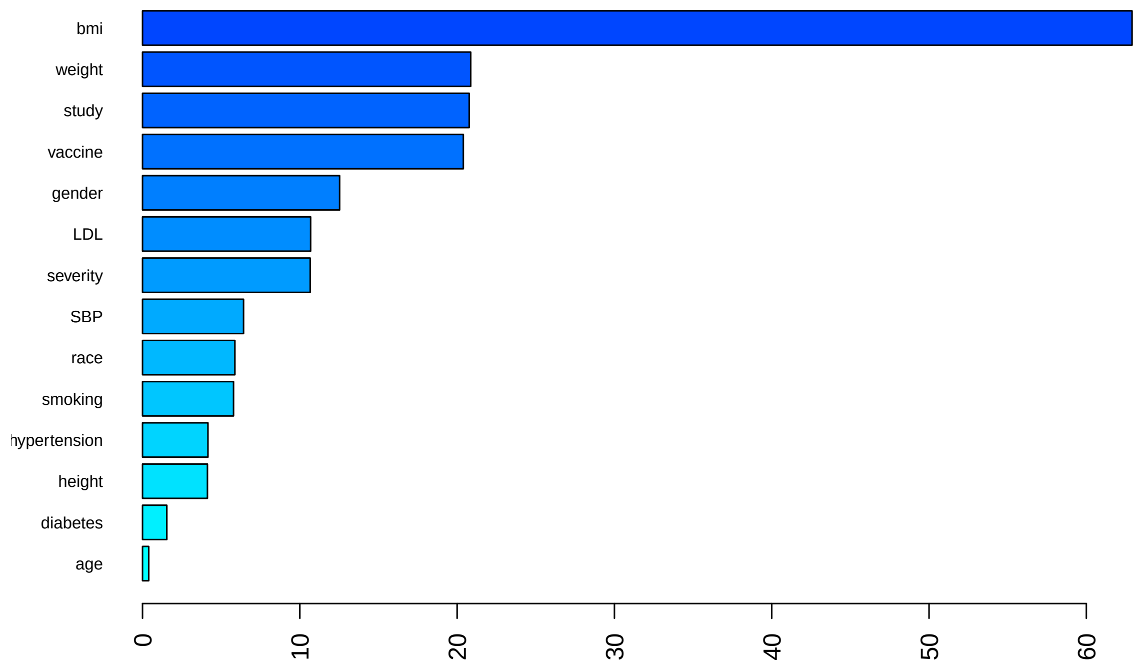
```
## Warning: The shape palette can deal with a maximum of 6 discrete values because
## more than 6 becomes difficult to discriminate; you have 10. Consider
## specifying shapes manually if you must have them.

## Warning: Removed 56 rows containing missing values (`geom_point()`).
```



```r
rf_model$bestTune
```

```
##     mtry splitrule min.node.size
## 122   13  variance             6
```

```r
# variable importance
set.seed(8)
rf.final.per <- ranger(recovery_time ~ . ,
                       train_data,
                       mtry = rf_model$bestTune[[1]],
                       splitrule = "variance",
                       min.node.size = rf_model$bestTune[[3]],
                       importance = "permutation",
                       scale.permutation.importance = TRUE)

barplot(sort(ranger::importance(rf.final.per), decreasing = FALSE),
        las = 2, horiz = TRUE, cex.names = 0.7,
        col = colorRampPalette(colors = c("cyan","blue"))(19))
```



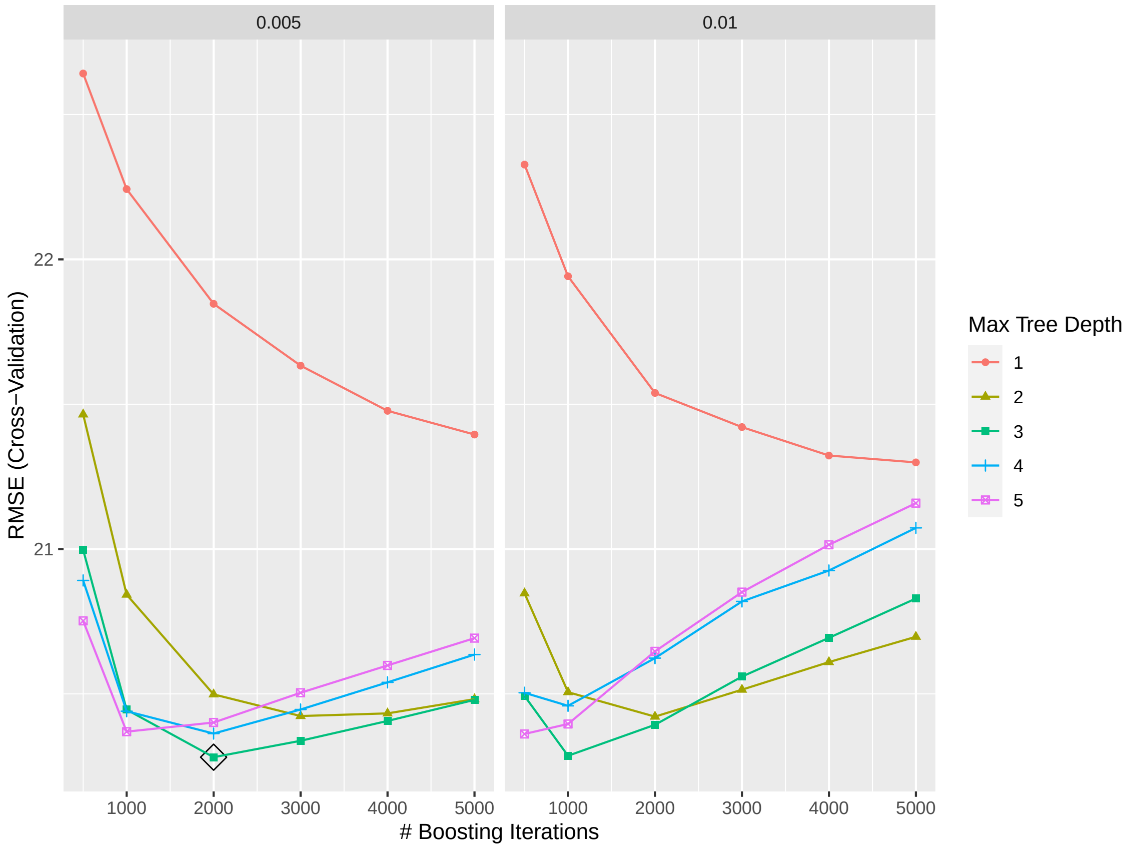
```r
# view performance on the test set (RMSE)
rf_test_pred <- predict(rf_model, newdata = test_data) # test dataset
rf_test_rmse <- sqrt(mean((rf_test_pred - test_y)^2))
sprintf("test error for Random Forest is: %.3f", rf_test_rmse)
```

```
## [1] "test error for Random Forest is: 21.965"
```

Boosting

```r
gbm.grid <- expand.grid(n.trees = c(500,1000,2000,3000,4000,5000),
                        interaction.depth = 1:5,
                        shrinkage = c(0.005,0.01),
                        n.minobsinnode = c(1))
no_cores <- detectCores() - 1
```

```
cl <- makePSOCKcluster(no_cores)
registerDoParallel(cl)
set.seed(8)
gbm.fit = train(recovery_time~. ,
                  train_data,
                  tuneGrid = gbm.grid,
                  trControl = ctrl,
                  method = "gbm",
                  verbose = FALSE)
stopCluster(cl)
registerDoSEQ()

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



```
gbm.fit$bestTune
```

```
##    n.trees interaction.depth shrinkage n.minobsinnode
## 15    2000                 3     0.005              1
```

```
# train error

gbm.fit.predict = predict(gbm.fit, newdata = train_data)
RMSE(gbm.fit.predict, train_y)
```

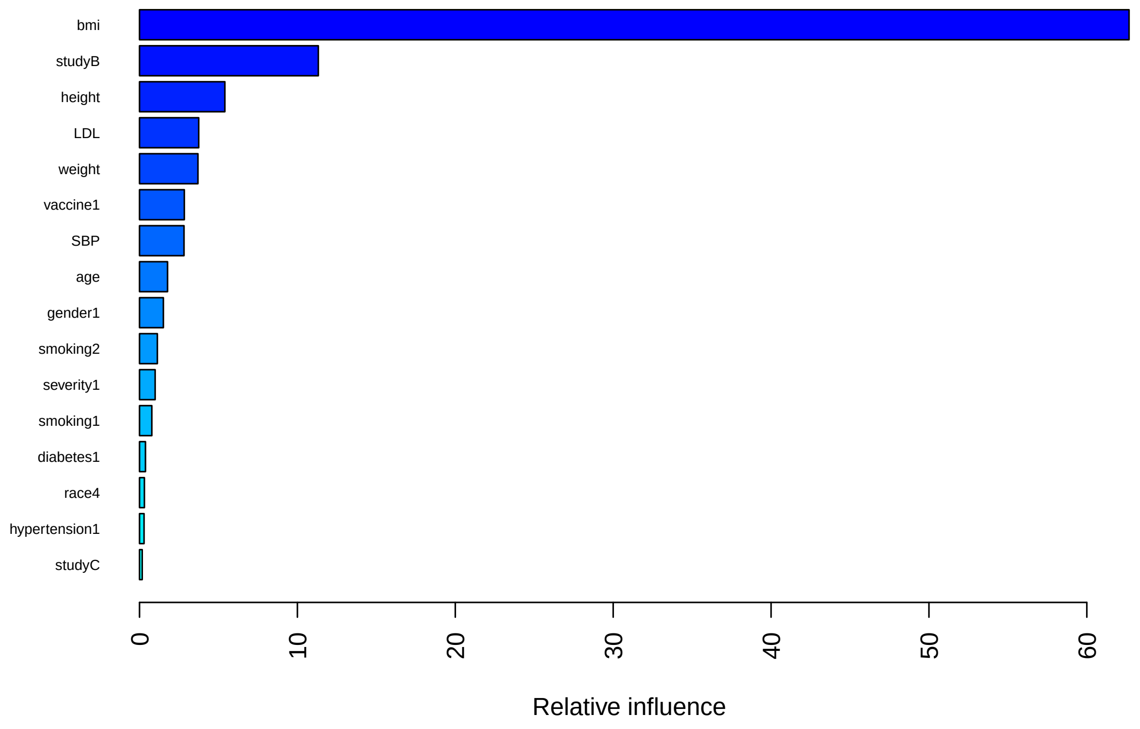
```
## [1] 17.48103
```

```
# test error
gbm.fit.predict = predict(gbm.fit, newdata = test_data)
```

```r
RMSE(gbm.fit.predict, test_y)
```

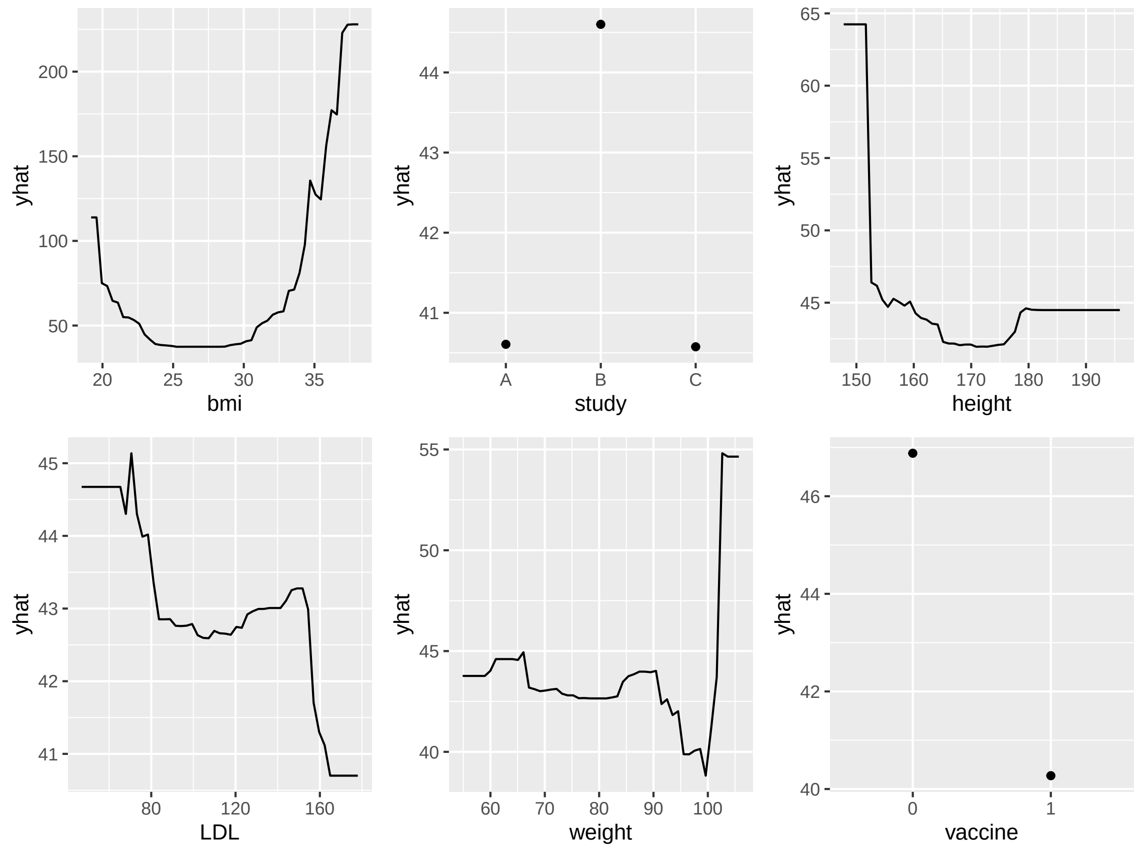
```
## [1] 21.36644
```

```r
#vip
summary(gbm.fit$finalModel, las = 2, cBars = 16, cex.names = 0.6)
```



```
##                         var     rel.inf
## bmi                     bmi 62.67390364
## studyB               studyB 11.32550304
## height               height  5.40662442
## LDL                     LDL  3.74887726
## weight               weight  3.70130262
## vaccine1           vaccine1  2.83797028
## SBP                     SBP  2.81893398
## age                     age  1.77559187
## gender1             gender1  1.51170747
## smoking2           smoking2  1.12956594
## severity1         severity1  0.98910314
## smoking1           smoking1  0.78002955
## diabetes1         diabetes1  0.37707597
## race4                 race4  0.30966831
## hypertension1 hypertension1  0.28792897
## studyC               studyC  0.17053920
## race3                 race3  0.09956841
## race2                 race2  0.05610592
```

```r
#pdp
features = c("bmi", "study", "height", "LDL", "weight", "vaccine")

pdps <- lapply(features, function(x) {
  partial(gbm.fit, pred.var = x, which.class = 2,
          prob = TRUE, plot = TRUE, plot.engine = "ggplot2")
})
grid.arrange(grobs = pdps,  ncol = 3)
```

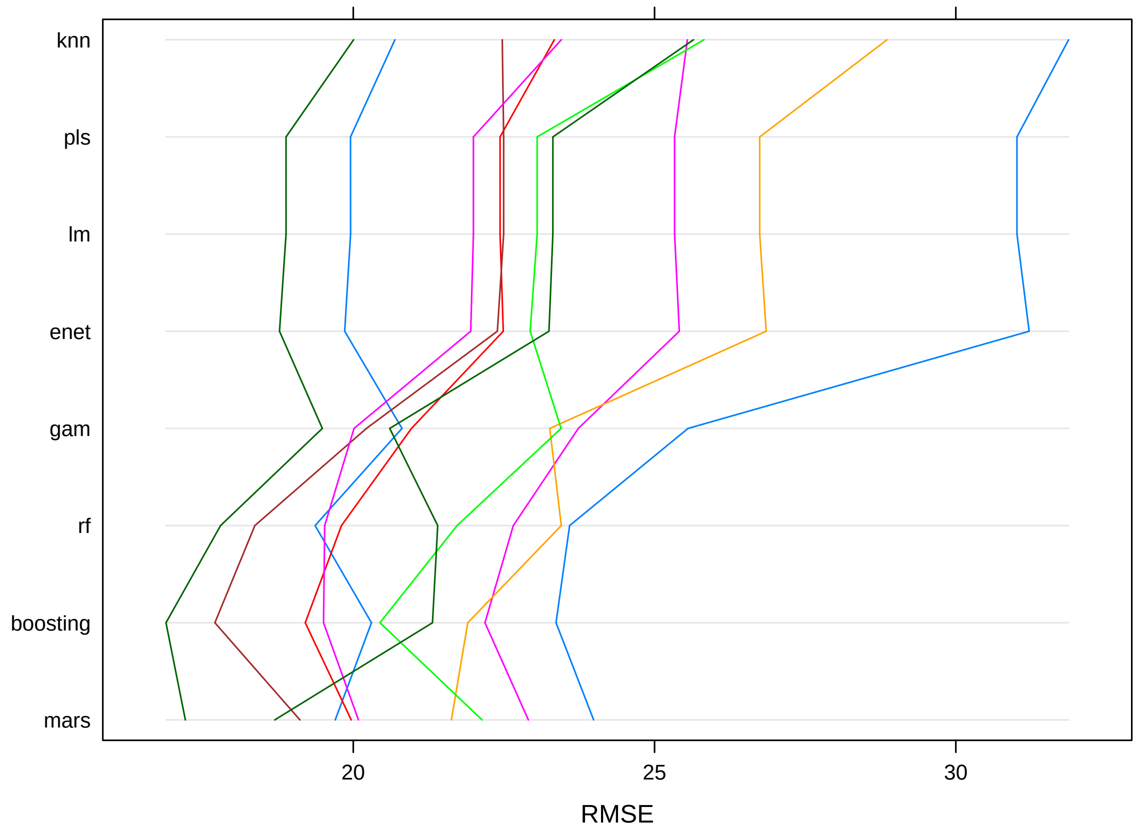


resampling on train

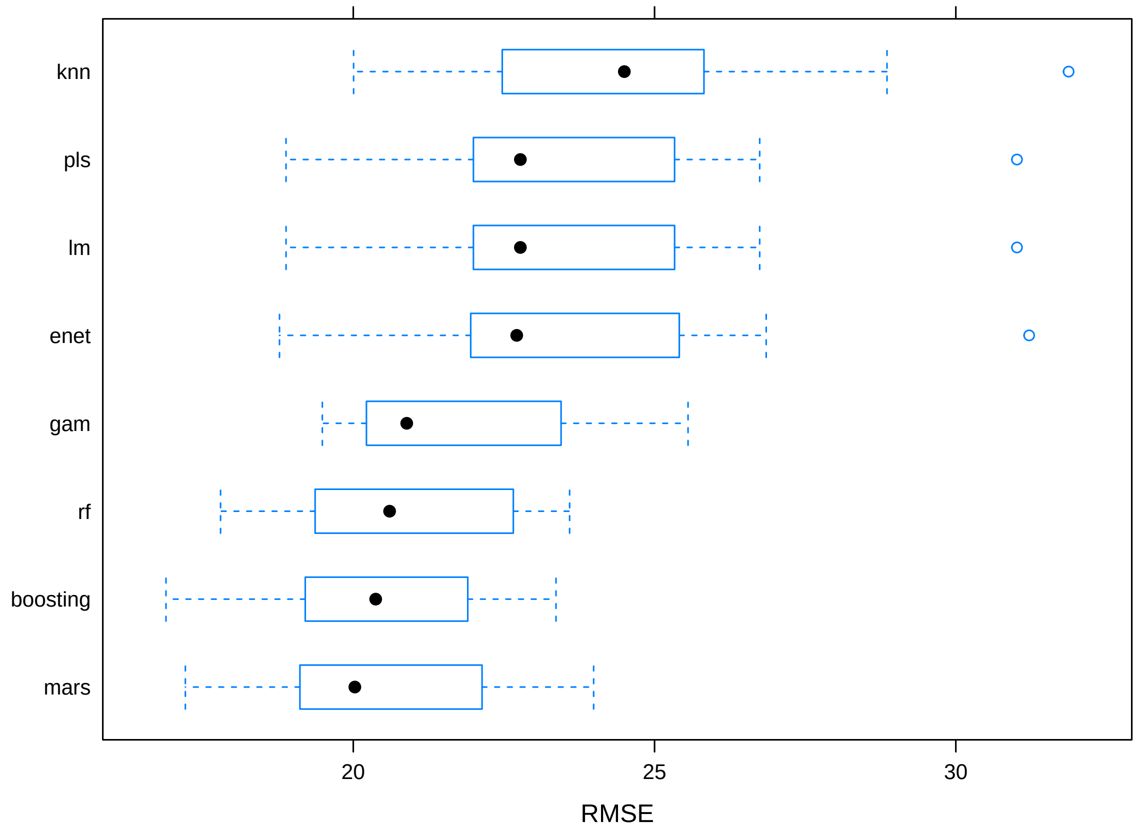
```
# parallel computing
no_cores <- detectCores() - 1
cl <- makePSOCKcluster(no_cores)
registerDoParallel(cl)
set.seed(8)

resamp <- resamples(list(lm = linear_model,
                         knn = knn_model,
                         enet = enet.fit.min,
                         pls = pls_model,
                         gam = gam_model,
                         mars = mars_model,
                         rf = rf_model,
                         boosting = gbm.fit))

stopCluster(cl)
registerDoSEQ()

summary(resamp)
```

```
##
## Call:
## summary.resamples(object = resamp)
##
## Models: lm, knn, enet, pls, gam, mars, rf, boosting
## Number of resamples: 10
##
## MAE
##              Min.  1st Qu.   Median     Mean  3rd Qu.     Max. NA's
## lm       13.76934 15.43334 15.76924 15.80693 16.17432 18.11764    0
## knn      14.06701 15.73153 16.09257 16.03670 16.46648 17.89633    0
## enet     13.69102 15.32867 15.68785 15.72506 16.12487 18.10713    0
## pls      13.76888 15.43393 15.76897 15.80691 16.17445 18.11772    0
## gam      13.19262 14.38982 14.82480 14.68947 15.13537 15.73301    0
## mars     12.27144 14.08073 14.54892 14.38932 14.86938 15.47013    0
## rf       13.28202 13.87283 14.49171 14.30696 14.74181 15.15497    0
## boosting 12.32434 13.76258 14.07635 13.93779 14.36728 15.05691    0
##
## RMSE
##              Min.  1st Qu.   Median     Mean  3rd Qu.     Max. NA's
## lm       18.88430 22.10438 22.77336 23.52201 24.82757 31.01445    0
## knn      20.00557 22.68863 24.49846 24.76979 25.77652 31.87127    0
## enet     18.77573 22.05979 22.71284 23.51269 24.86986 31.21659    0
## pls      18.88388 22.10432 22.77337 23.52193 24.82749 31.01461    0
## gam      19.48652 20.31487 20.88715 21.80966 23.40153 25.55548    0
## mars     17.21334 19.26111 20.02599 20.54374 22.01000 23.98902    0
## rf       17.79759 19.40633 20.60269 20.76831 22.42284 23.59035    0
## boosting 16.89195 19.27883 20.37222 20.28145 21.75394 23.36495    0
##
## Rsquared
##                Min.   1st Qu.    Median      Mean   3rd Qu.      Max. NA's
## lm       0.15262099 0.2417259 0.2664909 0.2612246 0.2814750 0.3695876    0
## knn      0.06890501 0.1229402 0.1601685 0.1838074 0.1914104 0.3999299    0
## enet     0.15157916 0.2419275 0.2660519 0.2606718 0.2821525 0.3650478    0
## pls      0.15266199 0.2417286 0.2664926 0.2612288 0.2814784 0.3695807    0
## gam      0.19032422 0.3458940 0.3645476 0.3822057 0.4249498 0.6033048    0
## mars     0.17813209 0.3790794 0.4295123 0.4310183 0.5145510 0.5980581    0
## rf       0.23449216 0.3940702 0.4288848 0.4227968 0.4520670 0.6156429    0
## boosting 0.21179764 0.4242251 0.4766269 0.4578489 0.5023122 0.6160659    0
```

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



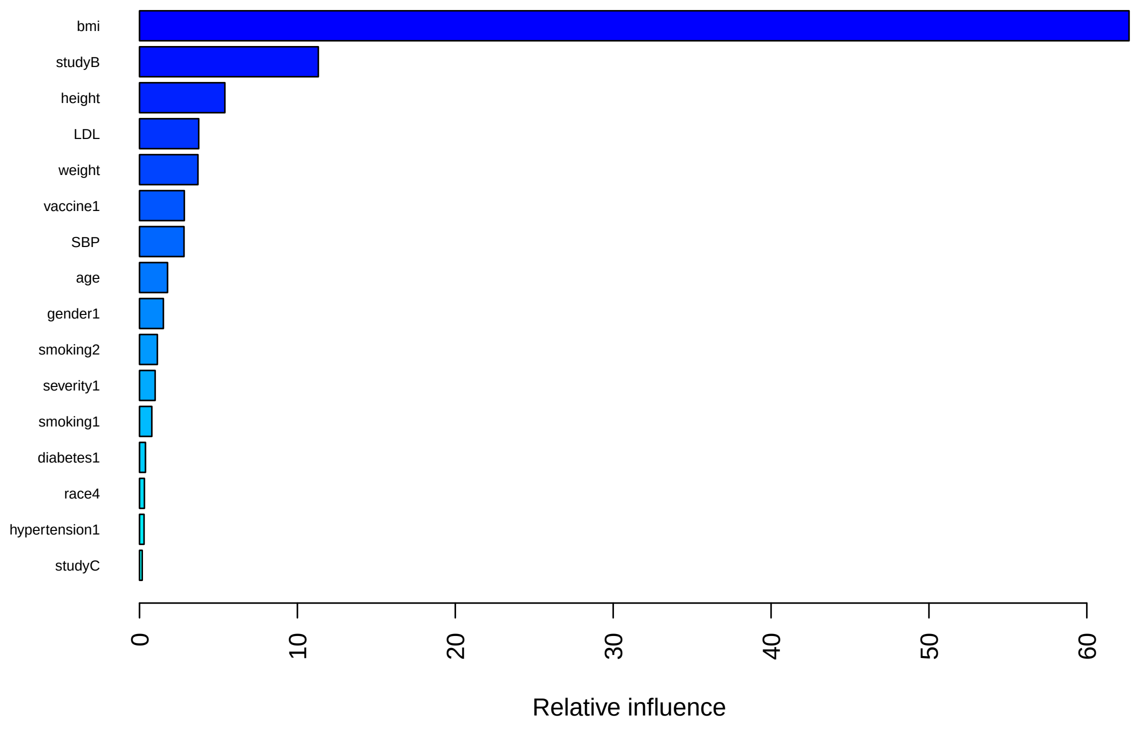
```r
bwplot(resamp, metric = "RMSE")
```



Final Model for Regression

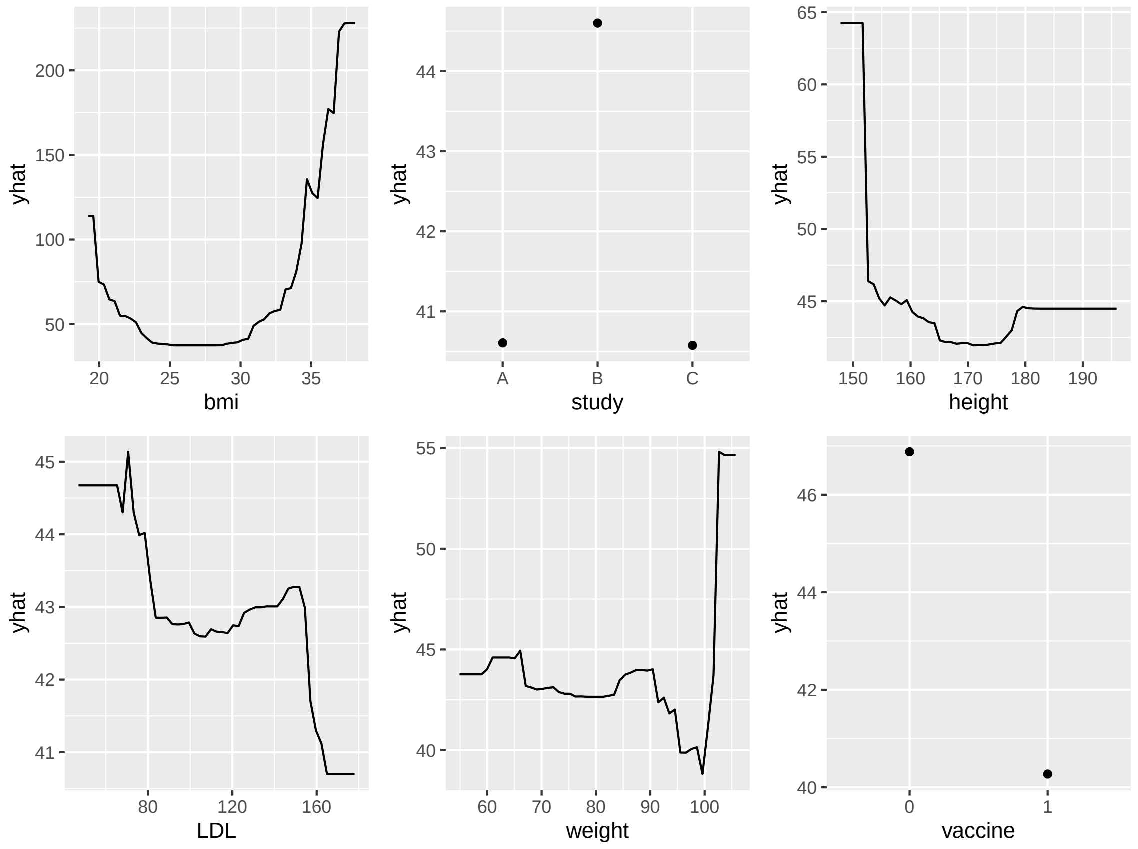
```
summary(gbm.fit$finalModel, las = 2, cBars = 16, cex.names = 0.6)
```

PDP plot

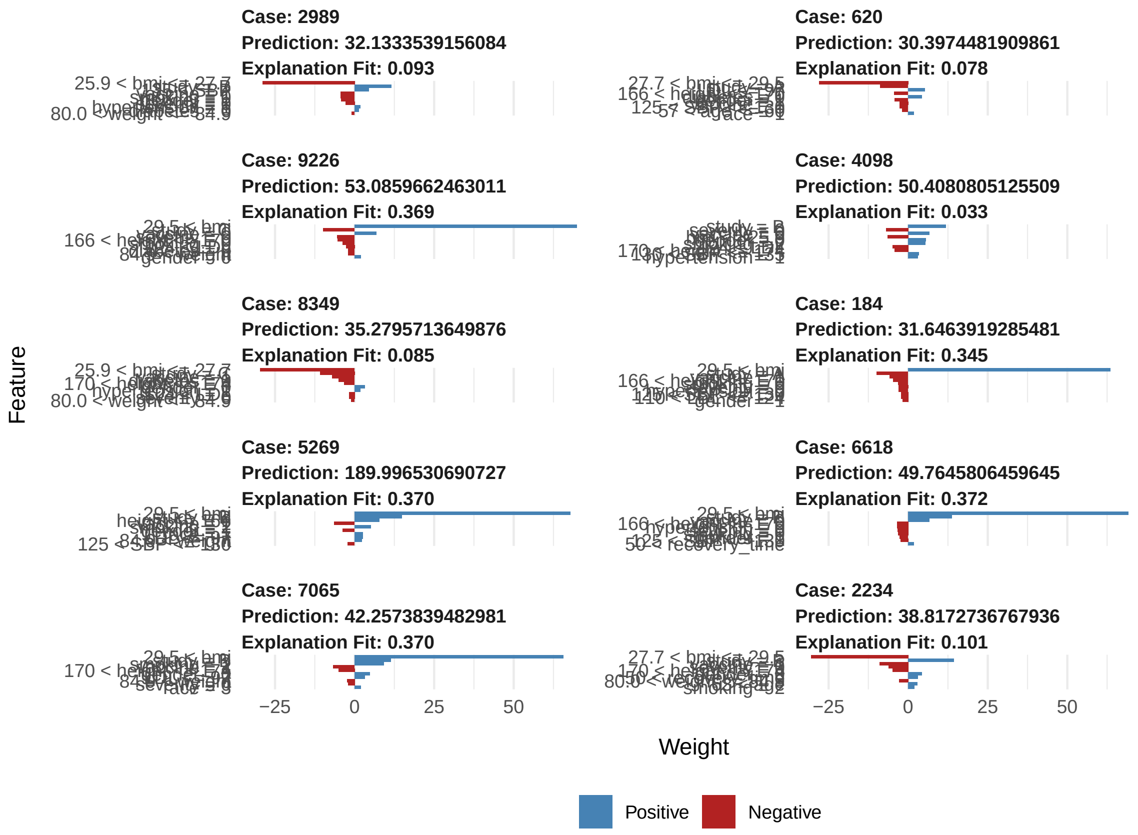


```
##                           var     rel.inf
## bmi                       bmi 62.67390364
## studyB                 studyB 11.32550304
## height                 height  5.40662442
## LDL                       LDL  3.74887726
## weight                 weight  3.70130262
## vaccine1             vaccine1  2.83797028
## SBP                       SBP  2.81893398
## age                       age  1.77559187
## gender1               gender1  1.51170747
## smoking2             smoking2  1.12956594
## severity1           severity1  0.98910314
## smoking1             smoking1  0.78002955
## diabetes1           diabetes1  0.37707597
## race4                   race4  0.30966831
## hypertension1 hypertension1  0.28792897
## studyC                 studyC  0.17053920
## race3                   race3  0.09956841
## race2                   race2  0.05610592
```

```
#pdp
features = c("bmi", "study", "height", "LDL", "weight", "vaccine")

pdps <- lapply(features, function(x) {
  partial(gbm.fit, pred.var = x, which.class = 2,
          prob = TRUE, plot = TRUE, plot.engine = "ggplot2")
})
grid.arrange(grobs = pdps,  ncol = 3)
```



```
#lime
explain_boosting <- lime(train_data, gbm.fit)
new_obs <- explain(train_data[1:10,], explain_boosting, n_features=10)

plot_features(new_obs)
```



Classification

Data Manipulation

We consider time to recovery as a binary outcome as long(>30 days) and short (<= 30 days).

```
#consider time to recovery as a binary outcome (>30 days vs. <= 30 days) and develop a prediction model
train_class =
  train_data %>%
  mutate(recovery_time = ifelse(recovery_time>30, "long", "short"))
test_class =
  test_data %>%
  mutate(recovery_time = ifelse(recovery_time>30, "long", "short"))

# matrix of predictors
x_train_class <- model.matrix(recovery_time~.,train_class)[,-1]
# vector of response
y_train_class <- train_class$recovery_time


# matrix of predictors
x_test_class <- model.matrix(recovery_time~.,test_class)[,-1]
# vector of response
y_test_class <- test_class$recovery_time


# ctrl for class
ctrl_class <- trainControl(method = "cv",
                     summaryFunction = twoClassSummary,
                     classProbs = TRUE)
```

Modeling Strategy

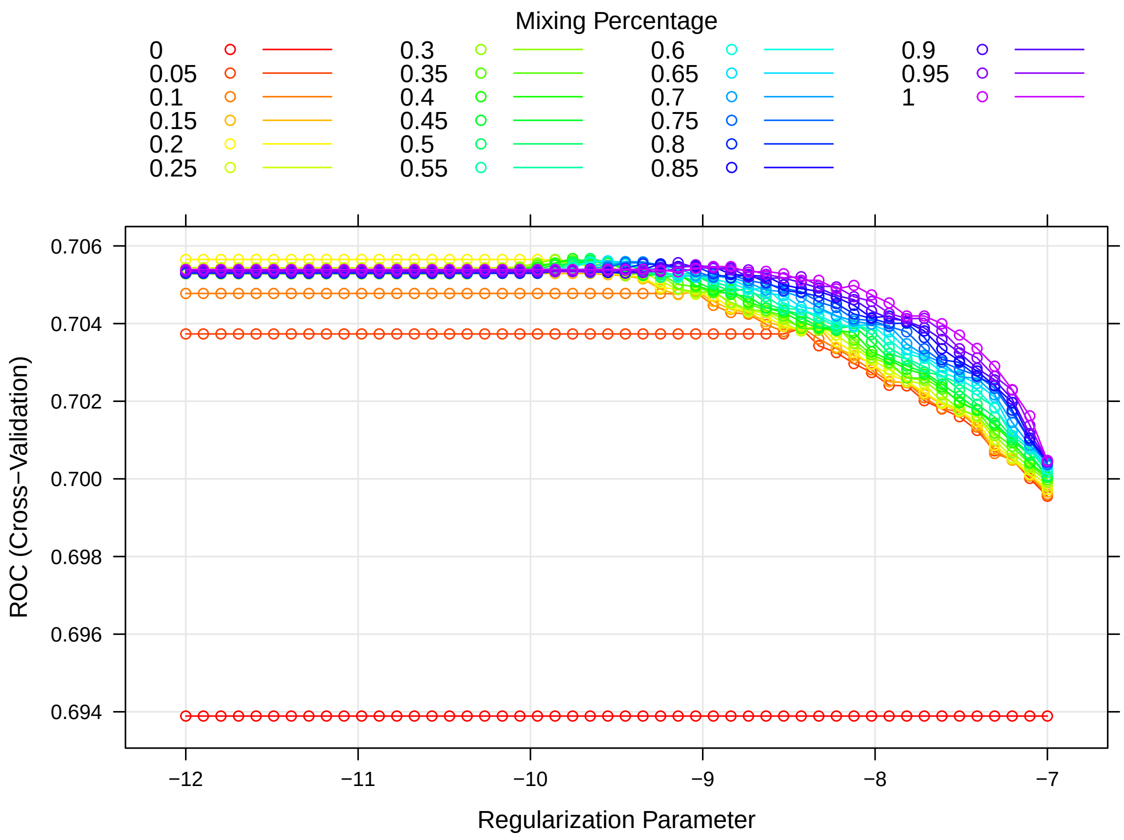
- **Penalized logistic regression**
- **Generalized additive model (GAM)**
- **Multivariate adaptive regression splines (MARS)**
- **Linear discriminant analysis (LDA)**
- **Random Forest**
- **Boosting**
- **Support Vector Machine (SVM with Linear and Radial Kernels)**

Penalized logistic regression

```
glmnGrid <- expand.grid(.alpha = seq(0, 1, length = 21),
                        .lambda = exp(seq(-12, -7, length = 50)))
set.seed(8)
model.glmn <- train(x = x_train_class,
                    y = y_train_class,
                    method = "glmnet",
                    tuneGrid = glmnGrid,
                    metric = "ROC",
                    trControl = ctrl_class)

model.glmn$bestTune
```

```
##     alpha       lambda
## 524   0.5 6.422865e-05
```

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

plot(model.glmn, par.settings = myPar, xTrans = function(x) log(x))
```



```
# view performance on the test set (accuracy)
glmn_class_test_pred <- predict(model.glmn, newdata=x_test_class) # test dataset
glmn_class_test_acc <- sum(glmn_class_test_pred==y_test_class)/length(y_test_class)
sprintf("test error for penalized logistic is: %.3f",1-glmn_class_test_acc)
```

```
## [1] "test error for penalized logistic is: 0.286"
```

Since the boundary value for λ is exp(-10)=4.54e-5 and exp(-5)=0.007, and the optimal lambda is not on the boundary. So local minimum is achieved.

Gam

```
# gam
set.seed(8)
model.gam <- train(x = x_train_class,
                   y = y_train_class,
                   method = "gam",
                   tuneGrid = data.frame(method = "GCV.Cp", select = c(TRUE,FALSE)),
                   metric = "ROC",
                   trControl = ctrl_class)

model.gam$bestTune
```

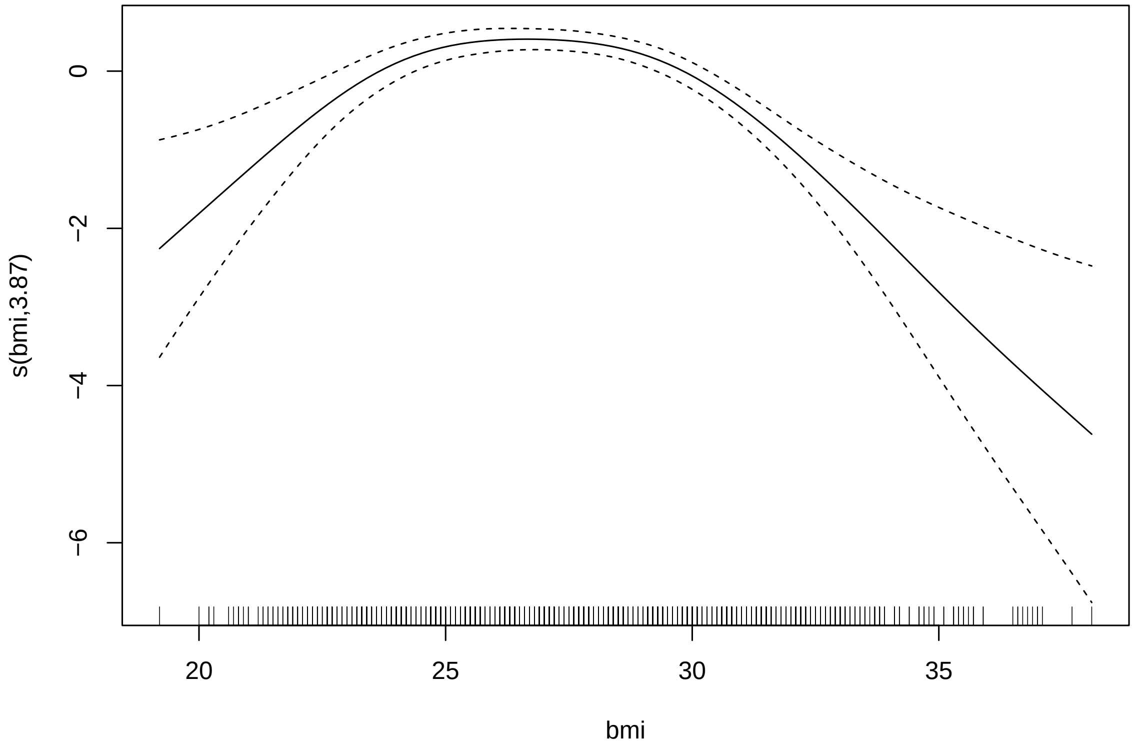
```
##   select method
## 2   TRUE GCV.Cp
```

```
model.gam$finalModel
```

```
##
```

```
## Family: binomial
## Link function: logit
##
## Formula:
## .outcome ~ gender1 + race2 + 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:
## 0.0002 3.0898 0.1982 3.8717 1.9808 0.0001  total = 22.14
##
## UBRE score: 0.07604226
```

```
#discover bmi and recovery time
plot(model.gam$finalModel, select = 4)
```



```
#train error
train.pred.gam <- predict(model.gam, newdata = x_train_class)
train.error.gam = 1-sum(train_class$recovery_time == train.pred.gam)/length(train_data$recovery_time)
sprintf("The train error for GAM is %.3f", train.error.gam)
```

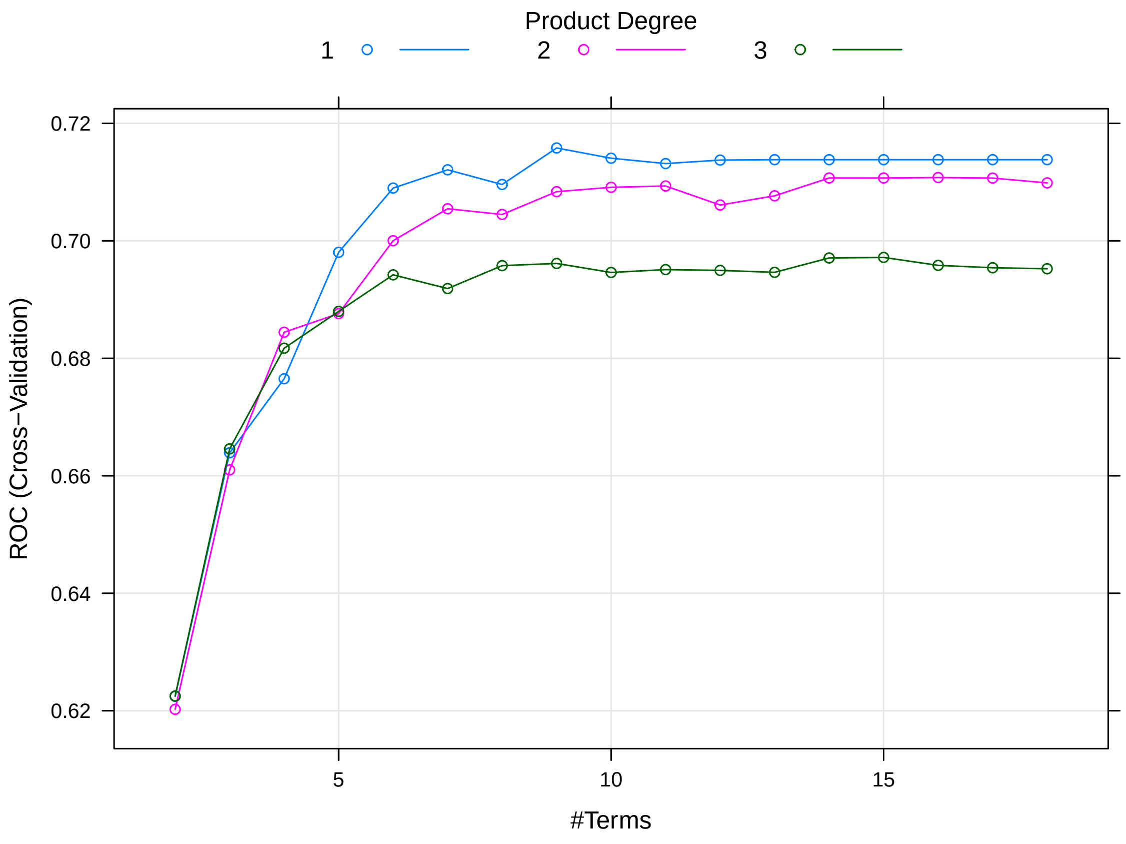
```
## [1] "The train error for GAM is 0.266"
```

```
#test error
test.pred.gam <- predict(model.gam, newdata = x_test_class)
test.error.gam = 1-sum(test_class$recovery_time == test.pred.gam)/length(test_class$recovery_time)
sprintf("The test error for GAM is %.3f", test.error.gam)
```

```
## [1] "The test error for GAM is 0.283"
```

MARS

```
set.seed(8)
mars.fit = train(x = x_train_class,
                        y =  y_train_class,
                         method = "earth",
                         tuneGrid = expand.grid(degree = 1:3,
                                                nprune = 2:18),
                         metric = "ROC",
                         trControl = ctrl_class)
plot(mars.fit)
```



```
#train error
train.pred.mars = predict(mars.fit , newdata = x_train_class)
train.error.mars = 1-sum(train_class$recovery_time == train.pred.mars)/length(train_data$recovery_time)
sprintf("The train error for MARS is %.3f", train.error.mars)
```

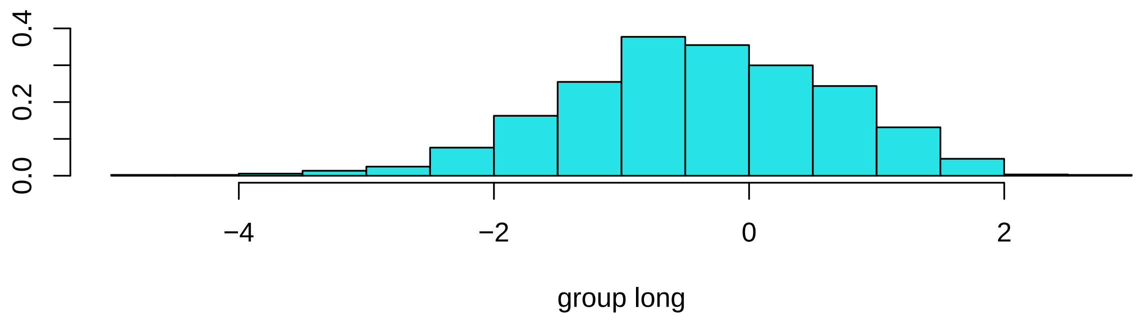
```
## [1] "The train error for MARS is 0.265"
```

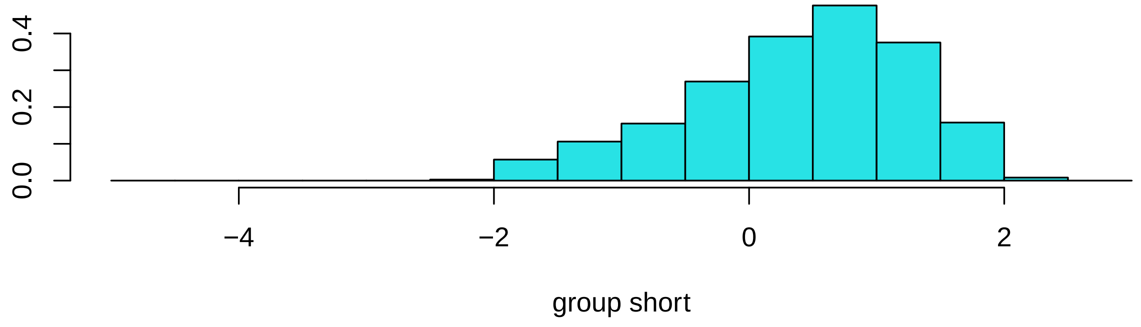
```
#test error
test.pred.mars = predict(mars.fit , newdata = x_test_class)
test.error.mars = 1-sum(test_class$recovery_time == test.pred.mars)/length(test_class$recovery_time)
sprintf("The test error for MARS is %.3f", test.error.mars)
```

```
## [1] "The test error for MARS is 0.280"
```

Linear discriminant analysis (LDA)

```r
set.seed(8)
# Using MASS
lda.fit <- lda(recovery_time~.,
               data = train_class)
plot(lda.fit)
```





```r
lda.fit$scaling
```

```
##                         LD1
## age           -0.005230071
## gender1        0.582852115
## race2          0.111644453
## race3         -0.015332625
## race4          0.078103928
## smoking1      -0.395459244
## smoking2      -0.628005874
## height        -0.497778576
## weight         0.538847538
## bmi           -1.636992668
## hypertension1 -0.368808467
## diabetes1     -0.053193708
## SBP            0.010681574
## LDL           -0.003381055
## vaccine1       0.854566384
## severity1     -0.726871127
## studyB         1.410574304
## studyC        -0.044449352
```

```
set.seed(8)
# Using caret
lda_model <- train(x_train_class, #train x
                   y_train_class, #train y
                   method = "lda",
                   metric = "ROC",
                   trControl = ctrl_class)
summary(lda_model)
```

```
##             Length Class      Mode
## prior        2     -none-     numeric
## counts       2     -none-     numeric
## means       36     -none-     numeric
## scaling     18     -none-     numeric
## lev          2     -none-     character
## svd          1     -none-     numeric
## N            1     -none-     numeric
## call         3     -none-     call
## xNames      18     -none-     character
## problemType  1     -none-     character
## tuneValue    1     data.frame list
## obsLevels    2     -none-     character
## param        0     -none-     list
```

```
#train error
train.pred.lda <- predict(lda_model, newdata = x_train_class)
train.error.lda = 1 - sum(train_class$recovery_time == train.pred.lda)/length(train_data$recovery_time)
sprintf("The train error for LDA is %.3f", train.error.lda)
```

```
## [1] "The train error for LDA is 0.277"
```

```
#test error
test.pred.lda <- predict(lda_model, newdata = x_test_class)
test.error.lda = 1 - sum(test_class$recovery_time == test.pred.lda)/length(test_class$recovery_time)
sprintf("The test error for LDA is %.3f", test.error.lda)
```

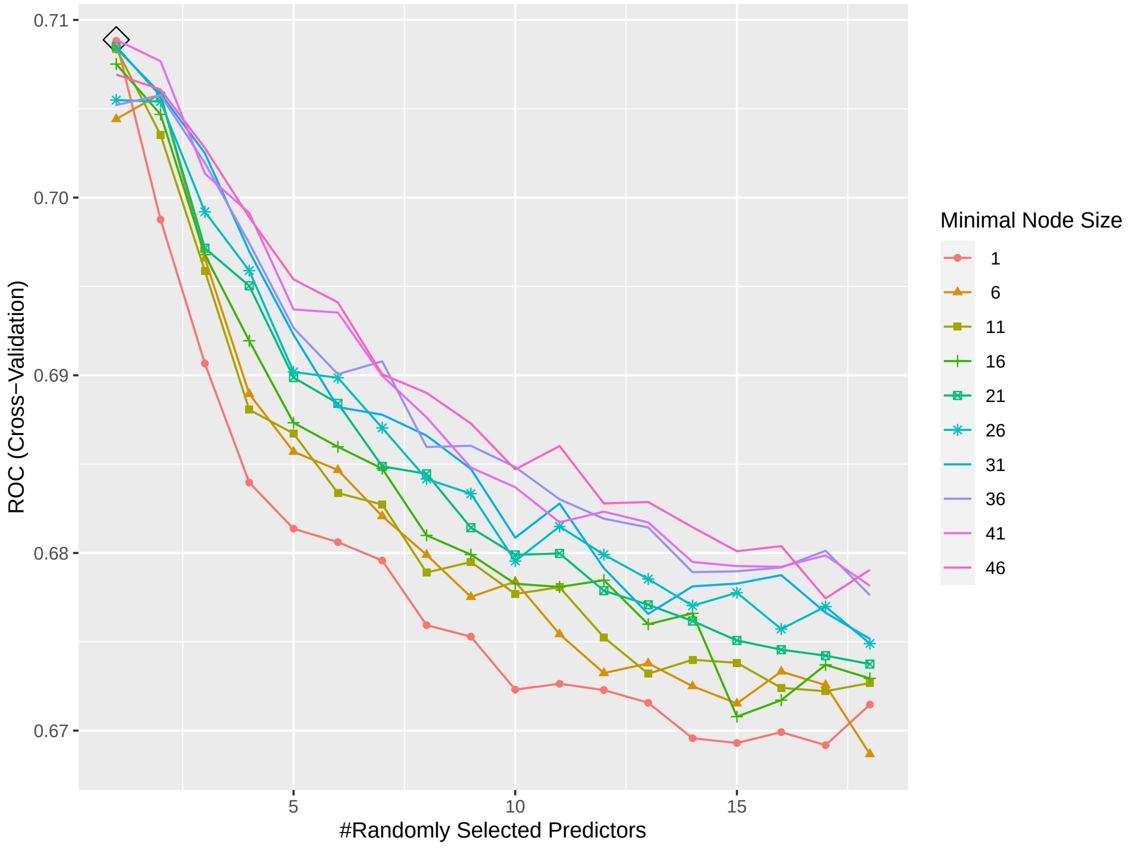
```
## [1] "The test error for LDA is 0.287"
```

Random Forest - Classification

```
cl <- makePSOCKcluster(no_cores)
registerDoParallel(cl)
rf.grid <- expand.grid(mtry = 1:18,
                       splitrule = "gini",
                       min.node.size = seq(from = 1, to = 50, by = 5))

set.seed(8)
rf_class_model <- train(x_train_class,
                        y_train_class,
                        method = "ranger",
                        importance = "permutation",
                        tuneGrid = rf.grid,
                        metric = "ROC",
                        trControl = ctrl_class)
stopCluster(cl)
```

```r
registerDoSEQ()

ggplot(rf_class_model, highlight = TRUE)
```

```
## Warning: The shape palette can deal with a maximum of 6 discrete values because
## more than 6 becomes difficult to discriminate; you have 10. Consider
## specifying shapes manually if you must have them.

## Warning: Removed 72 rows containing missing values (`geom_point()`).
```



```r
rf_class_model$bestTune
```

```
##   mtry splitrule min.node.size
## 9    1      gini            41
```

```r
#train error
train.pred.rf <- predict(lda_model, newdata = x_train_class)
train.error.ef = 1 - sum(train_class$recovery_time == train.pred.lda)/length(train_data$recovery_time)
sprintf("The train error for LDA is %.3f", train.error.lda)
```

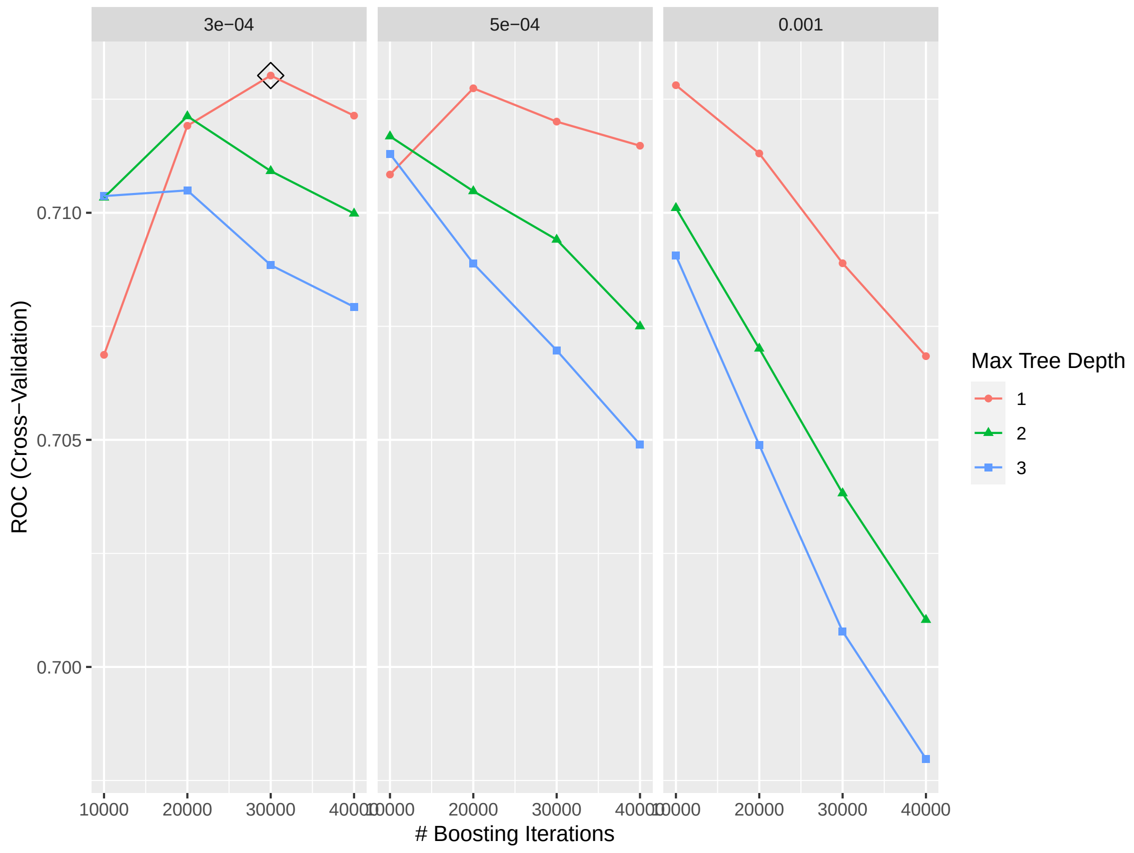
```
## [1] "The train error for LDA is 0.277"
```

```r
#test error
test.pred.rf <- predict(rf_class_model, newdata = x_test_class)
test.error.rf = 1 - sum(test_class$recovery_time == test.pred.rf)/length(test_class$recovery_time)
sprintf("The test error for Random Forest is %.3f", test.error.rf)
```

```
## [1] "The test error for Random Forest is 0.293"
```

Boosting

```
gbmA.grid = expand.grid(n.trees = c(10000,20000,30000,40000),
                        interaction.depth = 1:3,
                        shrinkage = c(0.0003,0.0005,0.001),
                        n.minobsinnode = 1)

cl <- makePSOCKcluster(no_cores)
registerDoParallel(cl)
set.seed(8)
gbmA.fit = train(recovery_time~. ,
                 train_class,
                 tuneGrid = gbmA.grid,
                 trControl = ctrl_class,
                 method = "gbm",
                 distribution = "adaboost",
                 metric = "ROC",
                 verbose = FALSE)

stopCluster(cl)
registerDoSEQ()

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



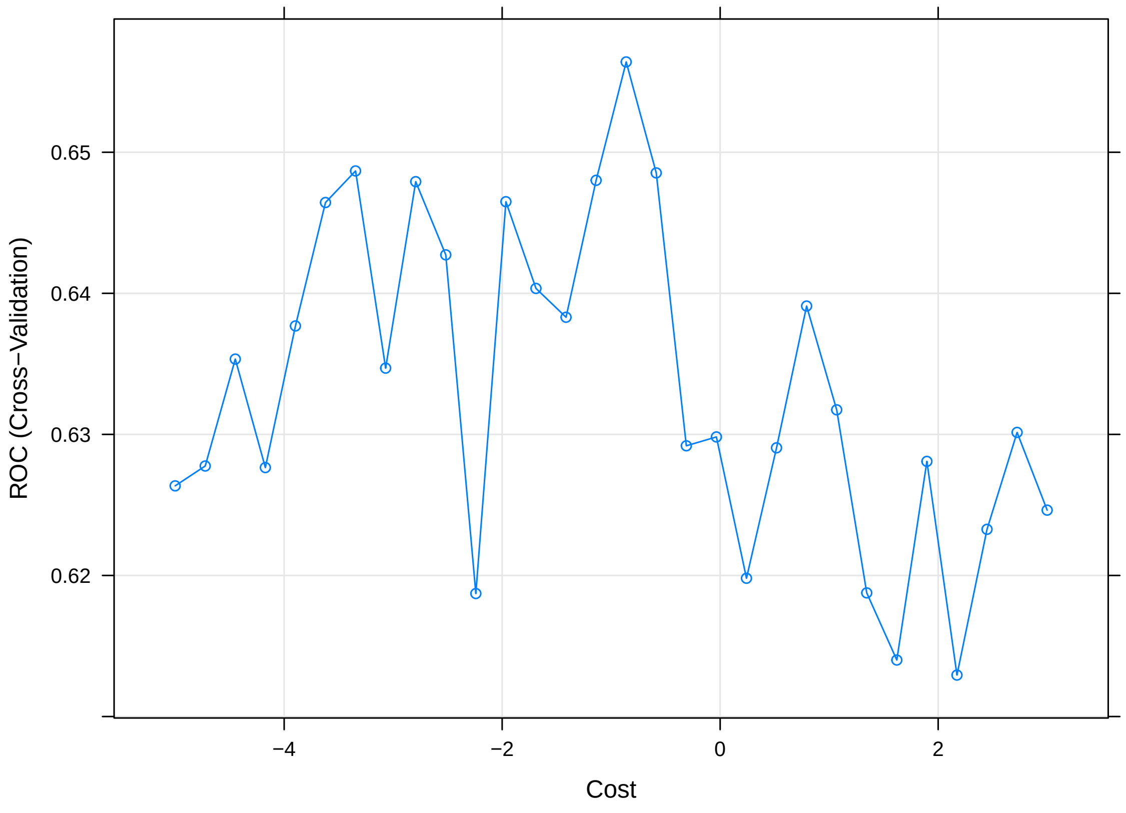
```
#train error
train.pred.boosting = predict(gbmA.fit , newdata = train_class, type = "raw")
train.error.boosting = 1-sum(train_class$recovery_time == train.pred.boosting)/length(train_data$recove
# sprintf("The train error for boosting is %.3f", train.pred.boosting)

#test error
test.pred.boosting = predict(gbmA.fit , newdata = test_class, type = "raw")
test.error.boosting = 1-sum(test_class$recovery_time == test.pred.boosting)/length(test_class$recovery_t
# sprintf("The test error for boosting is %.3f", train.pred.boosting)
```

linear SVM

```
# parallel computing
no_cores <- detectCores() - 1
cl <- makePSOCKcluster(no_cores)
registerDoParallel(cl)

# kernlab
set.seed(8)
svml.fit <- train(recovery_time ~ . ,
                  data = train_class,
                  method = "svmLinear",
                  tuneGrid = data.frame(C = exp(seq(-5,3,len=30))),
                  trControl = ctrl_class)
```

```
## maximum number of iterations reached 0.008313212 0.00758091
```

```
plot(svml.fit, highlight = TRUE, xTrans = log)
```



```
stopCluster(cl)
registerDoSEQ()
```

```
svml.fit$bestTune
```

```
##            C
## 16 0.4222875
```

```
#train error
train.pred.svml <- predict(svml.fit, newdata = train_class)
train.error.svml = 1-sum(train_class$recovery_time == train.pred.svml)/length(train_data$recovery_time)
sprintf("The train error for Support vector classifier is %.3f", train.error.svml)
```

```
## [1] "The train error for Support vector classifier is 0.292"
```

```
#test error
test.pred.svml <- predict(svml.fit, newdata = test_class)
test.error.svml = 1-sum(test_class$recovery_time == test.pred.svml)/length(test_class$recovery_time)
sprintf("The test error for Support vector classifier is %.3f", test.error.svml)
```

```
## [1] "The test error for Support vector classifier is 0.292"
```

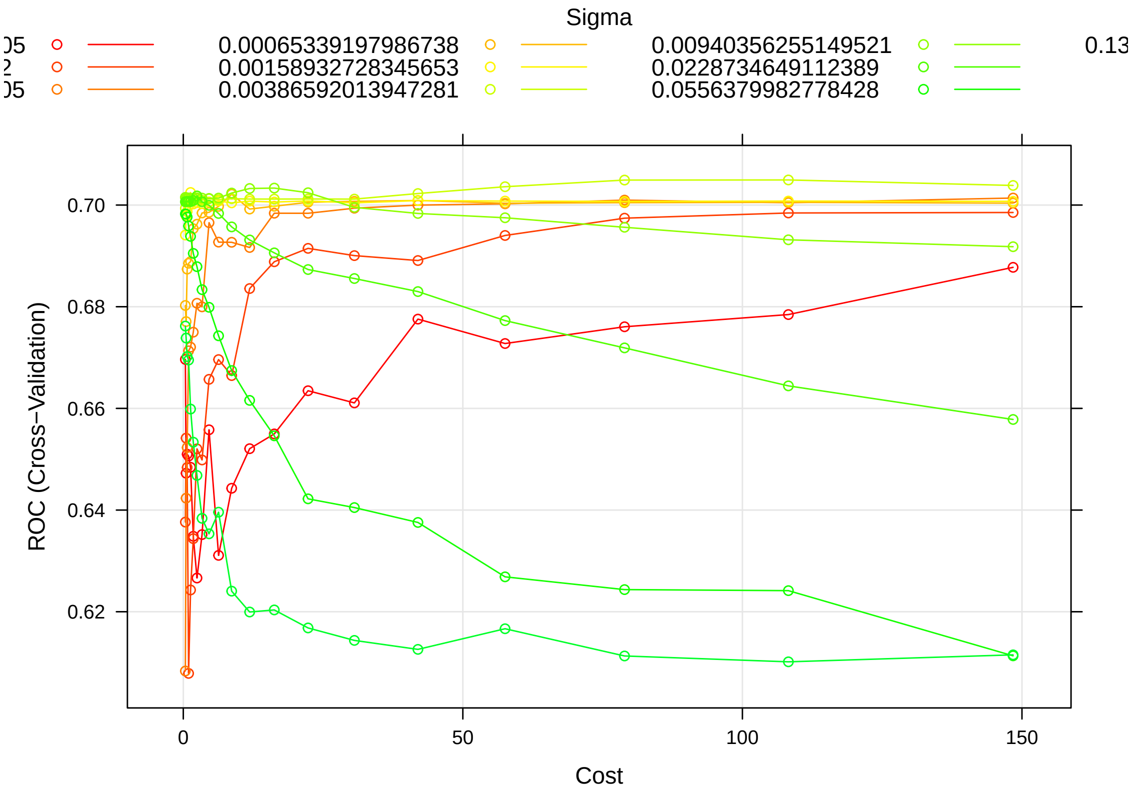
SVM with radial kernel

```
svmr.grid <- expand.grid(C = exp(seq(-1,5,len=20)),
                         sigma = exp(seq(-10,-2,len=10)))

# parallel computing
no_cores <- detectCores() - 1
cl <- makePSOCKcluster(no_cores)
registerDoParallel(cl)

# tunes over both cost and sigma
set.seed(8)
svmr.fit <- train(recovery_time ~ . ,
                  data = train_class,
                  method = "svmRadialSigma",
                  tuneGrid = svmr.grid,
                  trControl = ctrl_class)
```

```
## Warning in train.default(x, y, weights = w, ...): The metric "Accuracy" was not
## in the result set. ROC will be used instead.
```

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

```
stopCluster(cl)
registerDoSEQ()



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

plot(svmr.fit, highlight = TRUE, par.settings = myPar)
```



```r
svmr.fit$bestTune
```

```
##          sigma        C
## 186 0.00386592 108.2248
```

```r
#train error
train.pred.svmr <- predict(svmr.fit, newdata = train_class)
train.error.svmr = 1-sum(train_class$recovery_time == train.pred.svmr)/length(train_class$recovery_time
sprintf("The train error for Support vector Machine with radial kernel is %.3f", train.error.svmr)
```

```
## [1] "The train error for Support vector Machine with radial kernel is 0.253"
```

```r
#test error
test.pred.svmr <- predict(svmr.fit, newdata = test_class)
test.error.svmr = 1-sum(test_class$recovery_time == test.pred.svmr)/length(test_class$recovery_time)
sprintf("The test error for Support vector Machine with radial kernel is %.3f", test.error.svmr)
```

```
## [1] "The test error for Support vector Machine with radial kernel is 0.287"
```

After tuning, the cost in this range achieves local maximum accuracy. The value is not on the boundary, hence the local maximum accuracy is achieved. It takes a long time (aprox 30 min) to run so it may be hard to refine into a smaller grid.

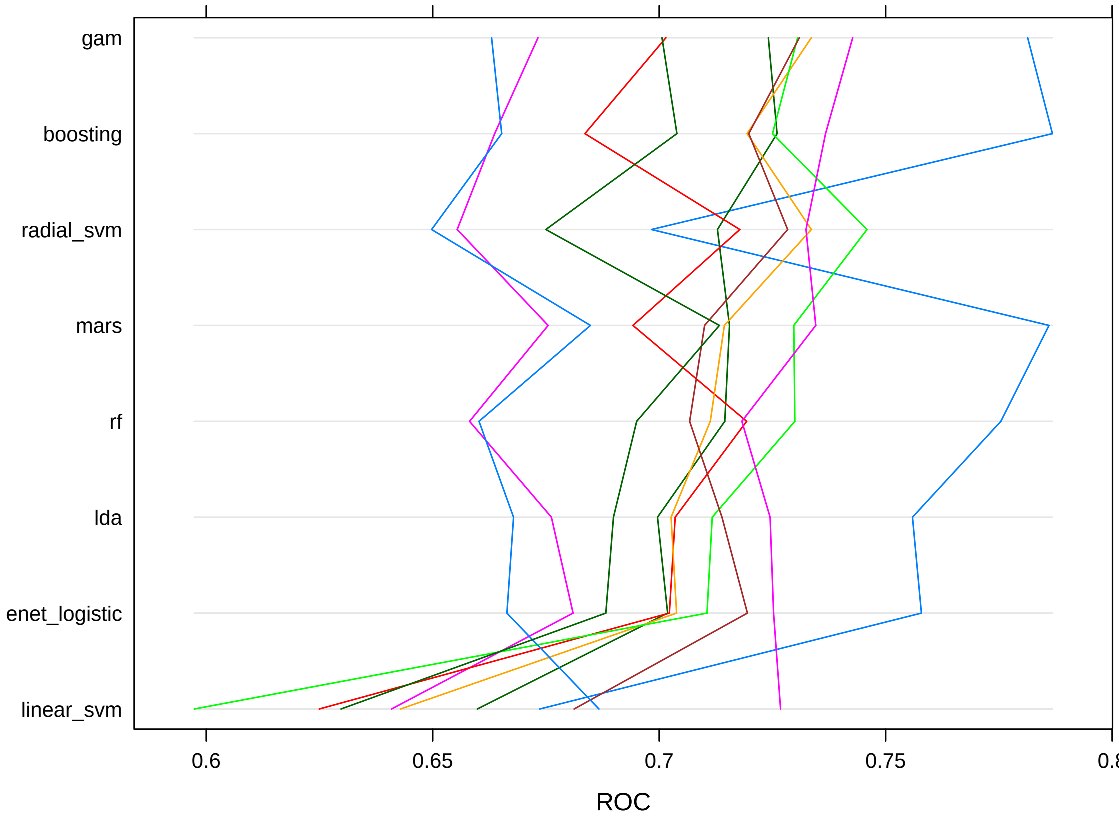
Resampling Results and Model Selection

```r
# parallel computing
no_cores <- detectCores() - 1
cl <- makePSOCKcluster(no_cores)
registerDoParallel(cl)

set.seed(8)
```

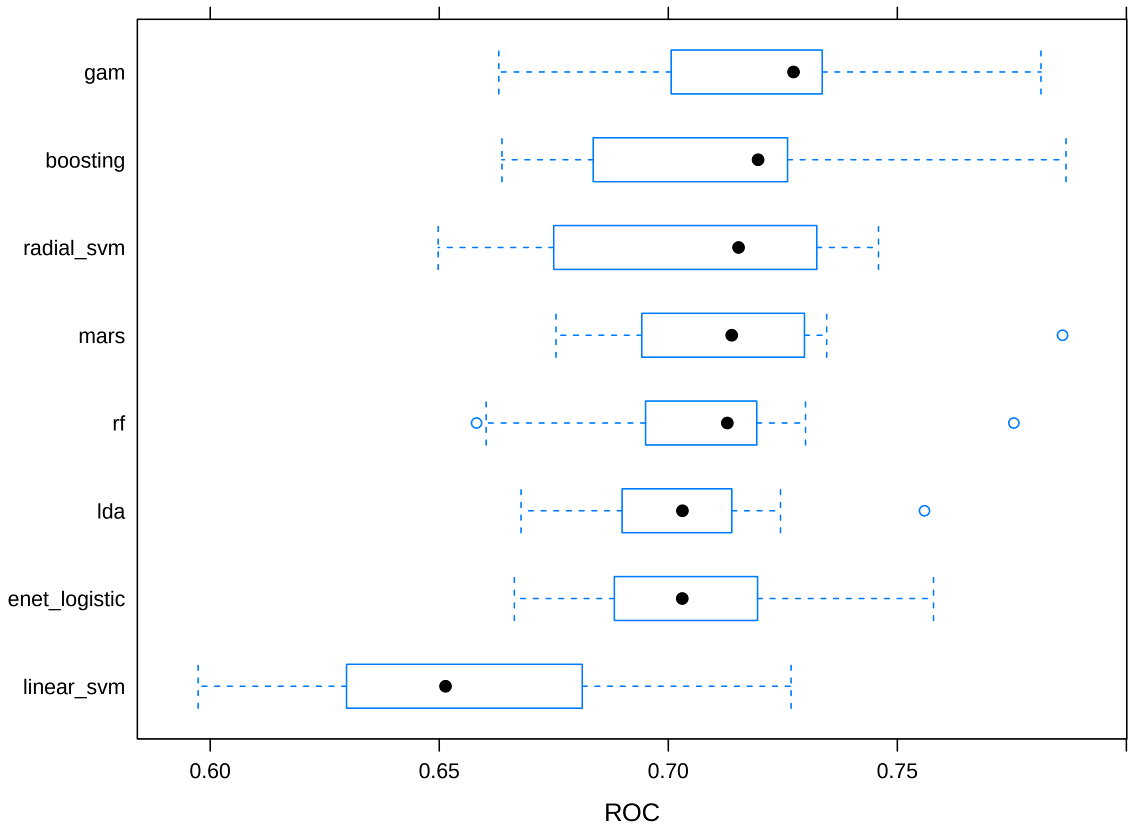
```r
resamp_class <- resamples(list(enet_logistic = model.glmn,
                         gam = model.gam,
                         mars = mars.fit,
                         lda = lda_model,
                         rf = rf_class_model,
                         boosting = gbmA.fit,
                         linear_svm = svml.fit,
                         radial_svm = svmr.fit))
stopCluster(cl)
registerDoSEQ()

summary(resamp_class)
```

```
##
## Call:
## summary.resamples(object = resamp_class)
##
## Models: enet_logistic, gam, mars, lda, rf, boosting, linear_svm, radial_svm
## Number of resamples: 10
##
## ROC
##                    Min.   1st Qu.    Median      Mean   3rd Qu.      Max. NA's
## enet_logistic 0.6663845 0.6916323 0.7030456 0.7056743 0.7172502 0.7578955    0
## gam           0.6629983 0.7008386 0.7273357 0.7181658 0.7329373 0.7813544    0
## mars          0.6754859 0.6981644 0.7138398 0.7158095 0.7261717 0.7860613    0
## lda           0.6678467 0.6923371 0.7030800 0.7045736 0.7133253 0.7559217    0
## rf            0.6581385 0.6979566 0.7128826 0.7088842 0.7190473 0.7754327    0
## boosting      0.6636805 0.6886796 0.7195946 0.7130213 0.7257773 0.7868205    0
## linear_svm    0.5973526 0.6325420 0.6513609 0.6564019 0.6793198 0.7267970    0
## radial_svm    0.6497614 0.6808119 0.7153345 0.7049381 0.7314020 0.7458827    0
##
## Sens
##                    Min.   1st Qu.    Median      Mean   3rd Qu.      Max. NA's
## enet_logistic 0.8882682 0.9016854 0.9299793 0.9236991 0.9410112 0.9606742    0
## gam           0.8651685 0.8867303 0.9157303 0.9130532 0.9353933 0.9606742    0
## mars          0.8820225 0.9007046 0.9073034 0.9124663 0.9186649 0.9606742    0
## lda           0.8932584 0.9073034 0.9271703 0.9270667 0.9438202 0.9662921    0
## rf            1.0000000 1.0000000 1.0000000 1.0000000 1.0000000 1.0000000    0
## boosting      0.9325843 0.9455307 0.9662921 0.9629810 0.9719101 0.9943820    0
## linear_svm    0.9831461 0.9943899 1.0000000 0.9955182 1.0000000 1.0000000    0
## radial_svm    0.8882682 0.9035136 0.9269663 0.9338271 0.9592697 0.9887640    0
##
## Spec
##                     Min.    1st Qu.    Median        Mean    3rd Qu.       Max.
## enet_logistic 0.17567568 0.18085894 0.2313032 0.217752684 0.24315068 0.27027027
## gam           0.20270270 0.21959459 0.2448167 0.268196964 0.32427805 0.36986301
## mars          0.17567568 0.21695668 0.2584228 0.270936690 0.33214550 0.36986301
## lda           0.12162162 0.17627730 0.2313032 0.211014439 0.24315068 0.27027027
## rf            0.00000000 0.00000000 0.0000000 0.000000000 0.00000000 0.00000000
## boosting      0.06756757 0.08820807 0.1095890 0.117049241 0.13217327 0.18918919
## linear_svm    0.00000000 0.00000000 0.0000000 0.009570529 0.02392632 0.02739726
## radial_svm    0.10958904 0.13231211 0.1891892 0.179563125 0.21283784 0.26027397
##               NA's
## enet_logistic    0
## gam                0
## mars               0
## lda                0
## rf                 0
## boosting           0
## linear_svm         0
## radial_svm         0
```

```
parallelplot(resamp_class, metric = "ROC")
```



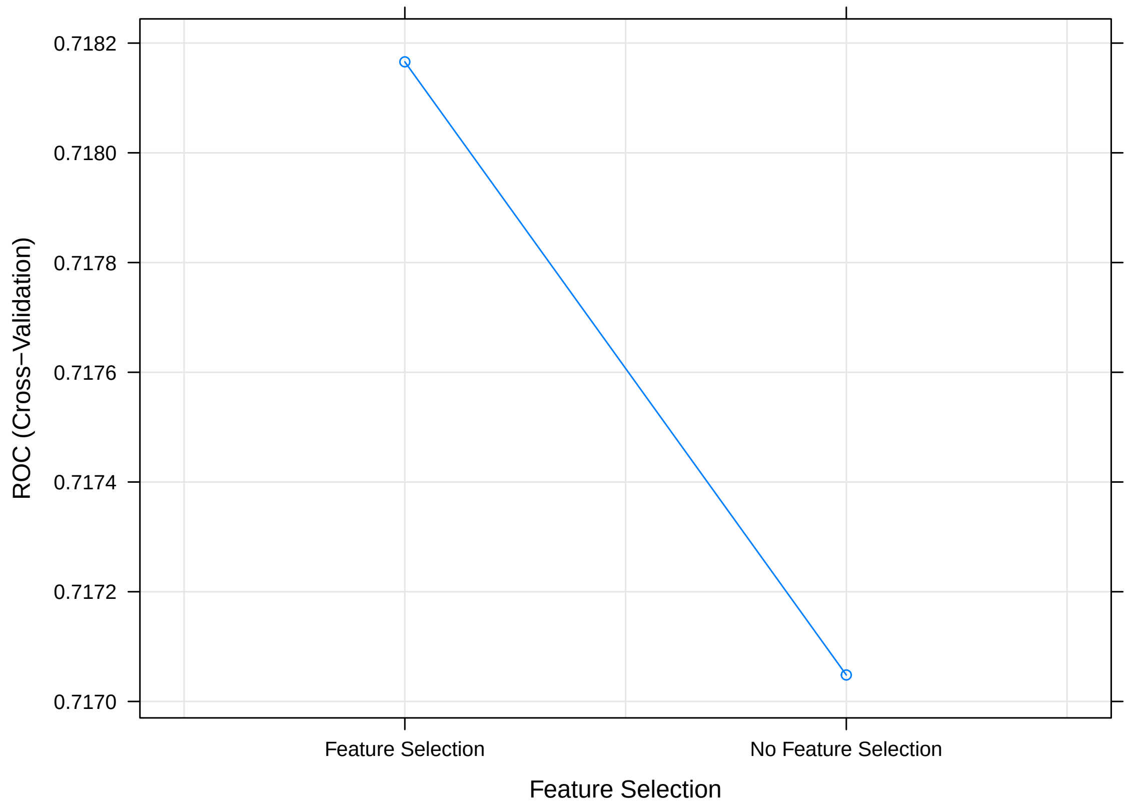
```
bwplot(resamp_class, metric = "ROC")
```



Final model for classification

```r
#feature selection or not
plot(model.gam)
```

GAM



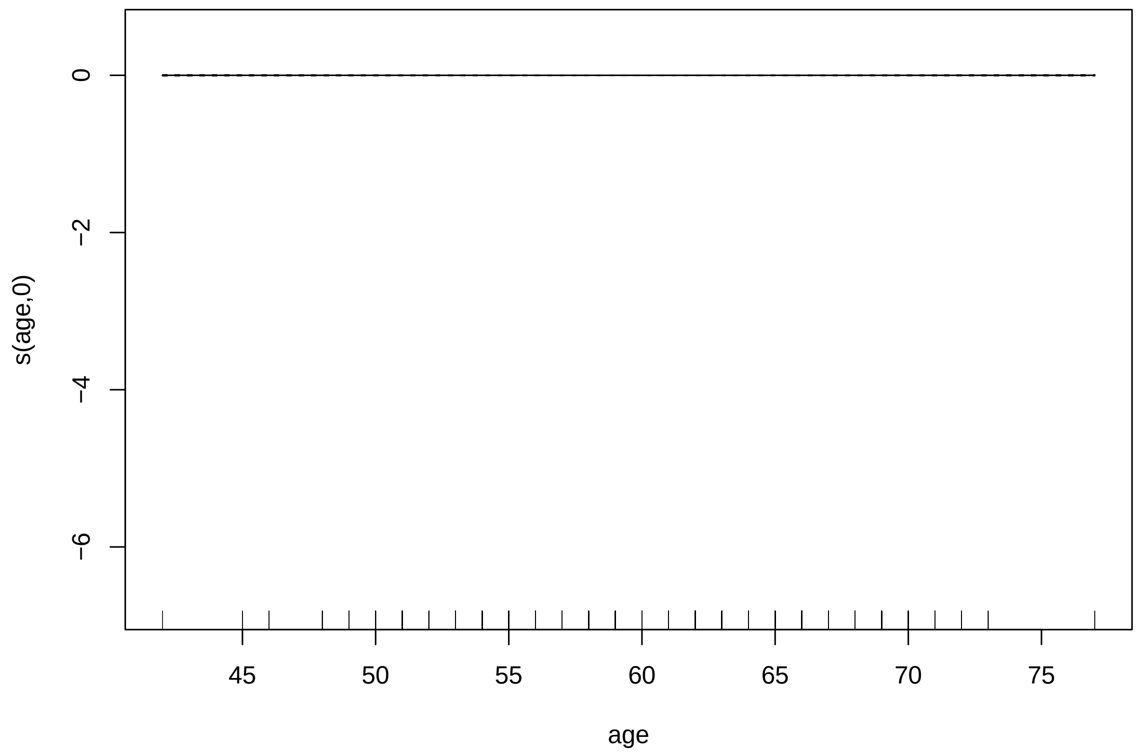
```r
#Formula and get the importance of each variable
summary(model.gam)
```

```
##
## Family: binomial
## Link function: logit
##
## Formula:
## .outcome ~ gender1 + race2 + race3 + race4 + smoking1 + smoking2 +
##     hypertension1 + diabetes1 + vaccine1 + severity1 + studyB +
##     studyC + s(age) + s(SBP) + s(LDL) + s(bmi) + s(height) +
##     s(weight)
##
## Parametric coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -2.07377    0.18672 -11.106  < 2e-16 ***
## gender1        0.47457    0.09509   4.991 6.01e-07 ***
## race2          0.04810    0.21813   0.221 0.825460
## race3         -0.06047    0.12015  -0.503 0.614738
## race4          0.07020    0.16087   0.436 0.662543
## smoking1      -0.33680    0.10828  -3.111 0.001867 **
## smoking2      -0.50352    0.16203  -3.108 0.001886 **
## hypertension1 -0.34676    0.20422  -1.698 0.089510 .
## diabetes1     -0.07480    0.12929  -0.579 0.562881
## vaccine1       0.69695    0.10061   6.927 4.29e-12 ***
## severity1     -0.61790    0.16782  -3.682 0.000232 ***
## studyB         1.18222    0.13684   8.639  < 2e-16 ***
## studyC         0.01115    0.17630   0.063 0.949592
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                 edf Ref.df Chi.sq p-value
## s(age)    1.899e-04      9  0.000  0.4443
## s(SBP)    3.090e+00      9  3.726  0.2920
## s(LDL)    1.982e-01      9  0.253  0.2577
## s(bmi)    3.872e+00      9 70.254  <2e-16 ***
## s(height) 1.981e+00      9  5.539  0.0416 *
## s(weight) 9.215e-05      9  0.000  0.9019
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.131   Deviance explained = 12.4%
## UBRE = 0.076042  Scale est. = 1         n = 2517
```

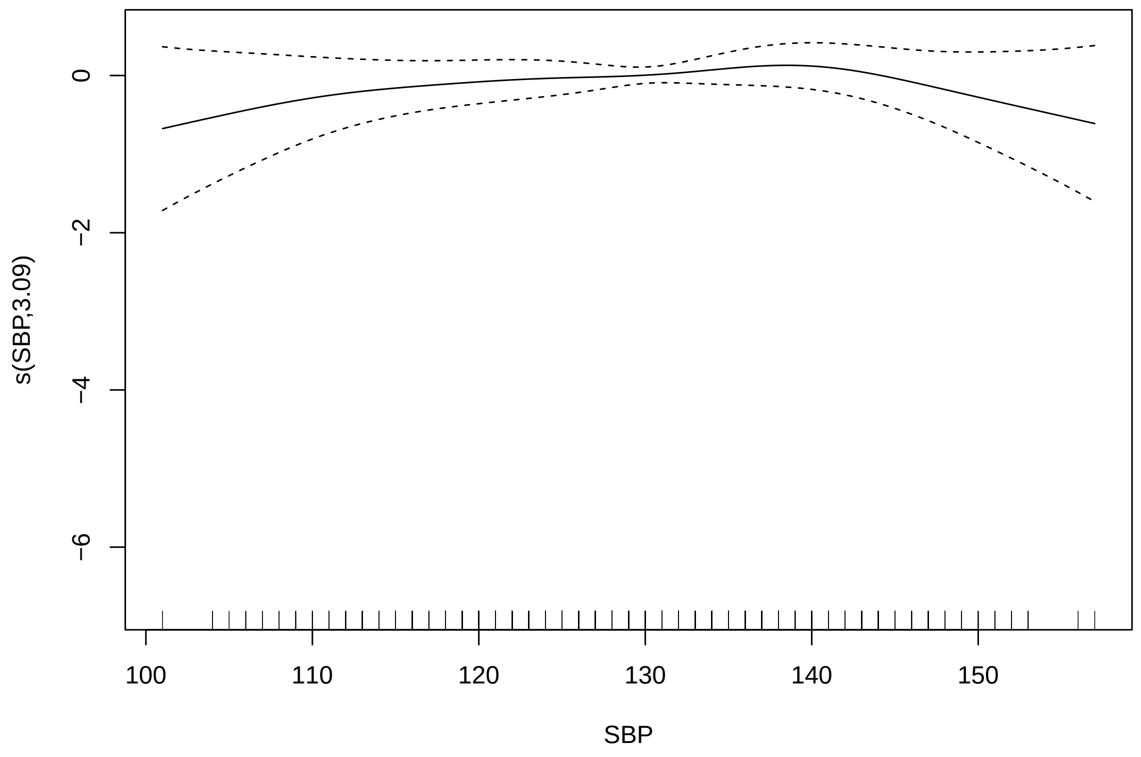
```
#degrees of freedom
model.gam$finalModel
```

```
##
## Family: binomial
## Link function: logit
##
## Formula:
## .outcome ~ gender1 + race2 + 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:
## 0.0002 3.0898 0.1982 3.8717 1.9808 0.0001  total = 22.14
##
## UBRE score: 0.07604226
```

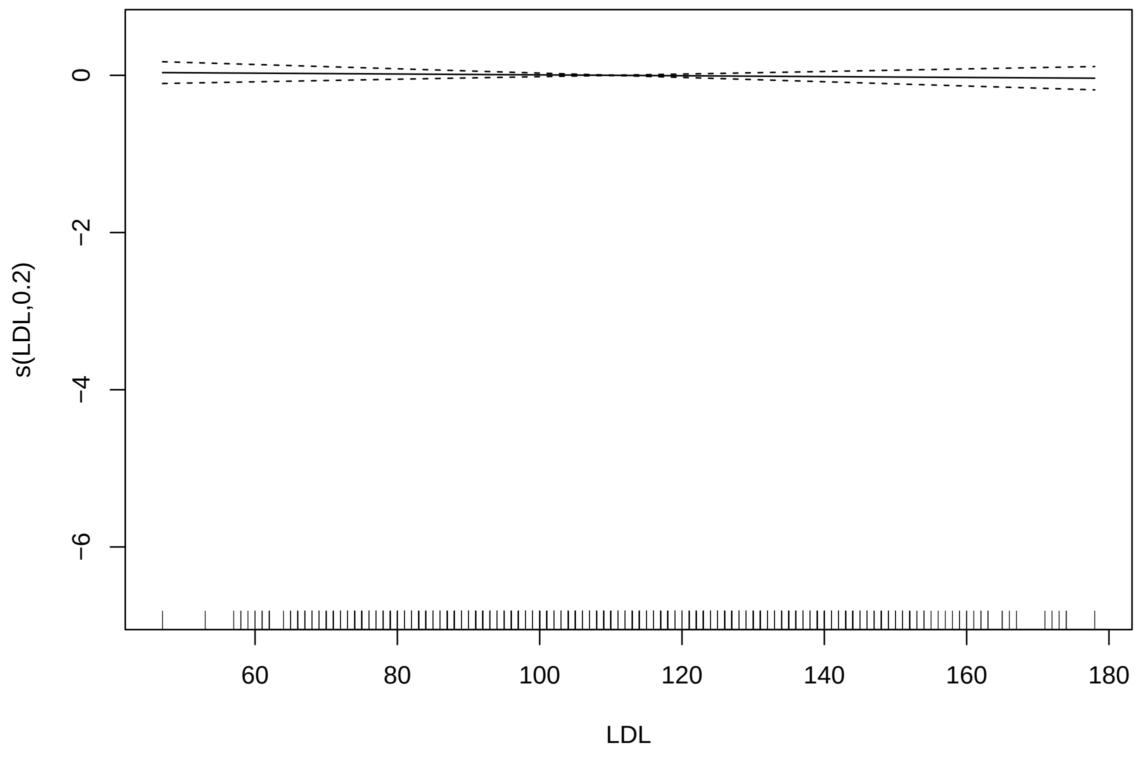
```
#discover age and recovery time, df = 0.0002
plot(model.gam$finalModel, select = 1)
```



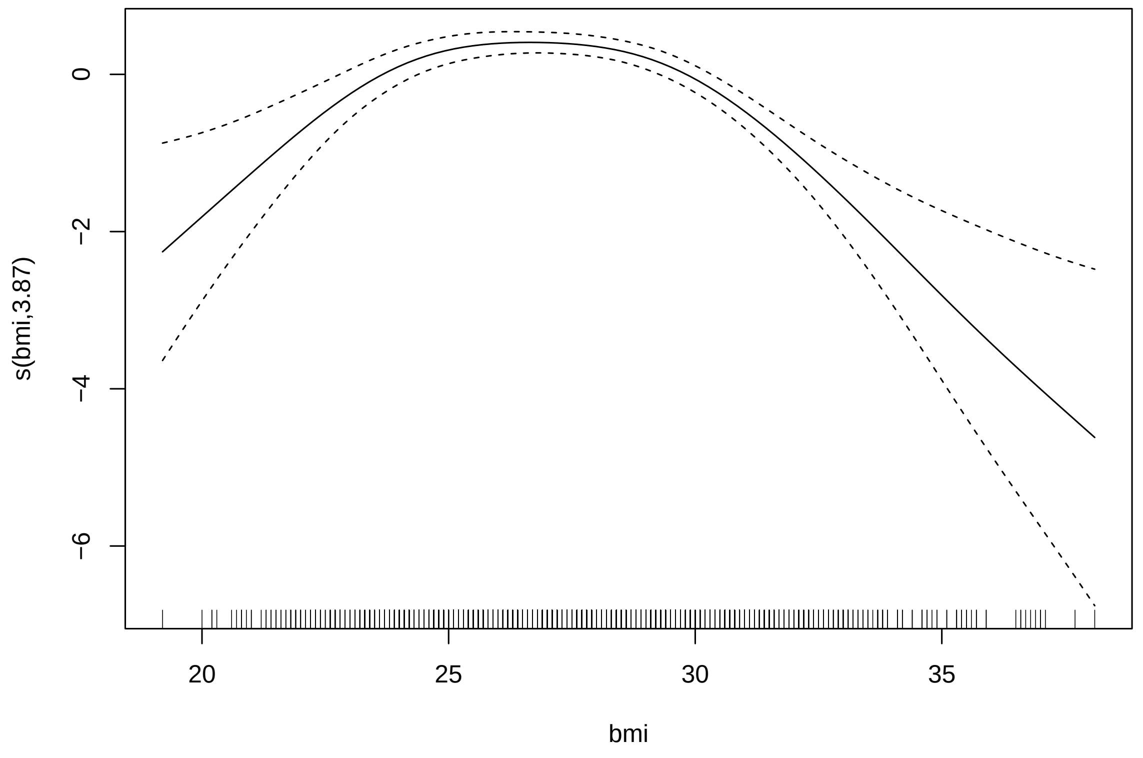
```
#discover sbp and recovery time
plot(model.gam$finalModel, select = 2)
```



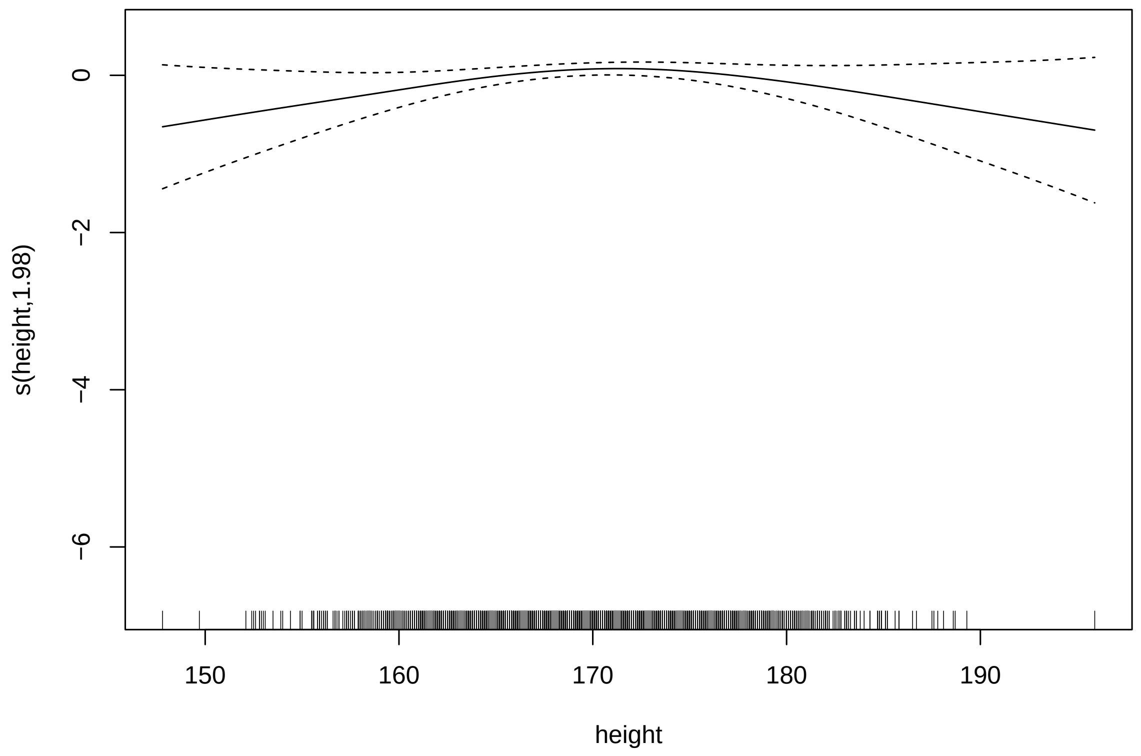
```
#discover ldl and recovery time
plot(model.gam$finalModel, select = 3)
```



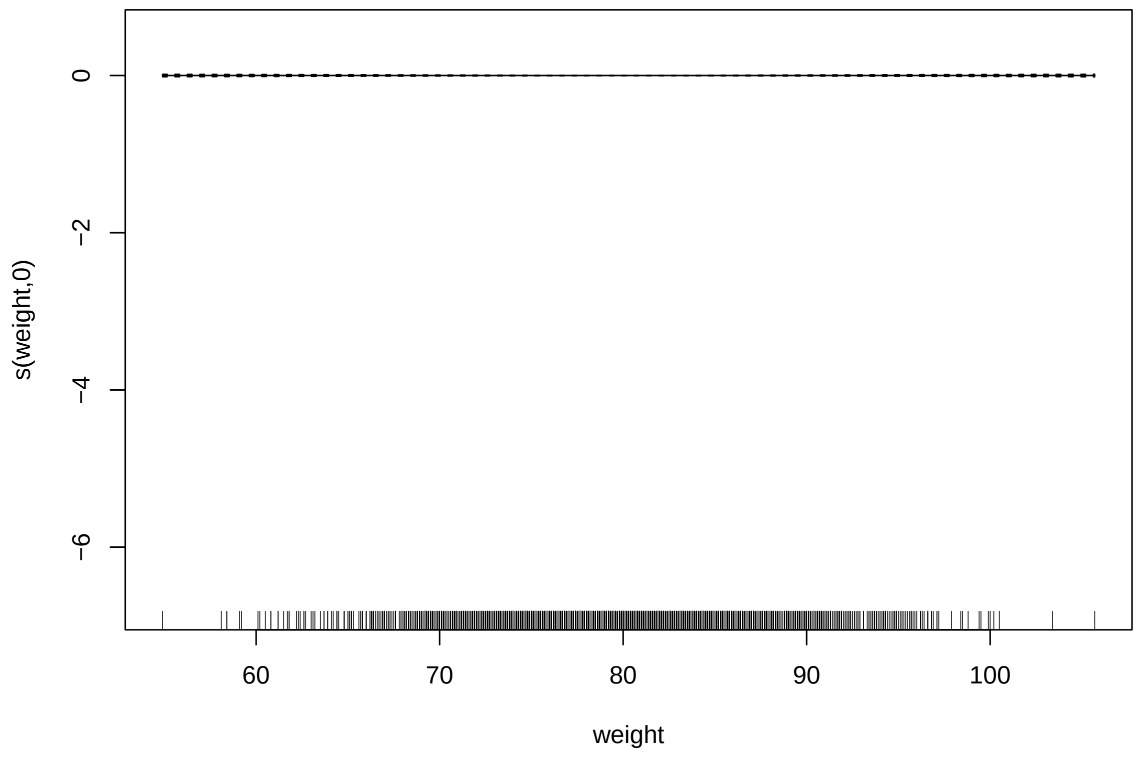
```r
#discover bmi and recovery time
plot(model.gam$finalModel, select = 4)
```



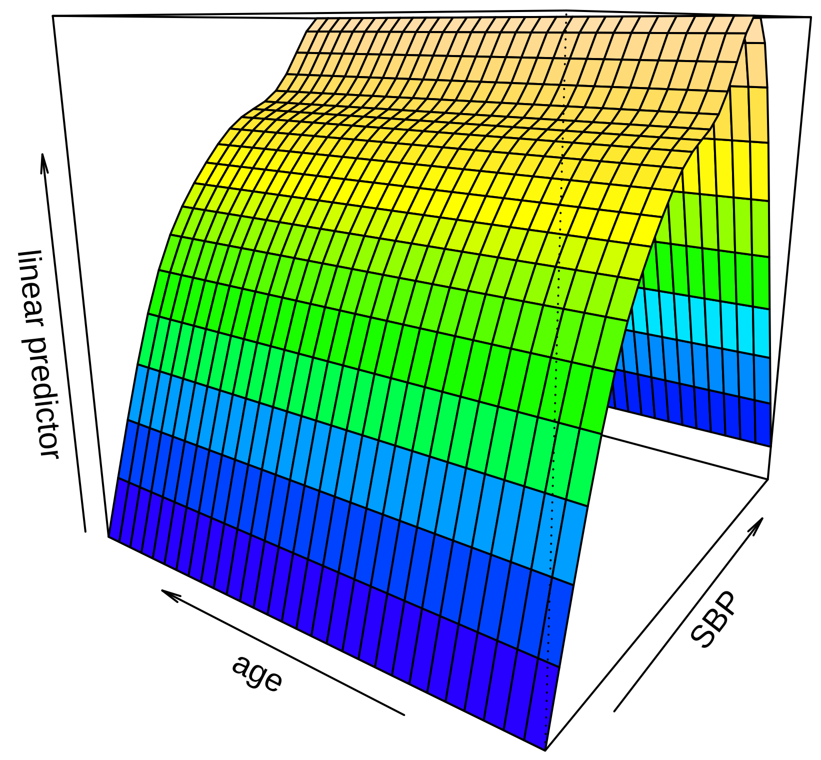
```r
#discover height and recovery time
plot(model.gam$finalModel, select = 5)
```



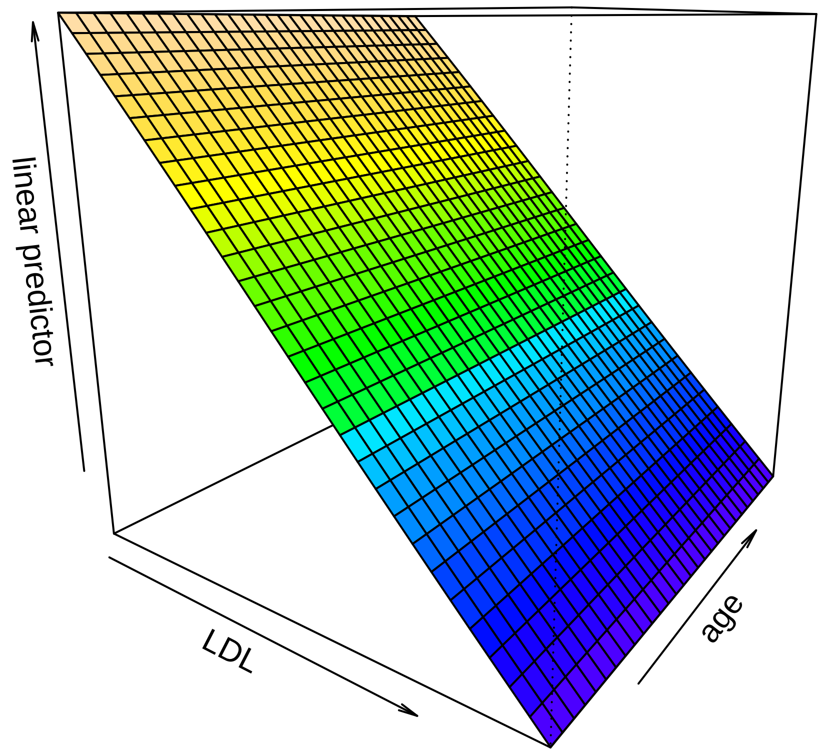
```r
#discover weight and recovery time, df = 0.0001
plot(model.gam$finalModel, select = 6)
```



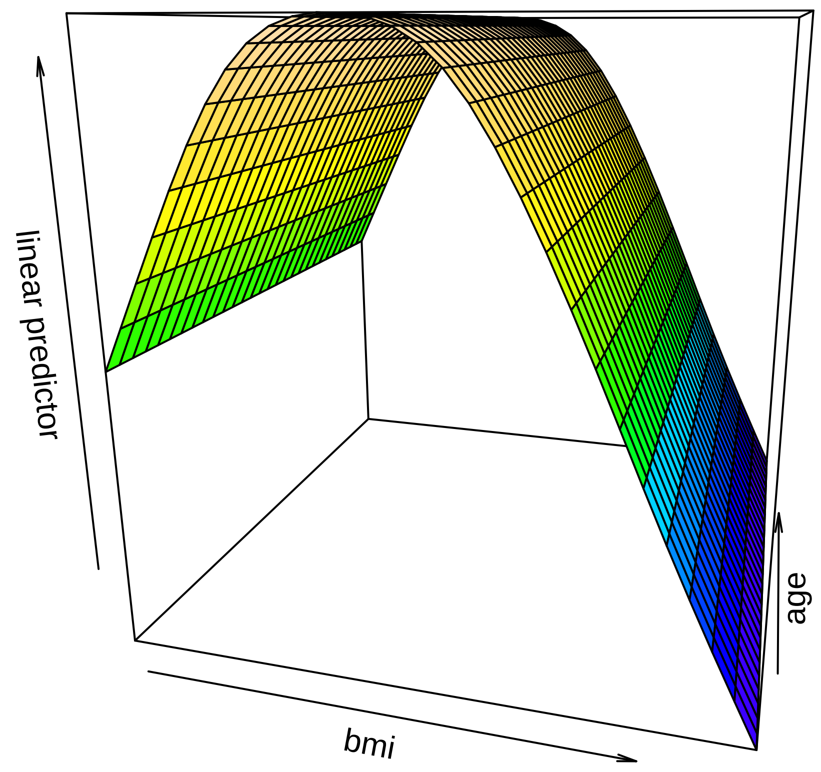
```r
#can also visualize the pairwise relation:
vis.gam(model.gam$finalModel, view=c("SBP","age"), color = "topo", theta = -55)
```



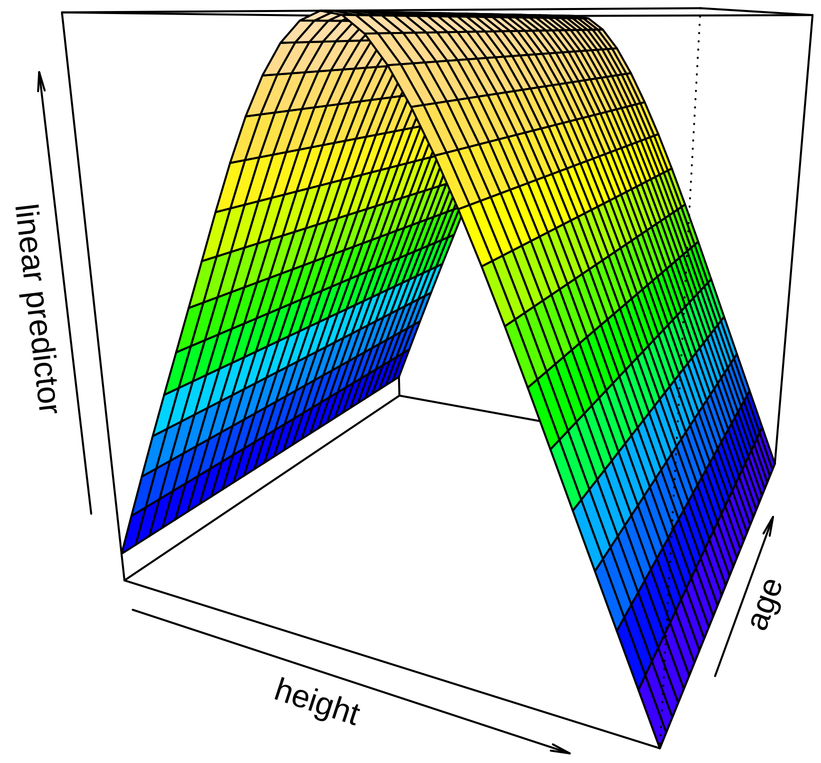
```
vis.gam(model.gam$finalModel, view=c("LDL","age"), color = "topo",  theta = 35)
```



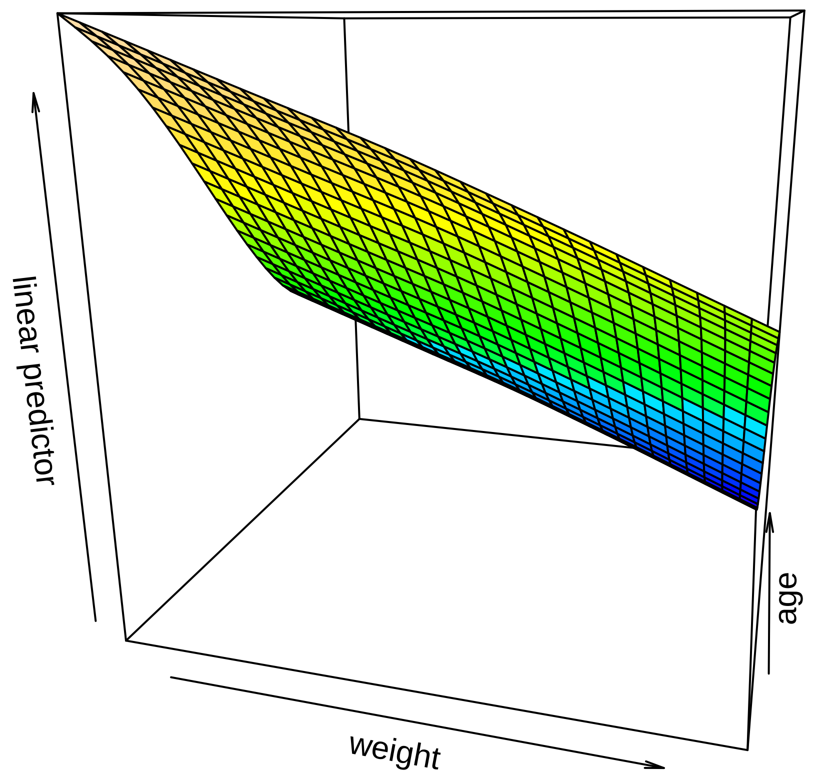
```
vis.gam(model.gam$finalModel, view=c("bmi","age"), color = "topo",  theta = 15)
```



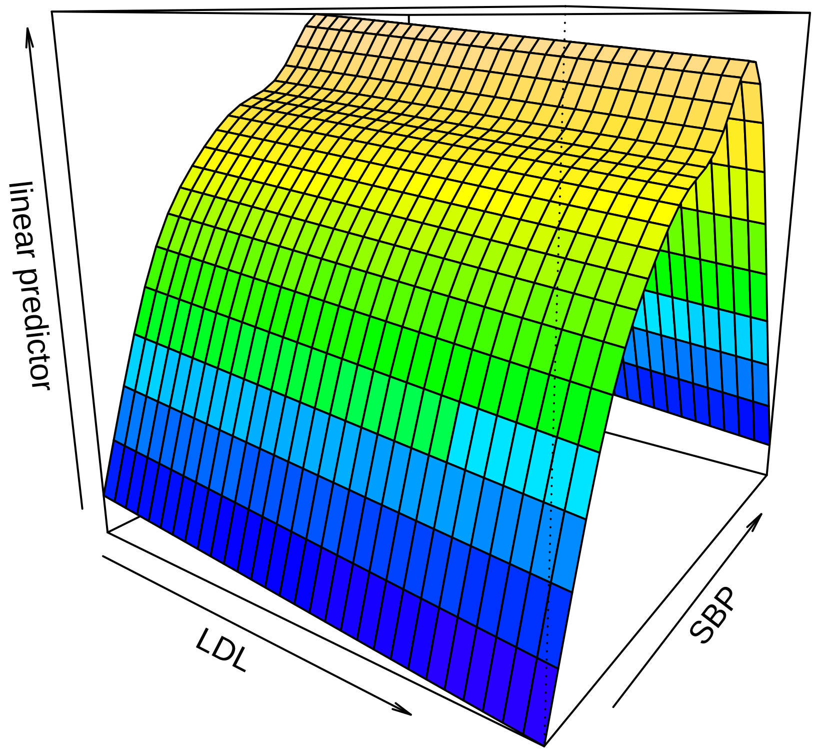
```
vis.gam(model.gam$finalModel, view=c("height","age"), color = "topo",  theta = 25)
```



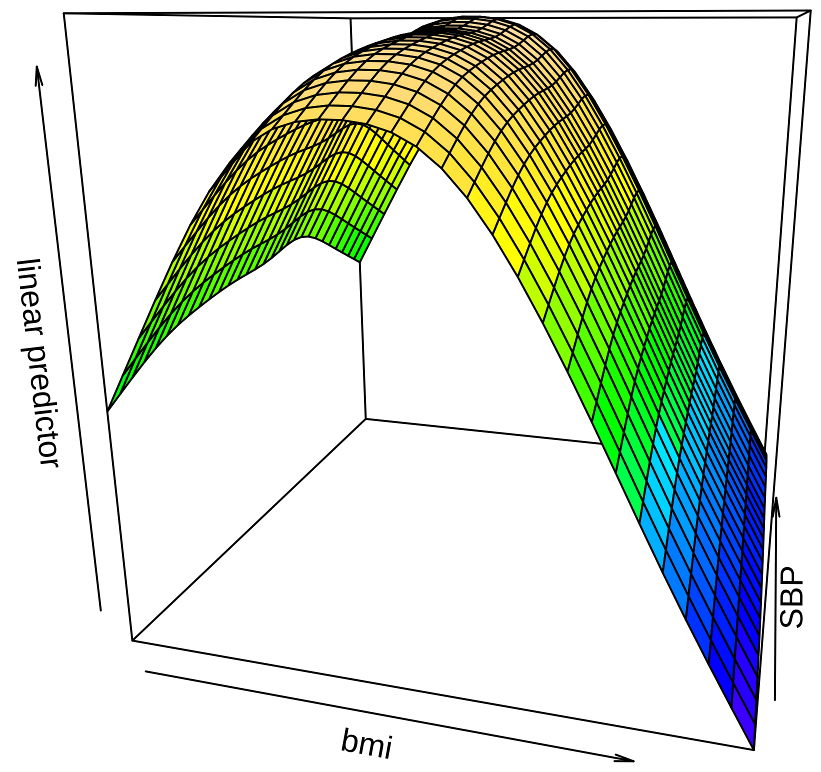
```
vis.gam(model.gam$finalModel, view=c("weight","age"), color = "topo",  theta = 15)
```



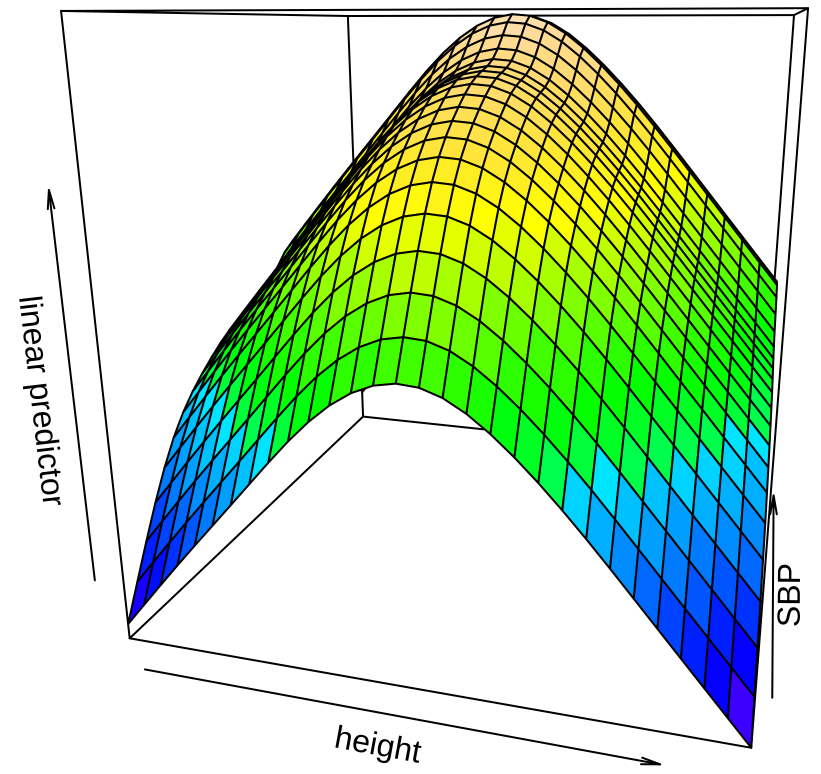
```
vis.gam(model.gam$finalModel, view=c("LDL","SBP"), color = "topo",  theta = 35)
```



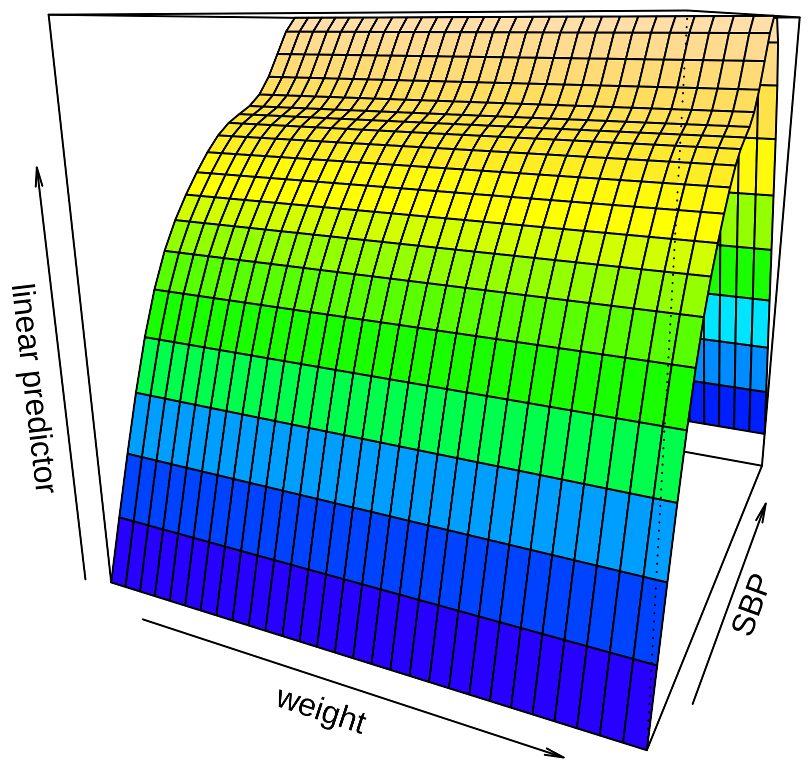
```
vis.gam(model.gam$finalModel, view=c("bmi","SBP"), color = "topo",  theta = 15)
```



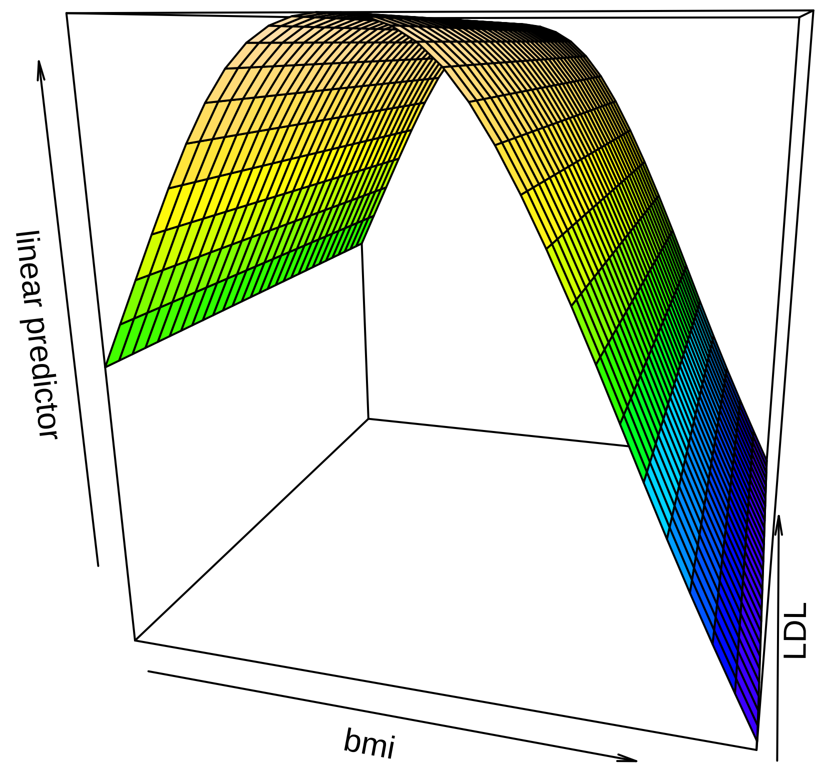
```r
vis.gam(model.gam$finalModel, view=c("height","SBP"), color = "topo",  theta = 15)
```



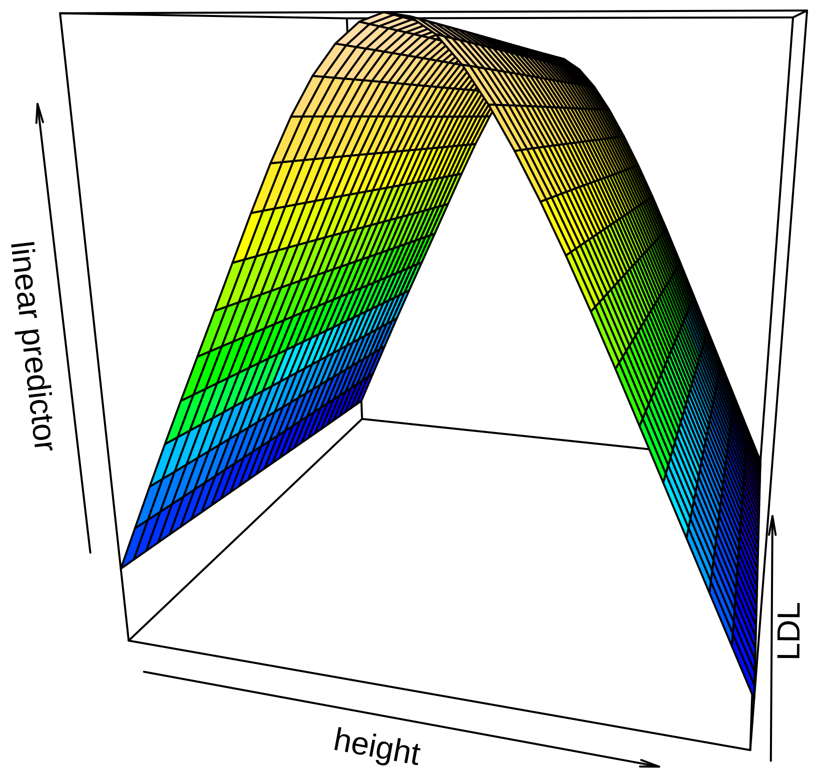
```r
vis.gam(model.gam$finalModel, view=c("weight","SBP"), color = "topo",  theta = 25)
```



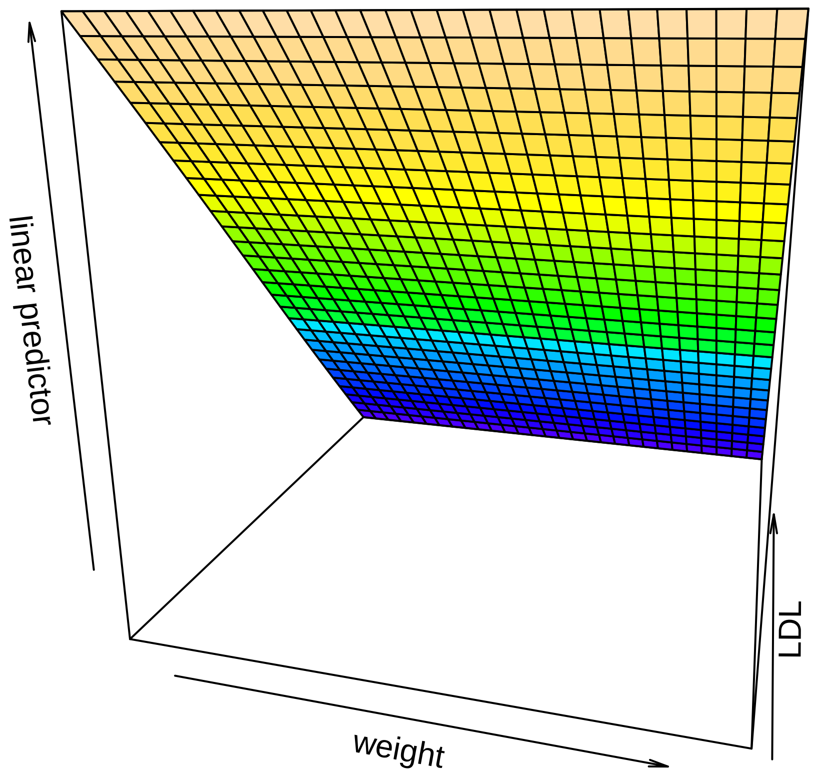
```
vis.gam(model.gam$finalModel, view=c("bmi","LDL"), color = "topo",  theta = 15)
```



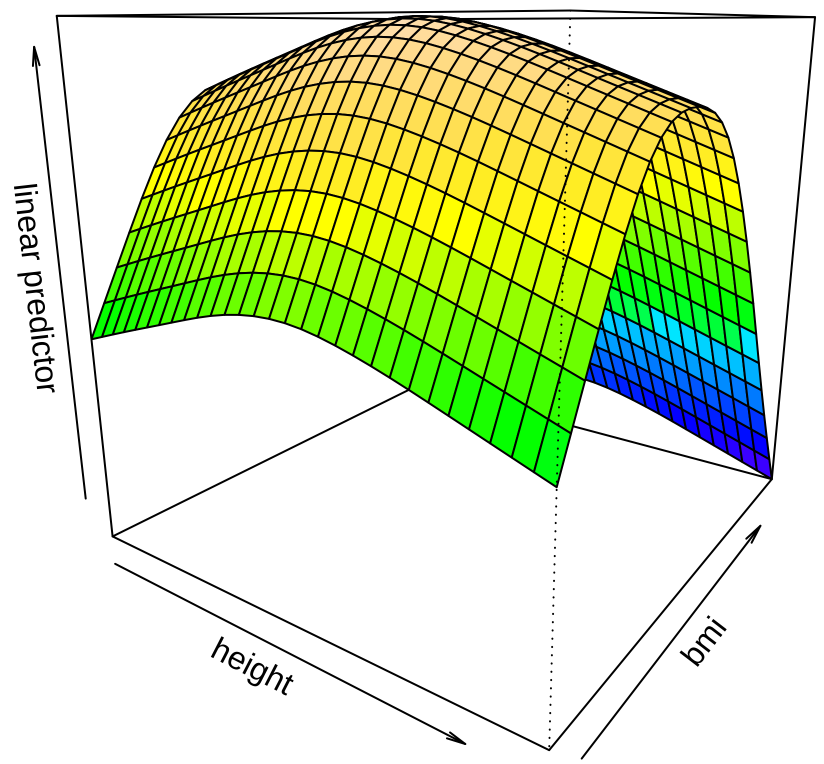
```
vis.gam(model.gam$finalModel, view=c("height","LDL"), color = "topo",  theta = 15)
```



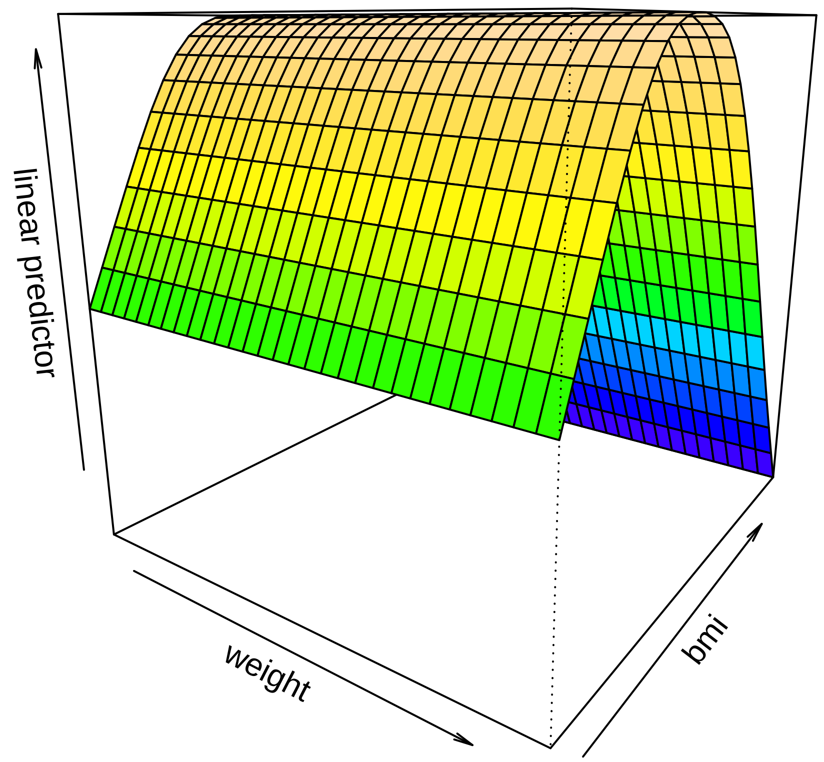
```r
vis.gam(model.gam$finalModel, view=c("weight","LDL"), color = "topo",  theta = 15)
```



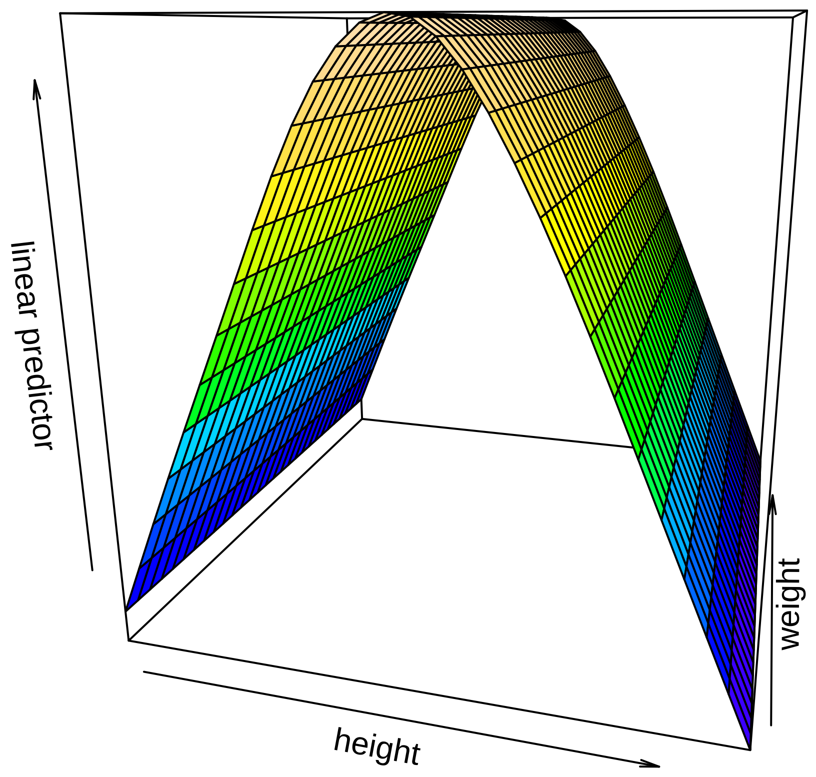
```r
vis.gam(model.gam$finalModel, view=c("height","bmi"), color = "topo",  theta = 35)
```



```
vis.gam(model.gam$finalModel, view=c("weight","bmi"), color = "topo",  theta = 35)
```



```
vis.gam(model.gam$finalModel, view=c("height","weight"), color = "topo",  theta = 15)
```


linear predictor
height
weight