Final Project

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```r
training_data <- training_data %>%
  janitor::clean_names() %>%
  dplyr::select(-id) %>%
  mutate(severity = case_match(as.numeric(severity),
                               1 ~ "Not Severe",
                               2 ~ "Severe"),
         severity = factor(severity),
         gender = case_match(gender,
                             1 ~ "Male",
                             0 ~ "Female"),
         race = case_match(as.numeric(race),
                           1 ~ "White",
                           2 ~ "Asian",
                           3 ~ "Black",
                           4 ~ "Hispanic"),
         smoking = case_match(as.numeric(smoking),
                              1 ~ "Never",
                              2 ~ "Former",
                              3 ~ "Current"),
         hypertension = case_match(hypertension,
                                   0 ~ "No",
                                   1 ~ "Yes"),
         diabetes = case_match(diabetes,
                               0 ~ "No",
                               1 ~ "Yes"),
         vaccine = case_match(vaccine,
                              0 ~ "Not Vaccinated",
                              1 ~ "Vaccinated")
         )
```

```r
test_data <- test_data %>%
  janitor::clean_names() %>%
  dplyr::select(-id) %>%
  mutate(severity = case_match(as.numeric(severity),
                               1 ~ "Not Severe",
                               2 ~ "Severe"),
         severity = factor(severity),
         gender = case_match(gender,
                             1 ~ "Male",
                             0 ~ "Female"),
         race = case_match(as.numeric(race),
                           1 ~ "White",
```

```r
                        2 ~ "Asian",
                        3 ~ "Black",
                        4 ~ "Hispanic"),
         smoking = case_match(as.numeric(smoking),
                           1 ~ "Never",
                           2 ~ "Former",
                           3 ~ "Current"),
         hypertension = case_match(hypertension,
                                0 ~ "No",
                                1 ~ "Yes"),
         diabetes = case_match(diabetes,
                            0 ~ "No",
                            1 ~ "Yes"),
         vaccine = case_match(vaccine,
                           0 ~ "Not Vaccinated",
                           1 ~ "Vaccinated")
         )
```

Exploratory analysis and data visualization

We will create box plots for continuous predictors such as Age, Height, Weight, BMI, Systolic blood pressure (SBP), LDL cholesterol (LDL), and Depression. These plots will show how these metrics vary with the severity of COVID-19.

```r
# Boxplot for Age vs. Severity
p1 <- ggplot(training_data, aes(x = factor(severity), y = age, fill = factor(severity))) +
  geom_boxplot() +
  labs(title = "Age vs. COVID-19 Severity", x = "Severity", y = "Age") +
  scale_fill_brewer(palette = "Set1")

# Boxplot for Height vs. Severity
p2 <- ggplot(training_data, aes(x = factor(severity), y = height, fill = factor(severity))) +
  geom_boxplot() +
  labs(title = "Height vs. COVID-19 Severity", x = "Severity", y = "Height") +
  scale_fill_brewer(palette = "Set1")

# Boxplot for Weight vs. Severity
p3 <- ggplot(training_data, aes(x = factor(severity), y = weight, fill = factor(severity))) +
  geom_boxplot() +
  labs(title = "Weight vs. COVID-19 Severity", x = "Severity", y = "Weight") +
  scale_fill_brewer(palette = "Set1")

# Boxplot for BMI vs. Severity
p4 <- ggplot(training_data, aes(x = factor(severity), y = bmi, fill = factor(severity))) +
  geom_boxplot() +
  labs(title = "BMI vs. COVID-19 Severity", x = "Severity", y = "BMI") +
  scale_fill_brewer(palette = "Set1")

# Boxplot for SBP vs. Severity
p5 <- ggplot(training_data, aes(x = factor(severity), y = sbp, fill = factor(severity))) +
  geom_boxplot() +
  labs(title = "Systolic Blood Pressure vs. COVID-19 Severity", x = "Severity", y = "Systolic BP") +
```

```r
  scale_fill_brewer(palette = "Set1")

# Boxplot for LDL vs. Severity
p6 <- ggplot(training_data, aes(x = factor(severity), y = ldl, fill = factor(severity))) +
  geom_boxplot() +
  labs(title = "LDL Cholesterol vs. COVID-19 Severity", x = "Severity", y = "LDL Cholesterol") +
  scale_fill_brewer(palette = "Set1")

# Boxplot for Depression vs. Severity
p7 <- ggplot(training_data, aes(x = factor(severity), y = depression, fill = factor(severity))) +
  geom_boxplot() +
  labs(title = "Depression vs. COVID-19 Severity", x = "Severity", y = "Depression") +
  scale_fill_brewer(palette = "Set1")
```

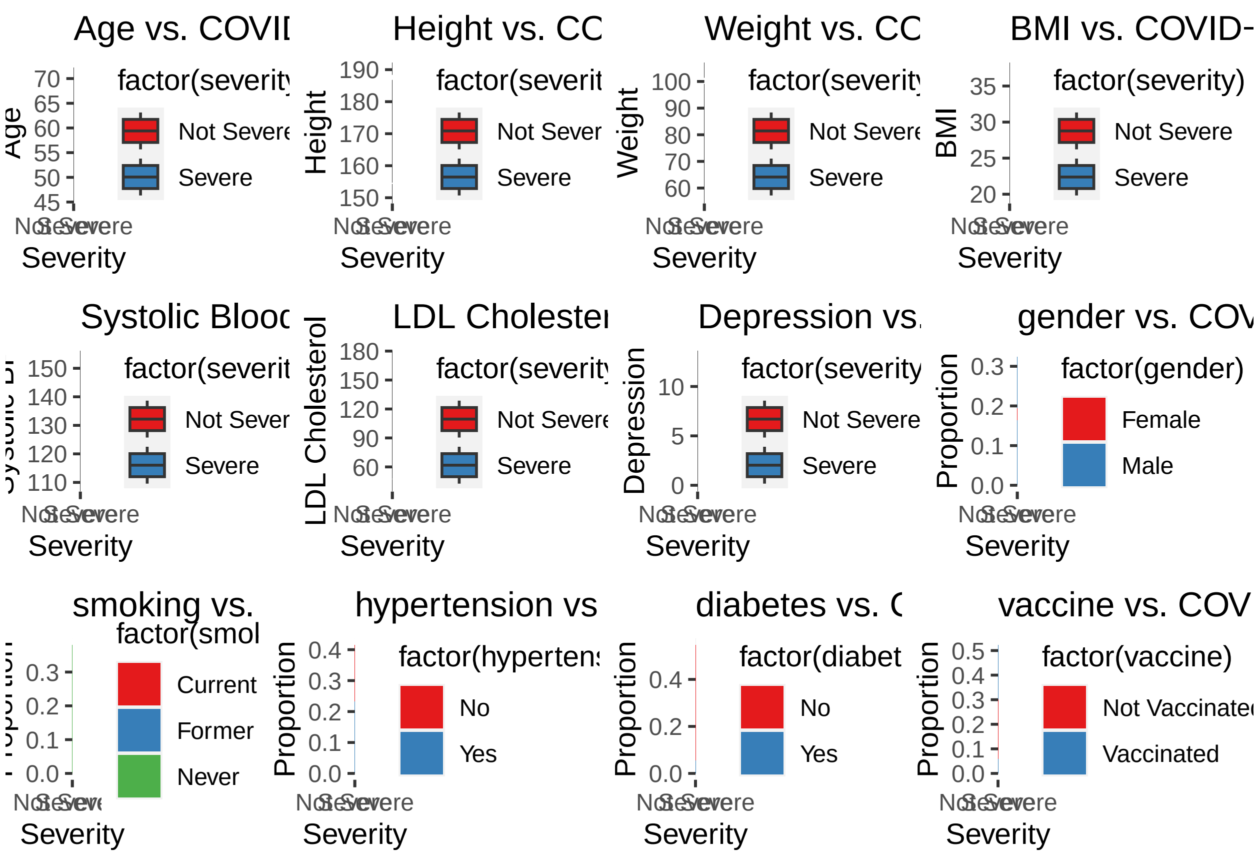
We will visualize the relationship between categorical predictors and severity. We will focus on gender, smoking status, hypertension, diabetes, and vaccination status. We will use bar plots showing the proportion within each severity category.

```r
# Function to create proportion bar plots
create_prop_plot <- function(data, varname) {
  plot <- data %>%
    group_by(severity, !!rlang::sym(varname)) %>%
    summarise(Count = n(), .groups = 'drop') %>%
    mutate(Prop = Count / sum(Count)) %>%
    ggplot(aes(x = factor(severity), y = Prop, fill = factor(!!rlang::sym(varname)))) +
    geom_bar(stat = "identity", position = position_dodge()) +
    labs(title = paste(varname, "vs. COVID-19 Severity"), x = "Severity", y = "Proportion") +
    scale_fill_brewer(palette = "Set1")

  return(plot)
}

# Proportion Bar Plots
p8 <- create_prop_plot(training_data, "gender")
p9 <- create_prop_plot(training_data, "smoking")
p10 <- create_prop_plot(training_data, "hypertension")
p11 <- create_prop_plot(training_data, "diabetes")
p12 <- create_prop_plot(training_data, "vaccine")
```

```r
plots_list <- list(p1, p2, p3, p4, p5, p6, p7, p8, p9, p10, p11, p12)
combined_plot <- grid.arrange(grobs = plots_list, ncol = 4, nrow = 3)
```




```
png("combined_plots.png", width = 2000, height = 1500)
grid.arrange(grobs = plots_list, ncol = 4, nrow = 3)
dev.off()
```

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

```
dat_continuous <- training_data %>%
  dplyr::select("age", "height", "weight", "bmi", "sbp", "ldl", "depression")
png("continuous_corrplot.png", width = 400, height = 300)

corrplot(cor(dat_continuous), method = 'number', type = 'lower')

dev.off()
```

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

Model Training

MARS

```r
set.seed(1)
mars_grid <- expand.grid(degree = 1:3,
                         nprune = 2:20)

ctrl <- trainControl(method = "cv",
                     number = 10,
                     summaryFunction = twoClassSummary,
                     classProbs = TRUE)

mars.fit <- train(make.names(severity) ~ .,
                  data = training_data,
                  method = "earth",
                  tuneGrid = mars_grid,
                  metric = "ROC",
                  trControl = ctrl)
```

```
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

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```
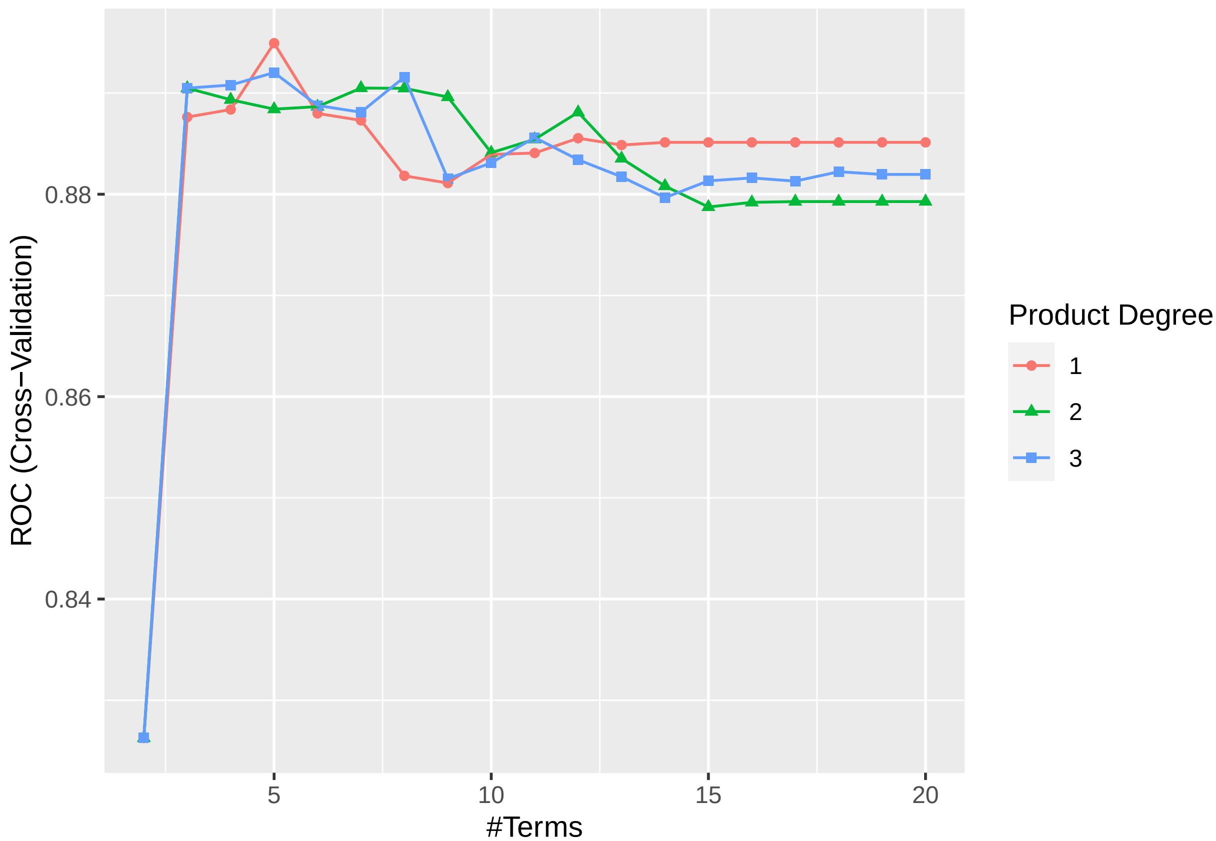

```r
ggplot(mars.fit)
```




```r
mars.fit$bestTune
```

```
##   nprune degree
## 4      5      1
```

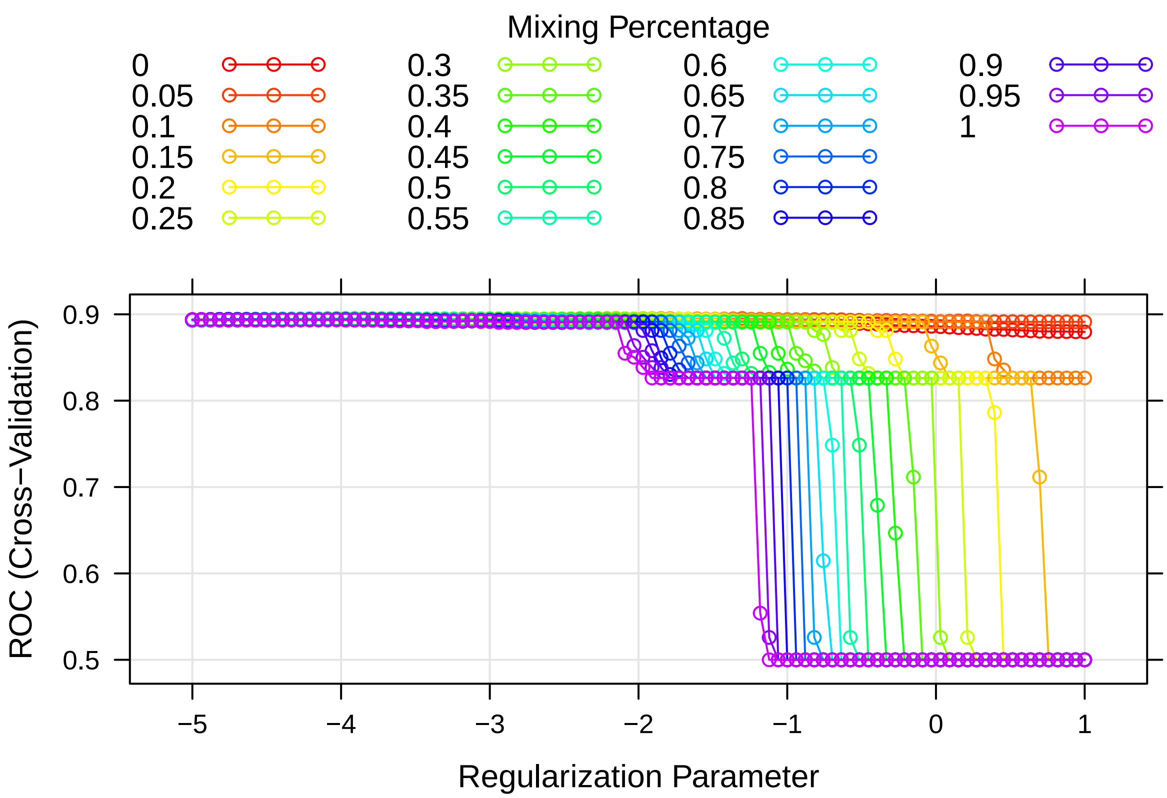
```r
coef(mars.fit$finalModel)
```

```
##       (Intercept) vaccineVaccinated        h(sbp-139)        h(139-sbp)
##        1.98341761       -3.50798169       -0.01515556       -0.13557595
##         h(bmi-27)
##        0.24293455
```

Penalized Logistic Regression

```r
set.seed(1)
glmnGrid <- expand.grid(.alpha = seq(0, 1, length = 21),
                        .lambda = exp(seq(-5, 1, length = 100)))

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

```r
                      summaryFunction = twoClassSummary,
                      classProbs = TRUE)

glmn.fit <- train(make.names(severity) ~.,
                  data = training_data,
                  method = "glmnet",
                  tuneGrid = glmnGrid,
                  metric = "ROC",
                  trControl = ctrl)

myCol <- rainbow(25)
myPar <- list(superpose.symbol = list(col = myCol),
              superpose.line = list(col = myCol))
plot(glmn.fit, par.settings = myPar, xTrans = function(x) log(x))
```




```r
glmn.fit$bestTune
```

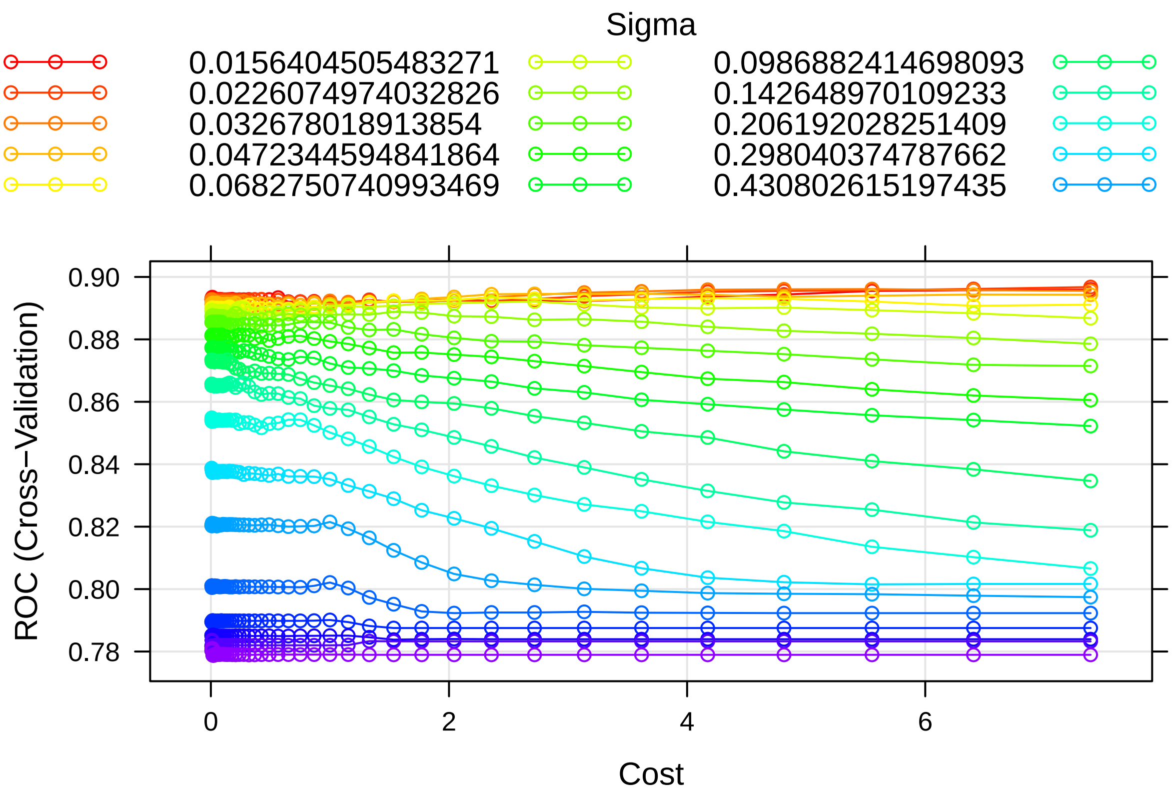
```
##     alpha     lambda
## 441   0.2 0.07609615
```

SVM

```r
set.seed(1)
svmr.grid <- expand.grid(C = exp(seq(-5, 2, len = 50)),
                         sigma = exp(seq(-6, 1, len = 20)))

ctrl <- trainControl(method = "cv",
                     number = 10,
                     summaryFunction = twoClassSummary,
                     classProbs = TRUE)

svmr.fit <- train(make.names(severity) ~ . ,
                  data = training_data,
                  method = "svmRadialSigma",
                  tuneGrid = svmr.grid,
                  metric = "ROC",
                  trControl = ctrl)
```

```
## maximum number of iterations reached 9.44953e-05 9.418661e-05maximum number of iterations reached 1.0
```

```r
myCol <- rainbow(25)
myPar <- list(superpose.symbol = list(col = myCol),
              superpose.line = list(col = myCol))
plot(svmr.fit, highlight = TRUE, par.settings = myPar)
```

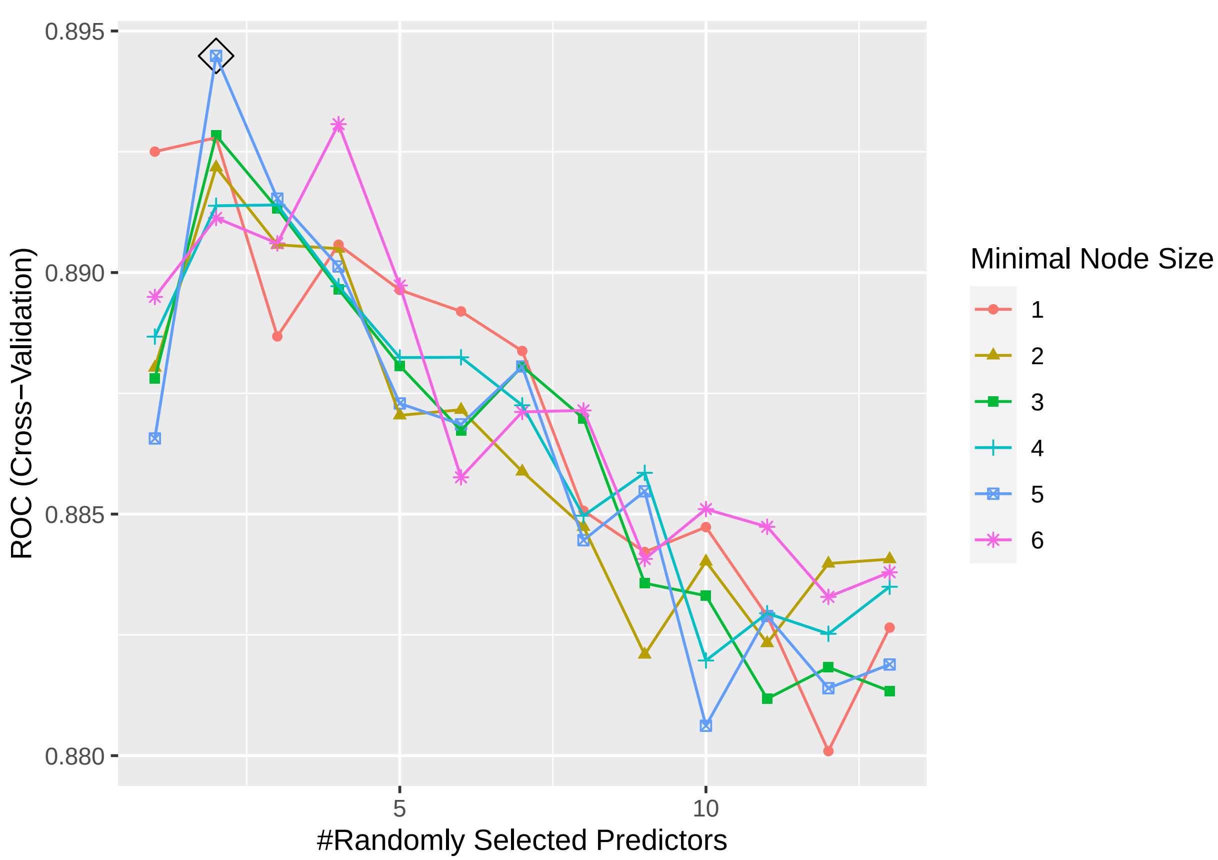


Random Forest

```r
set.seed(1)
rf.grid <- expand.grid(mtry = 1:13,
                       splitrule = "gini",
                       min.node.size = 1:6)

ctrl <- trainControl(method = "cv",
                     number = 10,
                     summaryFunction = twoClassSummary,
                     classProbs = TRUE)

rf.fit <- train(make.names(severity) ~ .,
                data = training_data,
                method = "ranger",
                tuneGrid = rf.grid,
                metric = "ROC",
                trControl = ctrl)
rf.fit$bestTune
```

```
##    mtry splitrule min.node.size
## 11    2      gini             5
```

```r
ggplot(rf.fit, highlight = TRUE)
```



LDA

```
set.seed(1)

ctrl <- trainControl(method = "cv",
                     number = 10,
                     summaryFunction = twoClassSummary,
                     classProbs = TRUE)

lda.fit <- train(make.names(severity) ~.,
                 data = training_data,
                 method = "lda",
                 metric = "ROC",
                 trControl = ctrl)

lda.fit$finalModel
```

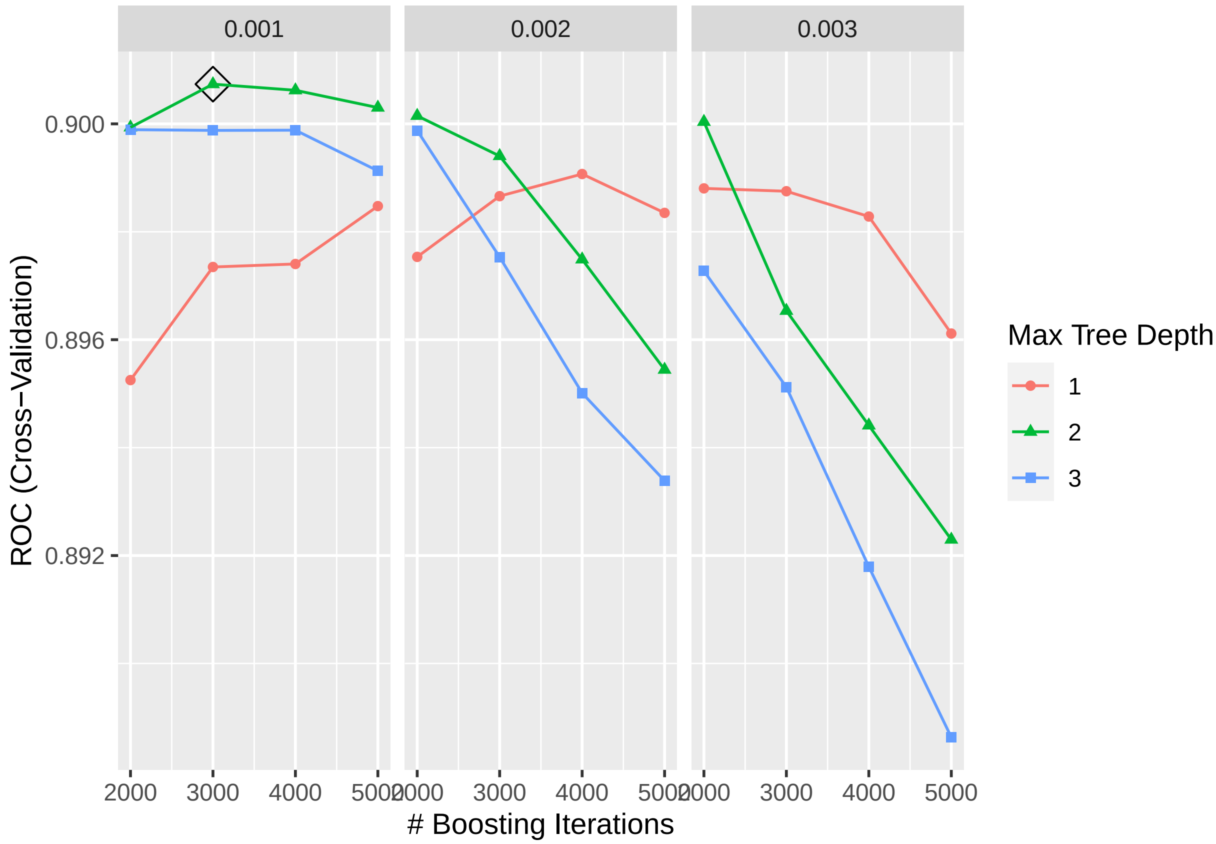
```
## Call:
## lda(x, grouping = y)
##
## Prior probabilities of groups:
## Not.Severe     Severe
##     0.6425     0.3575
##
## Group means:
##                 age genderMale raceBlack raceHispanic raceWhite smokingFormer
## Not.Severe 59.46887  0.5038911 0.2003891   0.09533074 0.6381323     0.3054475
## Severe     61.04545  0.4580420 0.1608392   0.10839161 0.6748252     0.3181818
##            smokingNever   height   weight      bmi diabetesYes hypertensionYes
## Not.Severe    0.5914397 170.1516 79.04125 27.35331   0.1498054       0.3540856
## Severe        0.5699301 169.7269 80.10245 27.86993   0.1538462       0.6503497
##                 sbp      ldl vaccineVaccinated depression
## Not.Severe 128.0272 108.4689         0.8132296   6.912451
## Severe     133.1224 113.4580         0.1608392   6.902098
##
## Coefficients of linear discriminants:
##                            LD1
## age                0.034385337
## genderMale        -0.236369596
## raceBlack          0.133771275
## raceHispanic       0.011221117
## raceWhite          0.126074229
## smokingFormer     -0.220509810
## smokingNever      -0.248324764
## height             0.067561771
## weight            -0.077322293
## bmi                0.301287096
## diabetesYes        0.144018177
## hypertensionYes    0.215120572
## sbp                0.036100853
## ldl                0.004588793
## vaccineVaccinated -2.478676582
## depression        -0.010600382
```

AdaBoost

```
set.seed(1)
gbmA.grid <- expand.grid(n.trees = c(2000,3000,4000,5000),
                         interaction.depth = 1:3,
                         shrinkage = c(0.001,0.002,0.003),
                         n.minobsinnode = 1)

ctrl <- trainControl(method = "cv",
                     number = 10,
                     summaryFunction = twoClassSummary,
                     classProbs = TRUE)

gbmA.fit <- train(make.names(severity) ~ .,
                  data = training_data,
                  method = "gbm",
                  tuneGrid = gbmA.grid,
                  metric = "ROC",
                  trControl = ctrl,
                  distribution = "adaboost",
                  verbose = FALSE)
gbmA.fit$bestTune
```

```
##   n.trees interaction.depth shrinkage n.minobsinnode
## 6    3000                 2     0.001              1
```

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



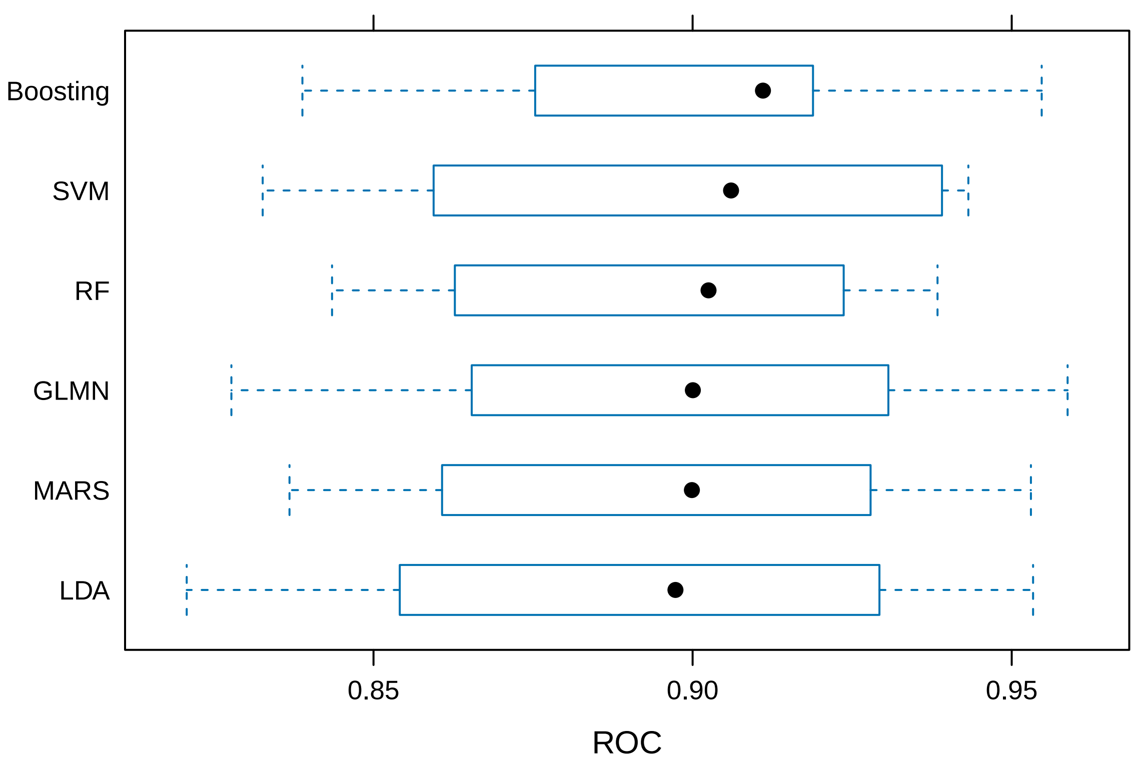
Compare all models

```
resamp <- resamples(list(MARS = mars.fit,
                         GLMN = glmn.fit,
                         SVM = svmr.fit,
                         RF = rf.fit,
                         LDA = lda.fit,
                         Boosting = gbmA.fit))
summary(resamp)
```

```
##
## Call:
## summary.resamples(object = resamp)
##
## Models: MARS, GLMN, SVM, RF, LDA, Boosting
## Number of resamples: 10
##
## ROC
##               Min.   1st Qu.    Median      Mean   3rd Qu.      Max. NA's
## MARS     0.8368347 0.8617374 0.8998836 0.8949289 0.9242048 0.9530088    0
## GLMN     0.8277311 0.8667531 0.9000364 0.8953483 0.9279149 0.9587559    0
## SVM      0.8326331 0.8639673 0.9060241 0.8967610 0.9359244 0.9432049    0
## RF       0.8435013 0.8629141 0.9024939 0.8944851 0.9221477 0.9383754    0
## LDA      0.8207283 0.8569460 0.8973124 0.8924337 0.9280664 0.9533469    0
```

```
## Boosting 0.8388594 0.8755656 0.9110222 0.9007355 0.9184898 0.9546991    0
##
## Sens
##               Min.   1st Qu.    Median      Mean   3rd Qu.      Max. NA's
## MARS     0.8431373 0.8461538 0.8725490 0.8834087 0.9128959 0.9607843    0
## GLMN     0.8461538 0.8634050 0.8823529 0.8970965 0.9226998 0.9803922    0
## SVM      0.7692308 0.8125000 0.8448341 0.8505279 0.8823529 0.9411765    0
## RF       0.8653846 0.9082768 0.9411765 0.9360106 0.9754902 0.9807692    0
## LDA      0.7500000 0.8076923 0.8350302 0.8407994 0.8725490 0.9411765    0
## Boosting 0.8653846 0.8829186 0.9019608 0.9164781 0.9558824 0.9807692    0
##
## Spec
##               Min.   1st Qu.    Median      Mean   3rd Qu.      Max. NA's
## MARS     0.6785714 0.7327586 0.7721675 0.7758621 0.8143473 0.8620690    0
## GLMN     0.6428571 0.7521552 0.7586207 0.7656404 0.8143473 0.8620690    0
## SVM      0.7142857 0.8001847 0.8423645 0.8284483 0.8608374 0.8965517    0
## RF       0.5714286 0.6813424 0.7413793 0.7270936 0.7789409 0.8275862    0
## LDA      0.7142857 0.8017241 0.8571429 0.8352217 0.8620690 0.8965517    0
## Boosting 0.6428571 0.6982759 0.7413793 0.7480296 0.7912562 0.8620690    0
```

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




```r
resamp_summary <- summary(resamp)

roc_summary <- as.data.frame(resamp_summary$statistics$ROC)
```

```r
roc_summary$Model <- rownames(roc_summary)
write.csv(roc_summary, "Roc_summary.csv", row.names = FALSE)
```

```r
png("Roc_boxplot.png", width = 400, height = 300)
bwplot(resamp, metric = "ROC")
dev.off()
```

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

```r
boosting.pred <- predict(gbmA.fit, newdata = test_data, type = "prob")
boosting.pred
```

```
##      Not.Severe     Severe
## 1    0.89630340 0.10369660
## 2    0.43313344 0.56686656
## 3    0.48536884 0.51463116
## 4    0.09701847 0.90298153
## 5    0.90786982 0.09213018
## 6    0.16864968 0.83135032
## 7    0.29994593 0.70005407
## 8    0.21075008 0.78924992
## 9    0.13076766 0.86923234
## 10   0.82659319 0.17340681
## 11   0.88841781 0.11158219
## 12   0.13667853 0.86332147
## 13   0.80671339 0.19328661
## 14   0.87902215 0.12097785
## 15   0.90451779 0.09548221
## 16   0.76508389 0.23491611
## 17   0.43040267 0.56959733
## 18   0.85820468 0.14179532
## 19   0.83302007 0.16697993
## 20   0.90749853 0.09250147
## 21   0.93204529 0.06795471
## 22   0.66431513 0.33568487
## 23   0.90224590 0.09775410
## 24   0.63228775 0.36771225
## 25   0.46271132 0.53728868
## 26   0.36734190 0.63265810
## 27   0.59463071 0.40536929
## 28   0.81730975 0.18269025
## 29   0.88712291 0.11287709
## 30   0.86823897 0.13176103
## 31   0.90730277 0.09269723
## 32   0.39872172 0.60127828
## 33   0.38333235 0.61666765
## 34   0.92901686 0.07098314
## 35   0.92442802 0.07557198
## 36   0.82882768 0.17117232
## 37   0.92975988 0.07024012
## 38   0.89737049 0.10262951
```

```
## 39  0.92412334 0.07587666
## 40  0.90447153 0.09552847
## 41  0.80911791 0.19088209
## 42  0.89197911 0.10802089
## 43  0.16119579 0.83880421
## 44  0.86505699 0.13494301
## 45  0.90463468 0.09536532
## 46  0.25120471 0.74879529
## 47  0.83158037 0.16841963
## 48  0.86855693 0.13144307
## 49  0.89904276 0.10095724
## 50  0.16234205 0.83765795
## 51  0.91067025 0.08932975
## 52  0.89465317 0.10534683
## 53  0.37343253 0.62656747
## 54  0.90610908 0.09389092
## 55  0.12278553 0.87721447
## 56  0.82262376 0.17737624
## 57  0.15771395 0.84228605
## 58  0.88992615 0.11007385
## 59  0.82794851 0.17205149
## 60  0.41472213 0.58527787
## 61  0.47594334 0.52405666
## 62  0.93578565 0.06421435
## 63  0.59317092 0.40682908
## 64  0.83680774 0.16319226
## 65  0.83380199 0.16619801
## 66  0.83583076 0.16416924
## 67  0.84462906 0.15537094
## 68  0.82533962 0.17466038
## 69  0.82769313 0.17230687
## 70  0.33682737 0.66317263
## 71  0.28624634 0.71375366
## 72  0.15022671 0.84977329
## 73  0.09694790 0.90305210
## 74  0.83721026 0.16278974
## 75  0.84263824 0.15736176
## 76  0.92562460 0.07437540
## 77  0.82965066 0.17034934
## 78  0.84491196 0.15508804
## 79  0.16538680 0.83461320
## 80  0.79523000 0.20477000
## 81  0.91967321 0.08032679
## 82  0.91734443 0.08265557
## 83  0.89476862 0.10523138
## 84  0.89444763 0.10555237
## 85  0.82213997 0.17786003
## 86  0.33064473 0.66935527
## 87  0.29481632 0.70518368
## 88  0.16952340 0.83047660
## 89  0.56554200 0.43445800
## 90  0.84461564 0.15538436
## 91  0.16653051 0.83346949
## 92  0.29974965 0.70025035
```

```
## 93  0.08620767 0.91379233
## 94  0.08550628 0.91449372
## 95  0.70556311 0.29443689
## 96  0.91067020 0.08932980
## 97  0.79940976 0.20059024
## 98  0.52096980 0.47903020
## 99  0.52738486 0.47261514
## 100 0.87533982 0.12466018
## 101 0.45085086 0.54914914
## 102 0.12700413 0.87299587
## 103 0.83689636 0.16310364
## 104 0.86151238 0.13848762
## 105 0.91107545 0.08892455
## 106 0.29365365 0.70634635
## 107 0.57086494 0.42913506
## 108 0.79878612 0.20121388
## 109 0.92424837 0.07575163
## 110 0.86046557 0.13953443
## 111 0.08615355 0.91384645
## 112 0.85219908 0.14780092
## 113 0.08603372 0.91396628
## 114 0.91194087 0.08805913
## 115 0.21730042 0.78269958
## 116 0.33543170 0.66456830
## 117 0.88932934 0.11067066
## 118 0.92045660 0.07954340
## 119 0.82824881 0.17175119
## 120 0.92836296 0.07163704
## 121 0.91000058 0.08999942
## 122 0.10885632 0.89114368
## 123 0.92837357 0.07162643
## 124 0.92734810 0.07265190
## 125 0.28608311 0.71391689
## 126 0.86104339 0.13895661
## 127 0.90264339 0.09735661
## 128 0.90530990 0.09469010
## 129 0.33398536 0.66601464
## 130 0.91513714 0.08486286
## 131 0.90832988 0.09167012
## 132 0.92321434 0.07678566
## 133 0.23457417 0.76542583
## 134 0.82805458 0.17194542
## 135 0.90947823 0.09052177
## 136 0.63393663 0.36606337
## 137 0.93141038 0.06858962
## 138 0.87155771 0.12844229
## 139 0.89921140 0.10078860
## 140 0.91955694 0.08044306
## 141 0.80501464 0.19498536
## 142 0.80820967 0.19179033
## 143 0.85839121 0.14160879
## 144 0.91764995 0.08235005
## 145 0.81786168 0.18213832
## 146 0.92854100 0.07145900
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## 147 0.33320542 0.66679458
## 148 0.80193426 0.19806574
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## 153 0.83439419 0.16560581
## 154 0.28949786 0.71050214
## 155 0.18781695 0.81218305
## 156 0.92054712 0.07945288
## 157 0.92957568 0.07042432
## 158 0.82460084 0.17539916
## 159 0.56796791 0.43203209
## 160 0.30046659 0.69953341
## 161 0.90844882 0.09155118
## 162 0.93377849 0.06622151
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## 166 0.54557646 0.45442354
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## 189 0.53967743 0.46032257
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## 191 0.23514521 0.76485479
## 192 0.20449541 0.79550459
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## 194 0.33885739 0.66114261
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## 196 0.83279144 0.16720856
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## 200 0.40622057 0.59377943
```