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

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2023-05-01

Contents

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
```

```r
# 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

```r
# 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	

```
skimr::skim(dat_2)
```

Table 4: Data summary

Name	dat_2
Number of rows	3587
Number of columns	15
Column type frequency:	
factor	9
numeric	6
Group variables	None

Variable type: factor

skim_variable	n_missing	complete_rate	ordered	n_unique	top_counts
recovery_time	0	1	FALSE	2	gre: 2534, les: 1053
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

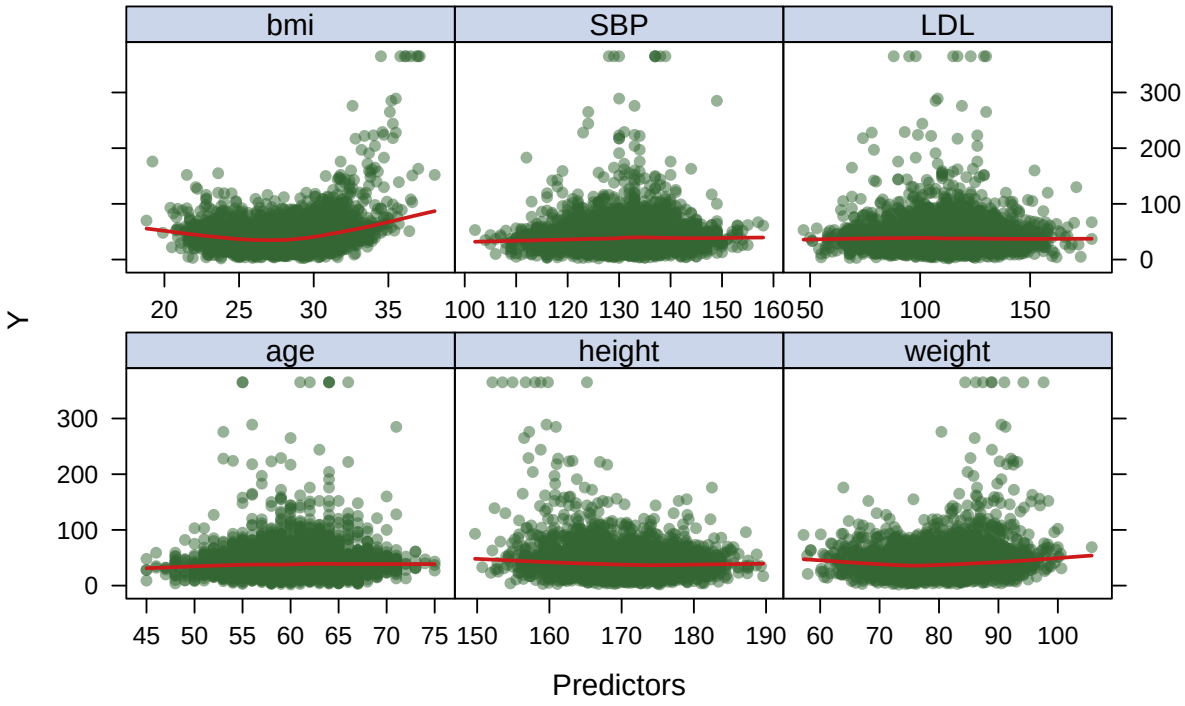
Variable type: numeric

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	p75	p100	hist
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"))
```

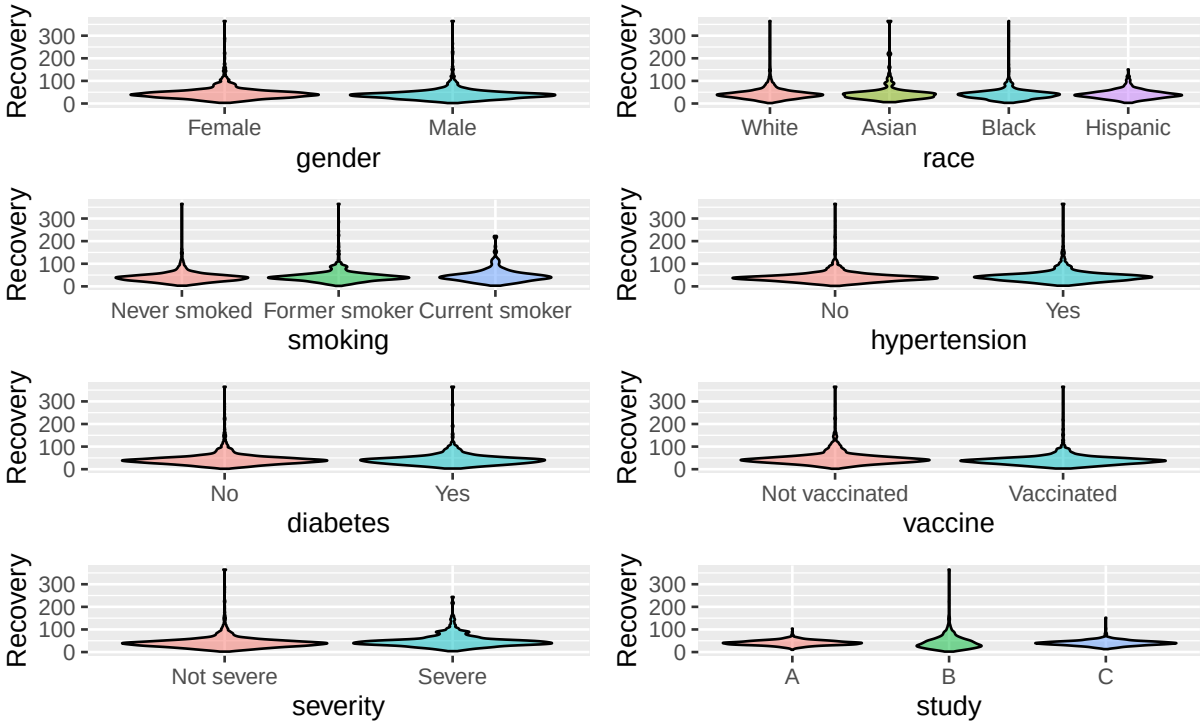
Figure 1.1. Lattice Plots for Continuous Variables in Primary Analysis




```
## 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')) +
```

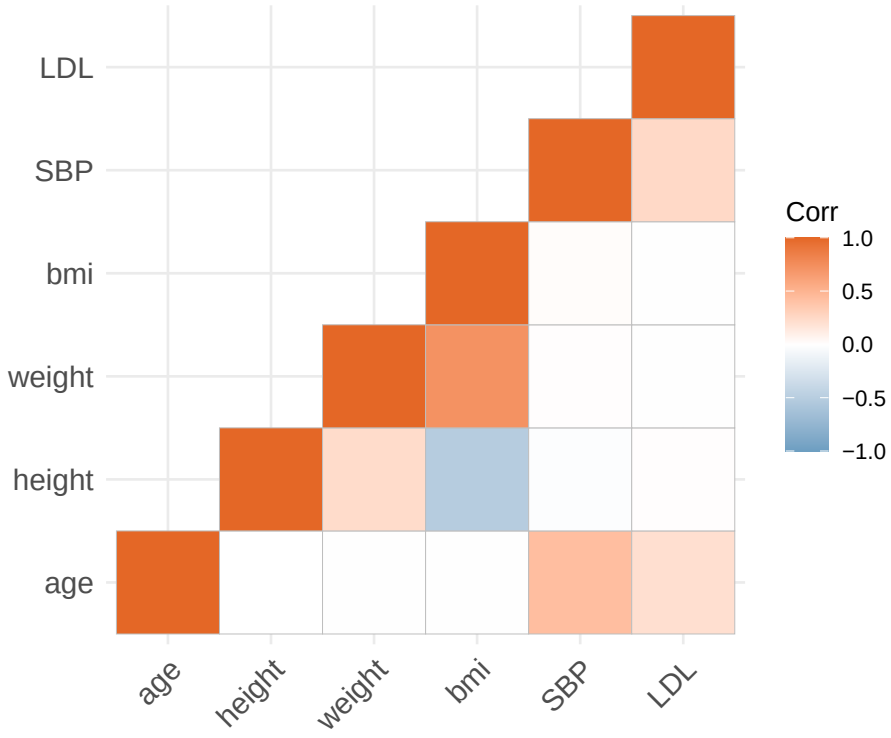
```
  theme(legend.position = "none")

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



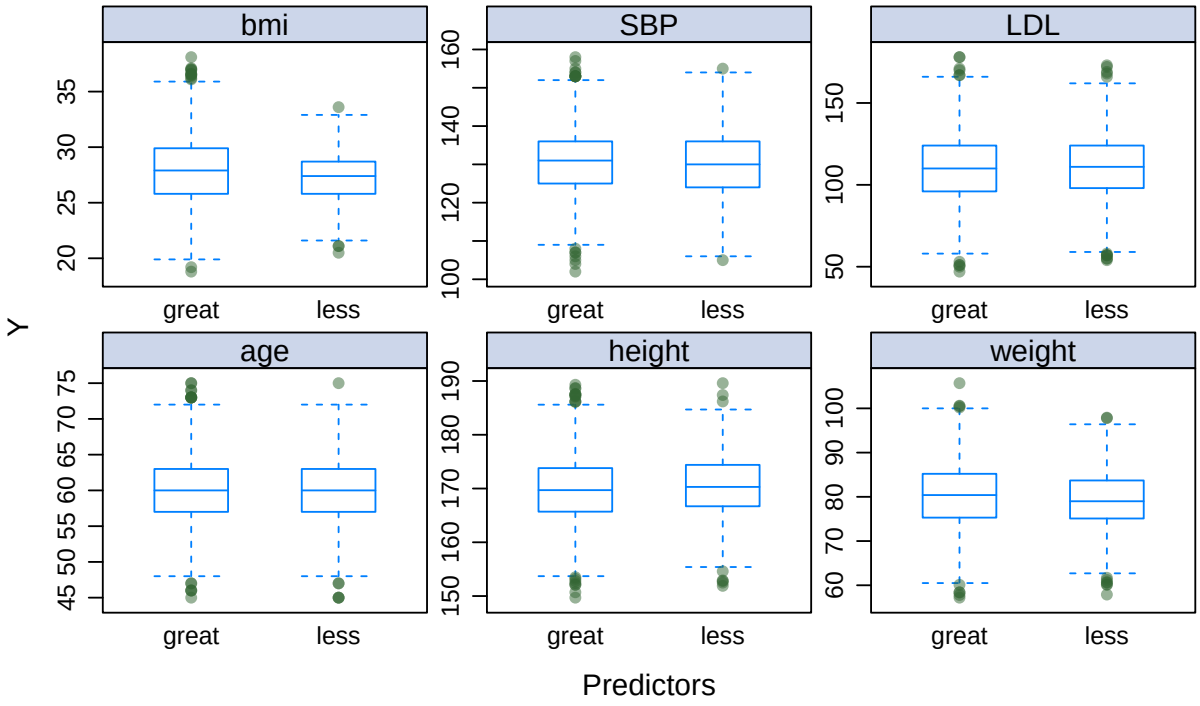

```
## Correlation matrix for continuous variables ONLY:
model.matrix( ~ 0+., data = dat %>% dplyr::select(age, height, weight, bmi, SBP, LDL)) %>%
  cor(use = "pairwise.complete.obs") %>%
  ggcorrplot::ggcorrplot(show.diag = T,
                         type = "lower",
                         lab =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

Figure 1.3. Correlation matrix for continuous datasat




```
# 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))
```

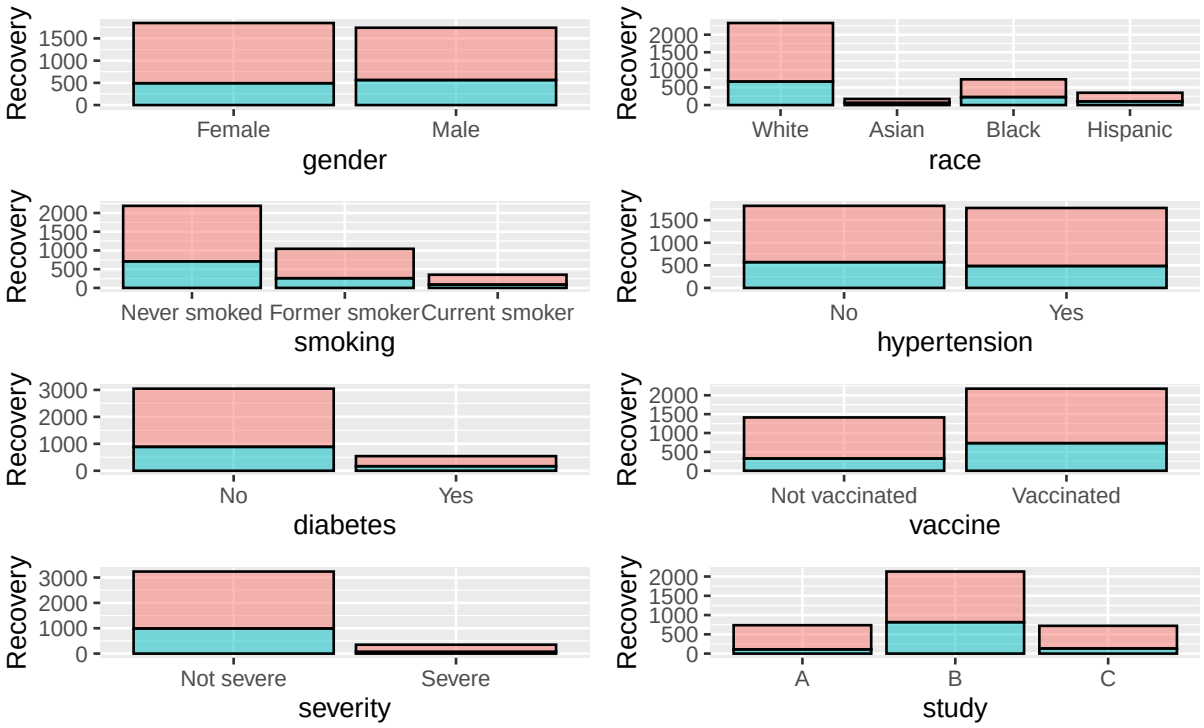
Figure 1.4. Lattice Plots for Continuous Variables in Secondary Analysis




```
## 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')) +
```

```r
  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_s
  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 and parallel computing setup:

```
ctrl = trainControl(method = "repeatedcv", number = 10, repeats = 5)
ctrl1 = trainControl(method = "repeatedcv",
                     summaryFunction = twoClassSummary,
                     classProbs = TRUE)
no_cores = detectCores() - 1
```

Primary Analysis

Recovery time as continuous variable.

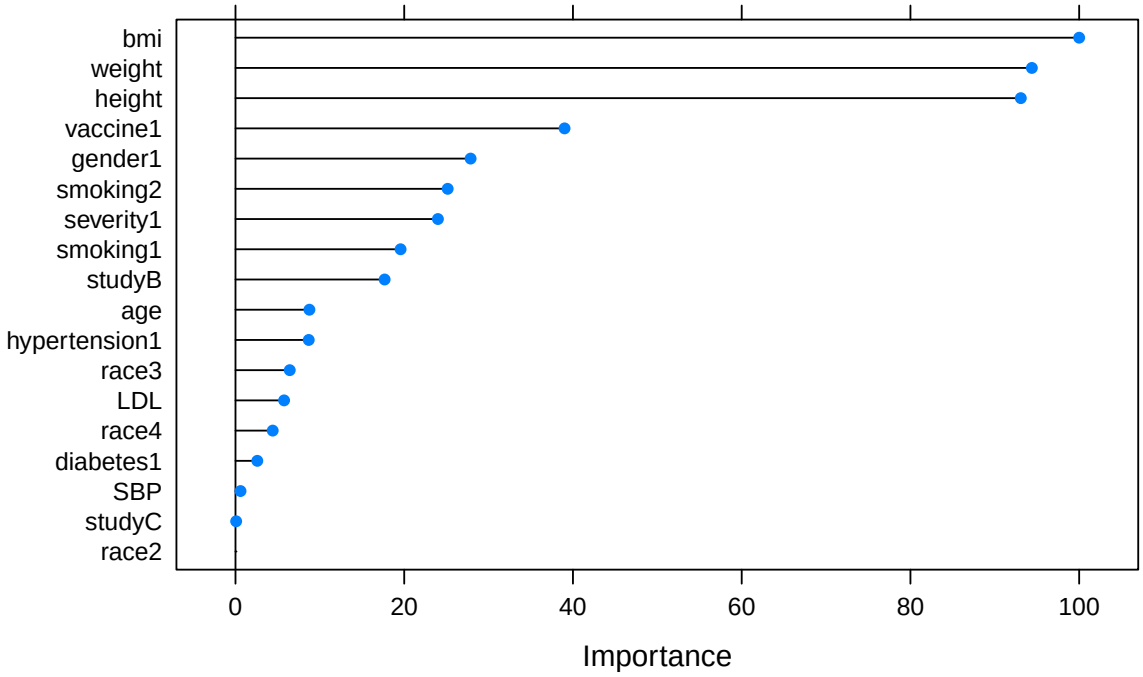
Linear methods:

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



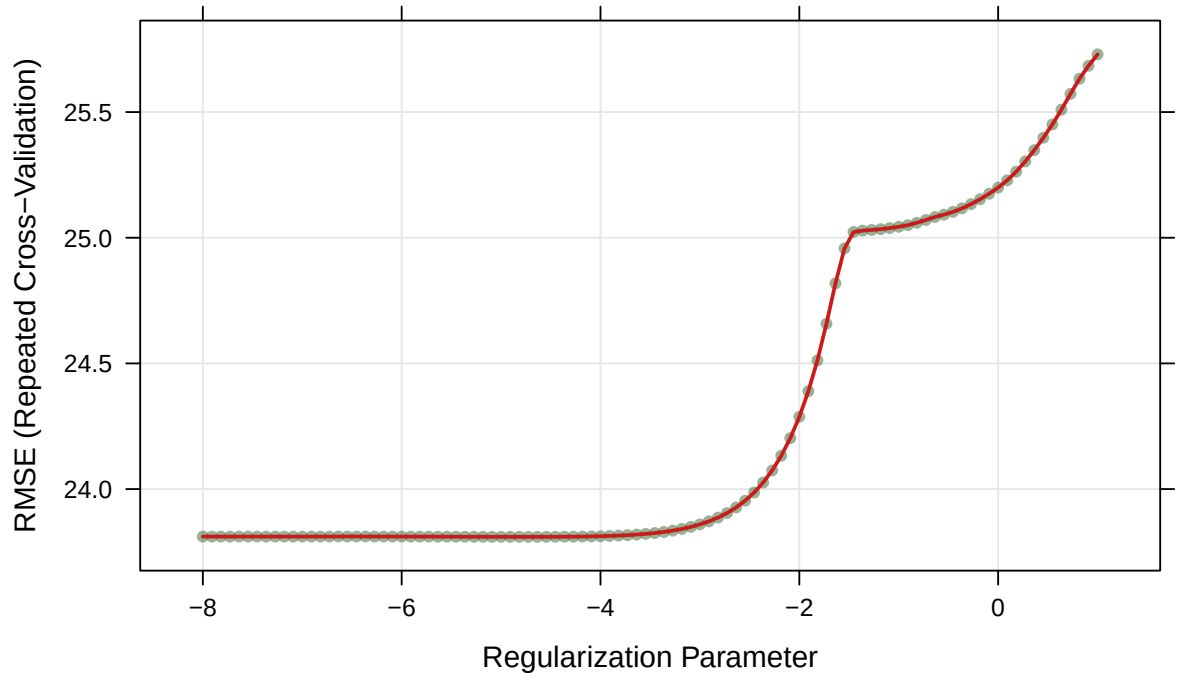

```
# Report the CV error:
lm$results$RMSE
## [1] 23.81421
```

[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
```

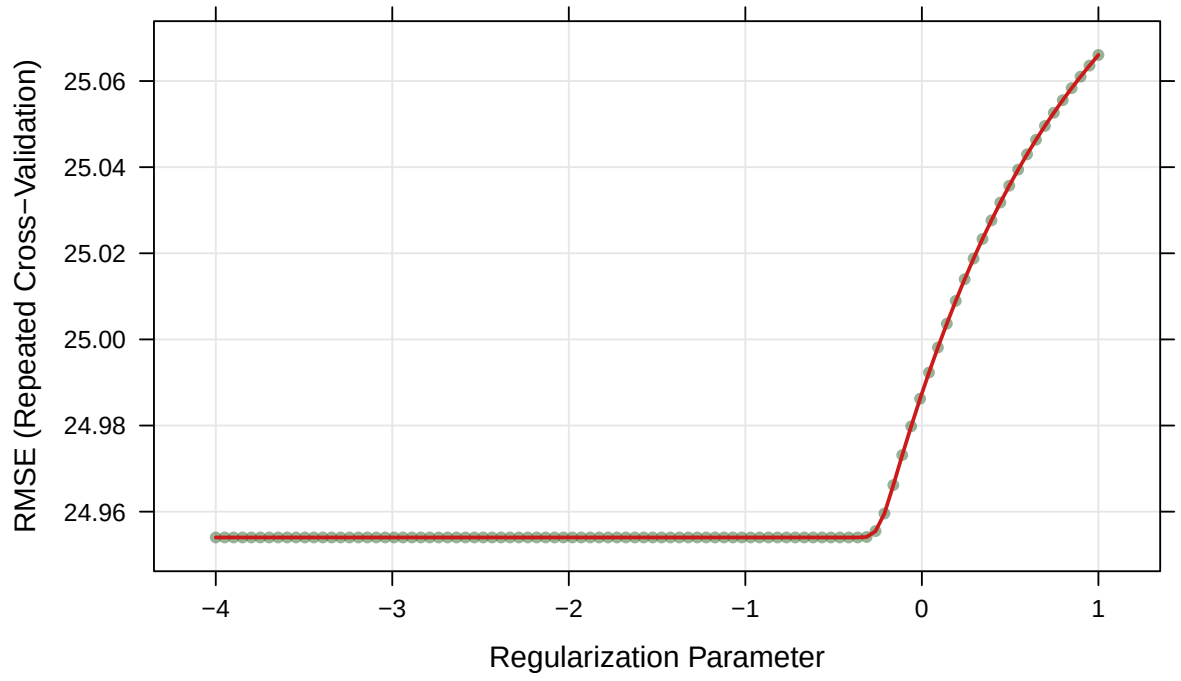
```
# Report the CV error:
lasso$results[37, ]$RMSE
## [1] 23.80994
```

[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)
```

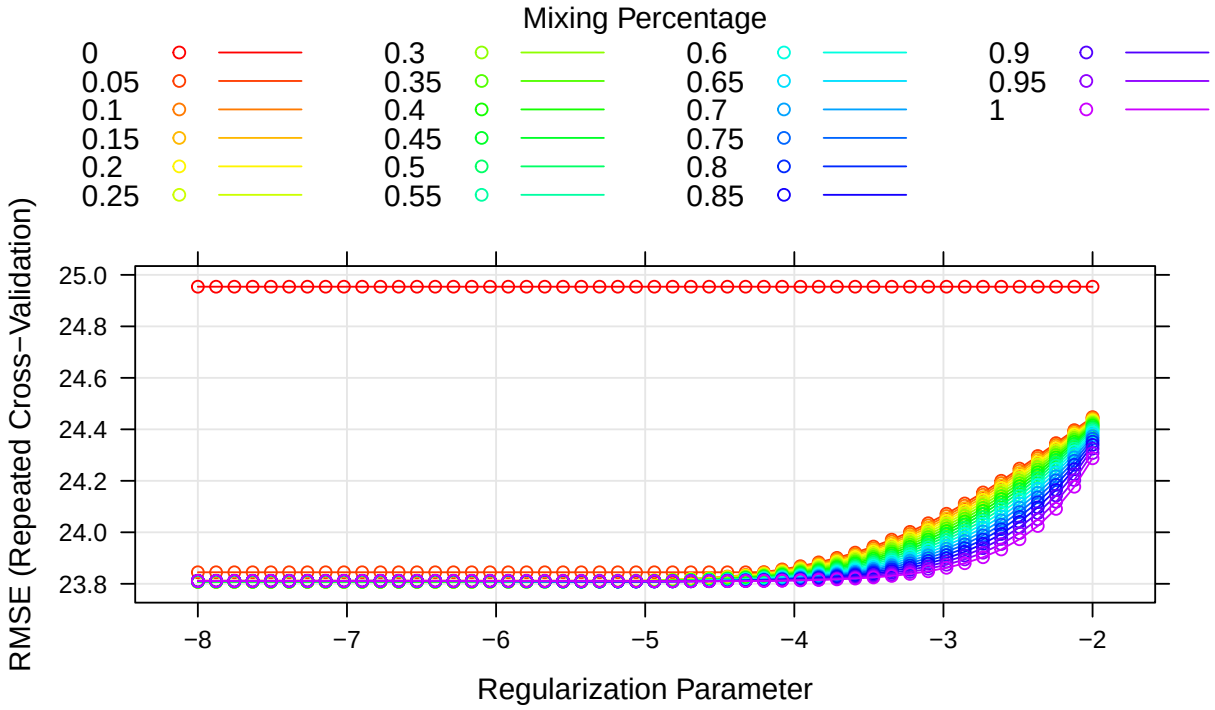
```
## 19 x 1 sparse Matrix of class "dgCMatrix"
##                          s1
## (Intercept)   -1.149931e+02
## age            2.064306e-01
## gender1       -4.932110e+00
## race2          1.218372e-01
## race3         -2.740022e+00
## race4         -1.799371e+00
## smoking1       4.007457e+00
## smoking2       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
```

[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(superpose.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
```

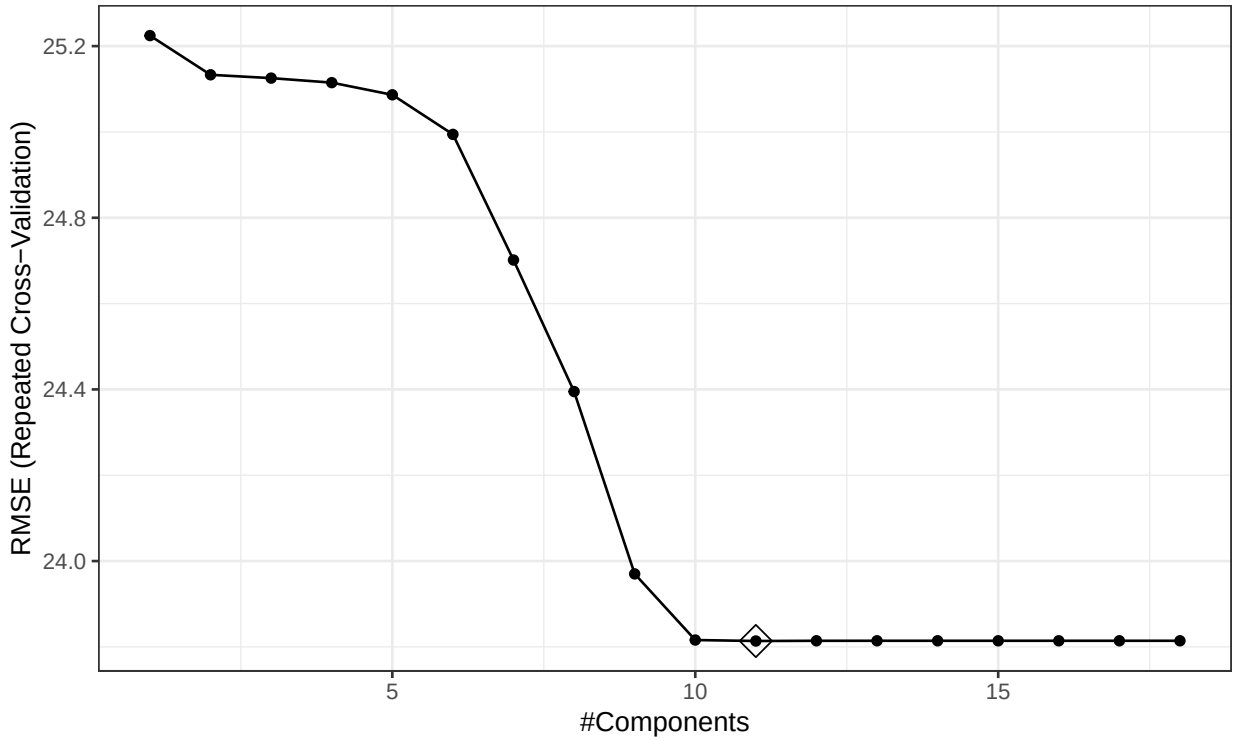
```
# Report the CV error:
enet$results[220, ]$RMSE
## [1] 23.80708
```

[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
```

[Describe the outputs above]

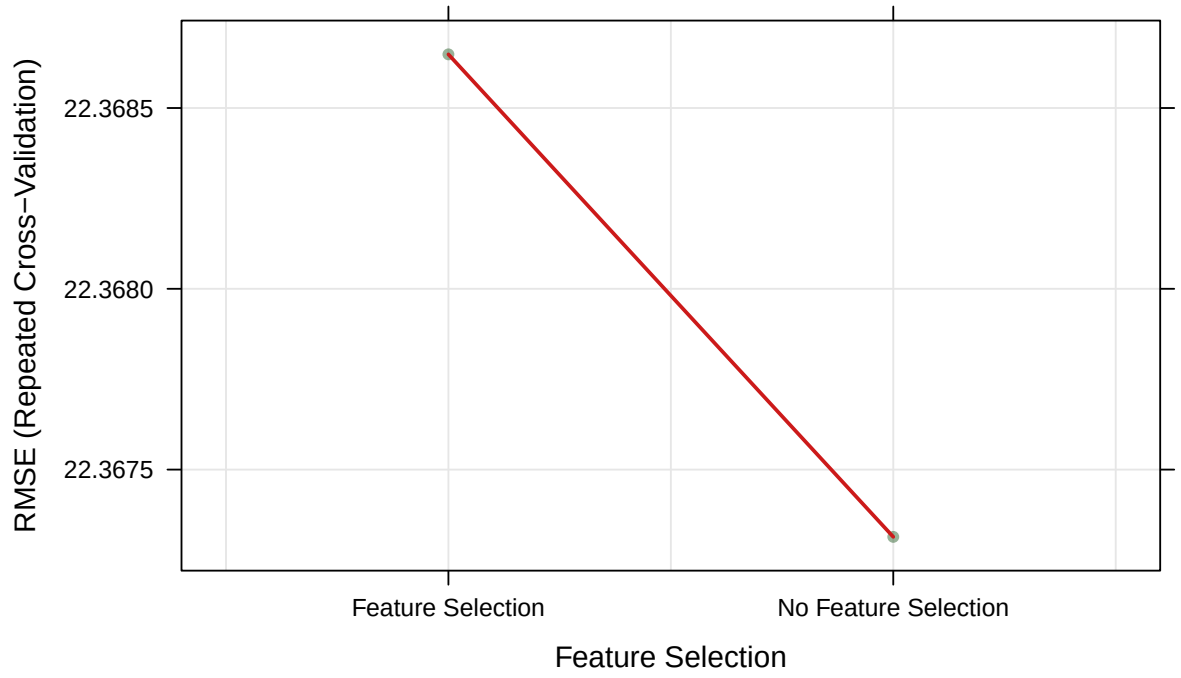
Nonlinear Methods:

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



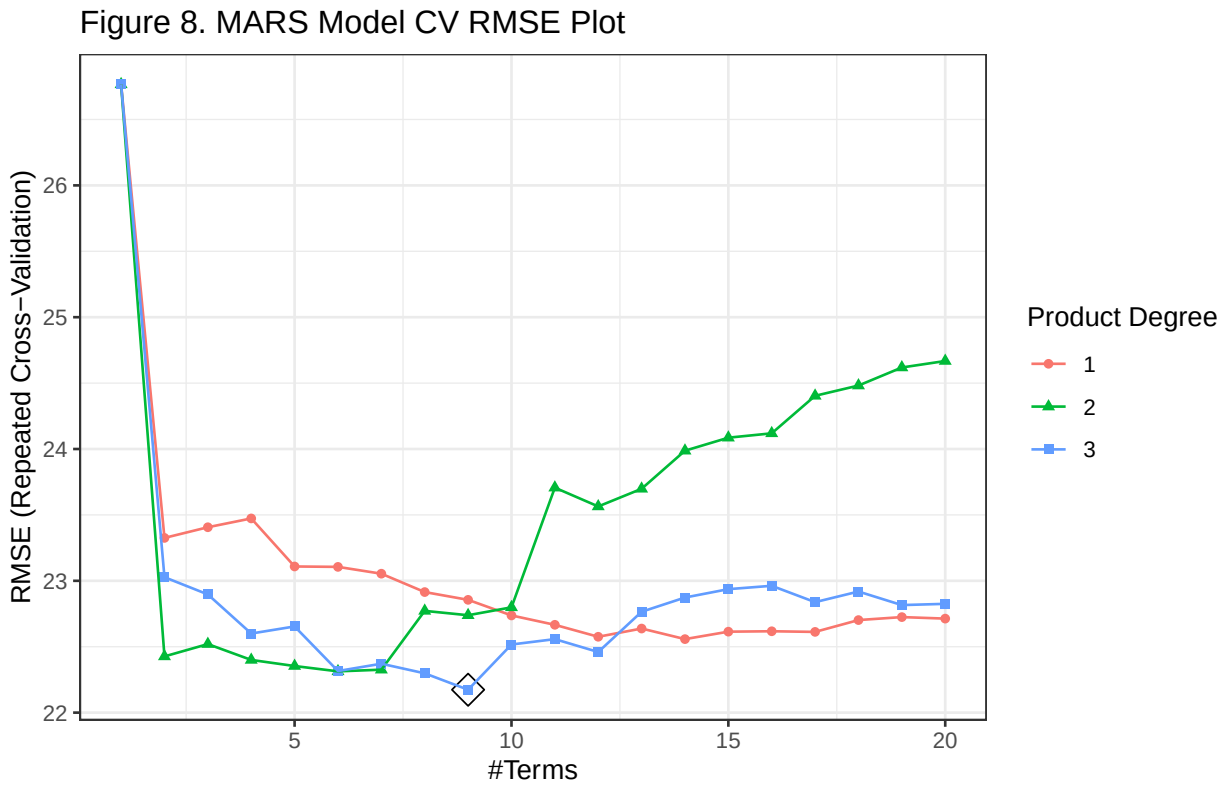

```
# Report the CV error:
gam$results$RMSE
## [1] 22.36731 22.36865
```

[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 prun
# Fit the MARS model:
cl = makePSOCKcluster(no_cores)
registerDoParallel(cl)
mars = train(x, y, # training dataset
             method = "earth",
             tuneGrid = mars_grid,
             trControl = ctrl)
stopCluster(cl)
registerDoSEQ()

# 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")
```



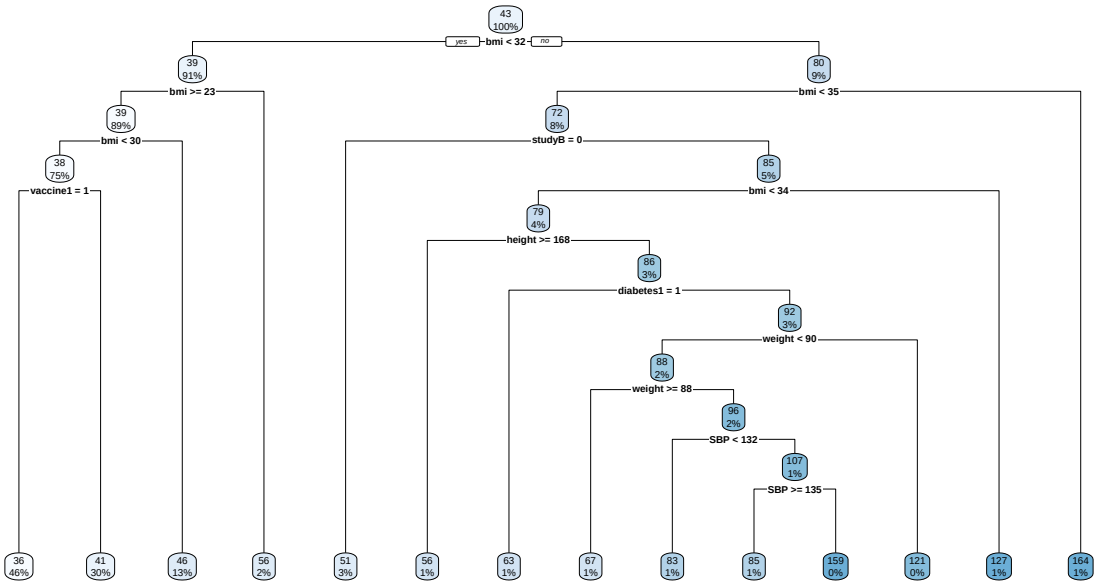

```
# Choose best tuning parameter value:
mars$bestTune
##    nprune degree
## 49      9      3

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

[Describe the outputs above]

Regression Tree:

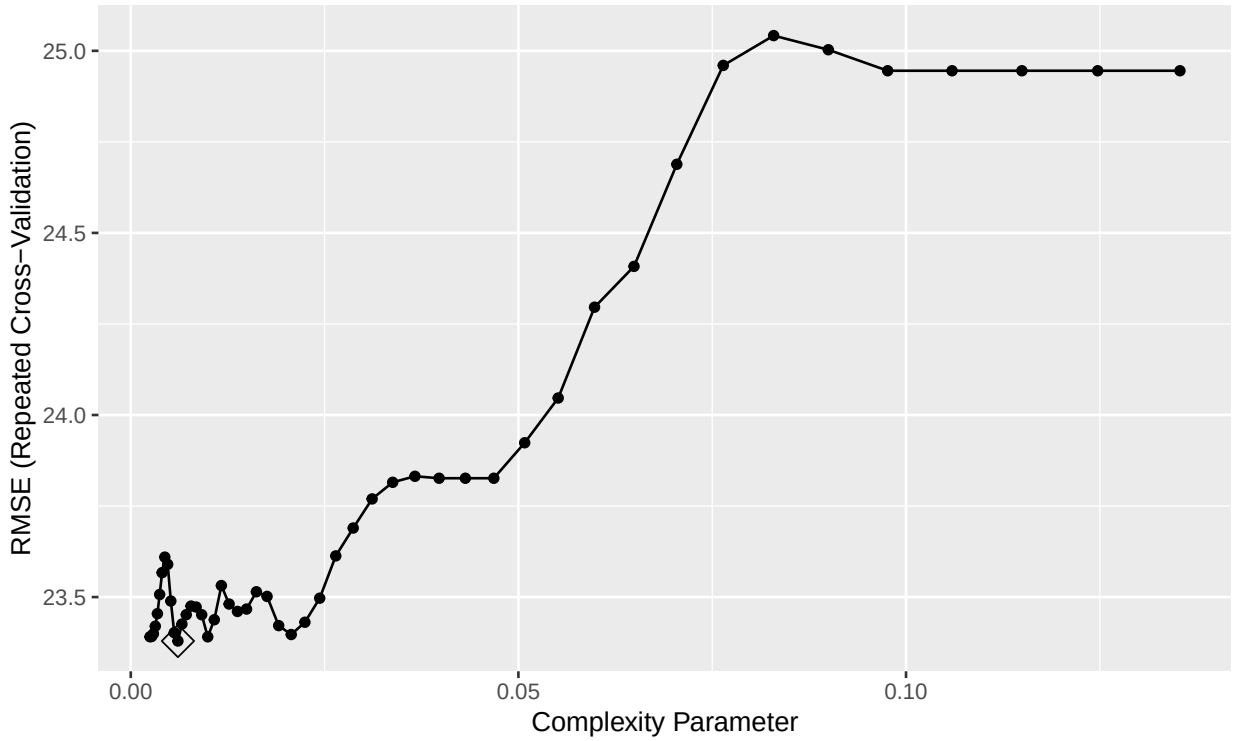
```
set.seed(3521)
# Fit the regression tree model:
cl = makePSOCKcluster(no_cores)
registerDoParallel(cl)
reg_tree = train(x, y, ## training dataset
                 method = "rpart",
                 tuneGrid = data.frame(cp = exp(seq(-6, -2, length = 50))),
                 trControl = ctrl)
stopCluster(cl)
registerDoSEQ()
# Plot the regression tree:
rpart.plot(reg_tree$finalModel, main = "Figure 9.1. Regression Tree")
```

Figure 9.1. Regression Tree




```
# Plot for tuning parameter selection:
ggplot(reg_tree, highlight = TRUE) + ggtitle("Figure 9.2 Regression Tree Model CV RMSE Plot")
```

Figure 9.2 Regression Tree Model CV RMSE Plot



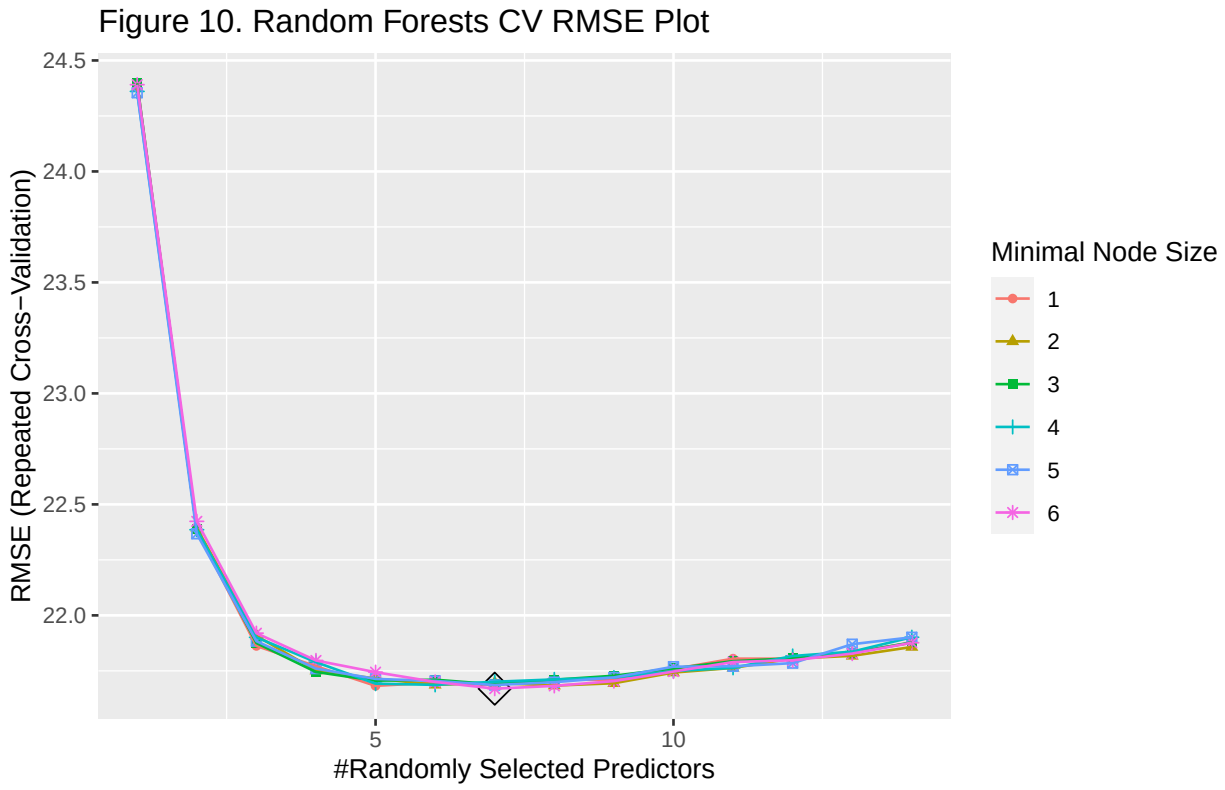

```
# Choose best tuning parameter value:
reg_tree$bestTune
##             cp
## 12 0.006084317

# Report the CV error:
reg_tree$results[12, ]$RMSE
## [1] 23.37935
```

[Describe the outputs above]

Random Forests:

```
set.seed(3521)
# Fit the random forest model:
rf.grid = expand.grid(mtry = 1:14, ## We have 14 predictors in training data in total
                      splitrule = "variance",
                      min.node.size = 1:6) ## large/small model flexibility
set.seed(3521)
cl = makePSOCKcluster(no_cores)
registerDoParallel(cl)
rf = train(x, y,
           method = "ranger",
           tuneGrid = rf.grid,
           trControl = ctrl)
stopCluster(cl)
```

```
registerDoSEQ()
# Plot for tuning parameter selection:
ggplot(rf, highlight = TRUE) + ggtitle("Figure 10. Random Forests CV RMSE Plot")
```



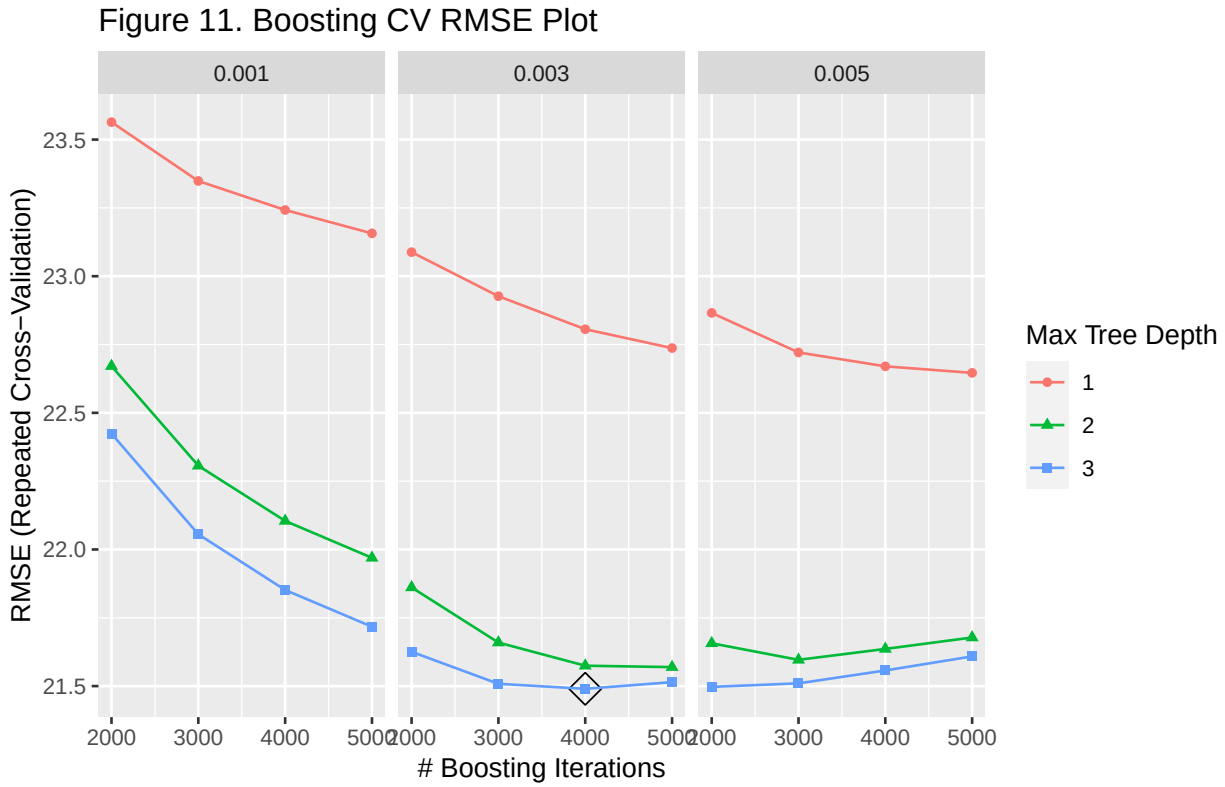

```
# Choose best tuning parameter value:
rf$bestTune
##    mtry splitrule min.node.size
## 42    7  variance             6

# Report the CV error:
rf$results[42, ]$RMSE
## [1] 21.6698
```

[Describe the outputs above]

Boosting:

```
set.seed(3521)
boosting.grid = expand.grid(n.trees = c(2000, 3000, 4000, 5000),
                        interaction.depth = 1:3,
                        shrinkage = c(0.001, 0.003, 0.005),
                        n.minobsinnode = 1)
set.seed(3521)
cl = makePSOCKcluster(no_cores)
registerDoParallel(cl)
```

```
boosting = train(x, y,
                 method = "gbm",
                 tuneGrid = boosting.grid,
                 trControl = ctrl,
                 verbose = FALSE)
stopCluster(cl)
registerDoSEQ()

# Plot for tuning parameter selection:
ggplot(boosting, highlight = TRUE) + ggtitle("Figure 11. Boosting CV RMSE Plot")
```




```
# Choose best tuning parameter value:
boosting$bestTune
##    n.trees interaction.depth shrinkage n.minobsinnode
## 23    4000                 3     0.003              1

# Report the CV error:
boosting$results[26, ]$RMSE
## [1] 21.49009
```

[Describe the outputs above]

Secondary Analysis

Logistic Model:

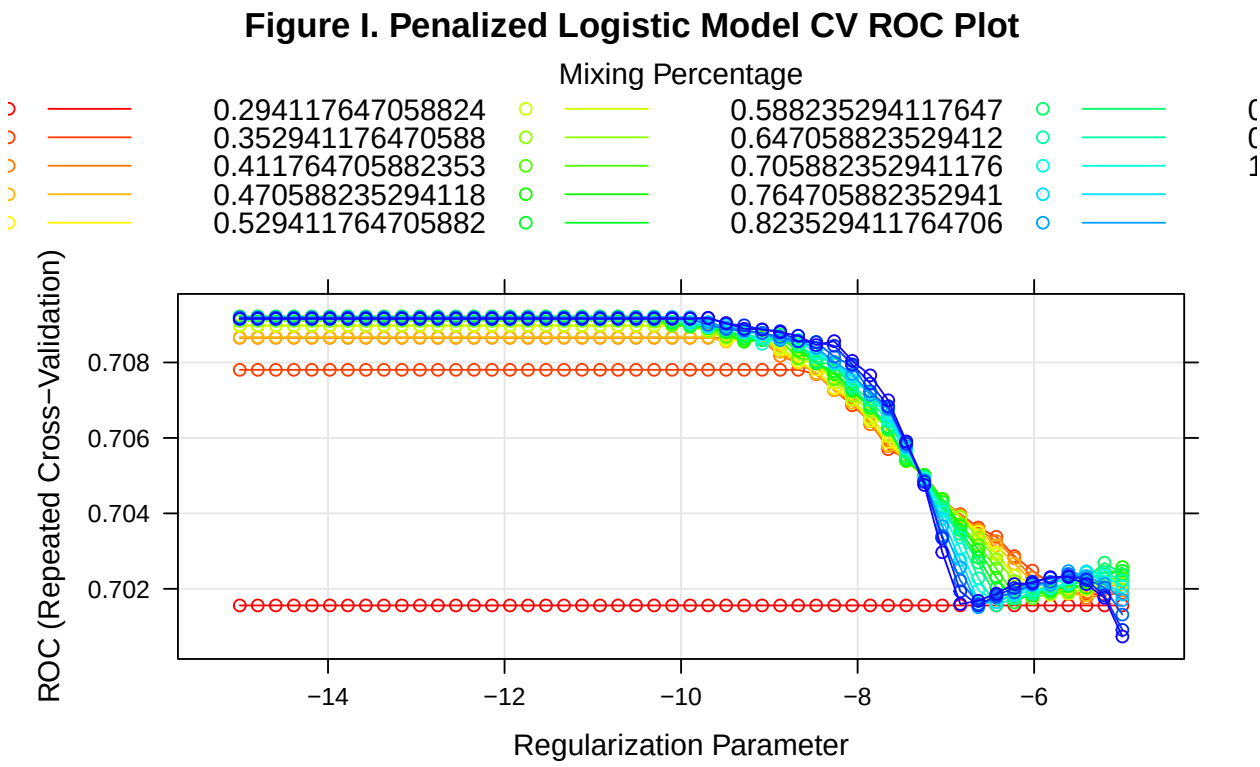
```
set.seed(3521)
glm = train(recovery_time ~ .,
            data = training_sec,
            method = "glm",
            metric = "ROC",
            trControl = ctrl1)
glm$finalModel
##
## Call:  NULL
##
## Coefficients:
##   (Intercept)            age        gender1          race2          race3
##     7.736e+01     -3.527e-02      2.843e-01      3.878e-01      1.411e-01
##         race4       smoking1       smoking2         height         weight
##     7.673e-03     -4.077e-01     -4.431e-01     -4.425e-01      4.718e-01
##           bmi  hypertension1      diabetes1            SBP            LDL
##    -1.453e+00     -1.643e-01      4.339e-02     -6.311e-05      4.684e-03
##      vaccine1      severity1         studyB         studyC
##     5.229e-01     -6.944e-01      1.335e+00      1.320e-01
##
## Degrees of Freedom: 2512 Total (i.e. Null);  2494 Residual
## Null Deviance:       3039
## Residual Deviance: 2725  AIC: 2763

# Report the CV ROC:
glm$results$ROC
## [1] 0.7095743
# Report the training error rate:
glm.train = predict(glm, newdata = training_sec)
glm_error = 1 - sum(y_sec == glm.train)/length(y_sec)
sprintf("The training error rate for logistic model is %.3f", glm_error)
## [1] "The training error rate for logistic model is 0.279"
```

[Describe the outputs above]

Penalized Logistic Model:

```
set.seed(3521)
glmnGrid = expand.grid(alpha = seq(0, 1, length = 18),
                       lambda = exp(seq(-15, -5, length = 50)))

glmn = train(recovery_time ~ .,
             data = training_sec,
             method = "glmnet",
             tuneGrid = glmnGrid,
             metric = "ROC",
```

```
            trControl = ctrl1)
# Plot for tuning parameter selection:
myCol = rainbow(25)
myPar = list(superpose.symbol = list(col = myCol),
       superpose.line = list(col = myCol))
plot(glmn, par.settings = myPar, xTran = function(x)log(x), highlight = T, main = "Figure I. Penalized
```

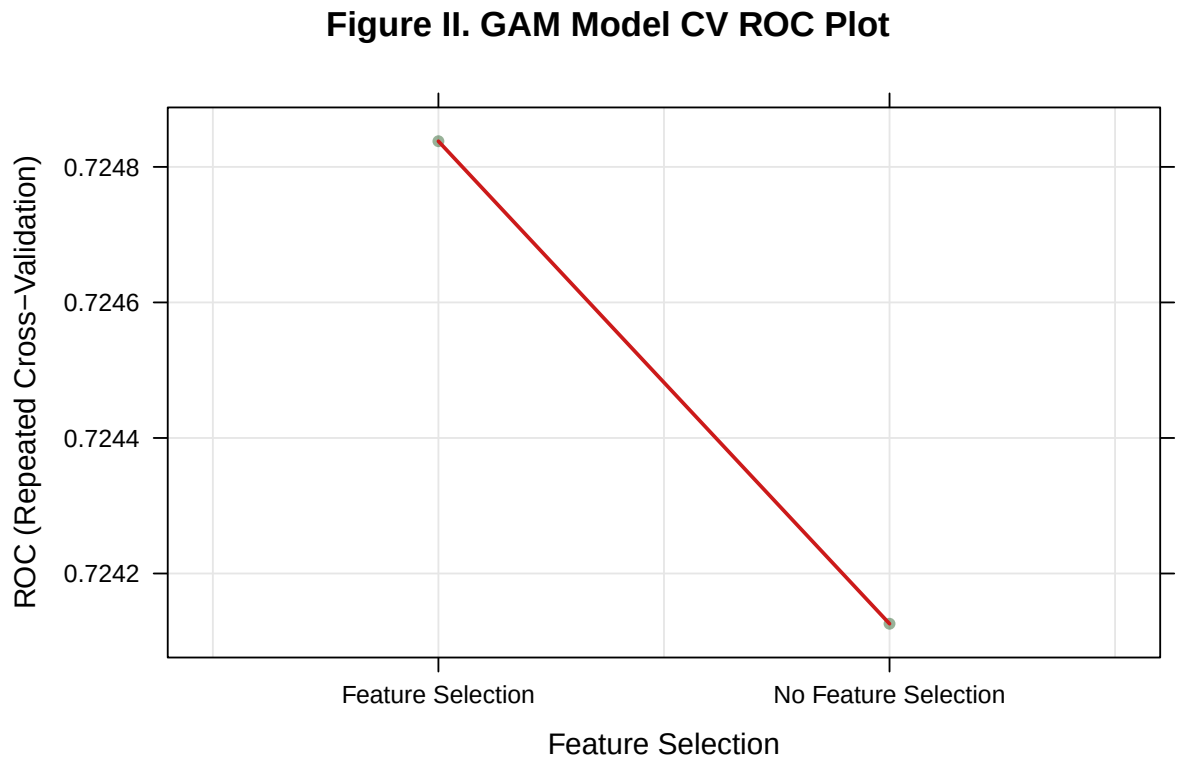



```
# Choose best tuning parameter value:
glmn$bestTune
##         alpha       lambda
## 422 0.4705882 2.222516e-05

# Report the CV ROC:
glmn$results[851, ]$ROC
## [1] 0.7091616
# Report the training error rate:
glmn.train = predict(glmn, newdata = training_sec)
glmn_error = 1 - sum(y_sec == glmn.train)/length(y_sec)
sprintf("The training error rate for penalized logistic model is %.3f", glmn_error)
## [1] "The training error rate for penalized logistic model is 0.278"
```

[Describe the outputs above]

GAM model for binary response:

```
set.seed(3521)
cl = makePSOCKcluster(no_cores)
registerDoParallel(cl)
gam_2 = train(recovery_time ~ .,
              data = training_sec,
              method = "gam",
              metric = "ROC",
              trControl = ctrl1)
stopCluster(cl)
registerDoSEQ()
# Plot for tuning parameter selection:
plot(gam_2, main = "Figure II. GAM Model CV ROC Plot")
```




```
# Report the final model:
gam_2$bestTune
##   select method
## 2   TRUE GCV.Cp
coef(gam_2$finalModel)
##   (Intercept)       gender1         race3         race4      smoking1
## -2.094415e+00  2.880745e-01  9.310134e-02  6.559474e-03 -4.371700e-01
##      smoking2 hypertension1     diabetes1      vaccine1     severity1
## -4.784380e-01 -1.857253e-01  1.970598e-02  5.356926e-01 -7.120308e-01
##        studyB        studyC      s(age).1      s(age).2      s(age).3
##  1.373336e+00  1.675730e-01 -3.547967e-04  1.690790e-03 -1.838724e-03
```

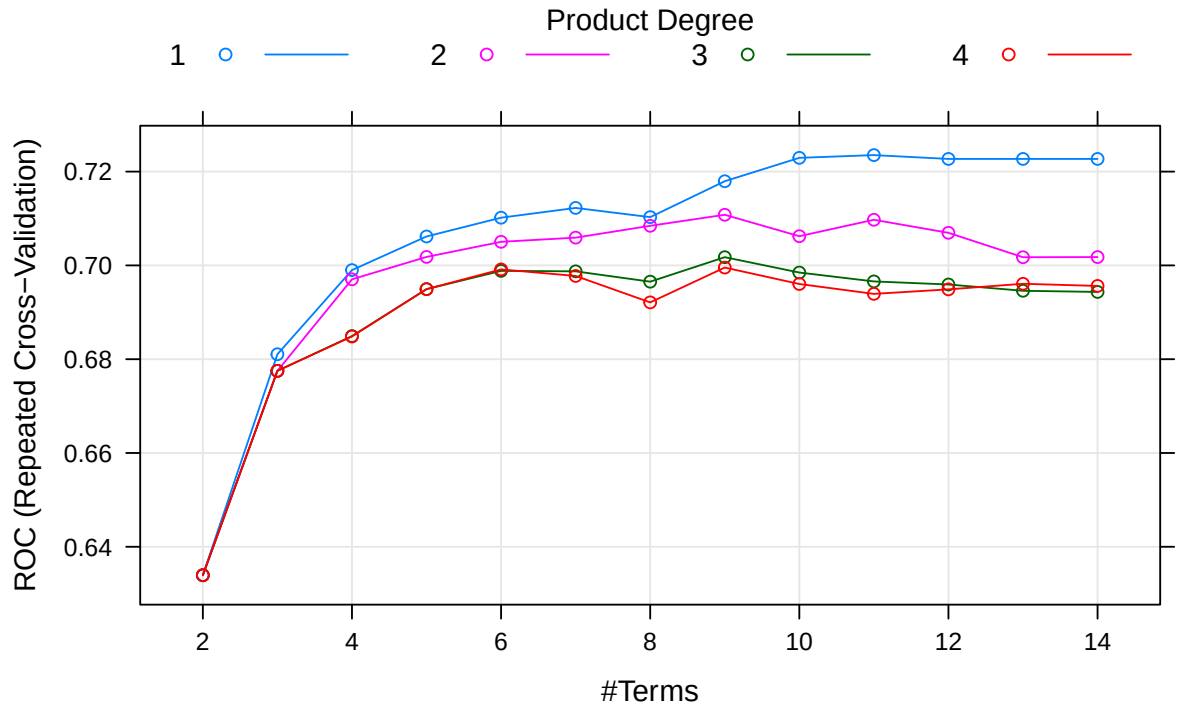
```
##      s(age).4      s(age).5      s(age).6      s(age).7      s(age).8
## -5.165523e-03  1.730323e-03 -4.076744e-03  2.181238e-03 -2.341176e-02
##      s(age).9      s(SBP).1      s(SBP).2      s(SBP).3      s(SBP).4
## -1.313838e-01  5.677327e-06  3.678094e-07 -1.373775e-07 -4.587642e-07
##      s(SBP).5      s(SBP).6      s(SBP).7      s(SBP).8      s(SBP).9
## -1.936734e-07  3.521817e-07  3.268165e-07  4.034795e-07  1.063455e-06
##      s(LDL).1      s(LDL).2      s(LDL).3      s(LDL).4      s(LDL).5
##  9.888402e-06  9.235410e-07  2.118225e-06 -5.184814e-07 -6.001575e-07
##      s(LDL).6      s(LDL).7      s(LDL).8      s(LDL).9      s(bmi).1
## -1.067971e-07  3.793180e-07 -2.515578e-06  6.736418e-02  2.008212e-01
##      s(bmi).2      s(bmi).3      s(bmi).4      s(bmi).5      s(bmi).6
##  6.053645e-02  4.628156e-02 -3.554393e-01  9.872649e-02  2.925849e-01
##      s(bmi).7      s(bmi).8      s(bmi).9   s(height).1   s(height).2
##  6.796104e-02  1.848588e+00 -2.913658e-01 -3.745810e-06 -1.490001e-08
##   s(height).3   s(height).4   s(height).5   s(height).6   s(height).7
##  7.316762e-07 -6.473545e-07  4.594748e-07  5.722461e-07  3.972392e-07
##   s(height).8   s(height).9   s(weight).1   s(weight).2   s(weight).3
## -2.537800e-06 -1.011582e-06  1.537831e-06  1.359224e-07  3.751313e-07
##   s(weight).4   s(weight).5   s(weight).6   s(weight).7   s(weight).8
##  3.344343e-07 -2.836629e-07 -2.968417e-07  2.050625e-07  1.225004e-06
##   s(weight).9
## -4.006080e-06

# Report the CV ROC:
gam_2$results[2, ]$ROC
## [1] 0.7248379
# Report the training error rate:
gam_2.train = predict(gam_2, newdata = training_sec)
gam_2_error = 1 - sum(y_sec == gam_2.train)/length(y_sec)
sprintf("The training error rate for GAM model is %.3f", gam_2_error)
## [1] "The training error rate for GAM model is 0.268"
```

[Describe the outputs above]

MARS model for binary response:

```
set.seed(3521)
cl = makePSOCKcluster(no_cores)
registerDoParallel(cl)
mars_2 = train(recovery_time ~ .,
               data = training_sec,
               method = "earth",
               tuneGrid = expand.grid(degree = 1:4, nprune = 2:14),
               metric = "ROC",
               trControl = ctrl1)
stopCluster(cl)
registerDoSEQ()
# Plot for tuning parameter selection:
plot(mars_2, main = "Figure III. MARS Model CV ROC Plot", highlight = T)
```

Figure III. MARS Model CV ROC Plot




```
# Report the final model:
mars_2$bestTune
##    nprune degree
## 10     11      1
coef(mars_2$finalModel)
## (Intercept)      studyB h(bmi-27.8) h(27.8-bmi)    vaccine1   severity1
##  -1.5347506   1.2977373  -0.4282987  -0.1841055   0.5316052  -0.7196799
##   h(61-age)    smoking1     gender1    smoking2
##   0.0590261  -0.4376436   0.2849957  -0.4923424

# Report the CV ROC:
mars_2$results[37, ]$ROC
## [1] 0.7235168
# Report the training error rate:
mars_2.train = predict(mars_2, newdata = training_sec)
mars_2_error = 1 - sum(y_sec == mars_2.train)/length(y_sec)
sprintf("The training error rate for MARS model is %.3f", mars_2_error)
## [1] "The training error rate for MARS model is 0.263"
```

[Describe the outputs above]

Linear discriminant analysis (LDA):

```
set.seed(3521)
lda = train(recovery_time ~ .,
```

```
            data = training_sec,
            method = "lda",
            metric = "ROC",
            trControl = ctrl1)
# Report the final model:
coef(lda$finalModel)
##                          LD1
## age           -4.414766e-02
## gender1        3.483168e-01
## race2          5.127539e-01
## race3          2.087032e-01
## race4          1.652280e-02
## smoking1      -5.093387e-01
## smoking2      -5.565945e-01
## height        -4.842308e-01
## weight         5.127571e-01
## bmi           -1.587689e+00
## hypertension1 -2.035363e-01
## diabetes1      5.532383e-02
## SBP           -7.703822e-06
## LDL            6.184843e-03
## vaccine1       6.694769e-01
## severity1     -7.851869e-01
## studyB         1.615000e+00
## studyC         1.104844e-01

# Report the CV ROC:
lda$results$ROC
## [1] 0.7100636
# Report the training error rate:
lda.train = predict(lda, newdata = training_sec)
lda_error = 1 - sum(y_sec == lda.train)/length(y_sec)
sprintf("The training error rate for LDA is %.3f", lda_error)
## [1] "The training error rate for LDA is 0.279"
```

[Describe the outputs above]

Quadratic discriminant analysis (QDA):

```
set.seed(3521)
qda = train(recovery_time ~ .,
            data = training_sec,
            method = "qda",
            metric = "ROC",
            trControl = ctrl1)
# Report the final model:
qda$finalModel
## Call:
## qda(x, grouping = y)
##
## Prior probabilities of groups:
```

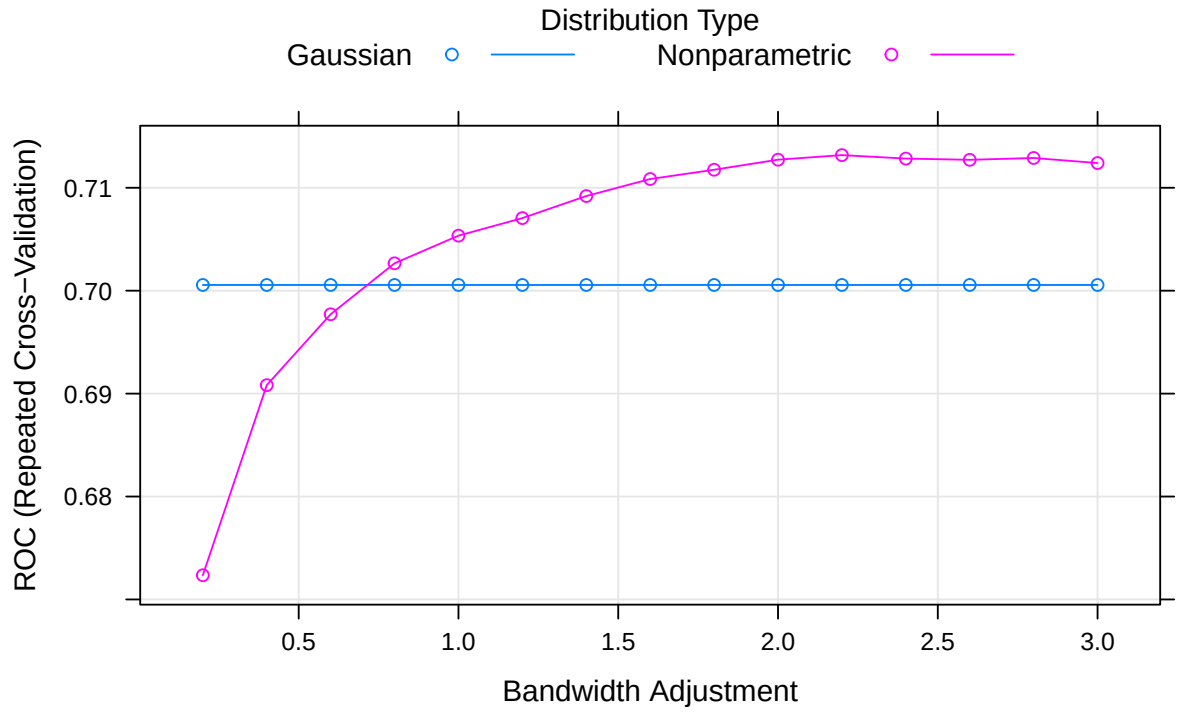
```
##    great     less
## 0.707123 0.292877
##
## Group means:
##            age   gender1      race2     race3      race4  smoking1   smoking2
## great 60.29994 0.4687676 0.04614519 0.1963984 0.09848059 0.3168261 0.10298255
## less  59.69429 0.5339674 0.05706522 0.2146739 0.09375000 0.2500000 0.08016304
##         height   weight      bmi hypertension1 diabetes1      SBP      LDL
## great 169.7715 80.20096 27.89994     0.5098481 0.1508160 130.5093 109.5937
## less  170.3648 79.04755 27.26454     0.4538043 0.1535326 129.6087 110.7527
##        vaccine1  severity1    studyB    studyC
## great 0.5751266 0.10635903 0.5160383 0.2341024
## less  0.6942935 0.05842391 0.7839674 0.1127717

# Report the CV ROC:
qda$results$ROC
## [1] 0.6965235
# Report the training error rate:
qda.train = predict(qda, newdata = training_sec)
qda_error = 1 - sum(y_sec == qda.train)/length(y_sec)
sprintf("The training error rate for QDA model is %.3f", qda_error)
## [1] "The training error rate for QDA model is 0.299"
```

[Describe the outputs above]

Naive Bayes:

```
set.seed(3521)
nbGrid = expand.grid(usekernel = c(FALSE, TRUE),
                     fL = 1,
                     adjust = seq(.2, 3, by = .2))
nb = train(recovery_time ~ .,
           data = training_sec,
           method = "nb",
           tuneGrid = nbGrid,
           metric = "ROC",
           trControl = ctrl1)
# Plot for tuning parameter selection:
plot(nb, main = "Figure IV. NB Model CV ROC Plot", highlight = T)
```

Figure IV. NB Model CV ROC Plot




```
# Report the final model:
nb$bestTune
##    fL usekernel adjust
## 26  1      TRUE    2.2

# Report the CV ROC:
nb$results[26, ]$ROC
## [1] 0.7131731
# Report the training error rate:
nb.train = predict(nb, newdata = training_sec)
nb_error = 1 - sum(y_sec == nb.train)/length(y_sec)
sprintf("The training error rate for Naive Bayes is %.3f", nb_error)
## [1] "The training error rate for Naive Bayes is 0.277"
```

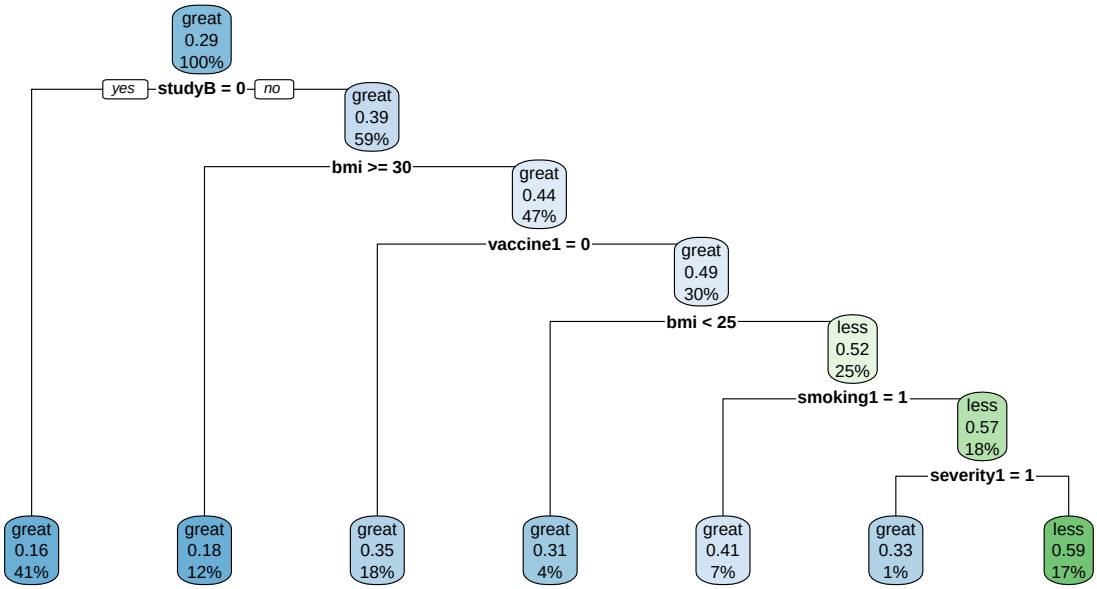
[Describe the outputs above]

Classfication tree:

```
set.seed(3521)
rpart = train(recovery_time ~ . ,
              data = training_sec,
              method = "rpart",
              tuneGrid = data.frame(cp = exp(seq(-6, -2, length = 50))),
              trControl = ctrl1,
              metric = "ROC")
```

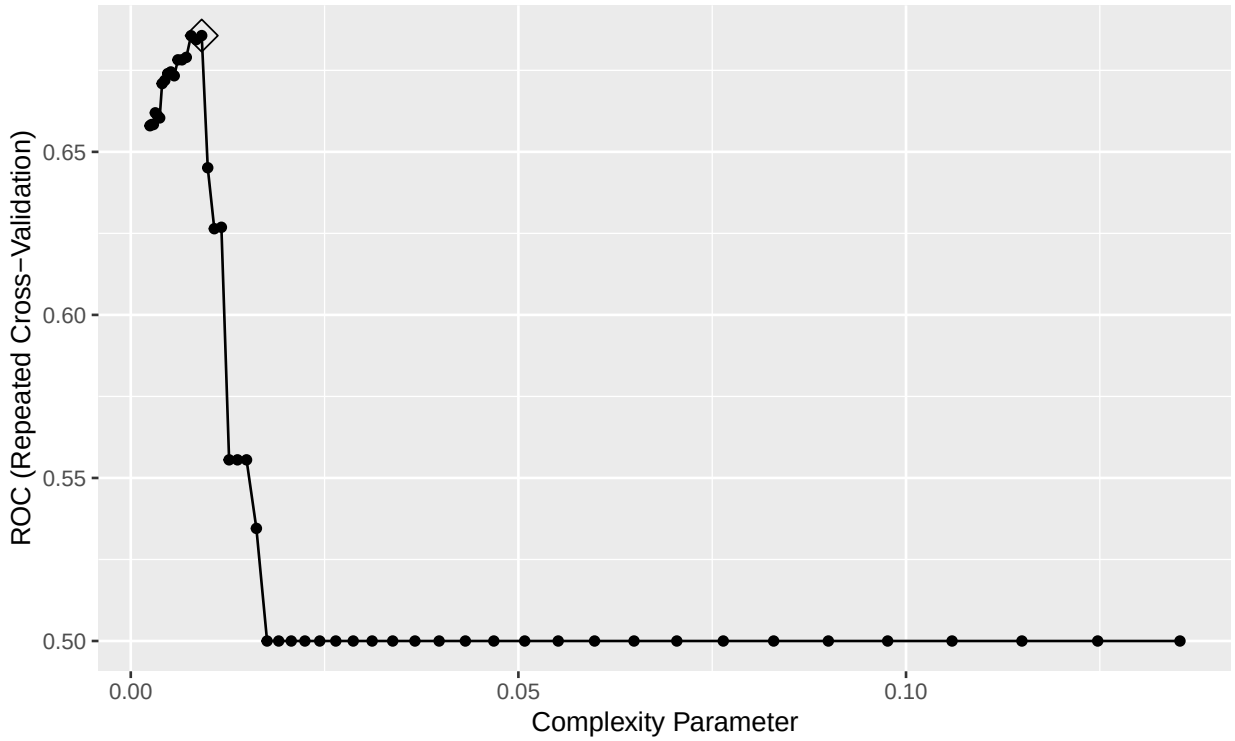
```
# Plot for classification tree:
rpart.plot(rpart$finalModel, main = "Figure V(I). Classification Tree")
```

Figure V(I). Classification Tree




```
# Plot for tuning parameter selection:
ggplot(rpart, highlight = TRUE) + ggtitle("Figure V(II). Classification Tree Model CV ROC Plot")
```

Figure V(II). Classification Tree Model CV ROC Plot



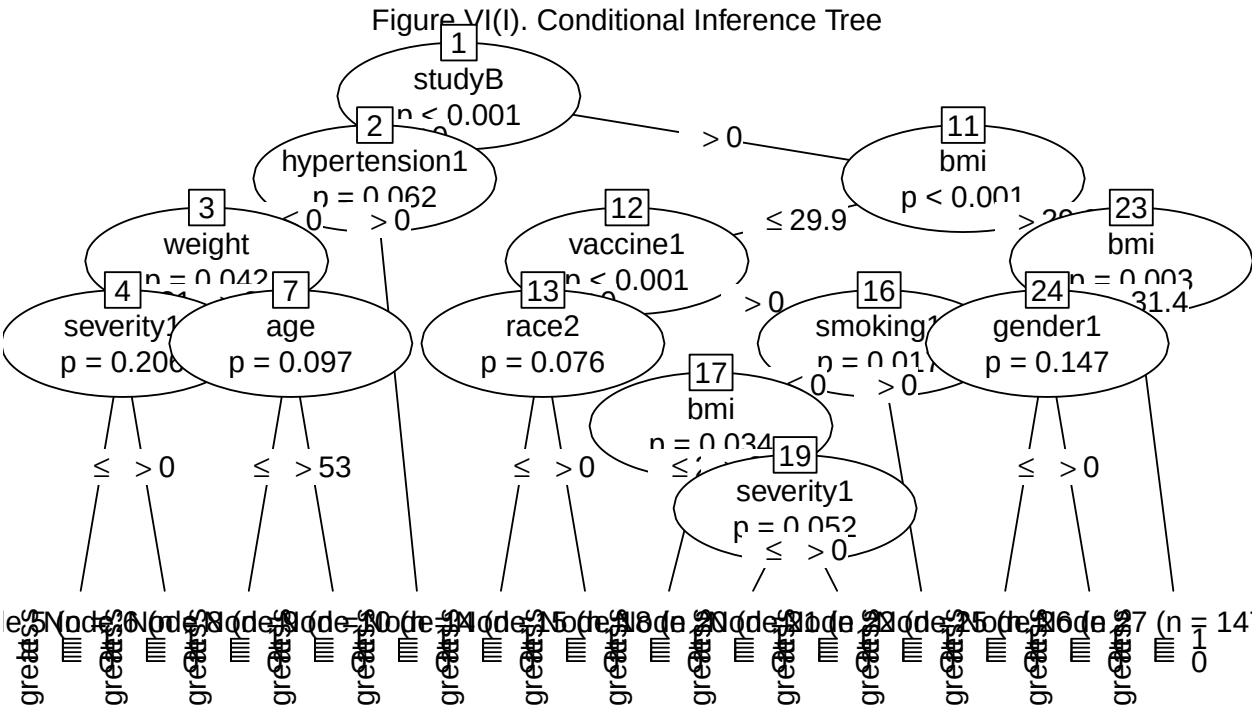

```
# Choose best tuning parameter value:
rpart$bestTune
##             cp
## 17 0.009151133

# Report the CV ROC
rpart$results[17, ]$ROC
## [1] 0.6856528
# Report the training error rate:
rpart.train = predict(rpart, newdata = training_sec)
rpart_error = 1 - sum(y_sec == rpart.train)/length(y_sec)
sprintf("The training error rate for classfication tree is %.3f", rpart_error)
## [1] "The training error rate for classfication tree is 0.265"
```

[Describe the outputs above]

Conditional Inference Tree:

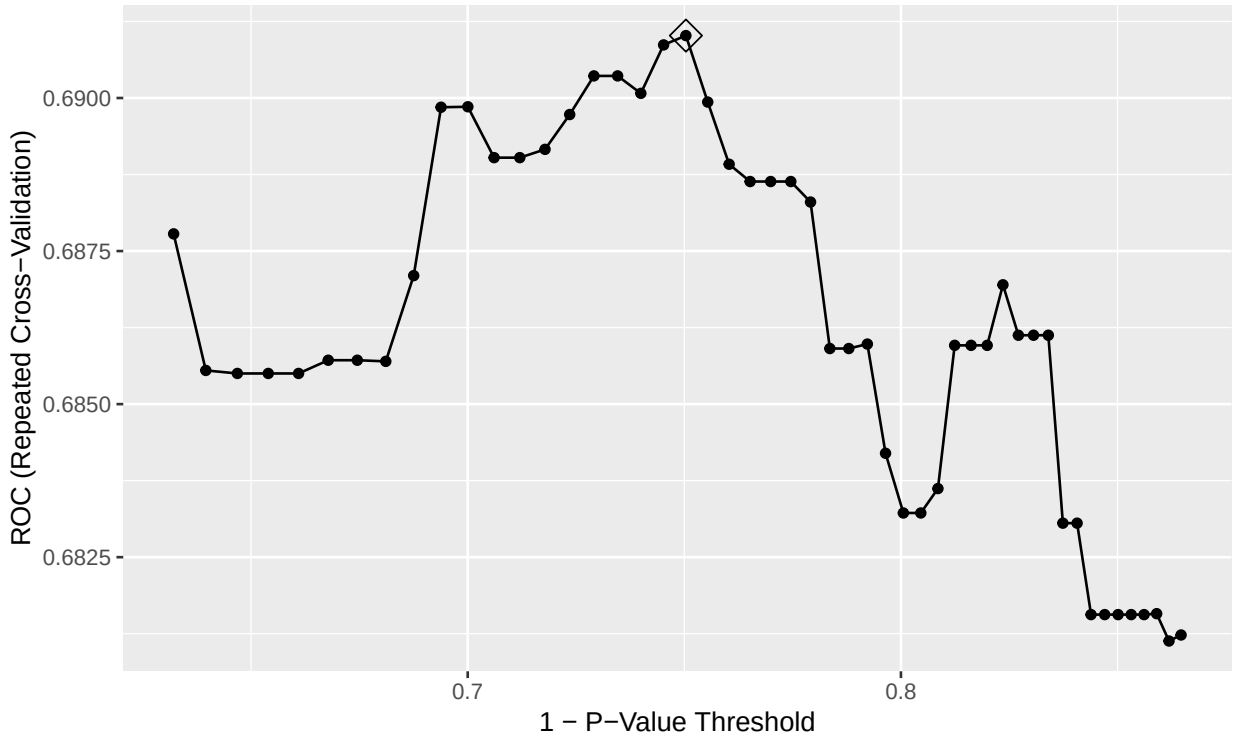
```
set.seed(3521)
ctree = train(recovery_time ~ . ,
                  data = training_sec,
                  method = "ctree",
                  tuneGrid = data.frame(mincriterion = 1 - exp(seq(-2, -1, length = 50))),
                  trControl = ctrl1,
                  metric = "ROC")
```

```
# Plot for CIT:
plot(ctree$finalModel, main = ("Figure VI(I). Conditional Inference Tree"))
```




```
# Plot for tuning parameter selection:
ggplot(ctree, highlight = T) + ggtitle("Figure VI(II). CIT Model CV ROC Plot")
```

Figure VI(II). CIT Model CV ROC Plot



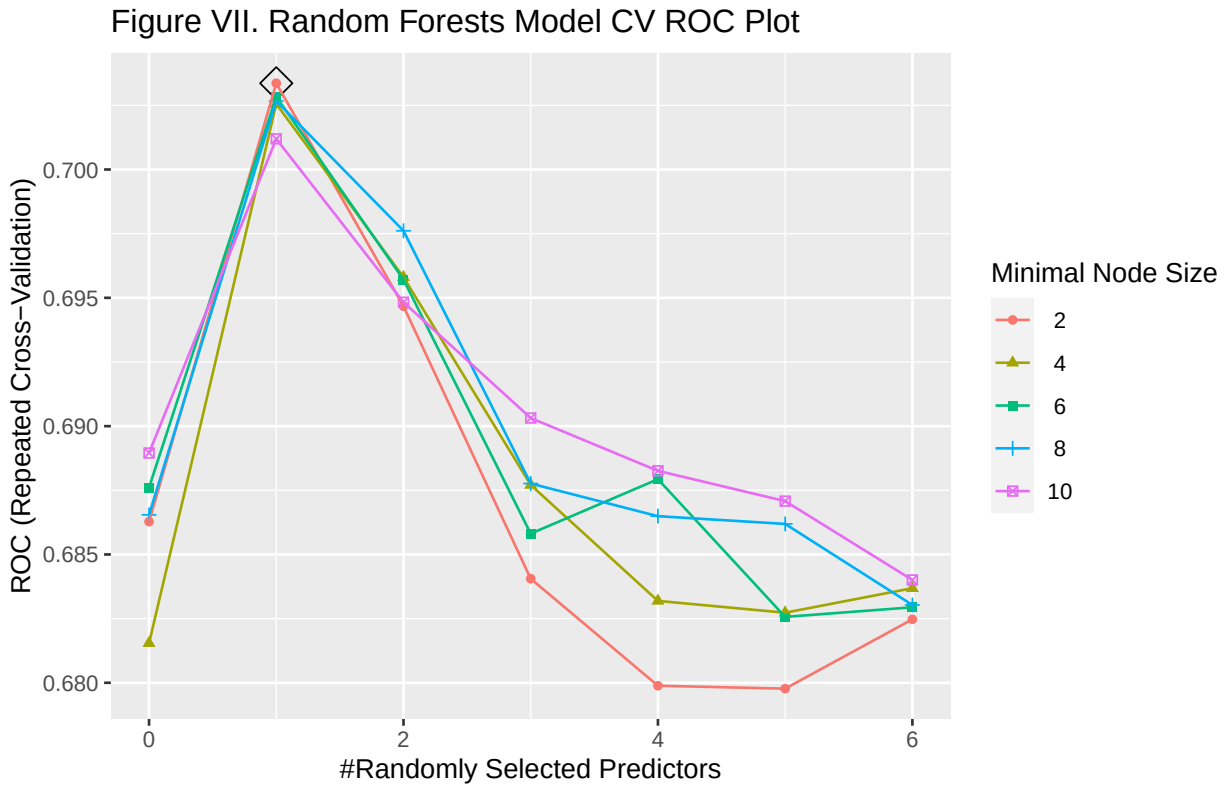

```
# Choose best tuning parameter value:
ctree$bestTune
##    mincriterion
## 20    0.7503649

# Report the CV ROC
ctree$results[20, ]$ROC
## [1] 0.6910193
# Report the training error rate:
ctree.train = predict(ctree, newdata = training_sec)
ctree_error = 1 - sum(y_sec == ctree.train)/length(y_sec)
sprintf("The training error rate for conditional inference tree is %.3f", ctree_error)
## [1] "The training error rate for conditional inference tree is 0.261"
```

[Describe the outputs above]

Random Forests for binary response:

```
rf.grid = expand.grid(mtry = 0:6,
                      splitrule = "gini",
                      min.node.size = seq(from = 2, to = 10, by = 2))
set.seed(3521)
cl = makePSOCKcluster(no_cores)
registerDoParallel(cl)
rf_2 = train(recovery_time ~ . ,
```

```
              data = training_sec,
              method = "ranger",
              tuneGrid = rf.grid,
              trControl = ctrl1,
              metric = "ROC")
stopCluster(cl)
registerDoSEQ()

# Plot for tuning parameter selection:
ggplot(rf_2, highlight = TRUE) + ggtitle("Figure VII. Random Forests Model CV ROC Plot")
```

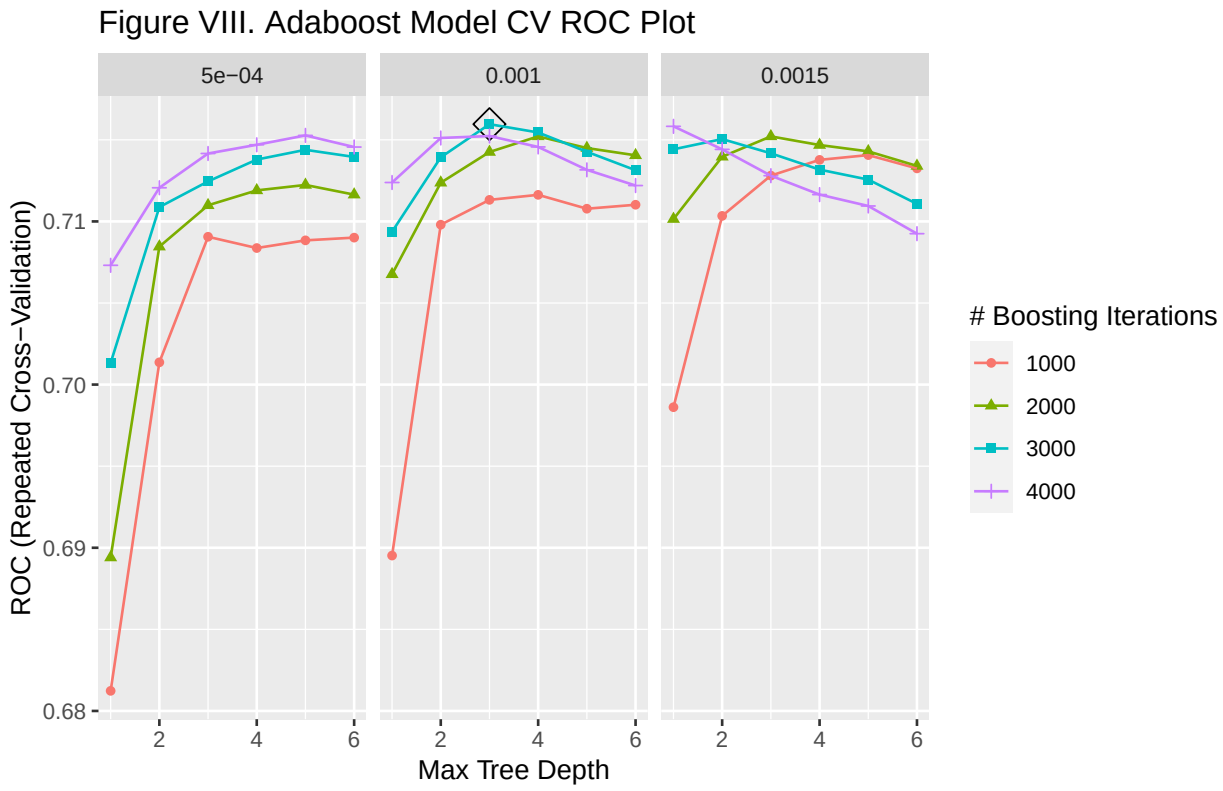



```
# Choose best tuning parameter value:
rf_2$bestTune
##   mtry splitrule min.node.size
## 6    1      gini             2

# Report the CV ROC
rf_2$results[6,]$ROC
## [1] 0.703361
# Report the training error rate:
rf_2.train = predict(rf_2, newdata = training_sec)
rf_2_error = 1 - sum(y_sec == rf_2.train)/length(y_sec)
sprintf("The training error rate for random forests is %.3f", rf_2_error)
## [1] "The training error rate for random forests is 0.293"
```

[Describe the outputs above]

Adaboost Model:

```
gbmA.grid = expand.grid(n.trees = c(1000, 2000, 3000, 4000),
                        interaction.depth = 1:6,
                        shrinkage = c(0.0005, 0.001, 0.0015),
                        n.minobsinnode = 1)
set.seed(3521)
cl = makePSOCKcluster(no_cores)
registerDoParallel(cl)
Adaboost = train(recovery_time ~ . ,
                 data = training_sec,
                 tuneGrid = gbmA.grid,
                 trControl = ctrl1,
                 method = "gbm",
                 distribution = "adaboost",
                 metric = "ROC",
                 verbose = FALSE)
stopCluster(cl)
registerDoSEQ()

# Plot for tuning parameter selection:
ggplot(Adaboost, highlight = TRUE) + ggtitle("Figure VIII. Adaboost Model CV ROC Plot")
```




```
# Choose best tuning parameter value:
Adaboost$bestTune
##    n.trees interaction.depth shrinkage n.minobsinnode
```

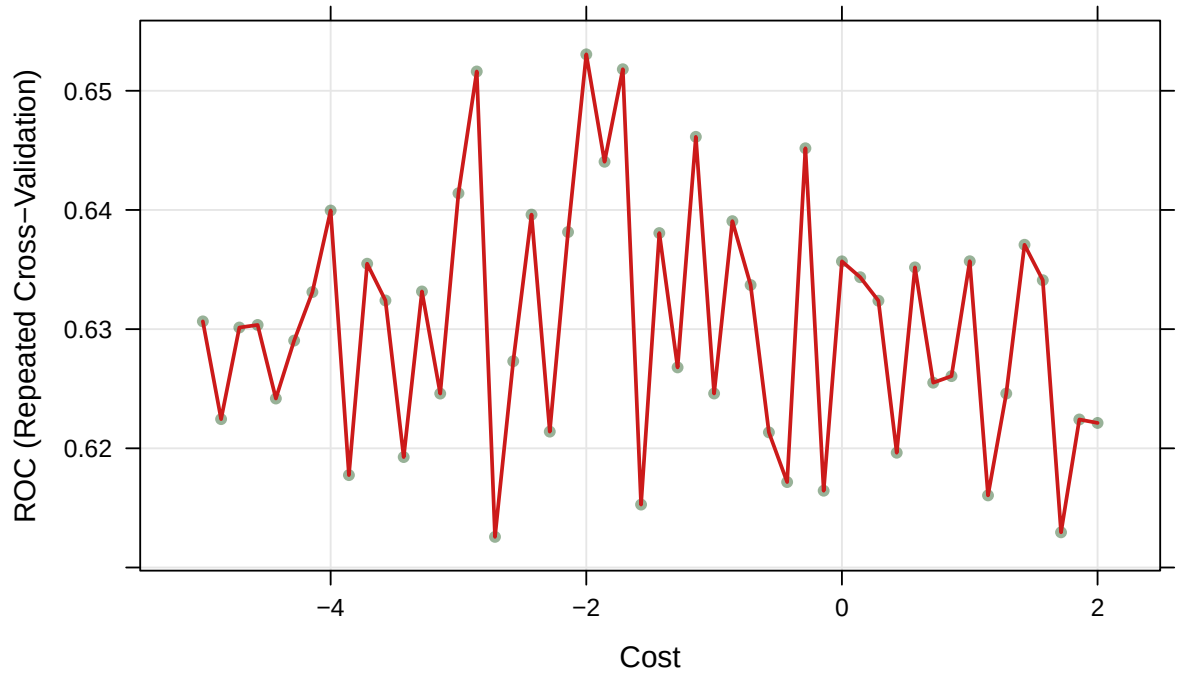
```
## 35    3000                 3     0.001              1

# Report the CV ROC:
Adaboost$results[44,]$ROC
## [1] 0.7159581
# Report the training error rate:
Adaboost.train = predict(Adaboost, newdata = training_sec)
Adaboost_error = 1 - sum(y_sec == Adaboost.train)/length(y_sec)
sprintf("The training error rate for Adaboost is %.3f", Adaboost_error)
## [1] "The training error rate for Adaboost is 0.275"
```

[Describe the outputs above]

Support Vector Machine (linear kernel):

```
set.seed(3521)
# kernlab
cl = makePSOCKcluster(no_cores)
registerDoParallel(cl)
svml = train(recovery_time ~ . ,
             training_sec,
             method = "svmLinear",
             tuneGrid = data.frame(C = exp(seq(-5, 2, len = 50))),
             trControl = ctrl1)
## maximum number of iterations reached 0.007078654 0.006600204
stopCluster(cl)
registerDoSEQ()
# Plot for tuning parameter selection:
plot(svml, highlight = TRUE, xTrans = log, main = ("Figure IX. SVM(linear) Model CV ROC Plot"))
```

Figure IX. SVM(linear) Model CV ROC Plot



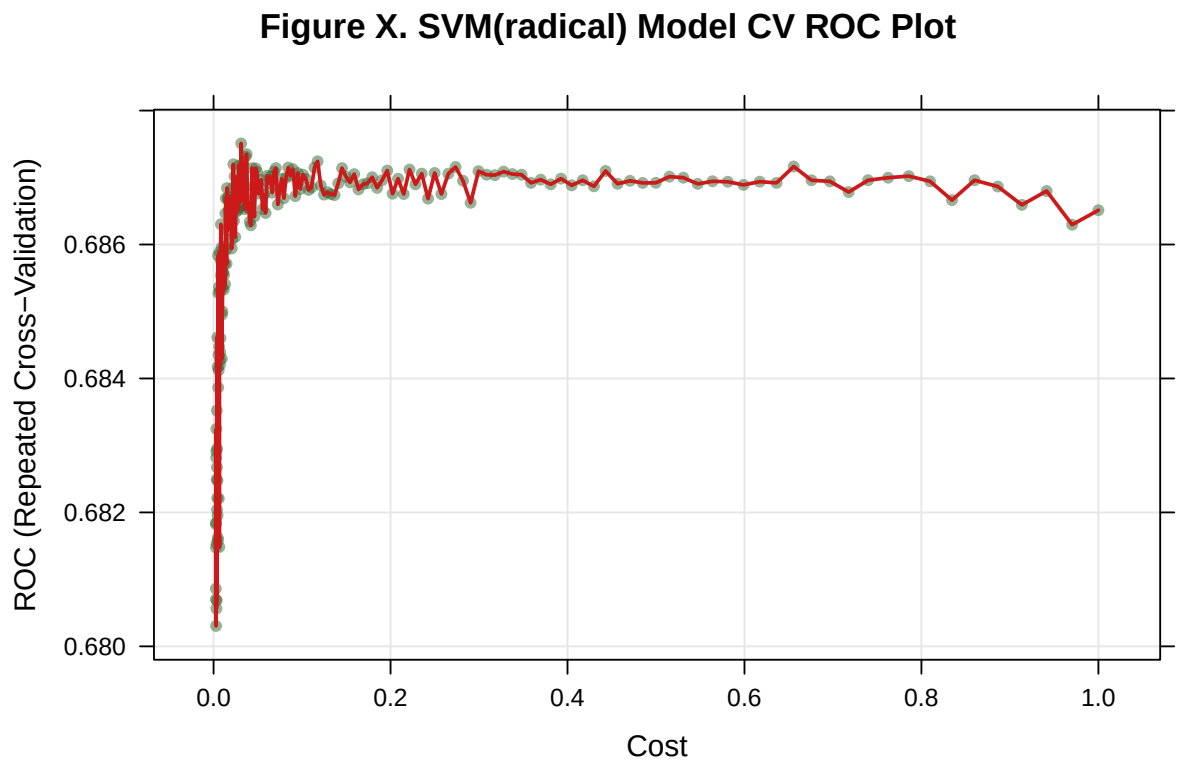

```
# Choose best tuning parameter value:
svml$bestTune
##            C
## 22 0.1353353

# Report the CV ROC:
svml$results[22, ]$ROC
## [1] 0.6530562
# Report the training error rate:
svml.train = predict(svml, newdata = training_sec)
svml_error = 1 - sum(y_sec == svml.train)/length(y_sec)
sprintf("The training error rate for SVM(linear) is %.3f", svml_error)
## [1] "The training error rate for SVM(linear) is 0.295"
```

[Describe the outputs above]

Support Vector Machine (radical kernel):

```
set.seed(3521)
cl = makePSOCKcluster(no_cores)
registerDoParallel(cl)
svmr = train(recovery_time ~ . ,
             training_sec,
             method = "svmRadialCost",
             tuneGrid = data.frame(C = exp(seq(-6, 0, len = 200))),
```

```
             trControl = ctrl1)
stopCluster(cl)
registerDoSEQ()
# Plot for tuning parameter selection:
myCol = rainbow(25)
myPar = list(superpose.symbol = list(col = myCol),
             superpose.line = list(col = myCol))
plot(svmr, highlight = TRUE, par.settings = myPar, main = "Figure X. SVM(radical) Model CV ROC Plot")
```




```
# Choose best tuning parameter value:
svmr$bestTune
##             C
## 85 0.03120002
# Report the CV ROC
svmr$results[85,]$ROC
## [1] 0.6875091
# Report the training error rate:
svmr.train = predict(svmr, newdata = training_sec)
svmr_error = 1 - sum(y_sec == svmr.train)/length(y_sec)
sprintf("The training error rate for SVM(radical) is %.3f", svmr_error)
## [1] "The training error rate for SVM(radical) is 0.263"
```

[Describe the outputs above]

Results:

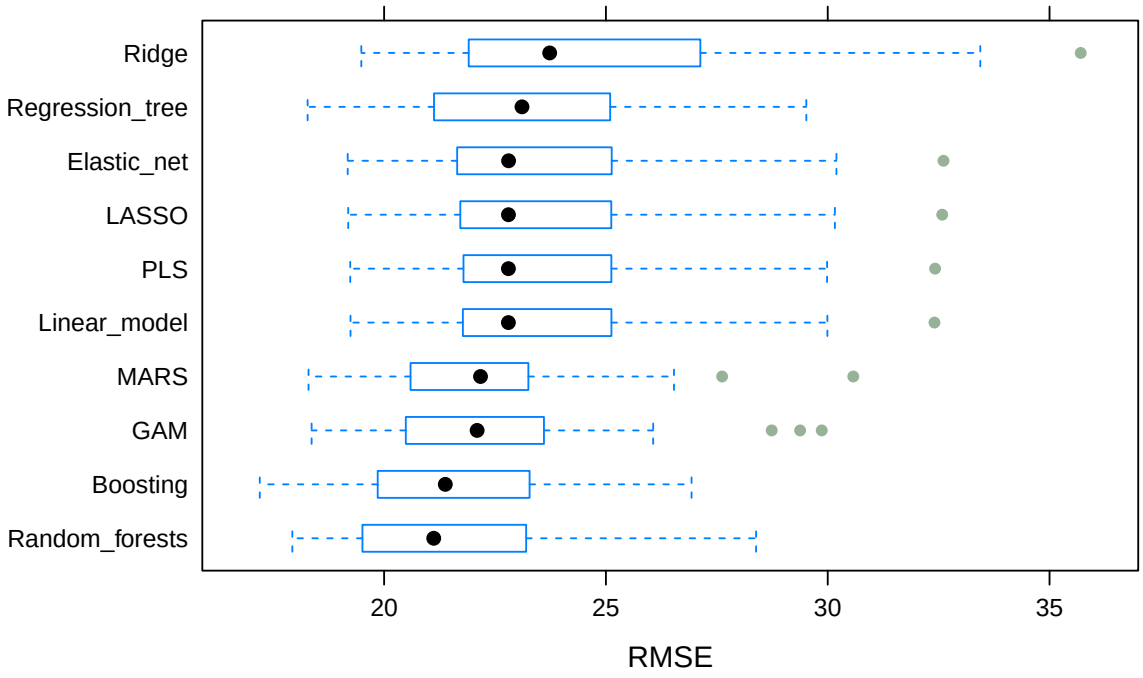
Model Comparison:

For Primary Analysis:

```
set.seed(3521)
# Resample all of the methods in primary analysis:
resamp1 = resamples(list(
  "Linear_model" = lm,
  "LASSO" = lasso,
  "Ridge" = ridge,
  "Elastic_net" = enet,
  "PLS" = pls,
  "GAM" = gam,
  "MARS" = mars,
  "Regression_tree" = reg_tree,
  "Random_forests" = rf,
  "Boosting" = boosting
  ))
summary(resamp1)
##
## Call:
## summary.resamples(object = resamp1)
##
## Models: Linear_model, LASSO, Ridge, Elastic_net, PLS, GAM, MARS, Regression_tree, Random_forests, Bo
## Number of resamples: 50
##
## MAE
##                     Min.  1st Qu.   Median     Mean  3rd Qu.     Max. NA's
## Linear_model    14.67066 15.48991 16.06302 16.07955 16.53136 18.59989    0
## LASSO           14.59644 15.45096 15.99727 16.02049 16.45200 18.61698    0
## Ridge           14.38506 15.47548 15.87450 16.14349 16.83170 19.21320    0
## Elastic_net     14.57525 15.43960 15.97740 16.00604 16.44358 18.62216    0
## PLS             14.66805 15.49701 16.05942 16.08032 16.52859 18.61425    0
## GAM             13.59118 14.63653 15.16649 15.26451 15.74815 17.93186    0
## MARS            13.29454 14.38035 14.93388 14.85769 15.29974 17.36569    0
## Regression_tree 13.22010 14.61298 15.37972 15.32896 15.93998 17.32648    0
## Random_forests  13.07957 13.91055 14.61469 14.60152 15.05324 17.06594    0
## Boosting        12.73787 13.82567 14.44318 14.47372 15.00029 16.51907    0
##
## RMSE
##                     Min.  1st Qu.   Median     Mean  3rd Qu.     Max. NA's
## Linear_model    19.24267 21.79072 22.80191 23.81421 25.11510 32.40665    0
## LASSO           19.19072 21.73038 22.80289 23.80994 25.11060 32.58078    0
## Ridge           19.48590 21.95264 23.73214 24.95401 26.99573 35.70395    0
## Elastic_net     19.17912 21.67101 22.80645 23.80708 25.11863 32.60958    0
## PLS             19.23641 21.79956 22.80225 23.81368 25.11166 32.42073    0
## GAM             18.36556 20.52376 22.09691 22.36731 23.56738 29.86491    0
## MARS            18.29645 20.63415 22.17322 22.17363 23.23657 30.57617    0
## Regression_tree 18.27611 21.20505 23.10804 23.37935 25.06393 29.51805    0
## Random_forests  17.93140 19.57875 21.11887 21.66980 23.18764 28.38505    0
```

```
## Boosting        17.19735 19.85962 21.37935 21.49009 23.24254 26.93013    0
##
## Rsquared
##                       Min.   1st Qu.    Median      Mean   3rd Qu.      Max.
## Linear_model    0.07678700 0.1653324 0.2191504 0.2198027 0.2795802 0.3579423
## LASSO           0.07709354 0.1649789 0.2189348 0.2195261 0.2776934 0.3527277
## Ridge           0.03016220 0.1169776 0.1425677 0.1396430 0.1632161 0.2475719
## Elastic_net     0.07721286 0.1648110 0.2185774 0.2194180 0.2767432 0.3513515
## PLS             0.07723723 0.1654364 0.2186331 0.2198240 0.2803928 0.3566991
## GAM             0.12552650 0.2620688 0.3109112 0.3206620 0.3825147 0.5369269
## MARS            0.06791574 0.2488748 0.3366009 0.3286455 0.4043277 0.6317201
## Regression_tree 0.05203186 0.2069548 0.2672614 0.2610381 0.3281899 0.5326210
## Random_forests  0.12816879 0.2775967 0.3654901 0.3481470 0.4201052 0.5362815
## Boosting        0.11760843 0.2757646 0.3449788 0.3589667 0.4516057 0.5960014
##                 NA's
## Linear_model       0
## LASSO              0
## Ridge              0
## Elastic_net        0
## PLS                0
## GAM                0
## MARS               0
## Regression_tree    0
## Random_forests     0
## Boosting           0
# RMSE plots for all models:
bwplot(resamp1,
       metric = "RMSE",
       main = "Figure 12. Primary Analysis: Model Comparison Plot Using RMSE")
```

Figure 12. Primary Analysis: Model Comparison Plot Using RMSE



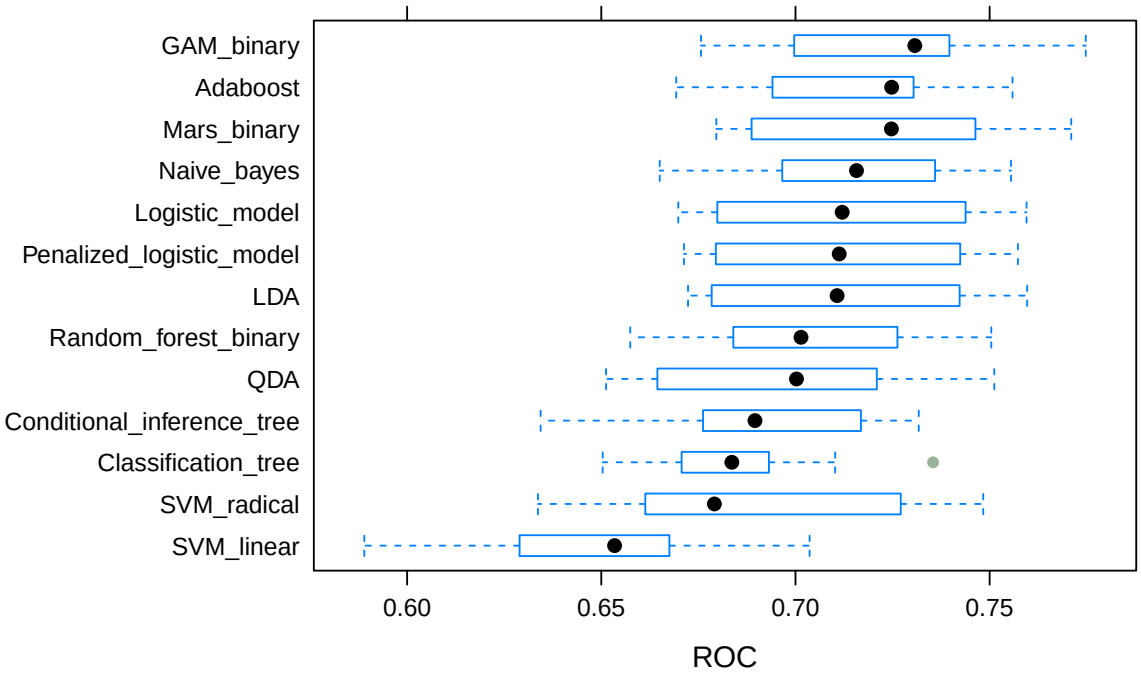
For Secondary Analysis:

```
set.seed(3521)
# Resample all of the methods in secondary analysis:
resamp2 = resamples(list(
  "Logistic_model" = glm,
  "Penalized_logistic_model" = glmn,
  "GAM_binary" = gam_2,
  "Mars_binary" = mars_2,
  "LDA" = lda,
  "QDA" = qda,
  "Naive_bayes" = nb,
  "Classification_tree" = rpart,
  "Conditional_inference_tree" = ctree,
  "Random_forest_binary" = rf_2,
  "Adaboost" = Adaboost,
  "SVM_linear" = svml,
  "SVM_radical" = svmr
  ))
summary(resamp2)
##
## Call:
## summary.resamples(object = resamp2)
##
## Models: Logistic_model, Penalized_logistic_model, GAM_binary, Mars_binary, LDA, QDA, Naive_bayes, Cl
## Number of resamples: 10
```

```
##
## ROC
##                                Min.   1st Qu.    Median      Mean   3rd Qu.
## Logistic_model             0.6698299 0.6816909 0.7120286 0.7095743 0.7363762
## Penalized_logistic_model   0.6712724 0.6814426 0.7112594 0.7092228 0.7358687
## GAM_binary                 0.6756757 0.7017803 0.7307370 0.7248379 0.7385734
## Mars_binary                0.6796234 0.6965818 0.7247028 0.7235168 0.7461700
## LDA                        0.6723353 0.6817607 0.7107197 0.7100636 0.7354306
## QDA                        0.6512299 0.6694437 0.7002606 0.6965235 0.7172734
## Naive_bayes                0.6650471 0.6980837 0.7157116 0.7131731 0.7332410
## Classification_tree        0.6503568 0.6714696 0.6836155 0.6856528 0.6922137
## Conditional_inference_tree 0.6343759 0.6780515 0.6895683 0.6910193 0.7123633
## Random_forest_binary       0.6574552 0.6849710 0.7014267 0.7033610 0.7241463
## Adaboost                   0.6692985 0.6951884 0.7247659 0.7159581 0.7300870
## SVM_linear                 0.5889766 0.6336666 0.6534191 0.6530562 0.6654053
## SVM_radical                0.6336845 0.6618395 0.6791257 0.6875091 0.7175166
##                                Max. NA's
## Logistic_model             0.7595044    0
## Penalized_logistic_model   0.7572726    0
## GAM_binary                 0.7747422    0
## Mars_binary                0.7710097    0
## LDA                        0.7596583    0
## QDA                        0.7511929    0
## Naive_bayes                0.7555025    0
## Classification_tree        0.7354236    0
## Conditional_inference_tree 0.7317416    0
## Random_forest_binary       0.7504233    0
## Adaboost                   0.7558873    0
## SVM_linear                 0.7036324    0
## SVM_radical                0.7483454    0
##
## Sens
##                                Min.   1st Qu.    Median      Mean   3rd Qu.
## Logistic_model             0.8587571 0.8832683 0.9213483 0.9155494 0.9409160
## Penalized_logistic_model   0.8757062 0.8928061 0.9267759 0.9211801 0.9452247
## GAM_binary                 0.8361582 0.8903304 0.9157303 0.9110296 0.9367978
## Mars_binary                0.8418079 0.9015584 0.9154923 0.9104869 0.9241573
## LDA                        0.8700565 0.8998524 0.9241573 0.9223037 0.9451295
## QDA                        0.6685393 0.7009855 0.7295436 0.7270710 0.7556180
## Naive_bayes                0.9887006 0.9957865 1.0000000 0.9977433 1.0000000
## Classification_tree        0.8418079 0.8843316 0.8957818 0.8969784 0.9073034
## Conditional_inference_tree 0.8418079 0.8621770 0.8873389 0.8924744 0.8974719
## Random_forest_binary       1.0000000 1.0000000 1.0000000 1.0000000 1.0000000
## Adaboost                   0.9491525 0.9746001 0.9859233 0.9802863 0.9887640
## SVM_linear                 0.9831461 0.9943582 0.9971910 0.9955024 1.0000000
## SVM_radical                0.8870056 0.9194915 0.9438202 0.9374913 0.9550562
##                                Max. NA's
## Logistic_model             0.9719101    0
## Penalized_logistic_model   0.9775281    0
## GAM_binary                 0.9550562    0
## Mars_binary                0.9662921    0
## LDA                        0.9775281    0
## QDA                        0.7696629    0
```

```
## Naive_bayes                 1.0000000    0
## Classification_tree         0.9438202    0
## Conditional_inference_tree 1.0000000    0
## Random_forest_binary        1.0000000    0
## Adaboost                    1.0000000    0
## SVM_linear                  1.0000000    0
## SVM_radical                 0.9719101    0
##
## Spec
##                                   Min.    1st Qu.     Median        Mean
## Logistic_model              0.10958904 0.18655128 0.22445391 0.222713810
## Penalized_logistic_model    0.09589041 0.17905405 0.21232877 0.213198815
## GAM_binary                  0.21621622 0.25763606 0.26527212 0.275823769
## Mars_binary                 0.22972973 0.26106072 0.29257682 0.292132544
## LDA                         0.09589041 0.16891892 0.21917808 0.213254350
## QDA                         0.50000000 0.54947242 0.56756757 0.570844132
## Naive_bayes                 0.00000000 0.00000000 0.00000000 0.002702703
## Classification_tree         0.21621622 0.27980378 0.31978897 0.311069974
## Conditional_inference_tree 0.01369863 0.31418919 0.32654572 0.303998519
## Random_forest_binary        0.00000000 0.00000000 0.00000000 0.000000000
## Adaboost                    0.02739726 0.04433543 0.06756757 0.073232136
## SVM_linear                  0.00000000 0.00000000 0.00000000 0.005423917
## SVM_radical                 0.10958904 0.13990189 0.17123288 0.173768974
##                                3rd Qu.       Max. NA's
## Logistic_model              0.25939467 0.29729730    0
## Penalized_logistic_model    0.25421140 0.29729730    0
## GAM_binary                  0.29794521 0.33783784    0
## Mars_binary                 0.32094595 0.35616438    0
## LDA                         0.26629026 0.28378378    0
## QDA                         0.58367271 0.65753425    0
## Naive_bayes                 0.00000000 0.01351351    0
## Classification_tree         0.33783784 0.41891892    0
## Conditional_inference_tree 0.34130877 0.43243243    0
## Random_forest_binary        0.00000000 0.00000000    0
## Adaboost                    0.08191411 0.16216216    0
## SVM_linear                  0.01013514 0.02702703    0
## SVM_radical                 0.19932432 0.25675676    0
# RMSE plots for all models:
bwplot(resamp2,
       metric = "ROC",
       main = "Figure XI. Secondary Analysis: Model Comparison Plot Using ROC")
```

Figure XI. Secondary Analysis: Model Comparison Plot Using ROC



From the outputs, we choose random forests for primary analysis and GAM model for secondary analysis.

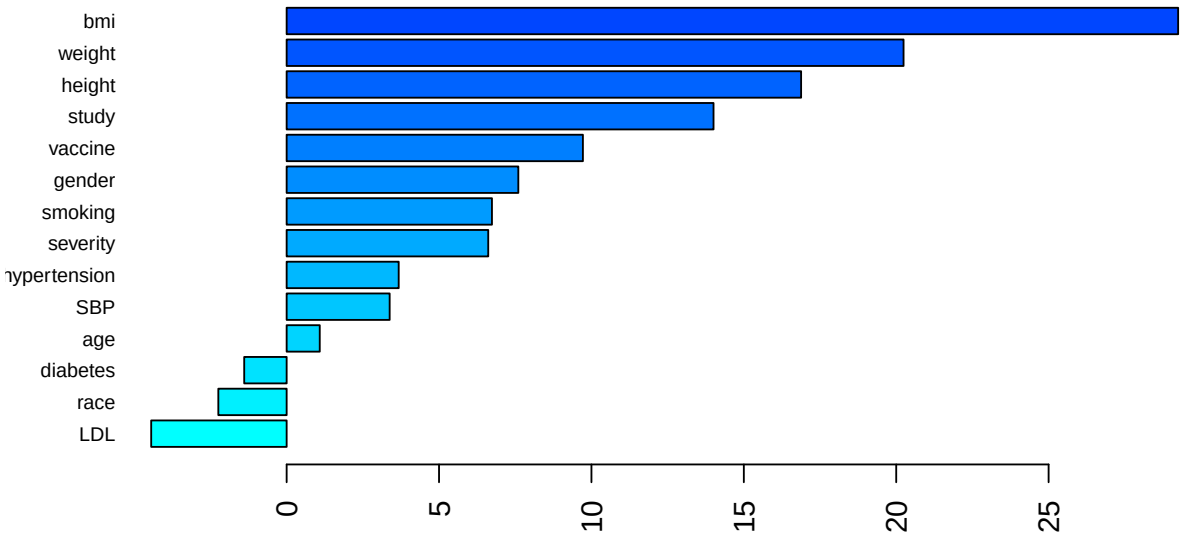
Final model interpretation

Primary analysis: (Random Forests)

Extract the variable importance:

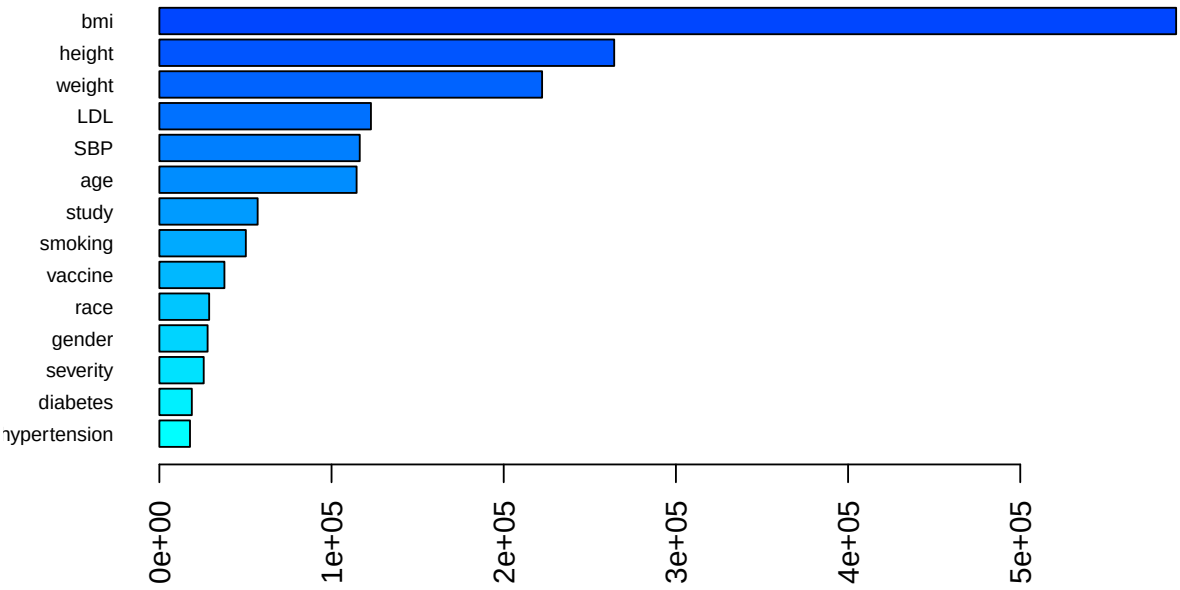
```
# Permutation:
set.seed(3521)
rf.per = ranger(recovery_time ~ .,
                data = training,
                mtry = rf$bestTune[[1]],
                splitrule = "variance",
                min.node.size = rf$bestTune[[3]],
                importance = "permutation",
                scale.permutation.importance = TRUE)
barplot(sort(importance(rf.per), decreasing = FALSE),
        las = 2, horiz = TRUE, cex.names = 0.7,
        col = colorRampPalette(colors = c("cyan", "blue"))(19),
        main = "Figure 10.1. Variable Importance by OOB permutation")
```

Figure 10.1. Variable Importance by OOB permutation




```
# Impurity:
set.seed(3521)
rf.imp = ranger(recovery_time ~ .,
                data = training,
                mtry = rf$bestTune[[1]],
                splitrule = "variance",
                min.node.size = rf$bestTune[[3]],
                importance = "impurity")
barplot(sort(importance(rf.imp), decreasing = FALSE),
        las = 2, horiz = TRUE, cex.names = 0.7,
        col = colorRampPalette(colors = c("cyan", "blue"))(19),
        main = "Figure 10.2. Variable Importance by Node Impurities")
```

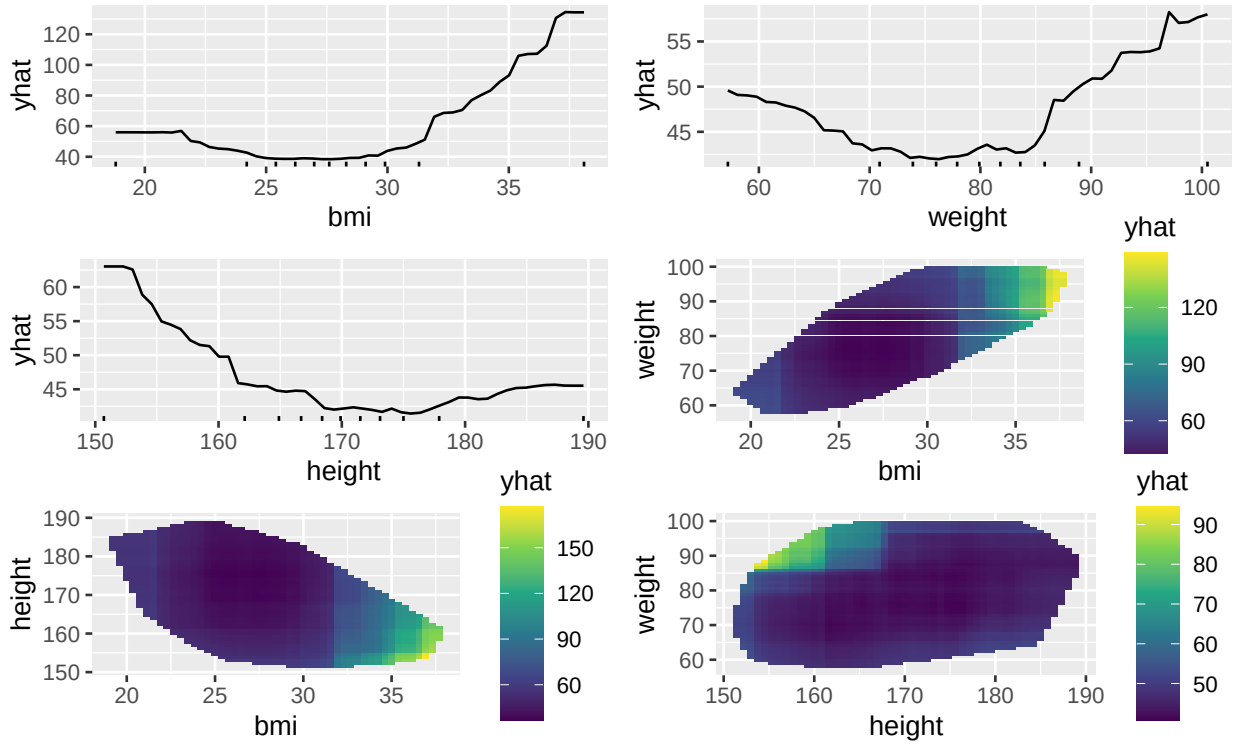
Figure 10.2. Variable Importance by Node Impurities



Partial dependence plots:

```
p1 = partial(rf, pred.var = "bmi",
     plot = TRUE, rug = TRUE,
     plot.engine = "ggplot")
p2 = partial(rf, pred.var = "weight",
     plot = TRUE, rug = TRUE,
     plot.engine = "ggplot")
p3 = partial(rf, pred.var = "height",
     plot = TRUE, rug = TRUE,
     plot.engine = "ggplot")
p4 = rf %>%
     partial(pred.var = c("bmi", "weight"), chull = TRUE) %>%
     autoplot(train = training, rug = TRUE)
p5 = rf %>%
     partial(pred.var = c("bmi", "height"), chull = TRUE) %>%
     autoplot(train = training, rug = TRUE)
p6 = rf %>%
     partial(pred.var = c("height", "weight"), chull = TRUE) %>%
     autoplot(train = training, rug = TRUE)
grid.arrange(p1, p2, p3, p4, p5, p6, nrow = 3, top = "Figure 10.3. Random Forests' PDPs for Important Va
```

Figure 10.3. Random Forests' PDPs for Important Variables

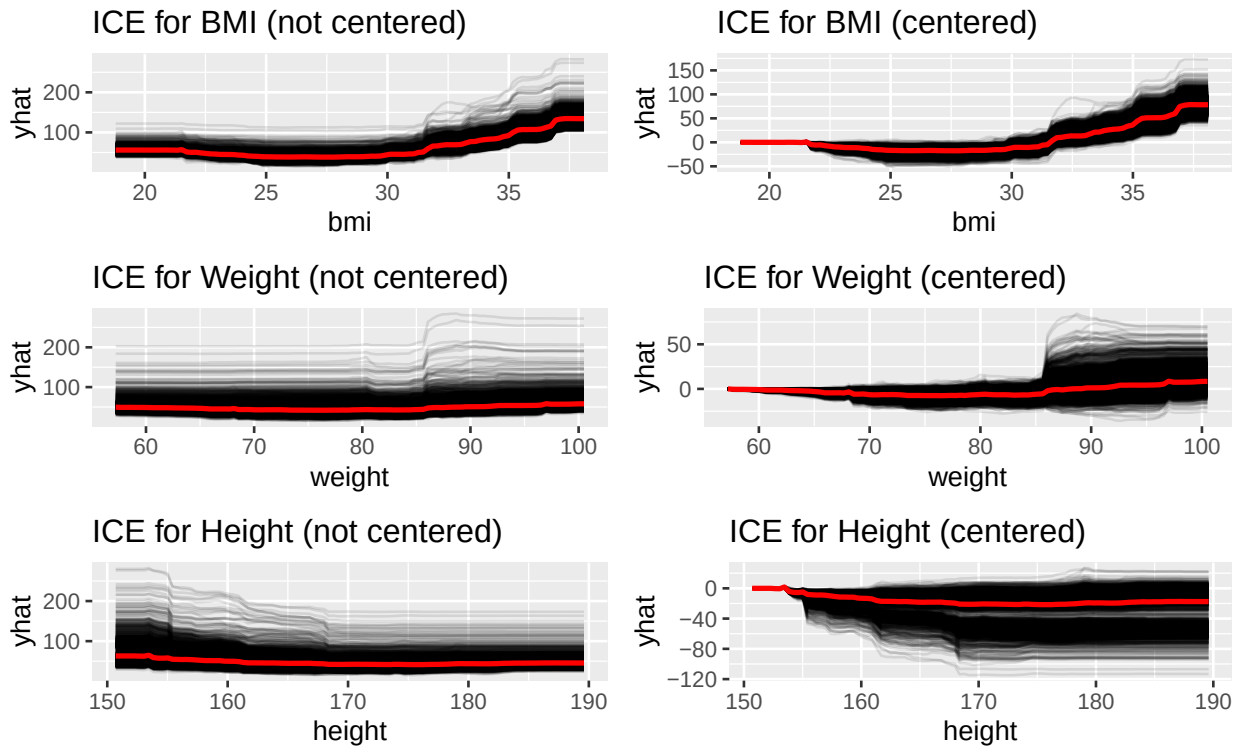


Individual conditional expectation curves (ICE):

```
ice1 = rf %>%
  partial(pred.var = "bmi",
          grid.resolution = 100,
          ice = TRUE) %>%
  autoplot(train = rf, alpha = 0.1) + ggtitle("ICE for BMI (not centered)")
ice2 = rf %>%
  partial(pred.var = "bmi",
          grid.resolution = 100,
          ice = TRUE) %>%
  autoplot(train = rf, alpha = 0.1, center = TRUE) + ggtitle("ICE for BMI (centered)")
ice3 = rf %>%
  partial(pred.var = "weight",
          grid.resolution = 100,
          ice = TRUE) %>%
  autoplot(train = rf, alpha = 0.1) + ggtitle("ICE for Weight (not centered)")
ice4 = rf %>%
  partial(pred.var = "weight",
          grid.resolution = 100,
          ice = TRUE) %>%
  autoplot(train = rf, alpha = 0.1, center = TRUE) + ggtitle("ICE for Weight (centered)")
ice5 = rf %>%
  partial(pred.var = "height",
          grid.resolution = 100,
          ice = TRUE) %>%
  autoplot(train = rf, alpha = 0.1) + ggtitle("ICE for Height (not centered)")
ice6 = rf %>%
```

```
  partial(pred.var = "height",
          grid.resolution = 100,
          ice = TRUE) %>%
  autoplot(train = rf, alpha = 0.1, center = TRUE) + ggtitle("ICE for Height (centered)")

grid.arrange(ice1, ice2, ice3, ice4, ice5, ice6, nrow = 3, top = "Figure 10.4. ICE for Importance Varial
```

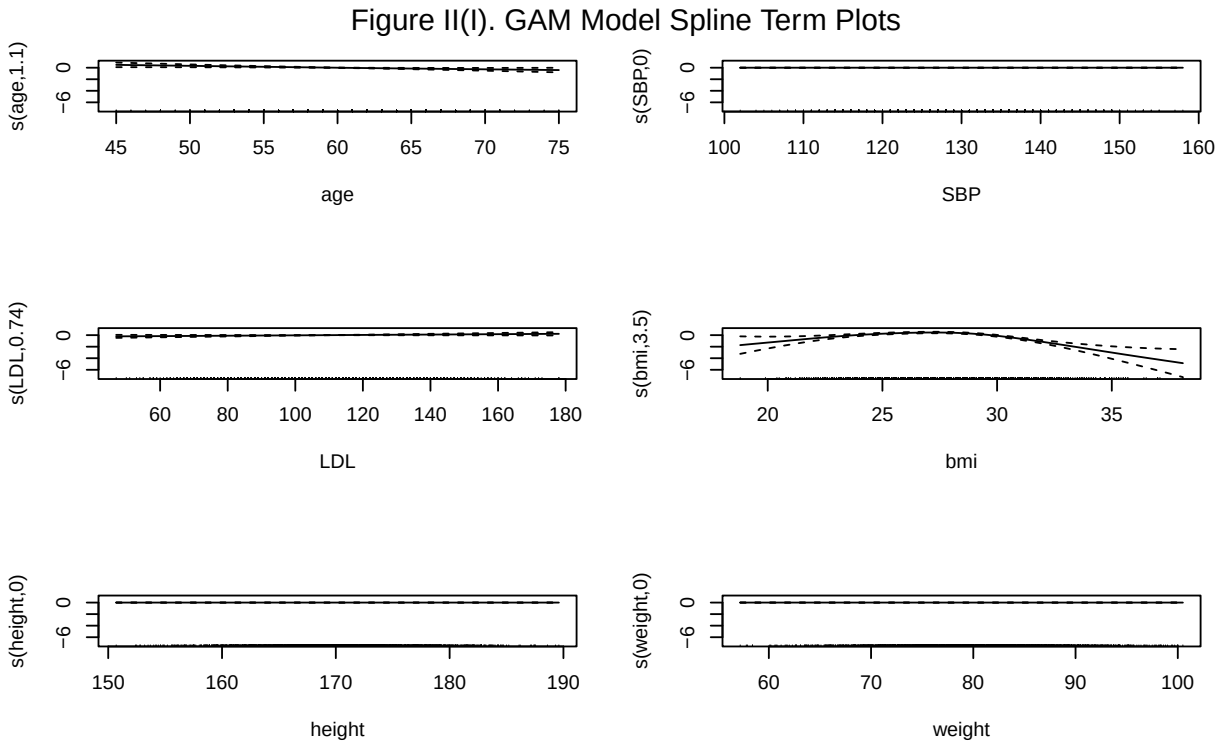
Figure 10.4. ICE for Importance Variables



Secondary analysis: (GAM model)

```
gam_2$finalModel
##
## Family: binomial
## Link function: logit
##
## 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:
## 1.1015 0.0003 0.7375 3.4962 0.0001 0.0001  total = 17.34
##
## UBRE score: 0.07088461
```

```r
par(mfrow = c(3, 2))
plot(gam_2$finalModel)
mtext("Figure II(I). GAM Model Spline Term Plots", side = 3, line = -3, outer = TRUE)
```



Report the training and test performance

Primary analysis:

```r
# Cross validation error:
rf$results[42, ]$RMSE
## [1] 21.6698
# Test error:
rf_pred = predict(rf, newdata = x2)
rf_mse = sqrt(mean((rf_pred - y2)^2))
rf_mse
## [1] 25.76281
```

Secondary analysis:

```r
# Training error rate:
gam_2.train = predict(gam_2, newdata = training_sec)
gam_2_error = 1 - sum(y_sec == gam_2.train)/length(y_sec)
gam_2_error
```

```
## [1] 0.2682053
# Test error rate:
gam_2.test = predict(gam_2, newdata = test_sec)
gam_2_error_t = 1 - sum(y2_sec == gam_2.test)/length(y2_sec)
gam_2_error_t
## [1] 0.2858473
```

Conclusions:

[show it in the report]