Final

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```r
library(tidyverse)
library(caret)
library(glmnet)
library(ISLR)
library(pls)
library(AppliedPredictiveModeling)
library(MASS)
library(e1071)
library(mlbench)
library(pROC)
library(arsenal)
library(visdat)
library(pdp)
library(vip)
library(randomForest)
library(ranger)
library(gbm)
library(e1071)
library(kernlab)
```

Introduction

Stroke is a serious life-threatening medical condition. According to the World Health Organization, stroke is the second leading cause of death globally. To better understand which factors correlate to the stroke event, our group find a stroke prediction dataset. This dataset contains twelve columns. The first column labels the unique identifier of the patient. The last column records the occurrence of stroke by 1 (Yes) or 0 (No). The other ten columns contain the observations of possible predictors.

Load, clean, and tidy data

```r
stroke = read_csv("./healthcare-dataset-stroke-data.csv") %>%
  mutate(
    bmi = as.numeric(bmi)
  ) %>%
  dplyr::select(-id, -Residence_type, -ever_married)

stroke1 = stroke %>%
  janitor::clean_names() %>%
  na.omit() %>%
  filter(
    bmi != "N/A",
    gender != "Other"
  ) %>%
  mutate(
    gender = recode(
      gender,
      "Male" = 0,
      "Female" = 1
    ),
```

```
    work_type = recode(
      work_type,
      "children" = 0,
      "Govt_job" = 1,
      "Never_worked" = 2,
      "Private" = 3,
      "Self-employed" = 4
    ),
    smoking_status = recode(
      smoking_status,
      "formerly smoked" = 0,
      "never smoked" = 1,
      "smokes" = 2,
      "Unknown" = 3
    ),
    stroke = recode(
      stroke,
     "0" = "No",
     "1" = "Yes"
    ),
    stroke = as.factor(stroke),
    gender = as.factor(gender),
    hypertension = as.factor(hypertension),
    heart_disease = as.factor(heart_disease),
    work_type = as.factor(work_type),
    smoking_status = as.factor(smoking_status)
  ) %>%
  relocate(
    age, avg_glucose_level, bmi
  )
```

Exploratory analysis/ visualization

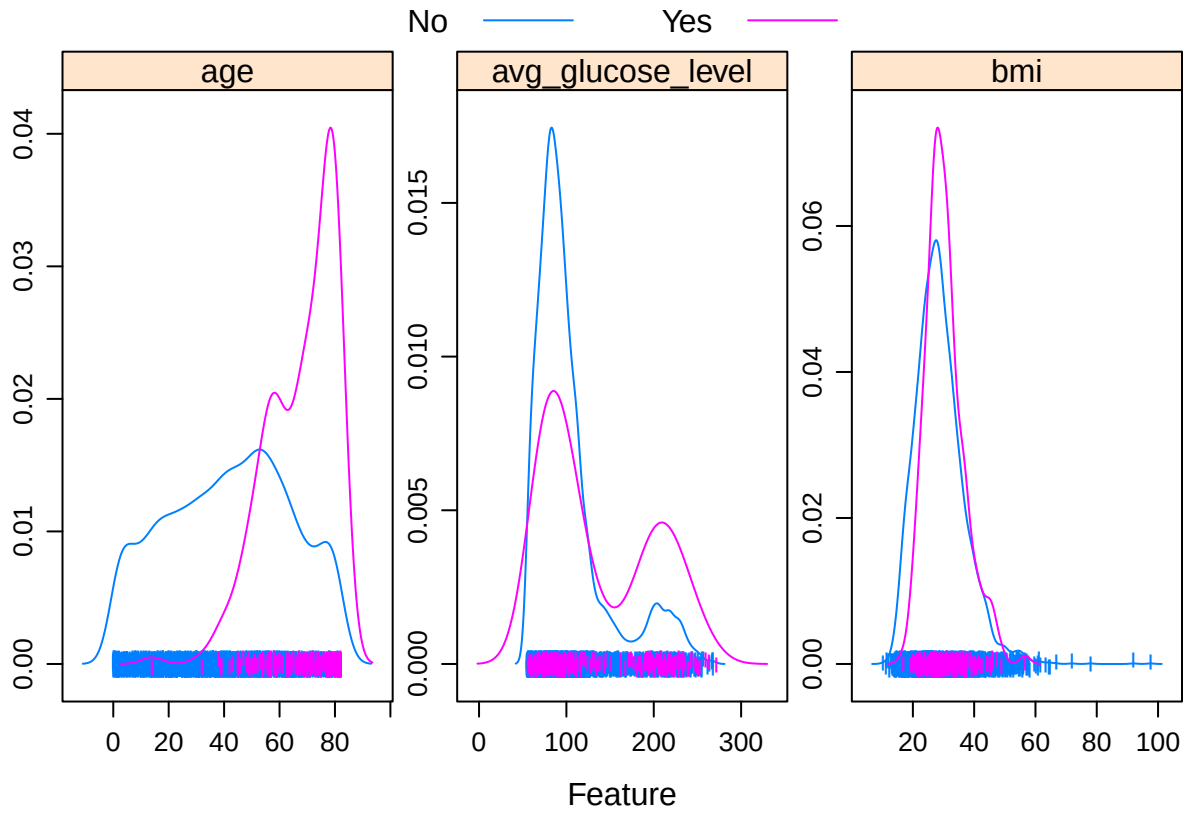
```
stats = tableby(stroke ~ gender + age + hypertension + heart_disease + work_type + avg_glucose_level + b

summary(stats, text = TRUE) %>% knitr::kable()
```

	0 (N=4861)	1 (N=249)	Total (N=5110)	p value
gender				0.790
- Female	2853 (58.7%)	141 (56.6%)	2994 (58.6%)	
- Male	2007 (41.3%)	108 (43.4%)	2115 (41.4%)	
- Other	1 (0.0%)	0 (0.0%)	1 (0.0%)	
age				< 0.001
- Mean (SD)	41.972 (22.292)	67.728 (12.727)	43.227 (22.613)	
- Range	0.080 - 82.000	1.320 - 82.000	0.080 - 82.000	
hypertension				< 0.001
- Mean (SD)	0.089 (0.285)	0.265 (0.442)	0.097 (0.297)	
- Range	0.000 - 1.000	0.000 - 1.000	0.000 - 1.000	
heart_disease				< 0.001
- Mean (SD)	0.047 (0.212)	0.189 (0.392)	0.054 (0.226)	

	0 (N=4861)	1 (N=249)	Total (N=5110)	p value
- Range	0.000 - 1.000	0.000 - 1.000	0.000 - 1.000	
work_type				< 0.001
- children	685 (14.1%)	2 (0.8%)	687 (13.4%)	
- Govt_job	624 (12.8%)	33 (13.3%)	657 (12.9%)	
- Never_worked	22 (0.5%)	0 (0.0%)	22 (0.4%)	
- Private	2776 (57.1%)	149 (59.8%)	2925 (57.2%)	
- Self-employed	754 (15.5%)	65 (26.1%)	819 (16.0%)	
avg_glucose_level				< 0.001
- Mean (SD)	104.796 (43.846)	132.545 (61.921)	106.148 (45.284)	
- Range	55.120 - 267.760	56.110 - 271.740	55.120 - 271.740	
bmi				0.003
- N-Miss	161	40	201	
- Mean (SD)	28.823 (7.908)	30.471 (6.329)	28.893 (7.854)	
- Range	10.300 - 97.600	16.900 - 56.600	10.300 - 97.600	
smoking_status				< 0.001
- formerly smoked	815 (16.8%)	70 (28.1%)	885 (17.3%)	
- never smoked	1802 (37.1%)	90 (36.1%)	1892 (37.0%)	
- smokes	747 (15.4%)	42 (16.9%)	789 (15.4%)	
- Unknown	1497 (30.8%)	47 (18.9%)	1544 (30.2%)	

```
featurePlot(x = stroke1[, 1:3],
            y = stroke1$stroke,
            scales = list(x = list(relation = "free"),
                          y = list(relation = "free")),
            plot = "density",
            pch = "|",
            auto.key = list(columns = 2),
            font = 2)
```



Models

```
set.seed(1)

indextrain <- createDataPartition(y = stroke1$stroke,
                                  p = 0.8,
                                  list = FALSE)

train = stroke1[indextrain, ]

test = stroke1[-indextrain, ]

x <- stroke1[indextrain, -c(9)]

y <- stroke1$stroke[indextrain] ###train

x2 <- stroke1[-indextrain, -c(9)]

y2 <- stroke1$stroke[-indextrain] ###test

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

GLM

```
model.glm = train(stroke ~ . ,
                  data = train,
                  method = 'glm',
                  metric = "ROC",
                  trControl = ctrl)

glm.pred.prob = predict(model.glm, newdata = x2, type = "prob")[,1]

glm.pred = rep("Yes", length(glm.pred.prob))

glm.pred[glm.pred.prob < 0.95] = "No"

confusionMatrix(data = as.factor(glm.pred),
                reference = y2,
                positive = "Yes")
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  No Yes
##        No  218  29
##        Yes 721  12
##
##                Accuracy : 0.2347
##                  95% CI : (0.2085, 0.2625)
##     No Information Rate : 0.9582
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : -0.0524
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 0.29268
##             Specificity : 0.23216
##          Pos Pred Value : 0.01637
##          Neg Pred Value : 0.88259
##              Prevalence : 0.04184
##          Detection Rate : 0.01224
##    Detection Prevalence : 0.74796
##       Balanced Accuracy : 0.26242
##
##        'Positive' Class : Yes
##
```

```
model.glm$bestTune
```

```
##   parameter
## 1      none
```

GLMN

```
glmn.grid <- expand.grid(.alpha = seq(0, 1, length = 6),
                         .lambda = exp(seq(-8, -2, length = 20)))

set.seed(1)

model.glmn <- train(x = data.matrix(x),
                    y = y,
                    method = "glmnet",
                    tuneGrid = glmn.grid,
                    metric = "ROC",
                    trControl = ctrl)

glmn.pred.prob = predict(model.glmn, newdata = data.matrix(x2), type = "prob")[,1]

glmn.pred = rep("Yes", length(glmn.pred.prob))

glmn.pred[glmn.pred.prob < 0.95] = "No"

confusionMatrix(data = as.factor(glmn.pred),
                reference = y2,
                positive = "Yes")
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  No Yes
##        No  231  30
##        Yes 708  11
##
##                Accuracy : 0.2469
##                  95% CI : (0.2202, 0.2752)
##     No Information Rate : 0.9582
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : -0.0545
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 0.26829
##             Specificity : 0.24601
##          Pos Pred Value : 0.01530
##          Neg Pred Value : 0.88506
##              Prevalence : 0.04184
##          Detection Rate : 0.01122
##    Detection Prevalence : 0.73367
##       Balanced Accuracy : 0.25715
##
##        'Positive' Class : Yes
##
```

```
model.glmn$bestTune
```

```
##    alpha      lambda
## 88   0.8 0.003059592
```

MARS

```
set.seed(1)

model.mars <- train(stroke ~ . ,
                    data = train,
                    method = "earth",
                    tuneGrid = expand.grid(degree = 1:3,
                                           nprune = 2:15),
                    metric = "ROC",
                    trControl = ctrl)

mars.pred.prob = predict(model.mars, newdata = x2, type = "prob")[,1]

mars.pred = rep("Yes", length(mars.pred.prob))

mars.pred[mars.pred.prob < 0.95] = "No"

confusionMatrix(data = as.factor(mars.pred),
                reference = y2,
                positive = "Yes")
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  No Yes
##        No  199  29
##        Yes 740  12
##
##                Accuracy : 0.2153
##                  95% CI : (0.1899, 0.2424)
##     No Information Rate : 0.9582
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : -0.0533
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 0.29268
##             Specificity : 0.21193
##          Pos Pred Value : 0.01596
##          Neg Pred Value : 0.87281
##              Prevalence : 0.04184
##          Detection Rate : 0.01224
##    Detection Prevalence : 0.76735
##       Balanced Accuracy : 0.25231
```

```
##
##        'Positive' Class : Yes
##
```

```
model.mars$bestTune
```

```
##   nprune degree
## 7      8      1
```

GAM

```
set.seed(1)

model.gam <- train(stroke ~ . ,
                   data = train,
                   method = "gam",
                   metric = "ROC",
                   trControl = ctrl)

gam.pred.prob = predict(model.gam, newdata = x2, type = "prob")[,1]

gam.pred = rep("Yes", length(gam.pred.prob))

gam.pred[gam.pred.prob < 0.95] = "No"

confusionMatrix(data = as.factor(gam.pred),
                reference = y2,
                positive = "Yes")
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  No Yes
##        No  241  32
##        Yes 698   9
##
##                Accuracy : 0.2551
##                  95% CI : (0.2281, 0.2836)
##     No Information Rate : 0.9582
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : -0.0597
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 0.219512
##             Specificity : 0.256656
##          Pos Pred Value : 0.012730
##          Neg Pred Value : 0.882784
##              Prevalence : 0.041837
##          Detection Rate : 0.009184
```

```
##    Detection Prevalence : 0.721429
##       Balanced Accuracy : 0.238084
##
##        'Positive' Class : Yes
##
```

```
model.gam$bestTune
```

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

LDA (from the midterm, LDA is the best among LDA, QDA and KNN)

```
set.seed(1)

model.lda = train(x = data.matrix(x),
                  y = y,
                  method = "lda",
                  metric = "ROC",
                  trControl = ctrl)

lda.pred.prob = predict(model.lda, newdata = data.matrix(x2), type = "prob")[,1]

lda.pred = rep("Yes", length(lda.pred.prob))

lda.pred[lda.pred.prob < 0.95] = "No"

confusionMatrix(data = as.factor(lda.pred),
                reference = y2,
                positive = "Yes")
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  No Yes
##        No  192  28
##        Yes 747  13
##
##                Accuracy : 0.2092
##                  95% CI : (0.1841, 0.236)
##     No Information Rate : 0.9582
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : -0.051
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 0.31707
##             Specificity : 0.20447
##          Pos Pred Value : 0.01711
##          Neg Pred Value : 0.87273
```

```
##              Prevalence : 0.04184
##          Detection Rate : 0.01327
##    Detection Prevalence : 0.77551
##       Balanced Accuracy : 0.26077
##
##        'Positive' Class : Yes
##
```

```
model.lda$bestTune
```

```
##   parameter
## 1      none
```

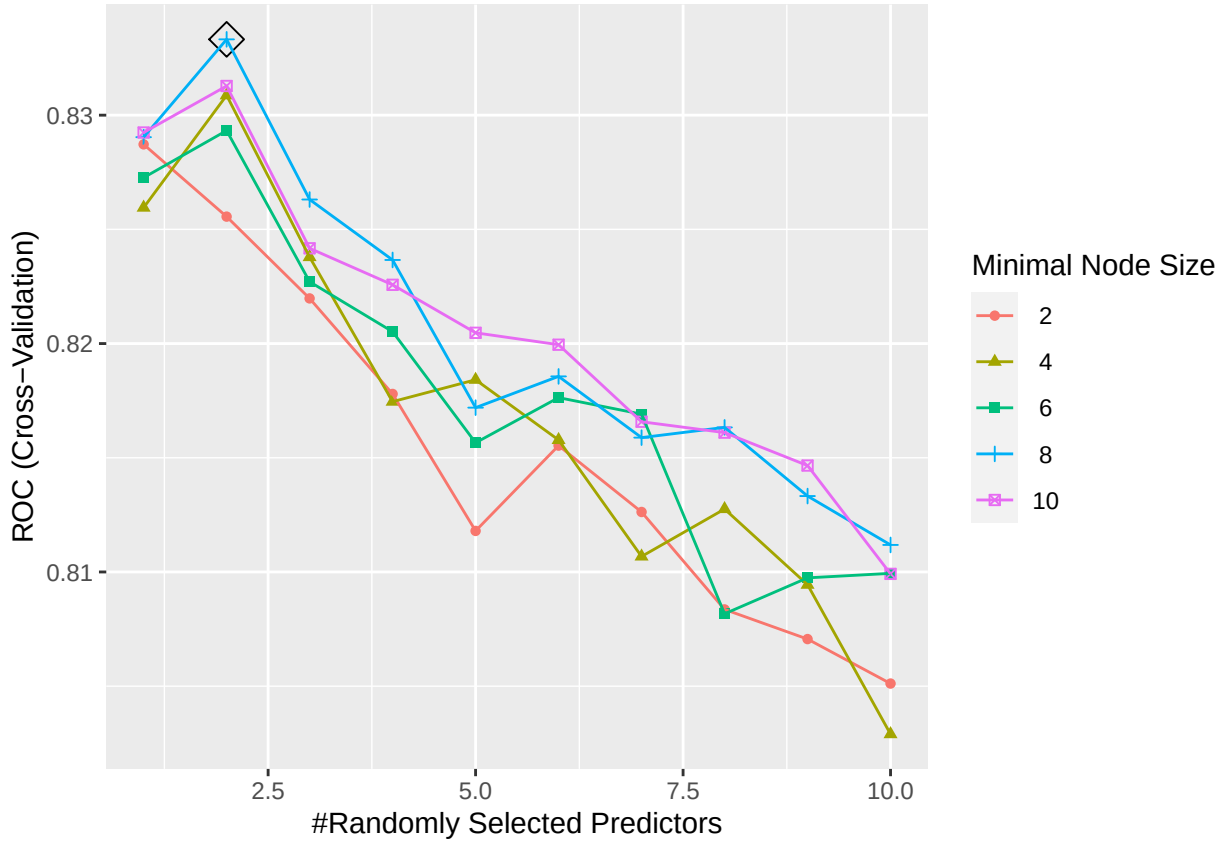
Random Forest

```
rf.grid <- expand.grid(mtry = 1:10,
                       splitrule = "gini",
                       min.node.size = seq(from = 2, to = 10, by = 2))

set.seed(1)

model.rf <- train(stroke ~ . ,
                  data = train,
                method = "ranger",
                tuneGrid = rf.grid,
                metric = "ROC",
                trControl = ctrl,
                importance = "permutation")

ggplot(model.rf, highlight = TRUE)
```




```
rf.pred.prob = predict(model.rf, newdata = x2, type = "prob")[,1]

rf.pred = rep("Yes", length(rf.pred.prob))

rf.pred[rf.pred.prob < 0.95] = "No"

confusionMatrix(data = as.factor(rf.pred),
                reference = y2,
                positive = "Yes")
```

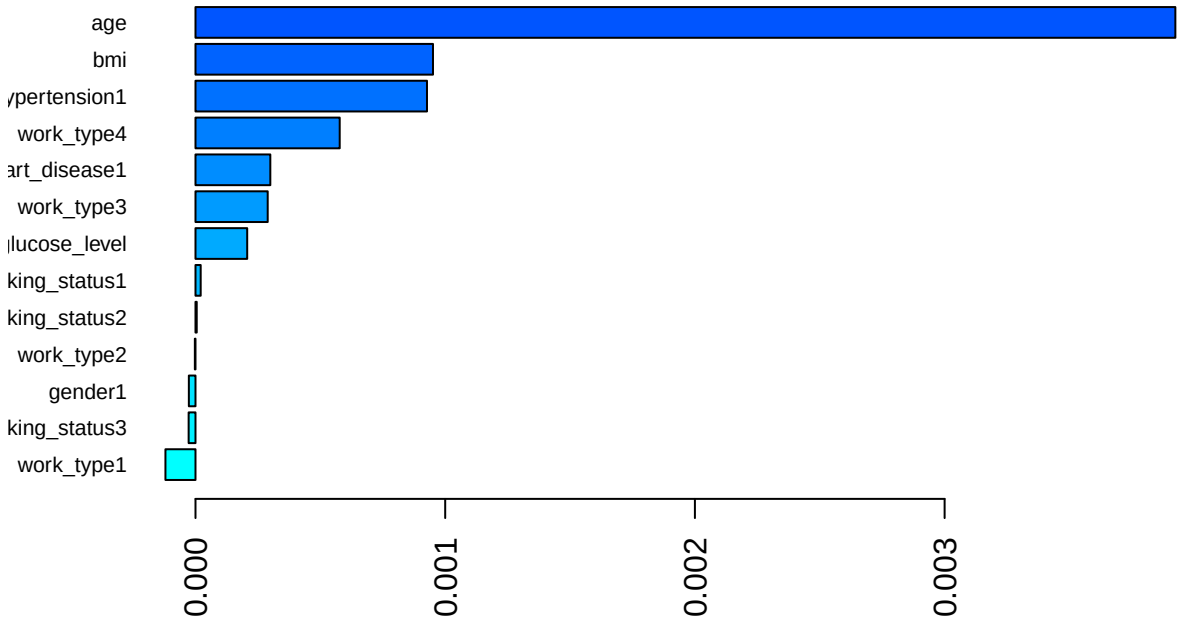
```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  No Yes
##        No  225  29
##        Yes 714  12
##
##                Accuracy : 0.2418
##                  95% CI : (0.2153, 0.2699)
##     No Information Rate : 0.9582
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : -0.052
##
##  Mcnemar's Test P-Value : <2e-16
```

```
##
##             Sensitivity : 0.29268
##             Specificity : 0.23962
##          Pos Pred Value : 0.01653
##          Neg Pred Value : 0.88583
##              Prevalence : 0.04184
##          Detection Rate : 0.01224
##    Detection Prevalence : 0.74082
##       Balanced Accuracy : 0.26615
##
##        'Positive' Class : Yes
##
```

```
model.rf$bestTune
```

```
##   mtry splitrule min.node.size
## 9    2      gini             8
```

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



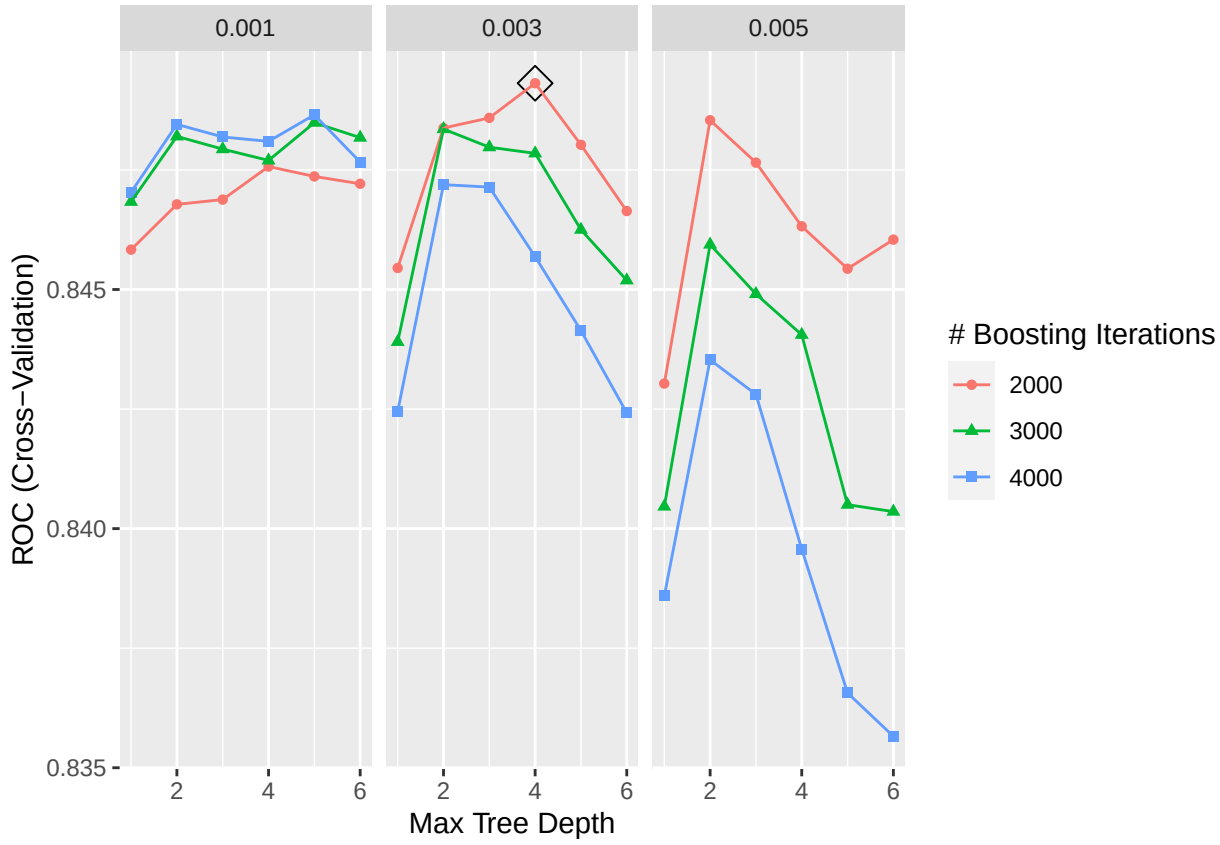
gbmA

```
gbmA.grid <- expand.grid(n.trees = c(2000,3000,4000),
                         interaction.depth = 1:6,
                         shrinkage = c(0.001,0.003,0.005),
                         n.minobsinnode = 1)

set.seed(1)

model.gbma <- train(stroke ~ . ,
                    data = train,
                    tuneGrid = gbmA.grid,
                    trControl = ctrl,
                    method = "gbm",
                    distribution = "adaboost",
                    metric = "ROC",
                    verbose = FALSE)

ggplot(model.gbma, highlight = TRUE)
```




```
test.pred.prob = predict(model.gbma, newdata = x2, type = "prob")[,1]

test.pred = rep("Yes", length(test.pred.prob))
```

```
test.pred[test.pred.prob < 0.95] = "No"

confusionMatrix(data = as.factor(test.pred),
                reference = y2,
                positive = "Yes")
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  No Yes
##        No  196  28
##        Yes 743  13
##
##                Accuracy : 0.2133
##                  95% CI : (0.188, 0.2403)
##     No Information Rate : 0.9582
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : -0.0508
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 0.31707
##             Specificity : 0.20873
##          Pos Pred Value : 0.01720
##          Neg Pred Value : 0.87500
##              Prevalence : 0.04184
##          Detection Rate : 0.01327
##    Detection Prevalence : 0.77143
##       Balanced Accuracy : 0.26290
##
##        'Positive' Class : Yes
##
```

```
model.gbma$bestTune
```

```
##    n.trees interaction.depth shrinkage n.minobsinnode
## 28    2000                 4     0.003              1
```

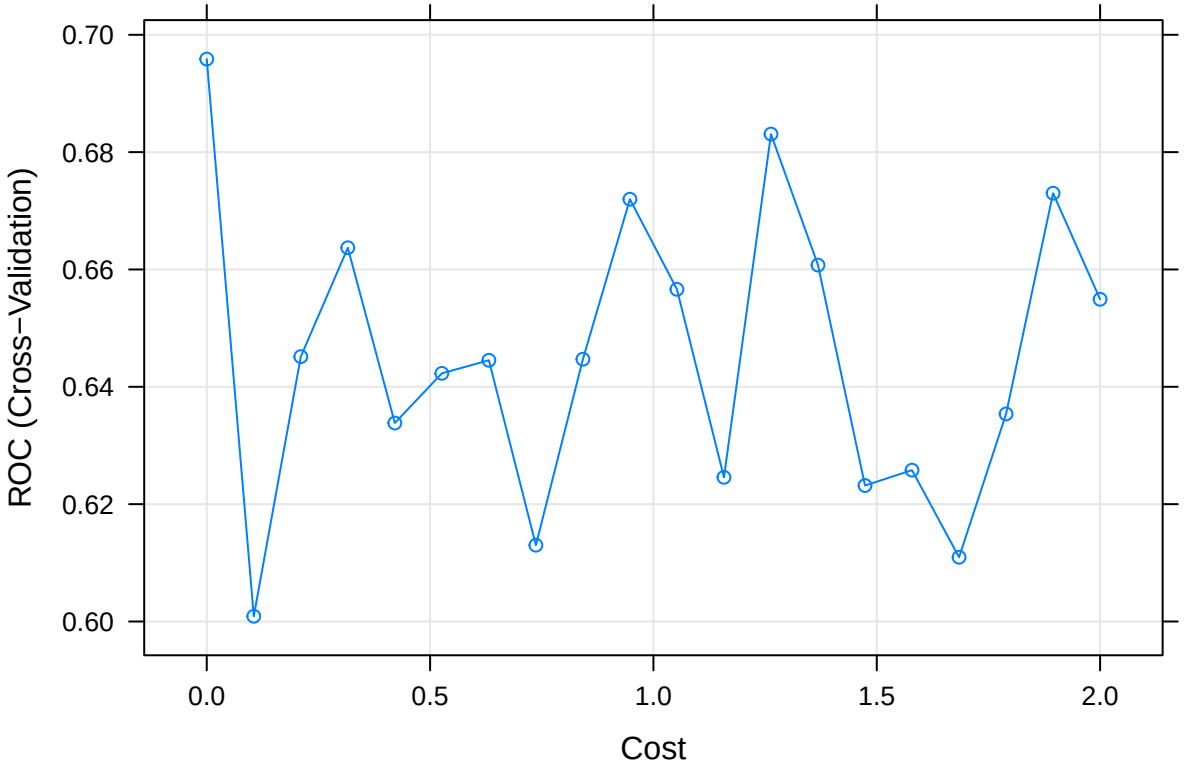
svml

```
set.seed(1)

model.svml <- train(stroke ~ . ,
                    data = train,
                    method = "svmLinear",
                    preProcess = c("center", "scale"),
                    tuneGrid = data.frame(C = exp(seq(0, 2,len = 20))),
                    metric = "ROC",
                    trControl = ctrl)
```

```
## maximum number of iterations reached 0.006147022 0.005760996maximum number of iterations reached 0.0
```

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




```
svml.pred.prob = predict(model.svml, newdata = x2, type = "prob")[,1]

svml.pred = rep("Yes", length(svml.pred.prob))

svml.pred[svml.pred.prob < 0.95] = "No"

confusionMatrix(data = as.factor(svml.pred),
                reference = y2,
                positive = "Yes")
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  No Yes
##        No   55   0
##        Yes 884  41
##
##                Accuracy : 0.098
##                  95% CI : (0.0801, 0.1183)
##     No Information Rate : 0.9582
##     P-Value [Acc > NIR] : 1
```

```
##
##                  Kappa : 0.0052
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 1.00000
##             Specificity : 0.05857
##          Pos Pred Value : 0.04432
##          Neg Pred Value : 1.00000
##              Prevalence : 0.04184
##          Detection Rate : 0.04184
##    Detection Prevalence : 0.94388
##       Balanced Accuracy : 0.52929
##
##        'Positive' Class : Yes
##
```

```
model.svml$bestTune
```

```
##   C
## 1 1
```

svmr

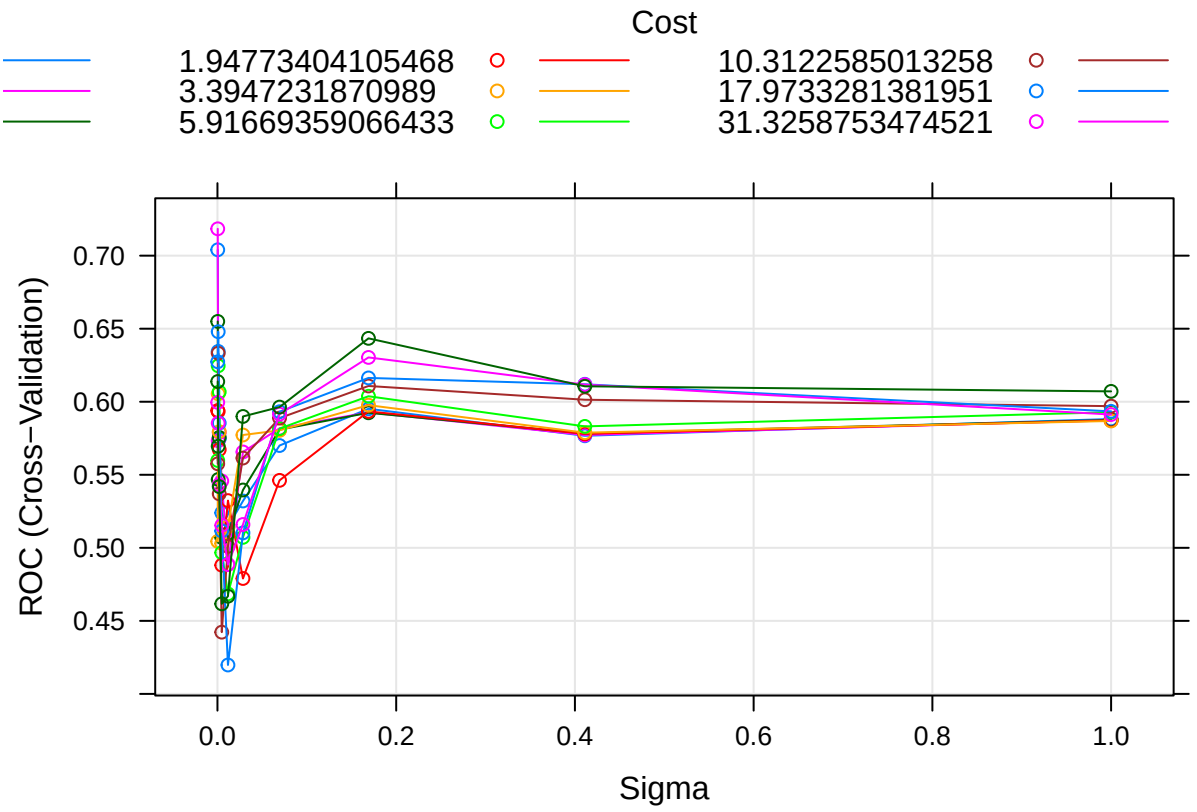
```
svmr.grid <- expand.grid(C = exp(seq(-1,4,len = 10)),
                         sigma = exp(seq(-8,0,len = 10)))

set.seed(1)

model.svmr <- train(stroke ~ . ,
                    data = train,
                    method = "svmRadialSigma",
                    preProcess = c("center", "scale"),
                    tuneGrid = svmr.grid,
                    trControl = ctrl)
```

```
## maximum number of iterations reached 0.00686392 0.006711329maximum number of iterations reached 0.00
```

```
plot(model.svmr, highlight = TRUE)
```




```
svmr.pred.prob = predict(model.svmr, newdata = x2, type = "prob")[,1]

svmr.pred = rep("Yes", length(svmr.pred.prob))

svmr.pred[svmr.pred.prob < 0.95] = "No"

confusionMatrix(data = as.factor(svmr.pred),
                reference = y2,
                positive = "Yes")
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  No Yes
##        No    0   0
##        Yes 939  41
##
##                Accuracy : 0.0418
##                  95% CI : (0.0302, 0.0563)
##     No Information Rate : 0.9582
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : 0
##
##  Mcnemar's Test P-Value : <2e-16
```

```
##
##             Sensitivity : 1.00000
##             Specificity : 0.00000
##          Pos Pred Value : 0.04184
##          Neg Pred Value :     NaN
##              Prevalence : 0.04184
##          Detection Rate : 0.04184
##    Detection Prevalence : 1.00000
##       Balanced Accuracy : 0.50000
##
##        'Positive' Class : Yes
##
```

```
model.svmr$bestTune
```

```
##           sigma         C
## 11 0.0003354626 0.6411804
```

Comparison

```
res <- resamples(list(glm = model.glm,
                      glmn = model.glmn,
                      mars = model.mars,
                      gam = model.gam,
                      lda = model.lda,
                      rf = model.rf,
                      gbmA = model.gbma,
                      svml = model.svml,
                      svmr = model.svmr))

summary(res)
```

```
##
## Call:
## summary.resamples(object = res)
##
## Models: glm, glmn, mars, gam, lda, rf, gbmA, svml, svmr
## Number of resamples: 10
##
## ROC
##           Min.   1st Qu.    Median      Mean   3rd Qu.      Max. NA's
## glm  0.7840758 0.8118742 0.8402691 0.8479809 0.8755867 0.9227159    0
## glmn 0.7510951 0.8341188 0.8586270 0.8507656 0.8754302 0.8969024    0
## mars 0.7291927 0.7933061 0.8578448 0.8343779 0.8720862 0.8922090    0
## gam  0.7553191 0.8254459 0.8594337 0.8477051 0.8768896 0.8936170    0
## lda  0.7270025 0.8254850 0.8400295 0.8362484 0.8595119 0.9161452    0
## rf   0.7350594 0.8057264 0.8349744 0.8333190 0.8572043 0.9152065    0
## gbmA 0.7711202 0.8287703 0.8545692 0.8493126 0.8748436 0.8889237    0
## svml 0.5314456 0.6267991 0.7093682 0.6958561 0.7503398 0.8160200    0
## svmr 0.6336436 0.6933080 0.7010325 0.7183941 0.7483182 0.8086671    0
```

```
##
## Sens
##            Min.  1st Qu.    Median      Mean   3rd Qu. Max. NA's
## glm  1.0000000 1.000000 1.0000000 1.0000000 1.0000000    1    0
## glmn 1.0000000 1.000000 1.0000000 1.0000000 1.0000000    1    0
## mars 0.9973404 1.000000 1.0000000 0.9997340 1.0000000    1    0
## gam  1.0000000 1.000000 1.0000000 1.0000000 1.0000000    1    0
## lda  0.9787234 0.987367 0.9933511 0.9912234 0.9946809    1    0
## rf   1.0000000 1.000000 1.0000000 1.0000000 1.0000000    1    0
## gbmA 1.0000000 1.000000 1.0000000 1.0000000 1.0000000    1    0
## svml 1.0000000 1.000000 1.0000000 1.0000000 1.0000000    1    0
## svmr 1.0000000 1.000000 1.0000000 1.0000000 1.0000000    1    0
##
## Spec
##      Min. 1st Qu.     Median       Mean    3rd Qu.   Max. NA's
## glm     0       0 0.00000000 0.00000000 0.00000000 0.0000    0
## glmn    0       0 0.00000000 0.00000000 0.00000000 0.0000    0
## mars    0       0 0.00000000 0.00000000 0.00000000 0.0000    0
## gam     0       0 0.00000000 0.00000000 0.00000000 0.0000    0
## lda     0       0 0.02941176 0.04264706 0.05882353 0.1875    0
## rf      0       0 0.00000000 0.00000000 0.00000000 0.0000    0
## gbmA    0       0 0.00000000 0.00000000 0.00000000 0.0000    0
## svml    0       0 0.00000000 0.00000000 0.00000000 0.0000    0
## svmr    0       0 0.00000000 0.00000000 0.00000000 0.0000    0
```

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