

# P8106 Final Project: Predicting COVID-19 Recovery Time and Identifying Significant Risk Factors

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# Background

[Check the report]

## Data:

[Description check the report]

```
# For primary analysis:
# Dataset Loading:
load("data/recovery.Rdata")

set.seed(3521) # Runze Cui's uni(2183):
# Create a first random sample of 2000 participants:
dat1 <- dat[sample(1:10000, 2000),]

set.seed(3555) # Yuchen Hua's uni(3555)
# Create a second random sample of 2000 participants:
dat2 <- dat[sample(1:10000, 2000),]

# Merged the two datasets and remove repeated observations:
dat <- unique(rbind(dat1, dat2))

# Get rid of the id variable from the merged dataset and do the data cleaning:
dat <- dat %>%
  select(-id) %>%
  mutate(gender = as.factor(gender)) %>%
  mutate(race = as.factor(race)) %>%
  mutate(smoking = as.factor(smoking)) %>%
  mutate(hypertension = as.factor(hypertension)) %>%
  mutate(diabetes = as.factor(diabetes)) %>%
  mutate(vaccine = as.factor(vaccine)) %>%
  mutate(severity = as.factor(severity)) %>%
  mutate(study = as.factor(study)) %>%
  na.omit() %>%
  relocate(recovery_time)

head(dat)
```

	recovery_time	age	gender	race	smoking	height	weight	bmi	hypertension
## 8158	52	61	0	1	1	169.9	87.6	30.4	0
## 3387	24	60	1	1	2	173.4	70.6	23.5	0
## 1709	36	60	1	1	1	178.2	79.9	25.1	0
## 4051	23	70	1	4	0	167.4	77.7	27.7	1
## 954	24	63	1	4	0	175.4	88.7	28.8	1
## 531	36	65	0	1	0	160.4	74.4	28.9	1
	diabetes	SBP	LDL	vaccine	severity	study			
## 8158	0	118	103	0	0	C			
## 3387	0	129	101	1	0	B			
## 1709	0	130	107	1	0	A			
## 4051	0	145	128	1	0	B			
## 954	0	131	100	0	0	A			
## 531	0	137	153	1	0	A			

```

# Separate the data as training and test data:
set.seed(3521)
# Specify rows of training data:
trRows <- createDataPartition(dat$recovery_time, p = 0.7, list = FALSE)

# Training data:
training <- dat[trRows, ]
## Covariates' matrix:
x <- model.matrix(recovery_time ~ ., dat)[trRows, -1]
## Response's vector:
y <- dat$recovery_time[trRows]

# Test data:
test <- dat[-trRows, ]
## Covariates' matrix:
x2 <- model.matrix(recovery_time ~ ., dat)[-trRows, -1]
## Response's vector:
y2 <- dat$recovery_time[-trRows]

# For secondary analysis:
dat_2 <- dat %>%
  mutate(recovery_time = ifelse(recovery_time > 30, "great", "less")) %>%
  mutate(recovery_time = as.factor(recovery_time))

# Training data:
training_sec <- dat_2[trRows, ]
## Covariates' matrix:
x_sec <- model.matrix(recovery_time ~ ., dat_2)[trRows, -1]
## Response's vector:
y_sec <- dat_2$recovery_time[trRows]

# Test data:
test_sec <- dat_2[-trRows, ]
## Covariates' matrix:
x2_sec <- model.matrix(recovery_time ~ ., dat_2)[-trRows, -1]
## Response's vector:
y2_sec <- dat_2$recovery_time[-trRows]

```

## Exploratory Analysis and Data Visualization

[Description check the report]

### Exploratory Analysis

```

# Summary statistics for whole dataset:
summary(dat)

```

```
## recovery_time      age      gender  race      smoking      height
## Min.      : 2.00    Min.      :45.00    0:1847    1:2332    0:2191    Min.      :149.7
## 1st Qu.: 28.00    1st Qu.:57.00    1:1740    2: 174    1:1044    1st Qu.:165.9
## Median : 39.00    Median :60.00          3: 731    2: 352    Median :169.9
## Mean      : 43.27    Mean      :60.09          4: 350          Mean      :169.9
## 3rd Qu.: 50.00    3rd Qu.:63.00          3rd Qu.:173.9
## Max.      :365.00    Max.      :75.00          Max.      :189.6
##      weight      bmi      hypertension diabetes      SBP
## Min.      : 57.20    Min.      :18.80    0:1817          0:3045    Min.      :102.0
## 1st Qu.: 75.20    1st Qu.:25.80    1:1770          1: 542    1st Qu.:125.0
## Median : 80.00    Median :27.70          Median :130.0
## Mean      : 79.93    Mean      :27.74          Mean      :130.3
## 3rd Qu.: 84.70    3rd Qu.:29.50          3rd Qu.:136.0
## Max.      :105.70    Max.      :38.10          Max.      :158.0
##      LDL      vaccine severity study
## Min.      : 47.0    0:1413    0:3236    A: 737
## 1st Qu.: 97.0    1:2174    1: 351    B:2129
## Median :110.0          C: 721
## Mean      :110.2
## 3rd Qu.:124.0
## Max.      :178.0
# Summary tables separated by continuous/categorical variables:
skimr::skim(dat)
```

Table 1: Data summary

Name	dat
Number of rows	3587
Number of columns	15
Column type frequency:	
factor	8
numeric	7
Group variables	None

#### Variable type: factor

skim_variable	n_missing	complete_rate	ordered	n_unique	top_counts
gender	0	1	FALSE	2	0: 1847, 1: 1740
race	0	1	FALSE	4	1: 2332, 3: 731, 4: 350, 2: 174
smoking	0	1	FALSE	3	0: 2191, 1: 1044, 2: 352
hypertension	0	1	FALSE	2	0: 1817, 1: 1770
diabetes	0	1	FALSE	2	0: 3045, 1: 542
vaccine	0	1	FALSE	2	1: 2174, 0: 1413
severity	0	1	FALSE	2	0: 3236, 1: 351
study	0	1	FALSE	3	B: 2129, A: 737, C: 721

#### Variable type: numeric

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	p75	p100	hist
recovery_time	0	1	43.27	29.57	2.0	28.0	39.0	50.0	365.0	
age	0	1	60.09	4.48	45.0	57.0	60.0	63.0	75.0	
height	0	1	169.94	6.00	149.7	165.9	169.9	173.9	189.6	
weight	0	1	79.93	7.02	57.2	75.2	80.0	84.7	105.7	
bmi	0	1	27.74	2.77	18.8	25.8	27.7	29.5	38.1	
SBP	0	1	130.28	7.96	102.0	125.0	130.0	136.0	158.0	
LDL	0	1	110.16	19.75	47.0	97.0	110.0	124.0	178.0	

## Data Visualization

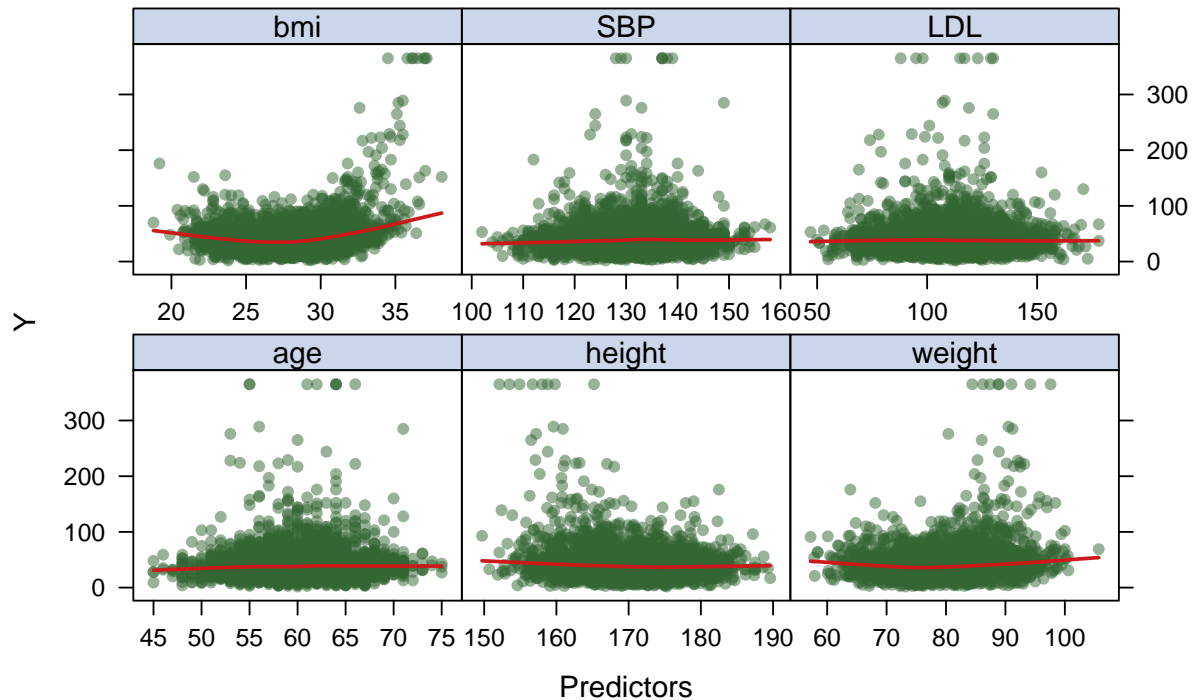
```

# For primary analysis:
## For continuous variables:
theme = trellis.par.get()
theme$plot.symbol$col = rgb(.2, .4, .2, .5)
theme$plot.symbol$pch = 16
theme$plot.line$col = rgb(.8, .1, .1, 1)
theme$plot.line$lwd = 2
theme$strip.background$col = rgb(.0, .2, .6, .2)
trellis.par.set(theme)

featurePlot(x = dat %>% dplyr::select(age, height, weight, bmi, SBP, LDL),
            y = dat$recovery_time,
            plot = "scatter",
            span = .5,
            labels = c("Predictors", "Y"),
            main = "Figure 1.1. Lattice Plots for Continuous Variables in Primary Analysis",
            type = c("p", "smooth"))

```

**Figure 1.1. Lattice Plots for Continuous Variables in Primary Analysis**



```
## For categorical variables:
gender_plot = dat %>%
  ggplot(aes(x = gender, y = recovery_time, fill = gender)) +
  geom_violin(color = "black", alpha = .5) +
  scale_x_discrete(labels = c('Female', 'Male')) +
  ylab("Recovery") +
  theme(legend.position = "none")

race_plot = dat %>%
  ggplot(aes(x = race, y = recovery_time, fill = race)) +
  geom_violin(color = "black", alpha = .5) +
  scale_x_discrete(labels = c('White', 'Asian', 'Black', 'Hispanic')) +
  ylab("Recovery") +
  theme(legend.position = "none")

smoking_plot = dat %>%
  ggplot(aes(x = smoking, y = recovery_time, fill = smoking)) +
  geom_violin(color = "black", alpha = .5) +
  scale_x_discrete(labels = c('Never smoked', 'Former smoker', 'Current smoker')) +
  ylab("Recovery") +
  theme(legend.position = "none")

hyper_plot = dat %>%
  ggplot(aes(x = hypertension, y = recovery_time, fill = hypertension)) +
  geom_violin(color = "black", alpha = .5) +
  ylab("Recovery") +
  scale_x_discrete(labels = c('No', 'Yes')) +
```

```

  theme(legend.position = "none")

diabetes_plot = dat %>%
  ggplot(aes(x = diabetes, y = recovery_time, fill = diabetes)) +
  geom_violin(color = "black", alpha = .5) +
  scale_x_discrete(labels = c('No', 'Yes')) +
  ylab("Recovery") +
  theme(legend.position = "none")

vac_plot = dat %>%
  ggplot(aes(x = vaccine, y = recovery_time, fill = vaccine)) +
  geom_violin(color = "black", alpha = .5) +
  scale_x_discrete(labels = c('Not vaccinated', 'Vaccinated')) +
  ylab("Recovery") +
  theme(legend.position = "none")

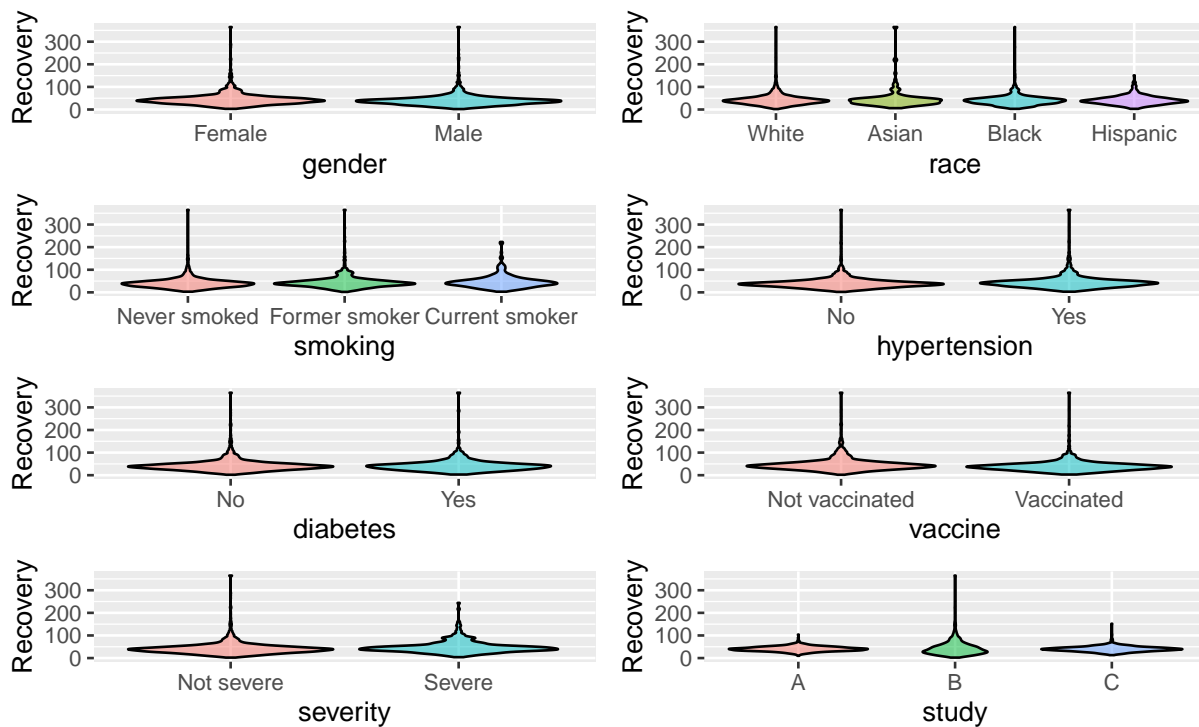
severity_plot = dat %>%
  ggplot(aes(x = severity, y = recovery_time, fill = severity)) +
  geom_violin(color = "black", alpha = .5) +
  scale_x_discrete(labels = c('Not severe', 'Severe')) +
  ylab("Recovery") +
  theme(legend.position = "none")

study_plot = dat %>%
  ggplot(aes(x = study, y = recovery_time, fill = study)) +
  geom_violin(color = "black", alpha = .5) +
  ylab("Recovery") +
  theme(legend.position = "none")

(gender_plot + race_plot + smoking_plot + hyper_plot) / (diabetes_plot + vac_plot + severity_plot + stu
plot_layout(guides = "collect") +
plot_annotation(title = "Figure 1.2. Violin Plots for Categorical Variables in Primary Analysis")

```

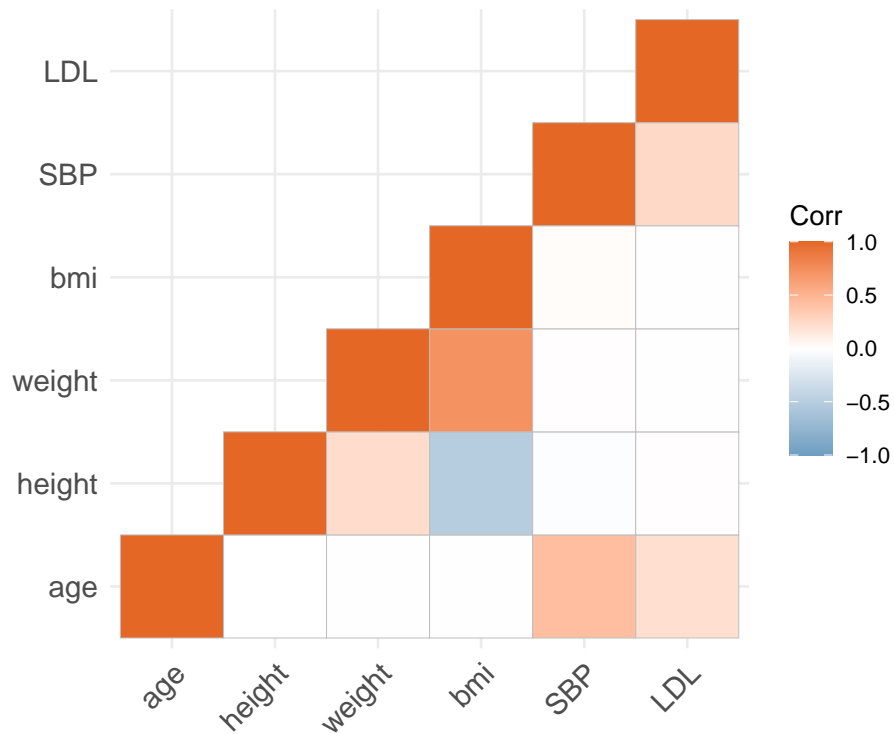
Figure 1.2. Violin Plots for Categorical Variables in Primary Analysis



```
## Correlation matrix for continuous variables ONLY:
model.matrix( ~ 0+., data = dat %>% dplyr::select(age, height, weight, bmi, SBP, LDL)) %>%
  cor(use = "pairwise.complete.obs") %>%
  ggcorrplot::ggcorrplot(show.diag = T,
                          type = "lower",
                          lab = F,
                          colors = c("#6D9EC1", "white", "#E46726")) +
  ggtitle("Figure 1.3. Correlation matrix for continuous datasat")
```



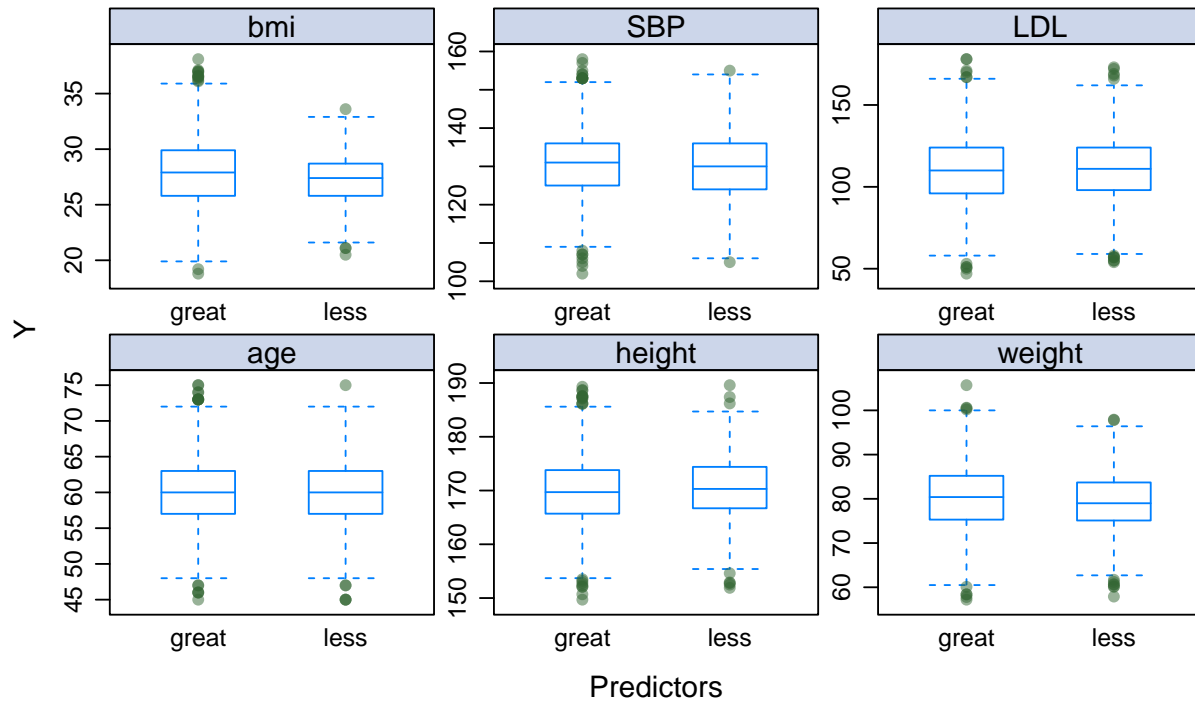
Figure 1.3. Correlation matrix for continuous dataset



```
# For secondary analysis:
## For continuous variables:
theme = trellis.par.get()
theme$plot.symbol$col = rgb(.2, .4, .2, .5)
theme$plot.symbol$pch = 16
theme$plot.line$col = rgb(.8, .1, .1, 1)
theme$plot.line$lwd = 2
theme$strip.background$col = rgb(.0, .2, .6, .2)
trellis.par.set(theme)

featurePlot(x = dat_2 %>% dplyr::select(age, height, weight, bmi, SBP, LDL),
            y = dat_2$recovery_time,
            plot = "box", pch = "|",
            scales = list(x = list(relation = "free"),
                          y = list(relation = "free")),
            labels = c("Predictors", "Y"),
            main = "Figure 1.4. Lattice Plots for Continuous Variables in Secondary Analysis",
            auto.key = list(columns = 2))
```

**Figure 1.4. Lattice Plots for Continuous Variables in Secondary Analysis**



```
## For categorical variables:
gender_plot_sec = dat_2 %>%
  ggplot(aes(x = gender, fill = recovery_time)) +
  geom_bar(color = "black", alpha = .5) +
  scale_x_discrete(labels = c('Female', 'Male')) +
  ylab("Recovery") +
  theme(legend.position = "none")

race_plot_sec = dat_2 %>%
  ggplot(aes(x = race, fill = recovery_time)) +
  geom_bar(color = "black", alpha = .5) +
  scale_x_discrete(labels = c('White', 'Asian', 'Black', 'Hispanic')) +
  ylab("Recovery") +
  theme(legend.position = "none")

smoking_plot_sec = dat_2 %>%
  ggplot(aes(x = smoking, fill = recovery_time)) +
  geom_bar(color = "black", alpha = .5) +
  scale_x_discrete(labels = c('Never smoked', 'Former smoker', 'Current smoker')) +
  ylab("Recovery") +
  theme(legend.position = "none")

hyper_plot_sec = dat_2 %>%
  ggplot(aes(x = hypertension, fill = recovery_time)) +
  geom_bar(color = "black", alpha = .5) +
  ylab("Recovery") +
  scale_x_discrete(labels = c('No', 'Yes')) +
```

```

theme(legend.position = "none")

diabetes_plot_sec = dat_2 %>%
  ggplot(aes(x = diabetes, fill = recovery_time)) +
  geom_bar(color = "black", alpha = .5) +
  scale_x_discrete(labels = c('No', 'Yes')) +
  ylab("Recovery") +
  theme(legend.position = "none")

vac_plot_sec = dat_2 %>%
  ggplot(aes(x = vaccine, fill = recovery_time)) +
  geom_bar(color = "black", alpha = .5) +
  scale_x_discrete(labels = c('Not vaccinated', 'Vaccinated')) +
  ylab("Recovery") +
  theme(legend.position = "none")

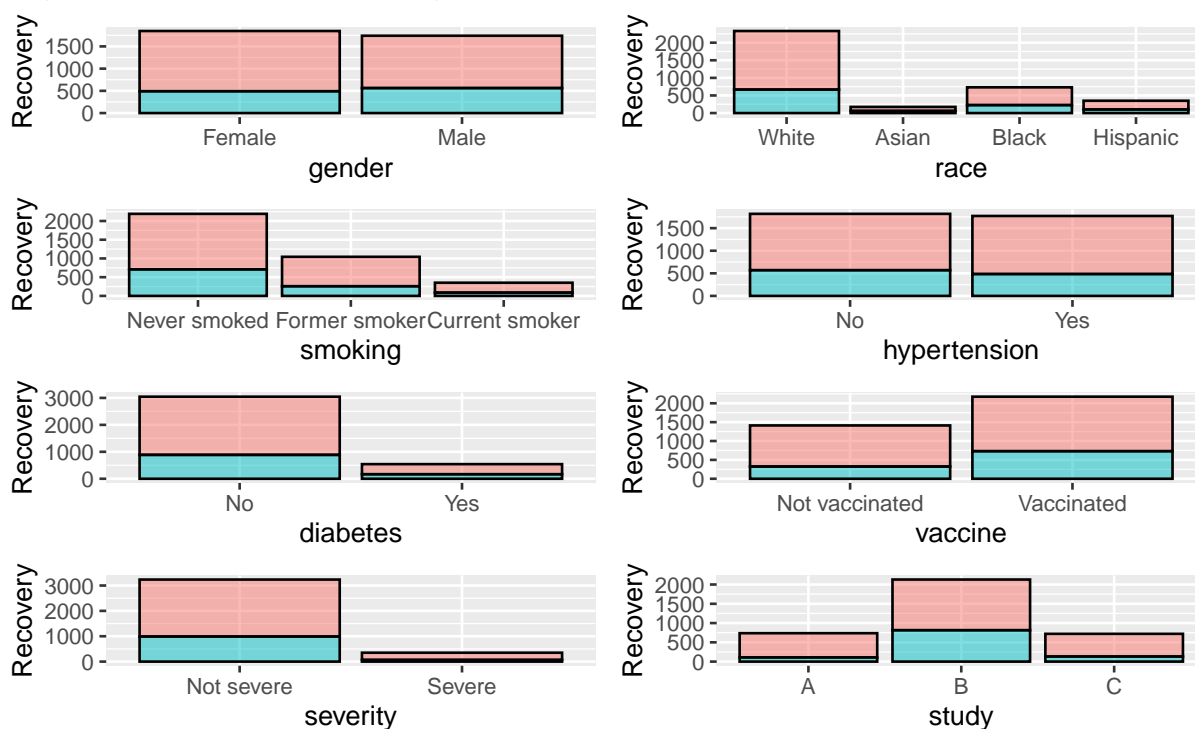
severity_plot_sec = dat_2 %>%
  ggplot(aes(x = severity, fill = recovery_time)) +
  geom_bar(color = "black", alpha = .5) +
  scale_x_discrete(labels = c('Not severe', 'Severe')) +
  ylab("Recovery") +
  theme(legend.position = "none")

study_plot_sec = dat_2 %>%
  ggplot(aes(x = study, fill = recovery_time)) +
  geom_bar(color = "black", alpha = .5) +
  ylab("Recovery") +
  theme(legend.position = "none")

(gender_plot_sec + race_plot_sec + smoking_plot_sec + hyper_plot_sec) / (diabetes_plot_sec + vac_plot_sec)
plot_layout(guides = "collect") +
plot_annotation(title = "Figure 1.5. Bar Plots for Categorical Variables in Secondary Analysis")

```

Figure 1.5. Bar Plots for Categorical Variables in Secondary Analysis



Note: Red is recovery time less than and equal to 30. Blue is greater than 30.

ctrl setting:

```
ctrl = trainControl(method = "repeatedcv", number = 10, repeats = 5)
ctrl1 = trainControl(method = "repeatedcv",
                     summaryFunction = twoClassSummary,
                     classProbs = TRUE)
```

## Primary Analysis

Recovery time as continuous variable.

### Linear methods:

Linear model:

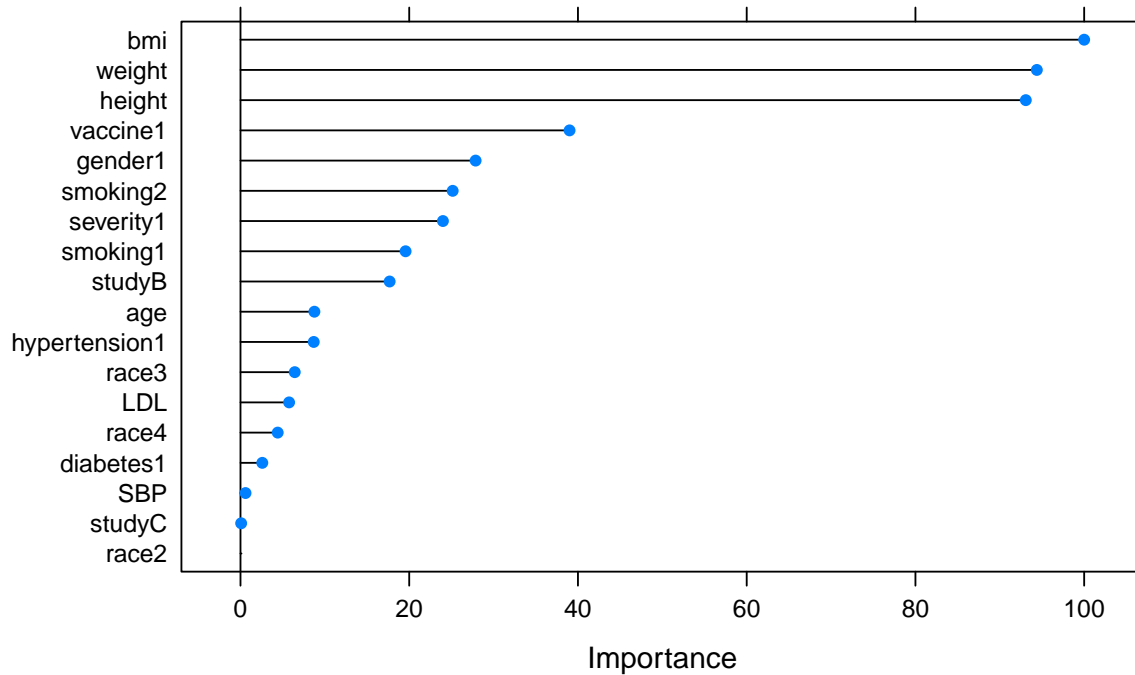
```
set.seed(3521)
# Fit a linear regression model:
lm = train(recovery_time ~ age + gender + race + smoking + height +
           weight + bmi + hypertension + diabetes + SBP +
           LDL + vaccine + severity + study,
           data = training, ## use training dataset
           method = "lm",
           trControl = ctrl)
```

```

summary(lm)
##
## Call:
## lm(formula = .outcome ~ ., data = dat)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -62.043 -13.881  -1.317   10.006  236.072
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -2.460e+03  1.398e+02 -17.598 < 2e-16 ***
## age          2.353e-01  1.205e-01   1.952 0.051045 .
## gender1     -5.201e+00  9.521e-01  -5.462 5.17e-08 ***
## race2        7.627e-01  2.226e+00   0.343 0.731920
## race3       -1.850e+00  1.214e+00  -1.524 0.127587
## race4       -1.890e+00  1.639e+00  -1.153 0.248913
## smoking1     4.200e+00  1.067e+00   3.938 8.46e-05 ***
## smoking2     8.195e+00  1.651e+00   4.963 7.43e-07 ***
## height       1.433e+01  8.213e-01  17.442 < 2e-16 ***
## weight      -1.541e+01  8.717e-01 -17.682 < 2e-16 ***
## bmi          4.676e+01  2.499e+00  18.713 < 2e-16 ***
## hypertension1 3.050e+00  1.574e+00   1.938 0.052794 .
## diabetes1    -1.085e+00  1.328e+00  -0.817 0.413725
## SBP          -4.700e-02  1.039e-01  -0.452 0.651026
## LDL          -3.455e-02  2.466e-02  -1.401 0.161337
## vaccine1     -7.333e+00  9.768e-01  -7.508 8.33e-14 ***
## severity1     7.807e+00  1.644e+00   4.750 2.15e-06 ***
## studyB        4.365e+00  1.216e+00   3.590 0.000337 ***
## studyC       -5.355e-01  1.499e+00  -0.357 0.720955
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 23.81 on 2494 degrees of freedom
## Multiple R-squared:  0.2355, Adjusted R-squared:  0.23
## F-statistic: 42.68 on 18 and 2494 DF,  p-value: < 2.2e-16
# Importances:
plot(varImp(lm, scale = TRUE), main = "Figure 2. Linear Model Variable's Importance Plot")

```

**Figure 2. Linear Model Variable's Importance Plot**



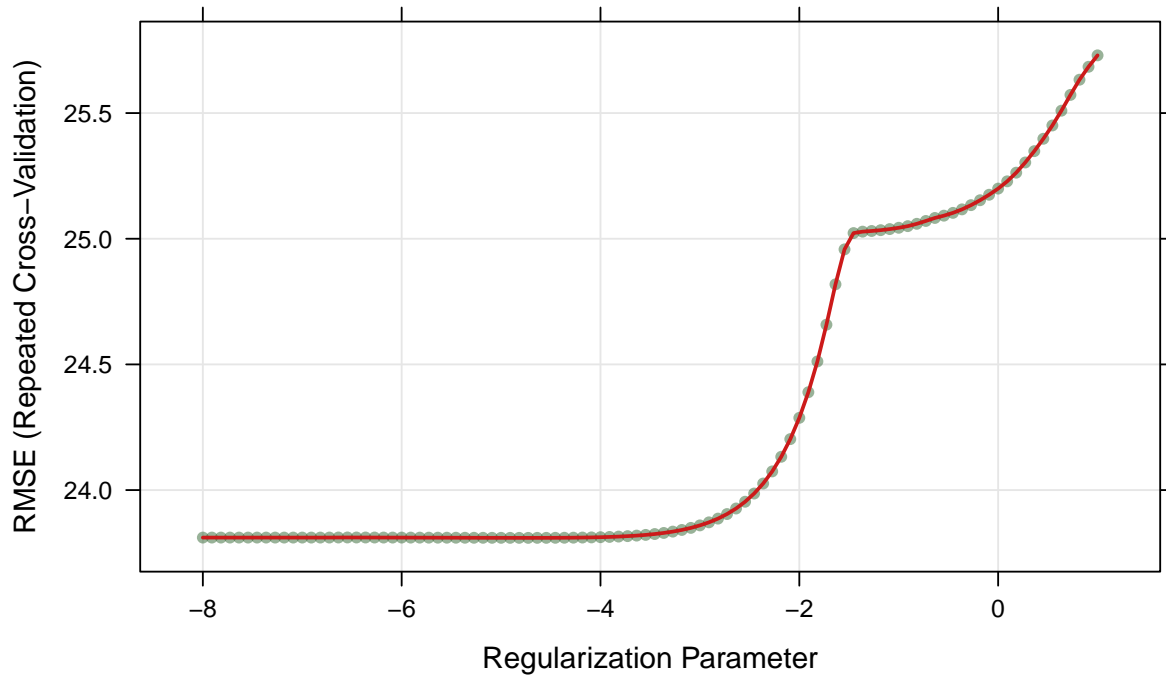
```
# Report the CV error:
lm$results$RMSE
## [1] 23.81421
# Report the test error:
lm_pred = predict(lm, newdata = test) ## Test dataset
lm_mse = sqrt(mean((lm_pred - y2)^2))
lm_mse
## [1] 29.06371
```

[Describe the outputs above]

**LASSO model:**

```
set.seed(3521)
# Fit a LASSO model:
lasso = train(x = x,
              y = y, ## training dataset
              method = "glmnet",
              tuneGrid = expand.grid(alpha = 1,
                                    lambda = exp(seq(-8, 1, length = 100))),
              trControl = ctrl)
# Plot for tuning parameter selection:
plot(lasso, xTrans = log, main = "Figure 3. LASSO Model CV RMSE Plot", highlight = T)
```

**Figure 3. LASSO Model CV RMSE Plot**



```
# Choose best tuning parameter value:
lasso$bestTune
##      alpha      lambda
## 37      1 0.008850576
# Report the coefficients after applying the best tuning parameter:
coef(lasso$finalModel, lasso$bestTune$lambda)
## 19 x 1 sparse Matrix of class "dgCMatrix"
##              s1
## (Intercept) -2.326105e+03
## age         2.302849e-01
## gender1     -5.174310e+00
## race2       6.917049e-01
## race3      -1.881002e+00
## race4      -1.852093e+00
## smoking1    4.170664e+00
## smoking2    8.130377e+00
## height     1.353195e+01
## weight     -1.457152e+01
## bmi        4.434163e+01
## hypertension1 2.956707e+00
## diabetes1   -1.028034e+00
## SBP        -3.873666e-02
## LDL        -3.421155e-02
## vaccine1   -7.301952e+00
## severity1   7.790966e+00
## studyB     4.368825e+00
## studyC     -4.916229e-01
```

```

# Report the CV error:
lasso$results[37, ]$RMSE
## [1] 23.80994
# Report the test error:
lasso_pred = predict(lasso, newdata = x2) ## Test dataset
lasso_mse = sqrt(mean((lasso_pred - y2)^2))
lasso_mse
## [1] 29.16892

```

[Describe the outputs above]

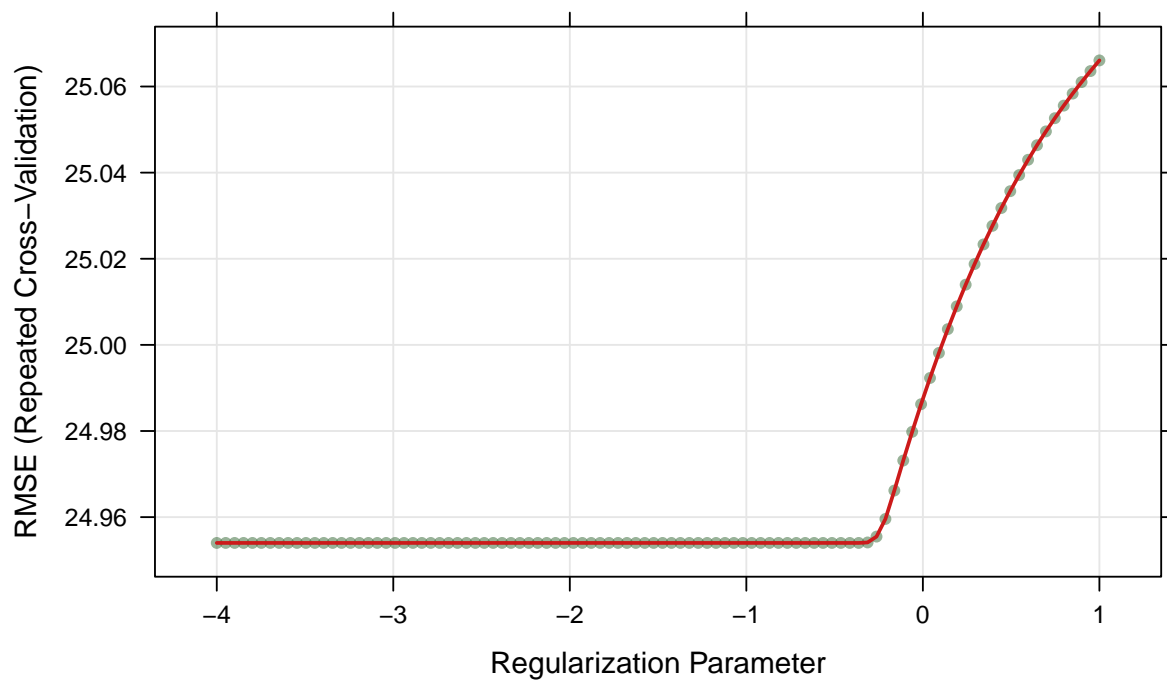
**Ridge model:**

```

set.seed(3521)
# Fit a ridge model:
ridge = train(x = x,
              y = y, ## training dataset
              method = "glmnet",
              tuneGrid = expand.grid(alpha = 0,
                                     lambda = exp(seq(-4, 1, length = 100))),
              trControl = ctrl)
# Plot for tuning parameter selection:
plot(ridge, xTrans = log, main = "Figure 4. Ridge Model CV RMSE Plot", highlight = T)

```

**Figure 4. Ridge Model CV RMSE Plot**





```

# Choose best tuning parameter value:
ridge$bestTune
##      alpha      lambda
## 73      0 0.6951439
# Report the coefficients after applying the best tuning parameter:
coef(ridge$finalModel, ridge$bestTune$lambda)
## 19 x 1 sparse Matrix of class "dgCMatrix"
##              s1
## (Intercept) -1.149931e+02
## age         2.064306e-01
## gender1     -4.932110e+00
## race2       1.218372e-01
## race3      -2.740022e+00
## race4      -1.799371e+00
## smoking1    4.007457e+00
## smoking2    7.504769e+00
## height     4.750406e-01
## weight     -6.857228e-01
## bmi        4.479836e+00
## hypertension1 2.800025e+00
## diabetes1   -4.992704e-01
## SBP        -2.006797e-04
## LDL        -3.530830e-02
## vaccine1   -6.887245e+00
## severity1   7.819336e+00
## studyB     4.395135e+00
## studyC     -2.104760e-01

# Report the CV error:
ridge$results[73, ]$RMSE
## [1] 24.95401
# Report the test error:
ridge_pred = predict(ridge, newdata = x2) ## Test dataset
ridge_mse = sqrt(mean((ridge_pred - y2)^2))
ridge_mse
## [1] 32.00583

```

[Describe the outputs above]

**Elastic net model:**

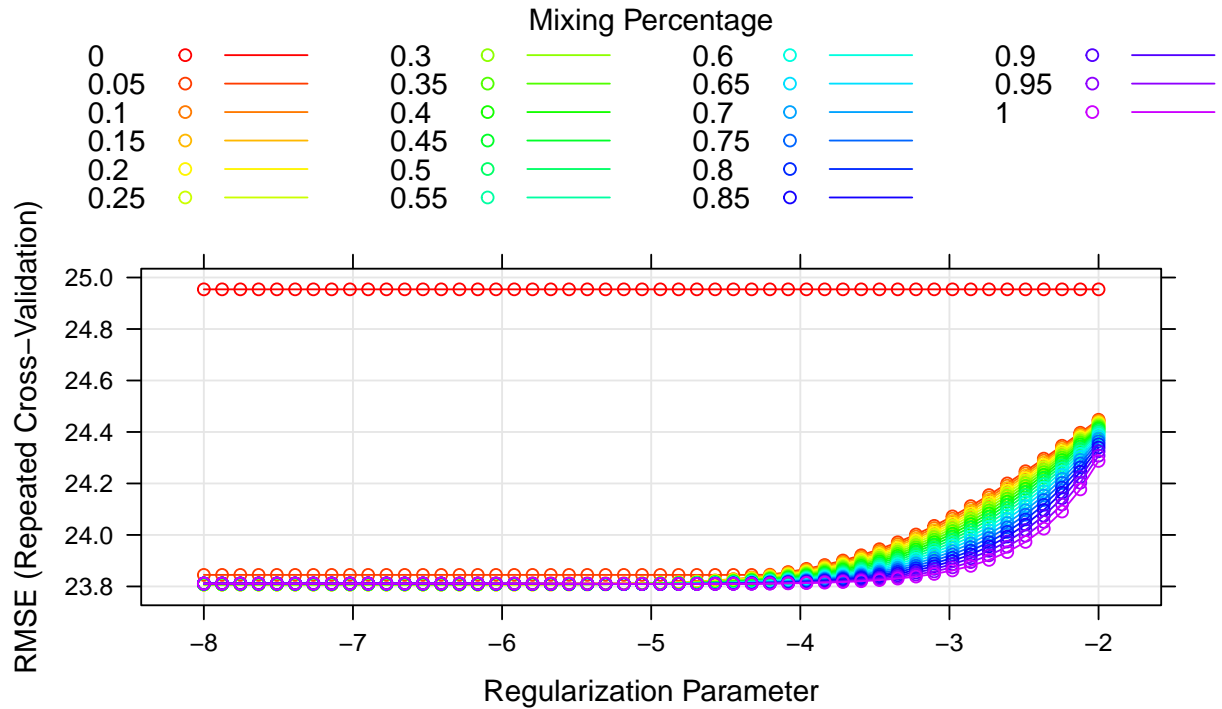
```

set.seed(3521)
# Fit a Elastic net model:
enet = train(x, y, ## training dataset
            method = "glmnet",
            tuneGrid = expand.grid(alpha = seq(0, 1, length = 21),
                                   lambda = exp(seq(-8, -2, length = 50))),
            trControl = ctrl)
# Plot for tuning parameters selection:
myCol = rainbow(25)
myPar = list(supерpose.symbol = list(col = myCol),

```

```
superpose.line = list(col = myCol))
plot(enet, par.settings = myPar, main = "Figure 5. Elastic Net Model CV RMSE Plot", xTrans = log)
```

**Figure 5. Elastic Net Model CV RMSE Plot**



```
# Choose best tuning parameter value:
enet$bestTune
##      alpha      lambda
## 220 0.2 0.003435924
# Report the coefficients after applying the best tuning parameter:
coef(enet$finalModel, enet$bestTune$lambda)
## 19 x 1 sparse Matrix of class "dgCMatrix"
##              s1
## (Intercept) -2.282729e+03
## age         2.333649e-01
## gender1     -5.189117e+00
## race2       7.082009e-01
## race3      -1.922687e+00
## race4      -1.886490e+00
## smoking1    4.193610e+00
## smoking2    8.158687e+00
## height     1.327902e+01
## weight     -1.430227e+01
## bmi        4.356889e+01
## hypertension1 3.037924e+00
## diabetes1   -1.039260e+00
## SBP        -4.372863e-02
## LDL        -3.464473e-02
## vaccine1   -7.312501e+00
```

```
## severity1      7.822090e+00
## studyB        4.381763e+00
## studyC        -4.985479e-01

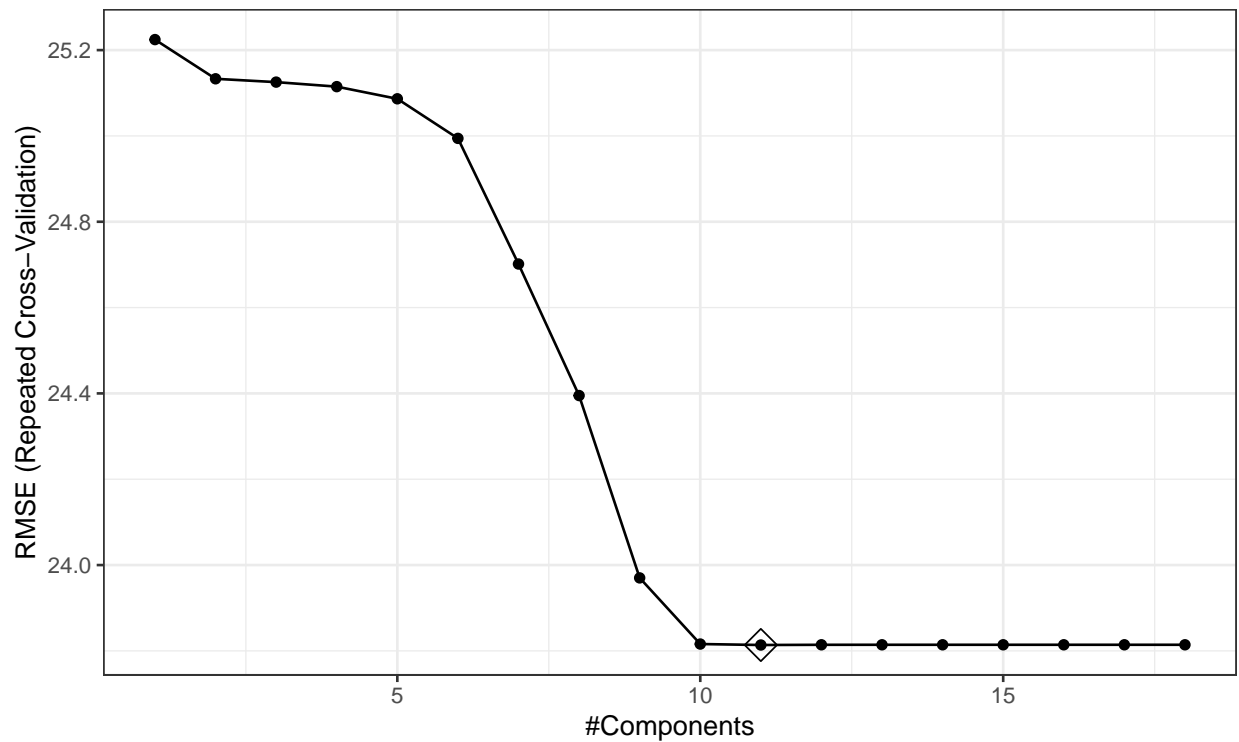
# Report the CV error:
enet$results[220, ]$RMSE
## [1] 23.80708
# Report the test error:
enet_pred = predict(enet, newdata = x2) ## Test dataset
enet_mse = sqrt(mean((enet_pred - y2)^2))
enet_mse
## [1] 29.20678
```

[Describe the outputs above]

Partial least squares model (PLS):

```
set.seed(3521)
# Fit a PLS model:
pls = train(x, y, ## training dataset
            method = "pls",
            tuneGrid = data.frame(ncomp = 1:18),
            trControl = ctrl,
            preprocess = c("center", "scale"))
summary(pls)
## Data:      X dimension: 2513 18
## Y dimension: 2513 1
## Fit method: oscorespls
## Number of components considered: 11
## TRAINING: % variance explained
##           1 comps  2 comps  3 comps  4 comps  5 comps  6 comps  7 comps
## X           9.44   16.31   26.35   31.00   35.86   41.51   45.81
## .outcome    12.45   13.46   13.57   13.71   13.99   14.69   16.91
##           8 comps  9 comps 10 comps 11 comps
## X           49.91   52.62   56.45   61.63
## .outcome    19.43   22.34   23.49   23.55
# Choose best tuning parameter value:
pls$bestTune
##      ncomp
## 11      11
# Plot for the number of components:
ggplot(pls, highlight = T) +
  theme_bw() +
  ggtitle("Figure 6. PLS Model CV RMSE Plot")
```

Figure 6. PLS Model CV RMSE Plot



```
# Report the CV error:
pls$results[11, ]$RMSE
## [1] 23.81368
# Report the test error:
pls_pred = predict(pls, newdata = x2) ## Test dataset
pls_mse = sqrt(mean((pls_pred - y2)^2))
pls_mse
## [1] 29.06252
```

[Describe the outputs above]

## Nonlinear Methods:

### Generalized additive model (GAM):

```
set.seed(3521)
# Fit a GAM model for all predictors:
gam = train(x, y, ## training dataset
            method = "gam",
            trControl = ctrl)
summary(gam)
##
## Family: gaussian
## Link function: identity
##
```

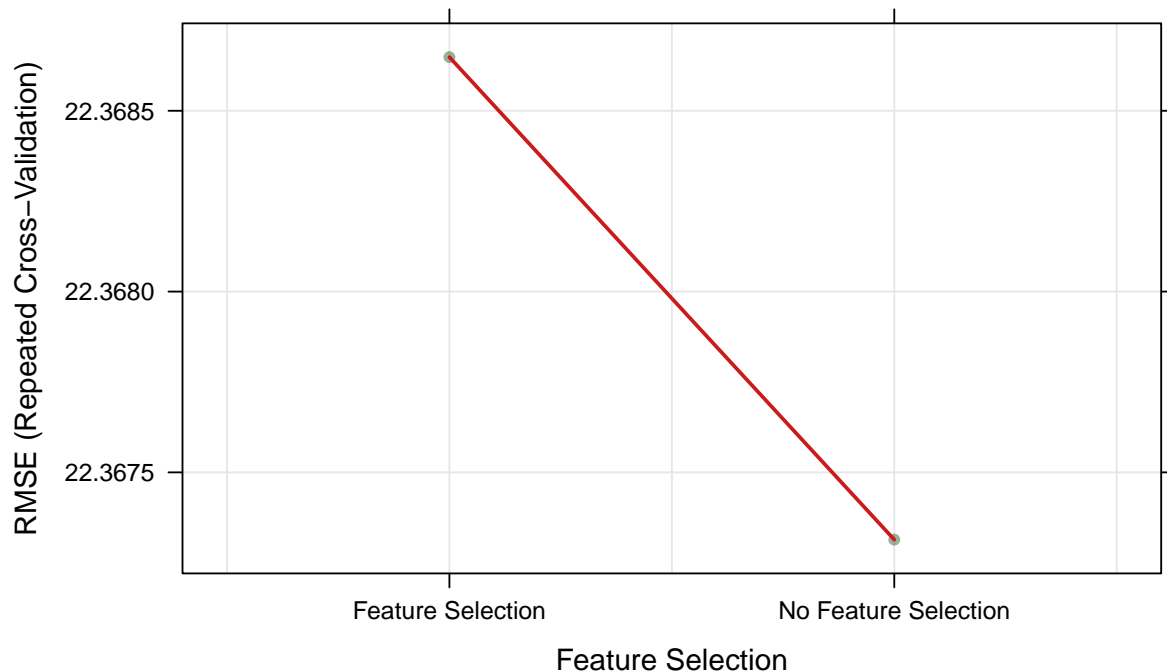
```

## Formula:
## .outcome ~ gender1 + 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)  43.2614      1.5011  28.820 < 2e-16 ***
## gender1      -4.8382      0.8761  -5.523 3.68e-08 ***
## race3        -1.9715      1.1066  -1.782 0.074945 .
## race4        -2.2377      1.5006  -1.491 0.136053
## smoking1      4.7304      0.9809   4.823 1.50e-06 ***
## smoking2      8.4125      1.5209   5.531 3.51e-08 ***
## hypertension1 4.0622      1.5700   2.587 0.009728 **
## diabetes1     -0.1520      1.2212  -0.124 0.900971
## vaccine1      -7.4441      0.8996  -8.275 < 2e-16 ***
## severity1      8.0127      1.5105   5.305 1.23e-07 ***
## studyB         3.9614      1.1211   3.533 0.000418 ***
## studyC        -1.1218      1.3803  -0.813 0.416468
## ---
## 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)        1.000  1.000  3.717 0.053976 .
## s(SBP)        2.033  2.564  1.853 0.161840
## s(LDL)        1.000  1.000  0.929 0.335229
## s(bmi)        8.079  8.737 84.927 < 2e-16 ***
## s(height)     1.000  1.000  0.591 0.442071
## s(weight)     6.720  7.840  3.688 0.000309 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.351   Deviance explained = 35.9%
## GCV = 483.87   Scale est. = 477.74      n = 2513
# Report the model:
gam$bestTune
##      select method
## 1 FALSE GCV.Cp
gam$finalModel
##
## Family: gaussian
## Link function: identity
##
## Formula:
## .outcome ~ gender1 + 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:
## 1.00 2.03 1.00 8.08 1.00 6.72 total = 31.83
##
## GCV score: 483.8652

```

```
# Plot for tuning parameter selection:
plot(gam, main = "Figure 7. GAM Model CV RMSE Plot")
```

**Figure 7. GAM Model CV RMSE Plot**



```
# Report the CV error:
gam$results$RMSE
## [1] 22.36731 22.36865
# Report the test error:
gam_pred = predict(gam, newdata = x2) ## Test dataset
gam_mse = sqrt(mean((gam_pred - y2)^2))
gam_mse
## [1] 25.85336
```

[Describe the outputs above]

## Multivariate adaptive regression spline (MARS) model

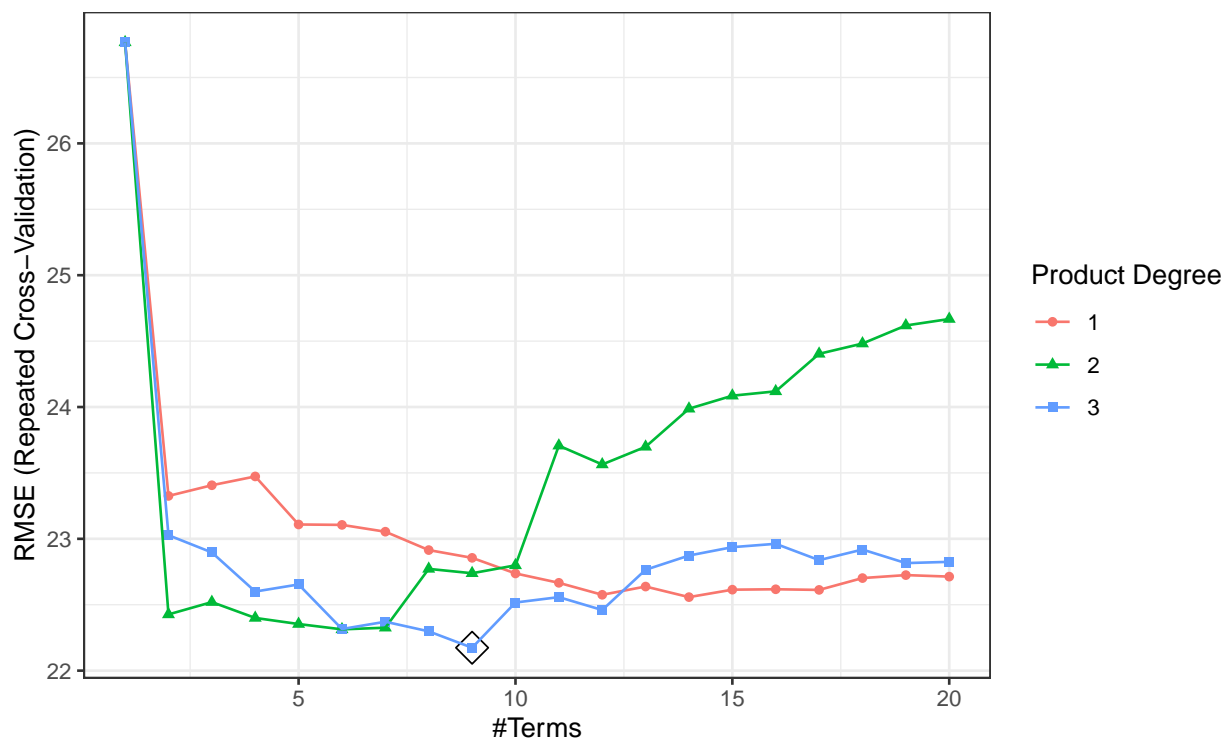
```
set.seed(3521)
# Create grid for two tuning parameters in MARS
mars_grid = expand.grid(degree = 1:3, ## number of possible product hinge functions
                        nprune = 1:20) ## the number of basis functions to be retained after the pruning
# Fit the MARS model:
mars = train(x, y, # training dataset
             method = "earth",
             tuneGrid = mars_grid,
```

```

trControl = ctrl)
# Report the coefficients:
coef(mars$finalModel)
##                (Intercept)                h(30.5-bmi)
##                12.631786                5.164229
##                h(bmi-30.5) * studyB      race2 * h(bmi-30.5) * studyB
##                22.177779                22.832642
##                vaccine1                h(bmi-25.4)
##                -7.057776                6.227136
## h(bmi-30.5) * h(SBP-128) * studyB h(bmi-30.5) * h(SBP-130) * studyB
##                24.889685                -18.901047
## h(bmi-30.5) * h(SBP-124) * studyB
##                -7.493282
# Plot for tuning parameter selection:
ggplot(mars, highlight = T) +
  theme_bw() +
  ggtitle("Figure 8. MARS Model CV RMSE Plot")

```

Figure 8. MARS Model CV RMSE Plot



```

# Choose best tuning parameter value:
mars$bestTune
##      nprune degree
## 49      9      3

# Report the CV error:
mars$results[27, ]$RMSE
## [1] 22.17363
# Report test error:

```

```

mars_pred = predict(mars, newdata = x2) ## Test dataset
mars_mse = sqrt(mean((mars_pred - y2)^2))
mars_mse
## [1] 27.02613

```

[Describe the outputs above]

## Secondary Analysis

```

ctrl1 = trainControl(method = "repeatedcv",
                     summaryFunction = twoClassSummary,
                     classProbs = TRUE)

ctrl = trainControl(method = "repeatedcv", number = 10, repeats = 5)

set.seed(3521)
# GLM fit
glm = train(x = x_sec,
            y = y_sec,
            method = "glm", metric = "ROC", trControl = ctrl1)

```