

Diabetes Prediction model

DS II Final team

Contents

Load Data	2
EDA	3
Summary statistics	3
Density plots (numerical covariates)	7
Bar plots (categorical covariates)	8
Partition-plots	9
Models	10
Prep/partition data	10
Linear models	11
Nonlinear models	13
trees/ SVM	15
Model comparison	31

```

library(RNHANES)
library(tidyverse)
library(summarytools)
library(leaps)
library(readr)
library(caret)
library(ggplot2)
library(patchwork)
library(mgcv)
library(nlme)
library(dplyr)
library(plyr)
library(AppliedPredictiveModeling)
library(dplyr)
library(scales)
library(pROC)
#library(MASS)
#library(klaR)
library(forcats)
library(visdat)
library(glmnet)
library(mlbench)
library(pROC)
library(pdp)
library(vip)
library(rpart.plot)
library(ranger)

```

Load Data

```
data_files <- nhanes_load_data(file_name = "DIQ_H", year = "2013-2014")
```

```

data_files <- data_files %>%
  left_join(nhanes_load_data("HDL_H", "2013-2014"), by = "SEQN") %>%
  left_join(nhanes_load_data("INS_H", "2013-2014"), by = "SEQN") %>%
  left_join(nhanes_load_data("TRIGLY_H", "2013-2014"), by = "SEQN") %>%
  left_join(nhanes_load_data("DEMO_H", "2013-2014"), by = "SEQN") %>%
  left_join(nhanes_load_data("BMX_H", "2013-2014"), by = "SEQN") %>%
  left_join(nhanes_load_data("OGTT_H", "2013-2014"), by = "SEQN") %>%
  left_join(nhanes_load_data("BPX_H", "2013-2014"), by = "SEQN") %>%
  left_join(nhanes_load_data("PAQ_H", "2013-2014"), by = "SEQN") %>%
  left_join(nhanes_load_data("DPQ_H", "2013-2014"), by = "SEQN") %>%
  left_join(nhanes_load_data("SLQ_H", "2013-2014"), by = "SEQN")

```

```
raw_data <- data_files %>%
```

```
  select(SEQN, RIAGENDR, RIDAGEYR, RIDRETH3, BMXBMI, LBDHDD, LBDLDL, LBXTR, LBXIN, LBXGLT, BPXSY1, BPXD
```

```

raw_data <- raw_data[raw_data$DIQ010 != 3 & raw_data$DIQ010 != 7 & raw_data$DIQ010 != 9, ] %>% mutate(
  drop_na(DIQ010)

```

```
colnames(raw_data) <- c("ID", "gender", "age", "race", "bmi", "hdl", "ldl", "triglyceride", "insulin",
  contrasts(raw_data$diabetes)
```

2 1 0 2 1

```
levels(raw_data$diabetes)[1] <- "yes"
levels(raw_data$diabetes)[2] <- "no"
contrasts(raw_data$diabetes)
```

no

yes 0 no 1

```
write.csv(raw_data, "final_data.csv")
```

EDA

Summary statistics

```
st_options(plain.ascii = FALSE,
  style = "rmarkdown",
  dfSummary.silent = TRUE,
  footnote = NA,
  subtitle.emphasis = FALSE)

dfSummary(raw_data[, -1], valid.col = FALSE)
```

Data Frame Summary

raw_data
Dimensions: 9578 x 18
Duplicates: 319

No	Variable	Stats / Values	Freqs (% of Valid)	Graph	Missing
1	gender	1. 1	4706 (49.1%)	IIIIIIII	0
	[factor]	2. 2	4872 (50.9%)	IIIIIIII	(0.0%)
2	age	Mean (sd) : 32.4 (23.9)	80 distinct values	:	0
	[numeric]	min < med < max:		::	(0.0%)
		1 < 28 < 80		:::	
		IQR (CV) : 41 (0.7)		:::::::::::	
				:::::::::::	
3	race	1. 1	1616 (16.9%)	III	0
	[factor]	2. 2	893 (9.3%)	I	(0.0%)
		3. 3	3449 (36.0%)	IIIIII	
		4. 4	2148 (22.4%)	IIII	
		5. 6	1033 (10.8%)	II	
		6. 7	439 (4.6%)		

No	Variable	Stats / Values	Freqs (% of Valid)	Graph	Missing
4	bmi [numeric]	Mean (sd) : 25.6 (7.9) min < med < max: 12.1 < 24.6 < 82.9 IQR (CV) : 10.4 (0.3)	436 distinct values	: .: : .: : .: :. .: : : .	706 (7.4%)
5	hdl [numeric]	Mean (sd) : 53.2 (15.2) min < med < max: 10 < 51 < 173 IQR (CV) : 19 (0.3)	116 distinct values	: : .: . .: : .: : .	2128 (22.2%)
6	ldl [numeric]	Mean (sd) : 106 (34.9) min < med < max: 14 < 103 < 375 IQR (CV) : 46 (0.3)	194 distinct values	: .: .: . .: : .: : : .	6553 (68.4%)
7	triglyceride [numeric]	Mean (sd) : 111.7 (115.9) min < med < max: 13 < 88 < 4233 IQR (CV) : 73 (1)	344 distinct values	: : : : :	6515 (68.0%)
8	insulin [numeric]	Mean (sd) : 13.4 (18.7) min < med < max: 0.1 < 9.3 < 682.5 IQR (CV) : 9.1 (1.4)	1716 distinct values	: : : : :	6567 (68.6%)
9	glucose [numeric]	Mean (sd) : 114 (45.5) min < med < max: 40 < 104 < 604 IQR (CV) : 44 (0.4)	227 distinct values	: .: .: .: .: :	7294 (76.2%)
10	bp_systolic [numeric]	Mean (sd) : 117.9 (18) min < med < max: 66 < 116 < 228 IQR (CV) : 20 (0.2)	71 distinct values	: .: .: .: :. .: : : .	2571 (26.8%)
11	bp_diastolic [numeric]	Mean (sd) : 65.7 (15) min < med < max: 0 < 66 < 122 IQR (CV) : 16 (0.2)	59 distinct values	: .: .: : .: : .: : : .	2571 (26.8%)
12	waist [numeric]	Mean (sd) : 86.9 (22.5) min < med < max: 40.2 < 87.4 < 177.9 IQR (CV) : 31.6 (0.3)	1030 distinct values	: .: .: : .: : : .: : : : .	1091 (11.4%)
13	lifestyle [numeric]	Mean (sd) : 478.5 (642.1) min < med < max: 0 < 480 < 9999 IQR (CV) : 300 (1.3)	36 distinct values	: : : : :	2625 (27.4%)

No	Variable	Stats / Values	Freqs (% of Valid)	Graph	Missing
14	education [factor]	1. 1	442 (7.9%)	I	3986 (41.6%)
		2. 2	761 (13.6%)	II	
		3. 3	1261 (22.6%)	III	
		4. 4	1715 (30.7%)	IIII	
		5. 5	1406 (25.1%)	IIII	
		6. 7	2 (0.0%)		
		7. 9	5 (0.1%)		
15	married [factor]	1. 1	2866 (51.3%)	IIIIIIII	3986 (41.6%)
		2. 2	419 (7.5%)	I	
		3. 3	637 (11.4%)	II	
		4. 4	170 (3.0%)		
		5. 5	1096 (19.6%)	III	
		6. 6	401 (7.2%)	I	
		7. 77	2 (0.0%)		
16	depression [numeric]	8. 99	1 (0.0%)		4343 (45.3%)
		Mean (sd) : 0.4 (0.8)	0 : 3955 (75.5%)	IIIIIIIIII	
		min < med < max:	1 : 876 (16.7%)	III	
		0 < 0 < 9	2 : 205 (3.9%)		
		IQR (CV) : 0 (2.1)	3 : 194 (3.7%)		
17	sleep [numeric]		7 : 2 (0.0%)		3300 (34.5%)
			9 : 3 (0.1%)		
		Mean (sd) : 7 (3.2)	12 distinct values	:	
		min < med < max:		:	
		2 < 7 < 99		:	
18	diabetes [factor]	IQR (CV) : 2 (0.5)		:	0 (0.0%)
				:	
				:	
		1. yes	737 (7.7%)	I	
		2. no	8841 (92.3%)	IIIIIIIIIIIIII	

```
# Delete high missing-data covariates
raw_data <- raw_data[-c(7:10)]
dfSummary(raw_data[, -1], valid.col = FALSE)
```

Data Frame Summary

raw_data
Dimensions: 9578 x 14
Duplicates: 319

No	Variable	Stats / Values	Freqs (% of Valid)	Graph	Missing
1	gender [factor]	1. 1	4706 (49.1%)	IIIIIIII	0 (0.0%)
		2. 2	4872 (50.9%)	IIIIIIII	
2	age [numeric]	Mean (sd) : 32.4 (23.9)	80 distinct values	:	0 (0.0%)
		min < med < max:		::	
		1 < 28 < 80		:::	
		IQR (CV) : 41 (0.7)		:::::::::::	
				:::::::::::	

No	Variable	Stats / Values	Freqs (% of Valid)	Graph	Missing
3	race [factor]	1. 1	1616 (16.9%)	III	0 (0.0%)
		2. 2	893 (9.3%)	I	
		3. 3	3449 (36.0%)	IIIIII	
		4. 4	2148 (22.4%)	IIII	
		5. 6	1033 (10.8%)	II	
		6. 7	439 (4.6%)		
4	bmi [numeric]	Mean (sd) : 25.6 (7.9)	436 distinct	:	706 (7.4%)
		min < med < max:	values	. : :	
		12.1 < 24.6 < 82.9		: : :	
		IQR (CV) : 10.4 (0.3)		: : : .	
5	hdl [numeric]	Mean (sd) : 53.2 (15.2)	116 distinct	:	2128 (22.2%)
		min < med < max:	values	:	
		10 < 51 < 173		. : .	
		IQR (CV) : 19 (0.3)		: : :	
6	bp_systolic [numeric]	Mean (sd) : 117.9 (18)	71 distinct values	:	2571 (26.8%)
		min < med < max:		: :	
		66 < 116 < 228		: :	
		IQR (CV) : 20 (0.2)		. : : .	
7	bp_diastolic [numeric]	Mean (sd) : 65.7 (15)	59 distinct values	:	2571 (26.8%)
		min < med < max:		: .	
		0 < 66 < 122		: : :	
		IQR (CV) : 16 (0.2)		: : :	
8	waist [numeric]	Mean (sd) : 86.9 (22.5)	1030 distinct	: : : : .	1091 (11.4%)
		min < med < max:	values	: .	
		40.2 < 87.4 < 177.9		: : :	
		IQR (CV) : 31.6 (0.3)		. : : :	
9	lifestyle [numeric]	Mean (sd) : 478.5 (642.1)	36 distinct values	: : : : : .	2625 (27.4%)
		min < med < max:		:	
		0 < 480 < 9999		:	
		IQR (CV) : 300 (1.3)		:	
10	education [factor]	1. 1	442 (7.9%)	I	3986 (41.6%)
		2. 2	761 (13.6%)	II	
		3. 3	1261 (22.6%)	IIII	
		4. 4	1715 (30.7%)	IIIIII	
		5. 5	1406 (25.1%)	IIII	
		6. 7	2 (0.0%)		
11	married [factor]	7. 9	5 (0.1%)		3986 (41.6%)
		1. 1	2866 (51.3%)	IIIIIIII	
		2. 2	419 (7.5%)	I	
		3. 3	637 (11.4%)	II	
		4. 4	170 (3.0%)		
		5. 5	1096 (19.6%)	III	
		6. 6	401 (7.2%)	I	
		7. 77	2 (0.0%)		
		8. 99	1 (0.0%)		

No	Variable	Stats / Values	Freqs (% of Valid)	Graph	Missing
12	depression [numeric]	Mean (sd) : 0.4 (0.8) min < med < max: 0 < 0 < 9 IQR (CV) : 0 (2.1)	0 : 3955 (75.5%) 1 : 876 (16.7%) 2 : 205 (3.9%) 3 : 194 (3.7%) 7 : 2 (0.0%) 9 : 3 (0.1%)	IIIIIIIIIIIIIIII III	4343 (45.3%)
13	sleep [numeric]	Mean (sd) : 7 (3.2) min < med < max: 2 < 7 < 99 IQR (CV) : 2 (0.5)	12 distinct values	: : : : :	3300 (34.5%)
14	diabetes [factor]	1. yes 2. no	737 (7.7%) 8841 (92.3%)	I IIIIIIIIIIIIIIIIIIII	0 (0.0%)

Density plots (numerical covariates)

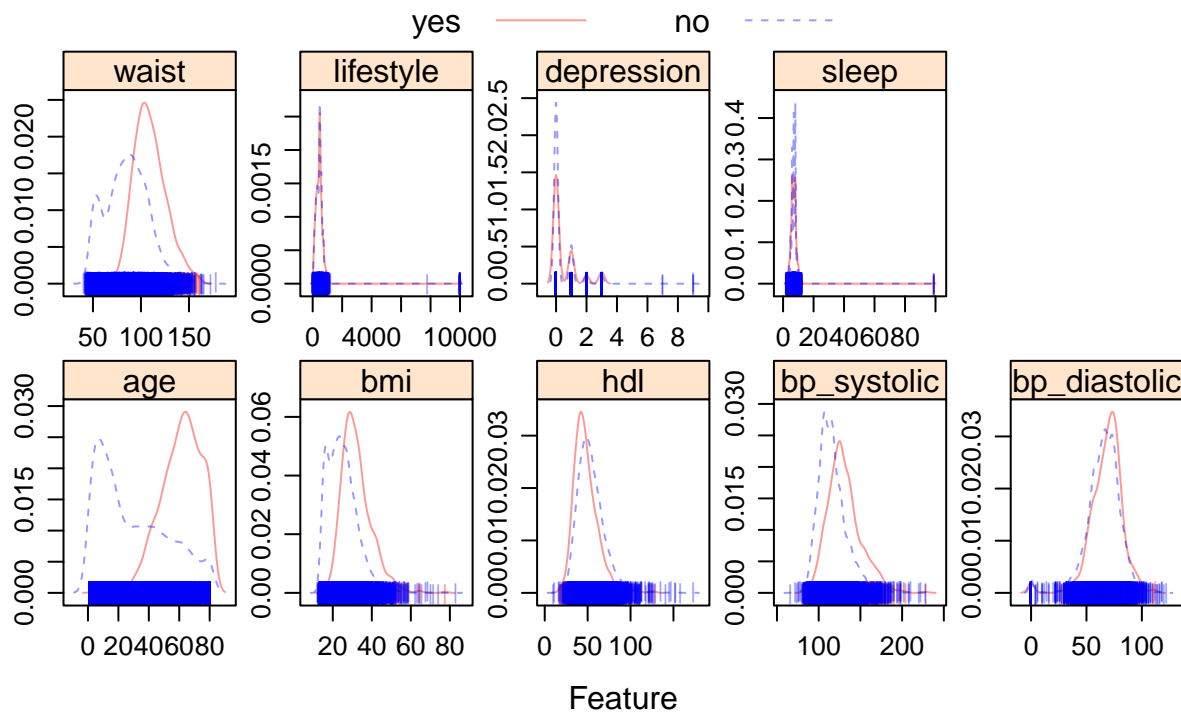
```

theme1 <- transparentTheme(trans = .4)
trellis.par.set(theme1)

raw_data <- raw_data %>%
  select(married, everything()) %>%
  select(education, everything()) %>%
  select(race, everything()) %>%
  select(gender, everything()) %>%
  select(ID, everything())

featurePlot(x = raw_data[, 6:14],
            y = raw_data$diabetes,
            scales = list(x = list(relation = "free"),
                          y = list(relation = "free")),
            plot = "density", pch = "|",
            auto.key = list(columns = 2))

```



Bar plots (categorical covariates)

```
diabetes_gender = ggplot(raw_data,
  aes(x = diabetes,
    fill = factor(gender,
      levels = c("1", "2"),
      labels = c("male", "female")))) +
  geom_bar(position = position_dodge(preserve = "single")) +
  scale_fill_brewer(palette = "Set2") +
  labs(fill = "gender")

diabetes_race = ggplot(raw_data,
  aes(x = diabetes,
    fill = factor(race,
      levels = c("1", "2", "3", "4", "6", "7"),
      labels = c("Mexican American", "Other Hispanic", "White", "Black", "Asian", "Other")))) +
  geom_bar(position = position_dodge(preserve = "single")) +
  scale_fill_brewer(palette = "Set2") +
  labs(fill = "race")

diabetes_education = ggplot(raw_data,
  aes(x = diabetes,
    fill = factor(education,
      levels = c("1", "2", "3", "4", "5"),
      labels = c("< 9th grade", "9 - 11 grade", "H.S./GED", "Some college", "College graduate")))) +
  geom_bar(position = position_dodge(preserve = "single")) +
  scale_fill_brewer(palette = "Set2") +
  labs(fill = "education")
```



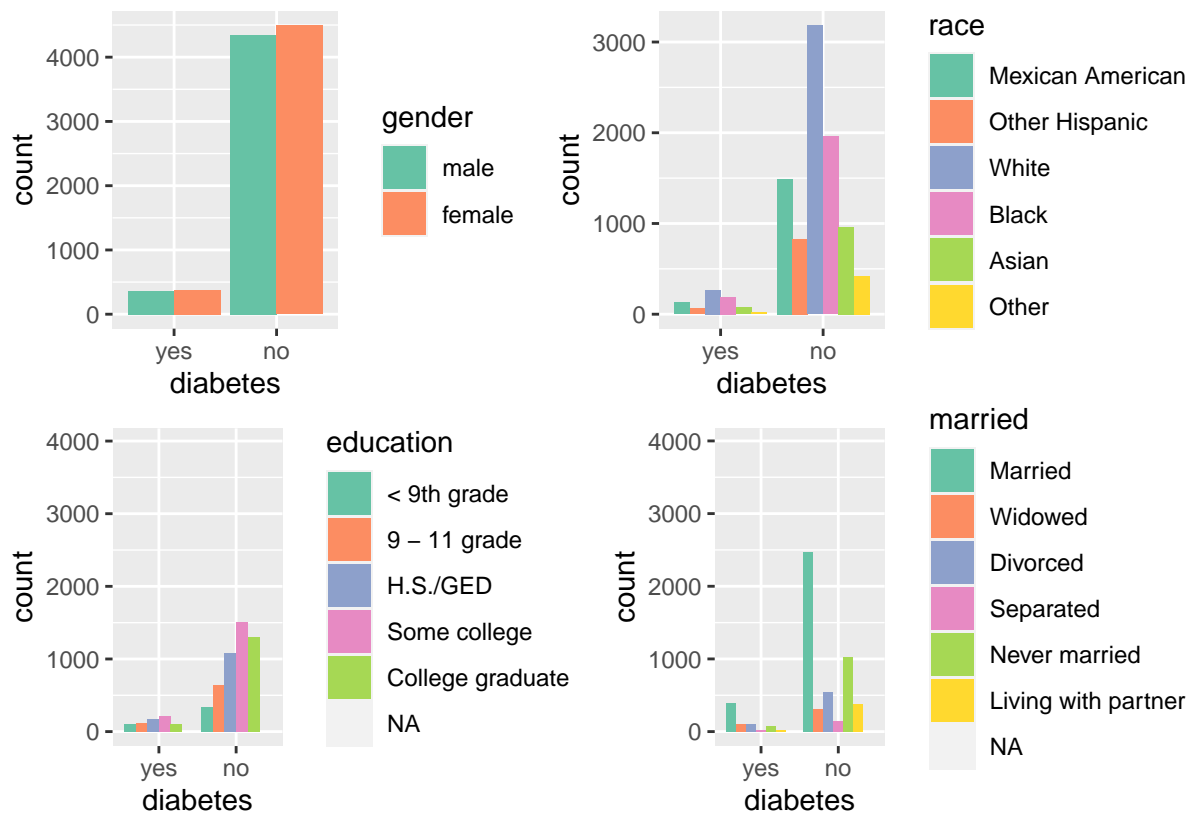
```

labs(fill = "education")

diabetes_married = ggplot(raw_data,
  aes(x = diabetes,
      fill = factor(married,
                    levels = c("1", "2", "3", "4", "5", "6"),
                    labels = c("Married", "Widowed", "Divorced", "Separated", "Never married", "Living with partner", "NA"))),
  geom_bar(position = position_dodge(preserve = "single"))) +
  scale_fill_brewer(palette = "Set2") +
  labs(fill = "married")

(diabetes_gender + diabetes_race) / (diabetes_education + diabetes_married)

```



Partition-plots

```

set.seed(1)
rowTrain <- createDataPartition(y = raw_data$diabetes,
  p = 0.7,
  list = FALSE)

# Exploratory analysis: LDA/QDA/NB based on every combination of two variables

# klaR::partimat(diabetes ~ age + bmi + hdl + bp_systolic + waist,

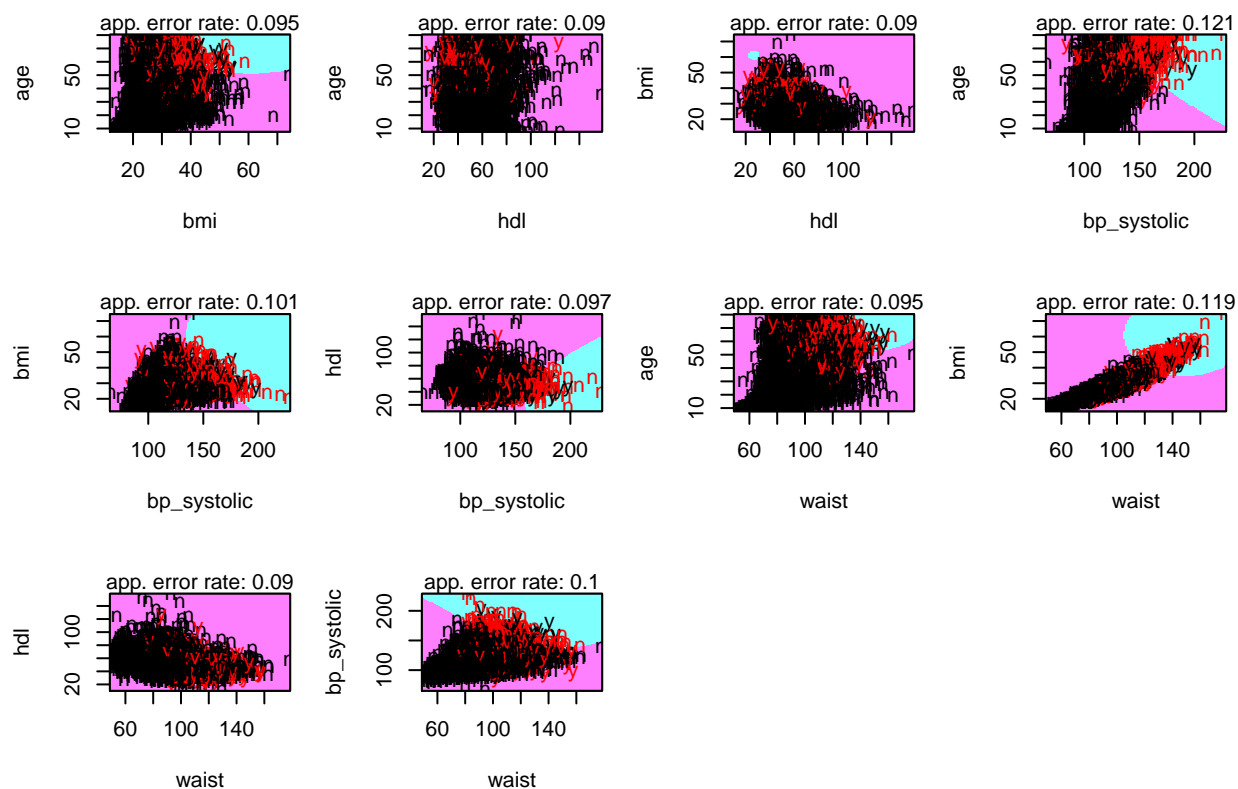
```

```
# data = raw_data, subset = rowTrain, method = "lda")

# klaR::partimat(diabetes ~ age + bmi + hdl + bp_systolic + waist,
# data = raw_data, subset = rowTrain, method = "qda")

klaR::partimat(diabetes ~ age + bmi + hdl + bp_systolic + waist,
data = raw_data, subset = rowTrain, method = "naiveBayes")
```

Partition Plot



Models

Prep/partition data

```
# Omit Missing data
diabetes_data <- na.omit(raw_data)

# Omit low-count subcategories
diabetes_data <- na.omit(diabetes_data) %>%
  filter(married != "77") %>%
  filter(education != "7") %>%
  filter(education != "9") %>%
  droplevels()
```

```

set.seed(1)
trainRows <- createDataPartition(diabetes_data$diabetes, p = 0.8, list = FALSE)

# training data
x <- diabetes_data[trainRows, -c(1, 15)]
y <- diabetes_data$diabetes[trainRows]

# test data
x2 <- diabetes_data[-trainRows, -c(1, 15)]
y2 <- diabetes_data$diabetes[-trainRows]

# Setup CV method
ctrl <- trainControl(method = "cv",
                      summaryFunction = twoClassSummary,
                      classProbs = TRUE)

```

Linear models

```

# glm
set.seed(1)

model.glm <- train(x = x,
                   y = y,
                   method = "glm",
                   metric = "ROC",
                   trControl = ctrl)

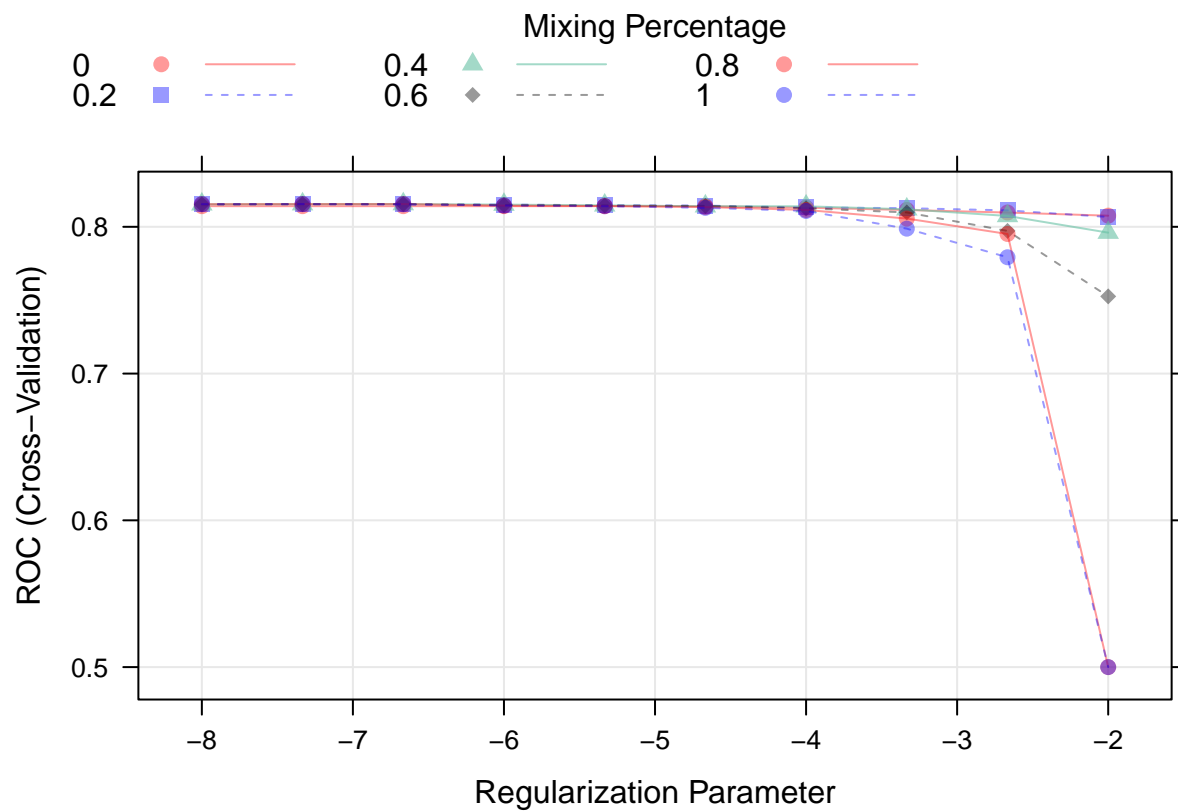
# glm.pred <- predict(model.glm, newdata = x2, type = "prob")[,2]
# roc.glm <- roc(y2, glm.pred)
# plot(roc.glm, legacy.axes = TRUE, print.auc = TRUE)
# plot(smooth(roc.glm), col = 4, add = TRUE)

# Penalized Logistic regression
glmGrid <- expand.grid(.alpha = seq(0, 1, length = 6),
                      .lambda = exp(seq(-8, -2, length = 10)))
set.seed(1)

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

plot(model.glmn, xTrans = function(x) log(x))

```



```
model.glmn$bestTune
```

```
alpha lambda 33 0.6 0.001272634
```

```
# glmn.pred <- predict(model.glmn, newdata = data.matrix(x2), type = "prob")[,2]
# roc.glmn <- roc(y2, glmn.pred)
# plot(roc.glmn, legacy.axes = TRUE, print.auc = TRUE)
# plot(smooth(roc.glmn), col = 4, add = TRUE)

# LDA
# set.seed(1)

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

# lda.pred <- predict(model.lda, newdata = data.matrix(x2), type = "prob")[,2]

# roc.lda <- roc(y2, lda.pred)
# plot(roc.lda, legacy.axes = TRUE, print.auc = TRUE)
# plot(smooth(roc.lda), col = 4, add = TRUE)
```

Nonlinear models

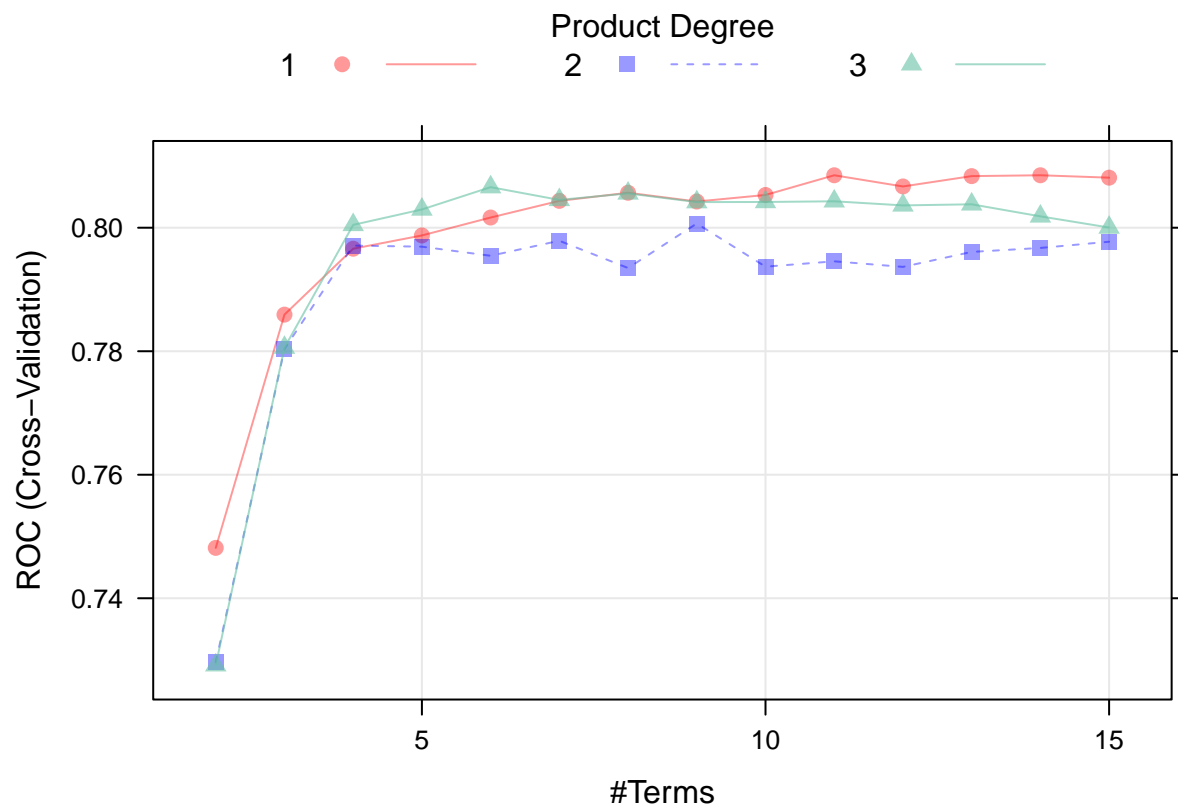
```
## Non-linear Logistic regression: GAM, MARS
# GAM
#set.seed(1)
#model.gam <- train(x = x,
#                    y = y,
#                    method = "gam",
#                    metric = "ROC",
#                    trControl = ctrl)

#model.gam$finalModel

# MARS
set.seed(1)

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

plot(model.mars)
```



```
coef(model.mars$finalModel)
```

(Intercept)	h(age-76)	h(76-age)	h(waist-88)
1.658285895	0.122437959	0.062661766	-0.055430289
h(74-hdl)	h(86-bp_diastolic)	race3	h(bmi-38.9)
-0.027315168	-0.012127252	0.549041828	0.150319736
married2	h(waist-104.2)	h(bmi-48.4)	education5
-0.214623872	0.005005836	-0.186737365	0.695318548
education3	education4		
0.440916855	0.367828136		

```
## Non-linear Discriminant analysis: QDA, Naive Bayes (NB)
```

```
# QDA = for continuous features
```

```
#set.seed(1)
```

```
#model.qda <- train(x = x,
```

```
#           y = y,
```

```
#           method = "qda",
```

```
#           metric = "ROC",
```

```
#           trControl = ctrl)
```

```
# NB
```

```
set.seed(1)
```

```
nbGrid <- expand.grid(usekernel = c(FALSE,TRUE),
```

```
                    fL = 1,
```

```
                    adjust = seq(.2, 2.5, by = .2))
```

```
model.nb <- train(x = x,
```

```
                y = y,
```

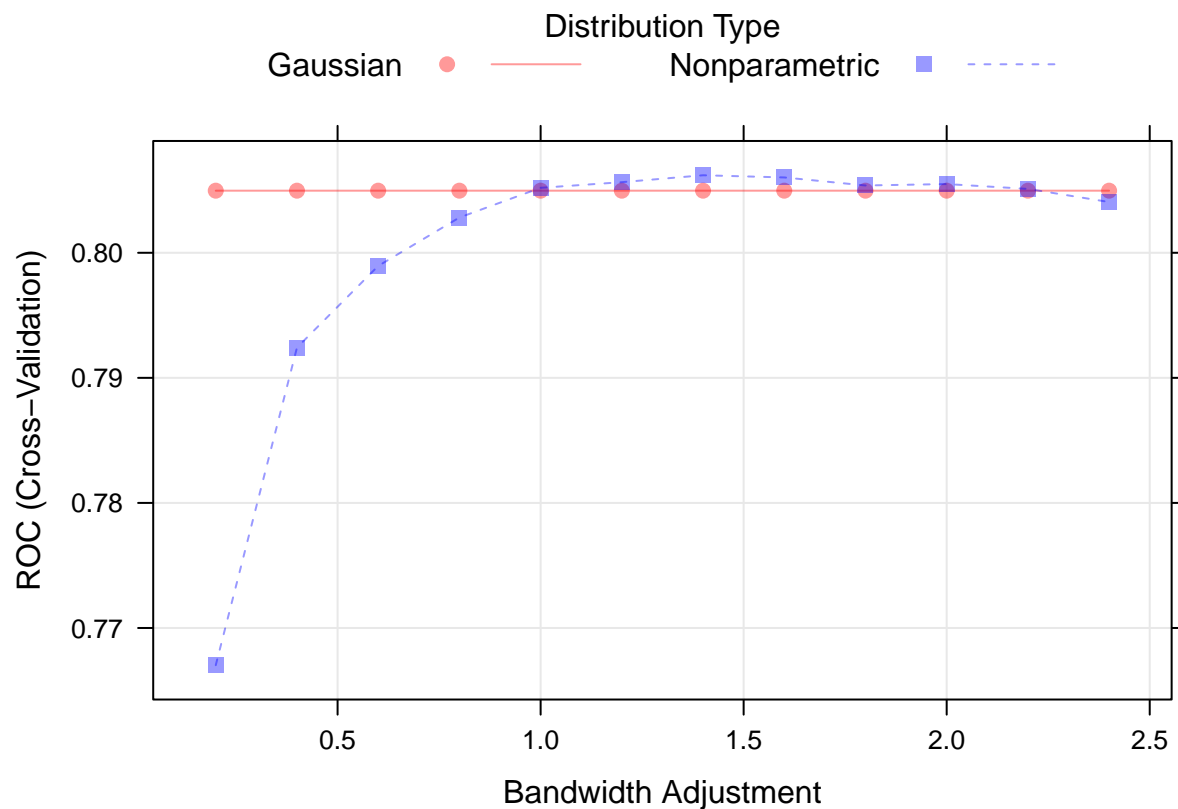
```
                method = "nb",
```

```
                tuneGrid = nbGrid,
```

```
                metric = "ROC",
```

```
                trControl = ctrl)
```

```
plot(model.nb)
```



trees/ SVM

```
## single tree. very useless
#set.seed(1)
#rpart.fit <- train(diabetes ~ . ,
#                   diabetes_data[trainRows,-1],
#                   method = "rpart",
#                   tuneGrid = data.frame(cp = exp(seq(-1,10, length = 500))),
#                   trControl = ctrl)
#ggplot(rpart.fit, highlight = TRUE)
#rpart.plot(rpart.fit$finalModel)

## random forest in caret

#rf_grid = expand.grid(mtry = 1:13,
#                      splitrule = "gini",
#                      min.node.size = seq(from = 2, to = 10, by = 2))

#set.seed(1)
#rf.fit = train(diabetes ~ . ,
#               diabetes_data[trainRows,-1],
#               method = "ranger",
#               tuneGrid = rf_grid,
#               metric = "ROC",
```

```

#           trControl = ctrl)

#ggplot(rf.fit, highlight = TRUE)

#set.seed(1)
#rf_final = ranger(diabetes ~ . ,
#                  diabetes_data[trainRows,-1],
#                  mtry = rf_fit$bestTune[[1]],
#                  min.node.size = rf_fit$bestTune[[3]],
#                  importance = "permutation",
#                  scale.permutation.importance = TRUE)
#rf_table=rf_final$variable.importance
#rf_final$prediction.error
#rfclass_pred = predict(rf_final, data = diabetes_data[-trainRows,-1], type = "response")$predictions
#rfconf = confusionMatrix(data = as.factor(rfclass_pred),
#                           reference = y2,
#                           positive = "yes")

#rf_err = (rfconf$table[1,2]+rfconf$table[2,1])/(rfconf$table[1,1]+rfconf$table[1,2]+rfconf$table[2,1]+

### gbm/gbma
#gbm_grid = expand.grid(n.trees = c(0,1000,2000,3000,4000,5000,6000),
#                       interaction.depth = 1:4,
#                       shrinkage = c(0.001,0.003,0.005),
#                       n.minobsinnode = c(1,10))

#set.seed(1)
#gbm_fit = train(diabetes ~ . ,
#                diabetes_data[trainRows,-1],
#                method = "gbm",
#                tuneGrid = gbm_grid,
#                trControl = ctrl,
#                verbose = FALSE)
#ggplot(gbm_fit, highlight = TRUE)
#summary(gbm_fit$finalModel)
#gbm_pred <- predict(gbm_fit, newdata = diabetes_data[-trainRows,], type = "prob")[,1]
#gbm_test_pred = rep("no", length(gbm_pred))
#gbm_test_pred[gbm_pred>0.5] = "yes"
#gbmconf = confusionMatrix(data = as.factor(gbm_test_pred),
#                           reference = diabetes_data$diabetes[-trainRows],
#                           positive = "yes")
#gbmconf$table
#gbm_err = (gbmconf$table[1,2]+gbmconf$table[2,1])/(gbmconf$table[1,1]+gbmconf$table[1,2]+gbmconf$table

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)
gbmA_fit <- train(diabetes ~ . ,
                  diabetes_data,
                  subset = trainRows,

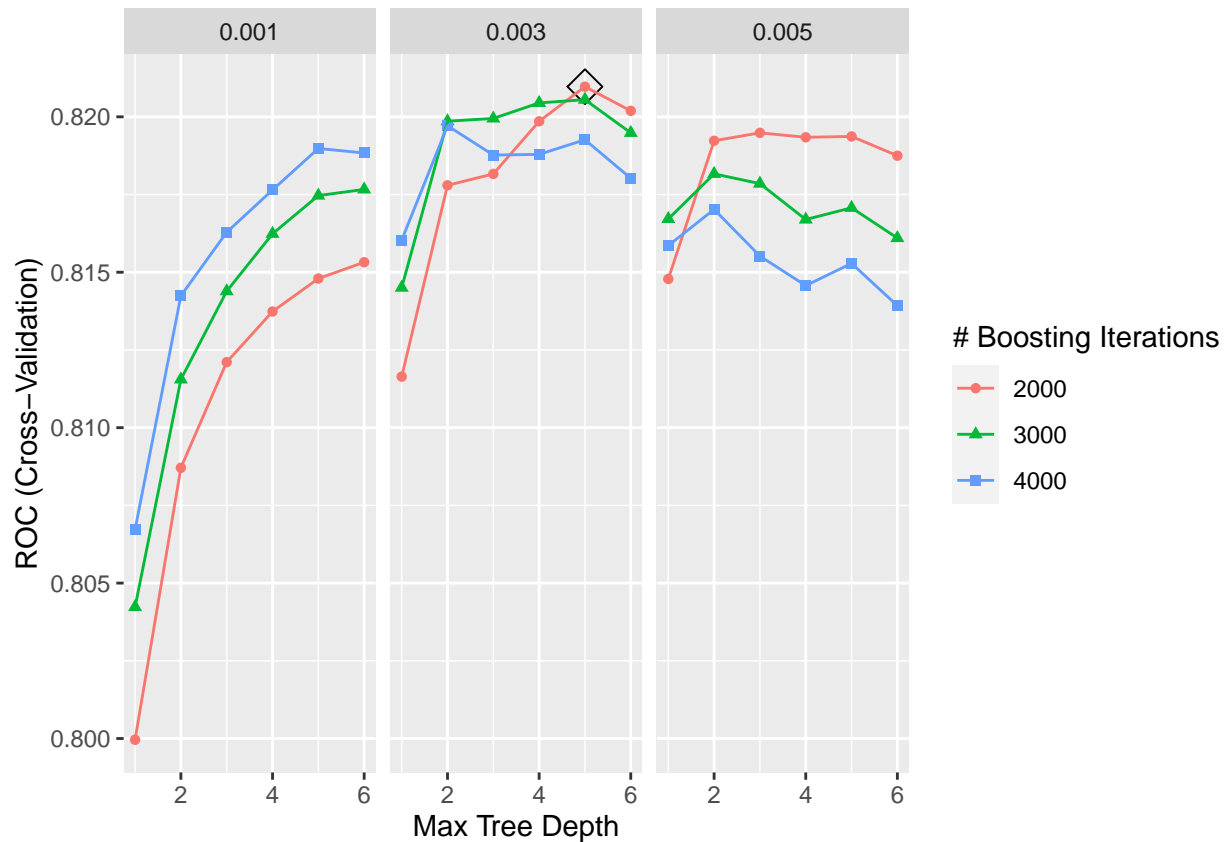
```



```

tuneGrid = gbmA_grid,
trControl = ctrl,
method = "gbm",
distribution = "adaboost",
metric = "ROC",
verbose = FALSE)
ggplot(gbmA.fit, highlight = TRUE)

```



```

#gbmA_pred <- predict(gbmA_fit, newdata = diabetes_data[-trainRows,], type = "prob")[,1]
#gbmA_test_pred = rep("no", length(gbmA_pred))
#gbmA_test_pred[gbmA_pred>0.5] = "yes"
#gbmAconf = confusionMatrix(data = as.factor(gbmA_test_pred),
#                             reference = diabetes_data$diabetes[-trainRows],
#                             positive = "yes")
#gbmAconf$table
#gbmA_err = (gbmAconf$table[1,2]+gbmAconf$table[2,1])/(gbmAconf$table[1,1]+gbmAconf$table[1,2]+gbmAconf$
# Comparing Ensemble methods
#res <- resamples(list(rf = rf.fit,
#                       gbm = gbm_fit,
#                       gbmA = gbmA_fit ))
#summary(res)
#bwplot(res, metric = "ROC")

```

```
## SVML/R
#ctrl <- trainControl(method = "cv")
# kernlab
set.seed(1)
svml.fit <- train(diabetes ~ . ,
                  data = diabetes_data[trainRows,],
                  method = "svmLinear",
                  #preProcess = c("center", "scale"),
                  tuneGrid = data.frame(C = exp(seq(0,2,len = 100))),
                  metric = "ROC",
                  trControl = ctrl)
```

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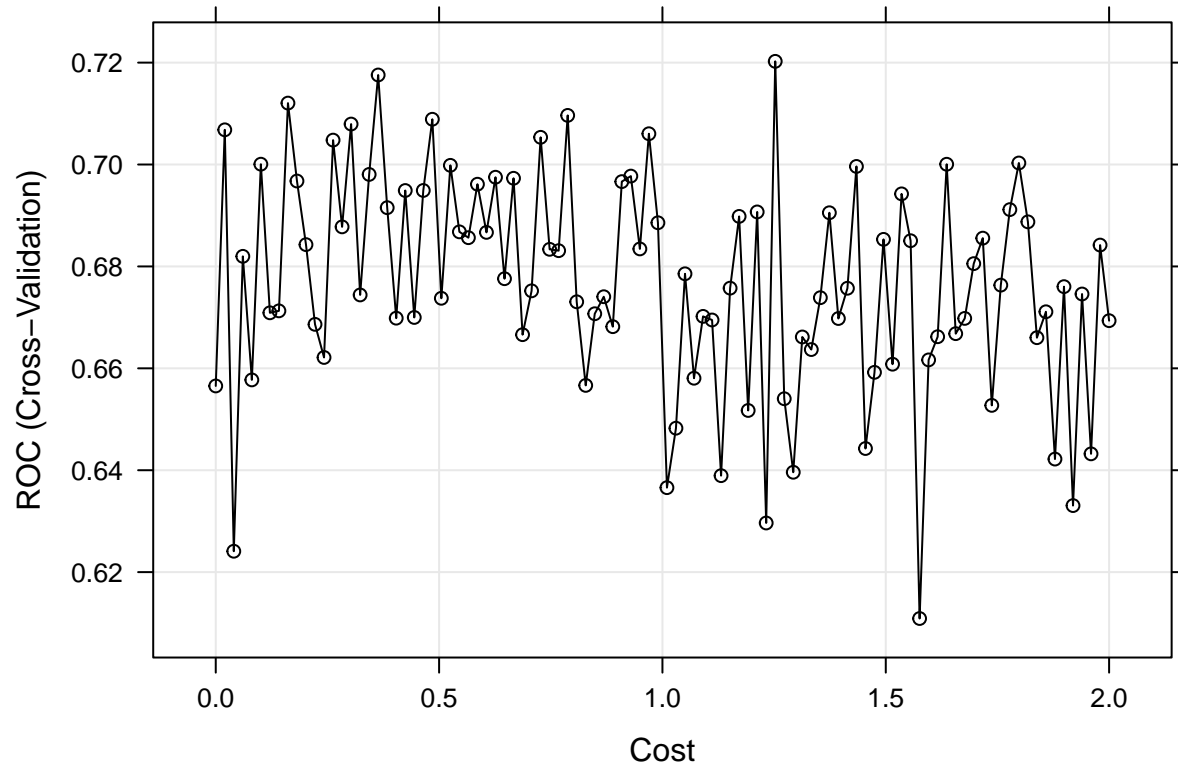
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 reached 0.008339732 -0.008039203maximum number of iterations reached 0.01185354 -0.01089943maximum
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 reached 0.009195617 -0.008859024maximum number of iterations reached 0.008526533 -0.00820679maximum
 number of iterations reached 0.005099481 -0.004957159maximum number of iterations reached 0.01111288
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 number of iterations reached 0.0104561 -0.009856496maximum number of iterations reached 0.009051564
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 0.008314487maximum number of iterations reached 0.005705987 -0.005573817maximum number of iterations
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 -0.01044614maximum number of iterations reached 0.009689951 -0.009195673maximum number of iterations
 reached 0.01136359 -0.01077797maximum number of iterations reached 0.01135118 -0.01071768maximum
 number of iterations reached 0.0123515 -0.0115294maximum number of iterations reached 0.01249418
 -0.01173077maximum number of iterations reached 0.006285307 -0.006129284maximum number of iterations
 reached 0.01070921 -0.009785008maximum number of iterations reached 0.01129159 -0.01072078maximum
 number of iterations reached 0.008810452 -0.008355197maximum number of iterations reached 0.007101167 -
 0.006824357maximum number of iterations reached 0.006880232 -0.006717914maximum number of iterations
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 number of iterations reached 0.008291298 -0.007986006maximum number of iterations reached 0.009983214
 -0.00950371maximum number of iterations reached 0.01016958 -0.009388264maximum number of iterations
 reached 0.01015727 -0.009517383maximum number of iterations reached 0.009481469 -0.008943468maximum
 number of iterations reached 0.009750607 -0.009253358maximum number of iterations reached 0.01238064
 -0.01150041maximum number of iterations reached 0.008775689 -0.008329354maximum number of iterations
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 -0.01115519maximum number of iterations reached 0.006366166 -0.006107237maximum number of iterations
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 0.009576708maximum number of iterations reached 0.009386937 -0.008939872maximum number of iterations
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reached 0.008238586 -0.007888968maximum number of iterations reached 0.01321204 -0.01201468maximum
 number of iterations reached 0.01272783 -0.01161828maximum number of iterations reached 0.007775836
 -0.007573947maximum number of iterations reached 0.01438731 -0.01339052maximum number of iterations
 reached 0.01082026 -0.01007114maximum number of iterations reached 0.008686117 -0.008287133maximum
 number of iterations reached 0.005261934 -0.005284852maximum number of iterations reached 0.009357461
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 number of iterations reached 0.004730914 -0.004688576maximum number of iterations reached 0.008325669
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 number of iterations reached 0.01441812 -0.01328546maximum number of iterations reached 0.01077093
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 number of iterations reached 0.01012285 -0.009653444maximum number of iterations reached 0.01293697
 -0.01172937maximum number of iterations reached 0.009454144 -0.009123214maximum number of iterations
 reached 0.01014908 -0.009794233maximum number of iterations reached 0.01130378 -0.01063457

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



```
#pred.suml <- predict(suml.fit, newdata = diabetes_data[-trainRows,])
#confusionMatrix(data = pred.suml,
#                  reference = diabetes_data$diabetes[-trainRows])

## radial
#sumr.grid <- expand.grid(C = exp(seq(-1,3,len = 10)),
#                          sigma = exp(seq(-4,0,len = 10)))

# tunes over both cost and sigma
#set.seed(1)
#sumr.fit <- train(diabetes ~ . ,
#                  diabetes_data,
#                  subset = trainRows,
#                  method = "sumRadialSigma",
#                  preProcess = c("center", "scale"),
#                  tuneGrid = sumr.grid,
#                  trControl = ctrl)
#plot(sumr.fit, highlight = TRUE)
#pred.sumr <- predict(sumr.fit, newdata = diabetes_data[-trainRows,])
#confusionMatrix(data = pred.sumr,
#                  reference = diabetes_data$diabetes[-trainRows])

# Comparing sum methods
#res <- resamples(list(suml = suml.fit,
#                       sumr = sumr.fit))
```

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

Model comparison

```
res <- resamples(list(GLM = model.glm,
                     GLMNET = model.glmn,
                     MARS = model.mars,
                     NB = model.nb,
                     gbmA = gbmA.fit,
                     svm1 = svm1.fit))

summary(res)
```

Call: summary.resamples(object = res)

Models: GLM, GLMNET, MARS, NB, gbmA, svm1 Number of resamples: 10

ROC Min. 1st Qu. Median Mean 3rd Qu. Max. NA's GLM 0.7623056 0.7861968 0.8276816 0.8196973 0.8465606 0.8756791 0 GLMNET 0.7671958 0.7860153 0.8182620 0.8155202 0.8457133 0.8632151 0 MARS 0.7704024 0.7818502 0.7989819 0.8084961 0.8296717 0.8719239 0 NB 0.7728447 0.7796216 0.7986685 0.8061999 0.8354096 0.8446480 0 gbmA 0.7675199 0.7941118 0.8181100 0.8209701 0.8562155 0.8644934 0 svm1 0.6611072 0.6902958 0.7109821 0.7202501 0.7249282 0.8312560 0

Sens Min. 1st Qu. Median Mean 3rd Qu. Max. NA's GLM 0.07142857 0.11904762 0.12929125 0.14147287 0.1607143 0.2325581 0 GLMNET 0.04761905 0.07142857 0.10575858 0.09905869 0.1183555 0.1627907 0 MARS 0.04761905 0.11904762 0.14285714 0.13909192 0.1578073 0.2325581 0 NB 0.16666667 0.22245293 0.30952381 0.28117386 0.3313953 0.3720930 0 gbmA 0.04761905 0.07142857 0.09413068 0.08732004 0.1110188 0.1190476 0 svm1 0.00000000 0.00000000 0.00000000 0.00000000 0.00000000 0.00000000 0

Spec Min. 1st Qu. Median Mean 3rd Qu. Max. NA's GLM 0.9730640 0.9772727 0.9815154 0.9831842 0.9898990 0.9966330 0 GLMNET 0.9697987 0.9806906 0.9898990 0.9858778 0.9898990 0.9932886 0 MARS 0.9697987 0.9747644 0.9831650 0.9828509 0.9882296 1.0000000 0 NB 0.9259259 0.9351852 0.9478114 0.9471855 0.9587542 0.9664430 0 gbmA 0.9764310 0.9898990 0.9932660 0.9902459 0.9932829 0.9966443 0 svm1 1.0000000 1.0000000 1.0000000 1.0000000 1.0000000 1.0000000 0

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

