

Use Logistic Regression and Classification to Explore the Impact of Supplemental Breast Imaging and False-positive Biopsy Rates among Young Breast Cancer Patients

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4/7/2020

import data

data cleaning

```
# race
screen <- screen %>% mutate(race_ethnicity = factor(race_ethnicity),
                           race_ethnicity = relevel(race_ethnicity,
                                                    ref = "Non-Hispanic White"))

# marital_status
screen <- screen %>% mutate(marital_final = factor(marital_final),
                           marital_final = relevel(marital_final,
                                                    ref = "Unmarried"))

# insurance
screen <- screen %>%
  mutate(insurance = recode(insurance,
                           "Medicare" = "public insur",
                           "Medicaid" = "public insur",
                           "Private insurance" = "private insur",
                           "Uninsured/Unknown" = "uninsured"),
         insurance = factor(insurance),
         insurance = relevel(insurance, ref = "private insur"))

# dx_year
dx_year <- screen %>% pull(dx_year)
dx_yr_cat <- rep(0, length(dx_year))
for (i in 1:length(dx_year)) {
  if (dx_year[i] < 2008) {
    dx_yr_cat[i] = "< 2008"
  } else if (dx_year[i] < 2011 & dx_year[i] >= 2008) {
    dx_yr_cat[i] = "2008-2011"
  } else if (dx_year[i] < 2014 & dx_year[i] >= 2011) {
    dx_yr_cat[i] = "2011-2013"
  } else {
    dx_yr_cat[i] = "> 2013"
  }
}
```

```

dx_yr_cat <- as.factor(dx_yr_cat) %>%
  relevel(ref = "< 2008")
screen <- screen %>%
  mutate(dx_year = dx_yr_cat)

# GT
screen <- screen %>% mutate(gt_final = recode(gt_final,
                                             "N" = "no",
                                             "Y Unknown" = "no",
                                             "Y unknown" = "no",
                                             "Y -" = "neg",
                                             "Y VUS" = "vus",
                                             "Y +" = "pos"),
                           gt_final = as.factor(gt_final),
                           gt_final = relevel(gt_final,ref = "no"))

# stage
screen <- screen %>% mutate(stage = factor(stage),
                           stage = relevel(stage,ref = "1"))

# FHX
screen <- screen %>% mutate(fhx = factor(fhx),
                           fhx = relevel(fhx,ref="No"))

# supp_screening
screen <- screen %>% mutate(supp_screening = factor(supp_screening),
                           supp_screening = relevel(supp_screening,ref = "no"))

# density_dx
screen <- screen %>% mutate(density_dx = recode(density_dx,
                                                "1" = "1",
                                                "2" = "1",
                                                "3" = "2",
                                                "4" = "2"),
                           density_dx = factor(density_dx),
                           density_dx = relevel(density_dx,ref = "1"))

# false positive
f_p <- pull(screen,false_positive)
f_p[which(is.na(f_p))] <- "N"
f_p <- as.factor(f_p) %>% relevel(ref = "N")
screen <- screen %>% mutate(false_positive = f_p)

dat <- screen %>% dplyr::select(ageatdiagnosis,race_ethnicity,
                              marital_final,insurance,stage,
                              fhx,dx_year,gt_final,supp_screening,
                              density_dx,false_positive)

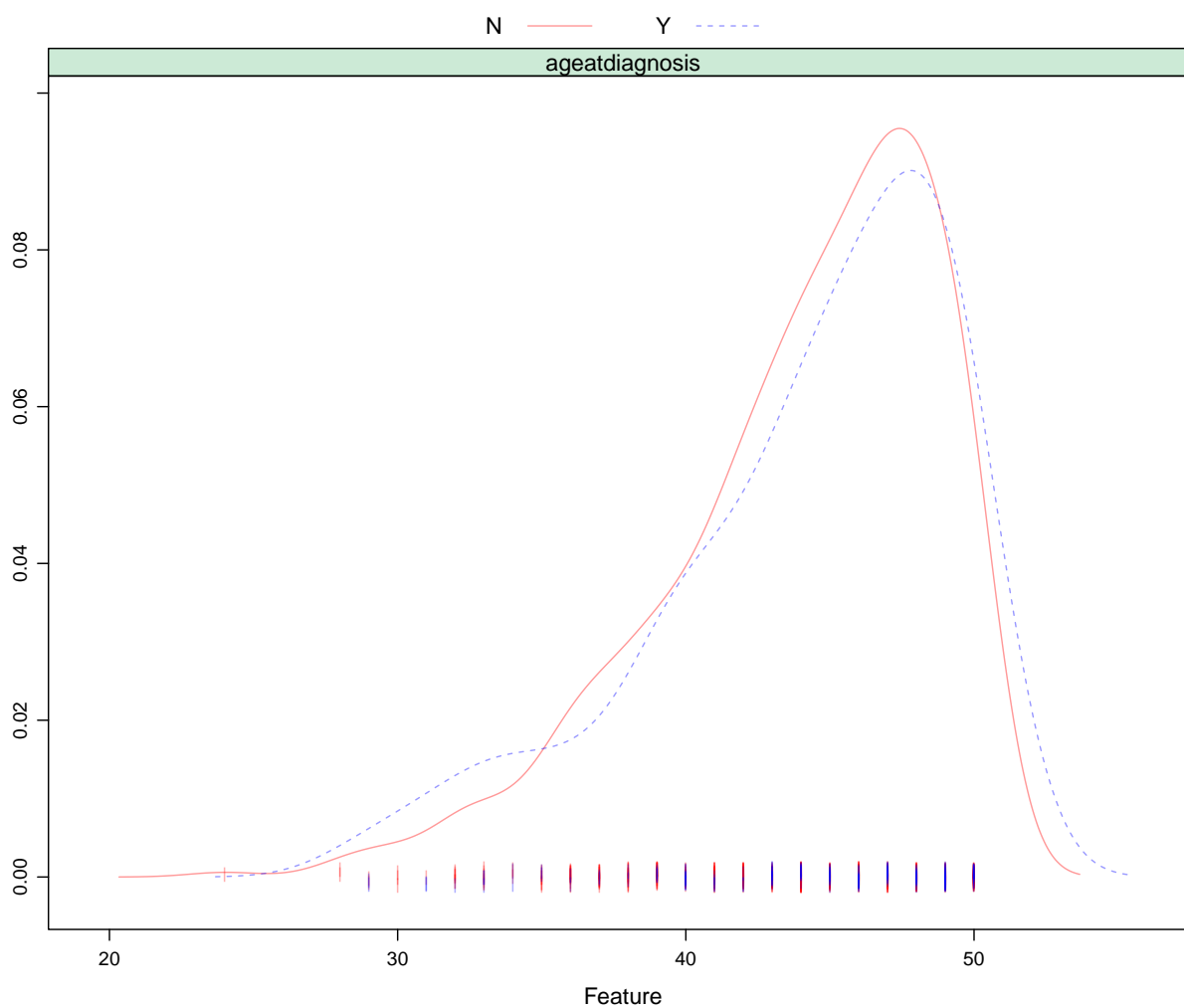
x <- model.matrix(false_positive~.,dat)[,-1]
y <- dat$false_positive

```

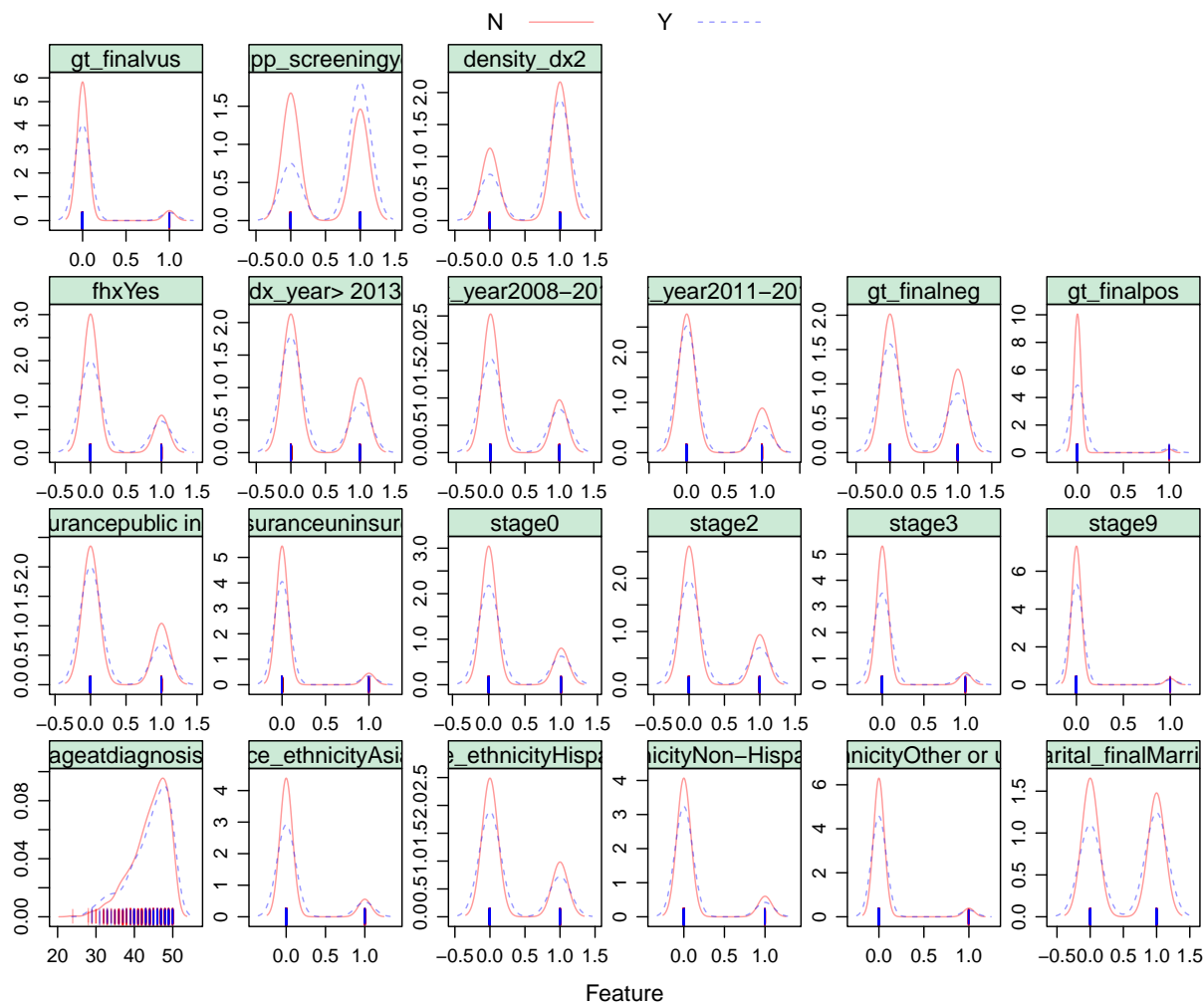
Visualization

```
theme1 <- transparentTheme(trans = 0.4)
theme1$strip.background$col <- rgb(0.0,0.6,0.2,0.2)
trellis.par.set(theme1)

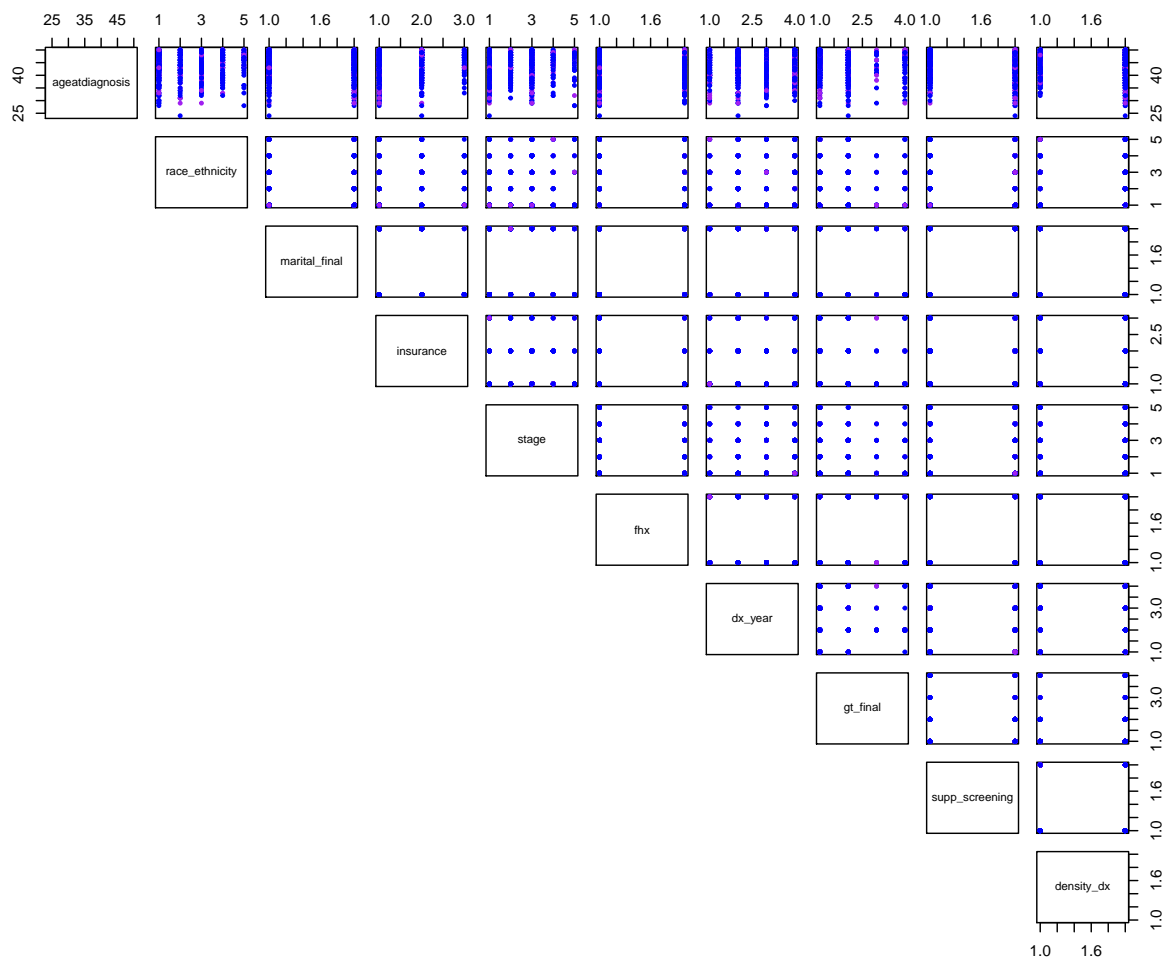
featurePlot(x = dat[,1],
            y = dat$false_positive,
            scales = list(x=list(relation = "free"),
                          y=list(relation = "free")),
            plot = "density", pch = "|",
            auto.key = list(columns = 2))
```



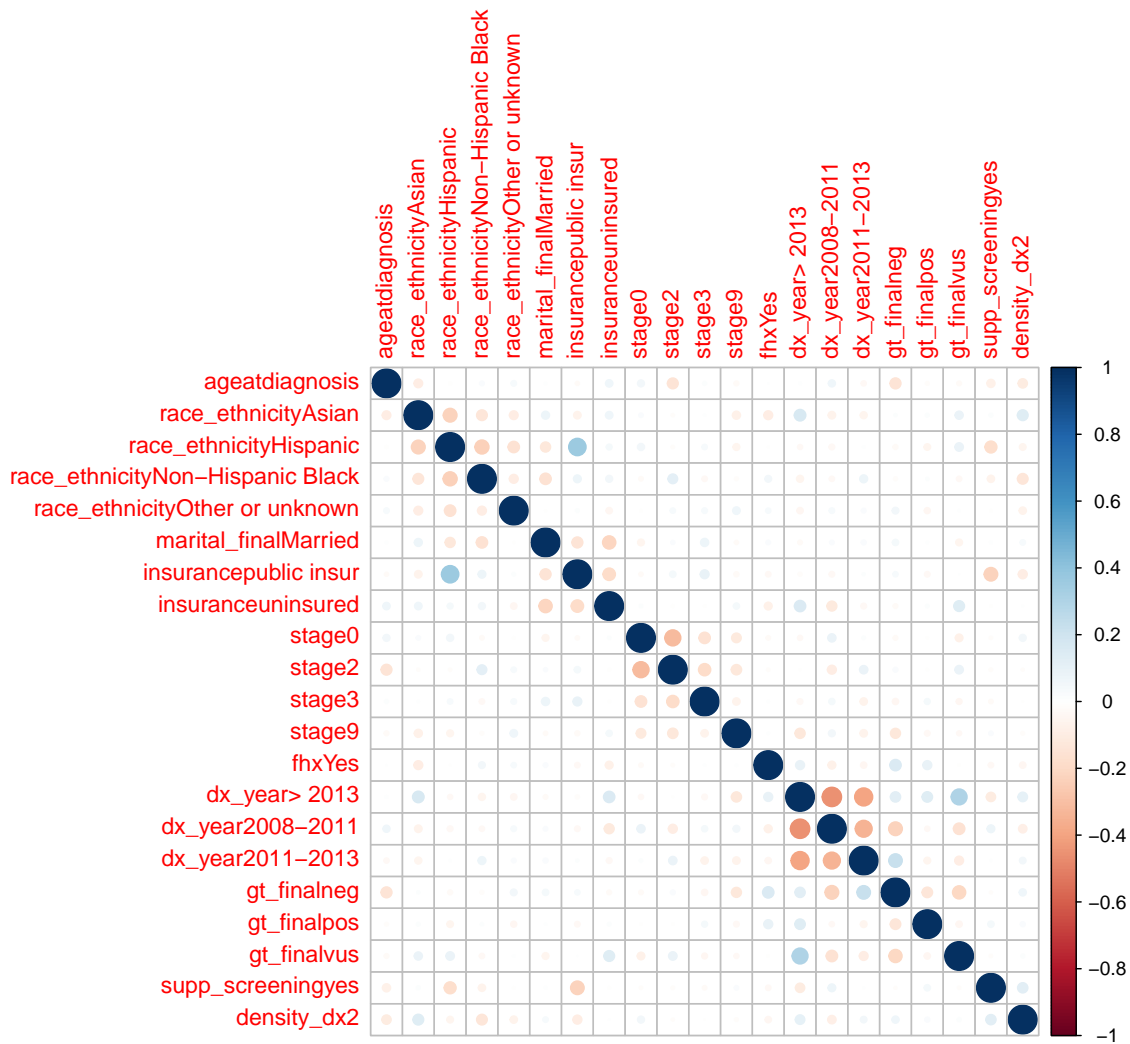
```
featurePlot(x = x,
            y = y,
            scales = list(x=list(relation = "free"),
                          y=list(relation = "free")),
            plot = "density", pch = "|",
            auto.key = list(columns = 2))
```



```
my_cols <- c("blue", "purple")
pairs(dat[,1:10], pch = 19, cex = 0.5,
      col = my_cols[dat$false_positive],
      lower.panel=NULL)
```



```
corrplot::corrplot(cor(x))
```



Models

```
set.seed(2)
rowTrain <- createDataPartition(y = dat$false_positive,
                                p = 2/3,
                                list = FALSE)

glm.fit <- glm(false_positive ~ .,
               data = dat,
               subset = rowTrain,
               family = binomial)

contrasts(dat$false_positive)
```

```
## Y
## N 0
## Y 1
```

```
summary(glm.fit)
```

```
##
## Call:
## glm(formula = false_positive ~ ., family = binomial, data = dat,
##      subset = rowTrain)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.2511  -0.6815  -0.5277  -0.3661   2.2919
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -4.96093     1.38596  -3.579 0.000344 ***
## ageatdiagnosis     0.06001     0.02813   2.134 0.032882 *
## race_ethnicityAsian    0.09521     0.41870   0.227 0.820126
## race_ethnicityHispanic  0.35975     0.35930   1.001 0.316704
## race_ethnicityNon-Hispanic Black 0.29901     0.41639   0.718 0.472691
## race_ethnicityOther or unknown -0.05186     0.68809  -0.075 0.939920
## marital_finalMarried    0.48597     0.27124   1.792 0.073193 .
## insurancepublic insur   -0.13301     0.34235  -0.389 0.697629
## insuranceuninsured     0.36026     0.46914   0.768 0.442530
## stage0                0.13503     0.33480   0.403 0.686714
## stage2                0.21899     0.32206   0.680 0.496518
## stage3                0.13424     0.47695   0.281 0.778357
## stage9               -0.84774     0.82166  -1.032 0.302195
## fhxYes                0.34024     0.30801   1.105 0.269322
## dx_year> 2013         -0.60174     0.41863  -1.437 0.150609
## dx_year2008-2011     -0.30961     0.38435  -0.806 0.420495
## dx_year2011-2013     -1.04183     0.44591  -2.336 0.019469 *
## gt_finalneg          0.14777     0.31660   0.467 0.640678
## gt_finalpos          0.55384     0.62190   0.891 0.373168
## gt_finalvus          0.63610     0.51891   1.226 0.220261
## supp_screeningyes     0.87265     0.27819   3.137 0.001707 **
## density_dx2          0.29503     0.28616   1.031 0.302539
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 444.05  on 454  degrees of freedom
## Residual deviance: 411.78  on 433  degrees of freedom
## AIC: 455.78
##
## Number of Fisher Scoring iterations: 4

test_pred_prob <- predict(glm.fit, newdata = dat[-rowTrain,],
                          type = "response")
test_pred <- rep("N",length(test_pred_prob))
test_pred[test_pred_prob>0.5] <- "Y"

caret::confusionMatrix(data = as.factor(test_pred),
                       reference = dat$false_positive[-rowTrain],
```

```
positive = "Y")
```

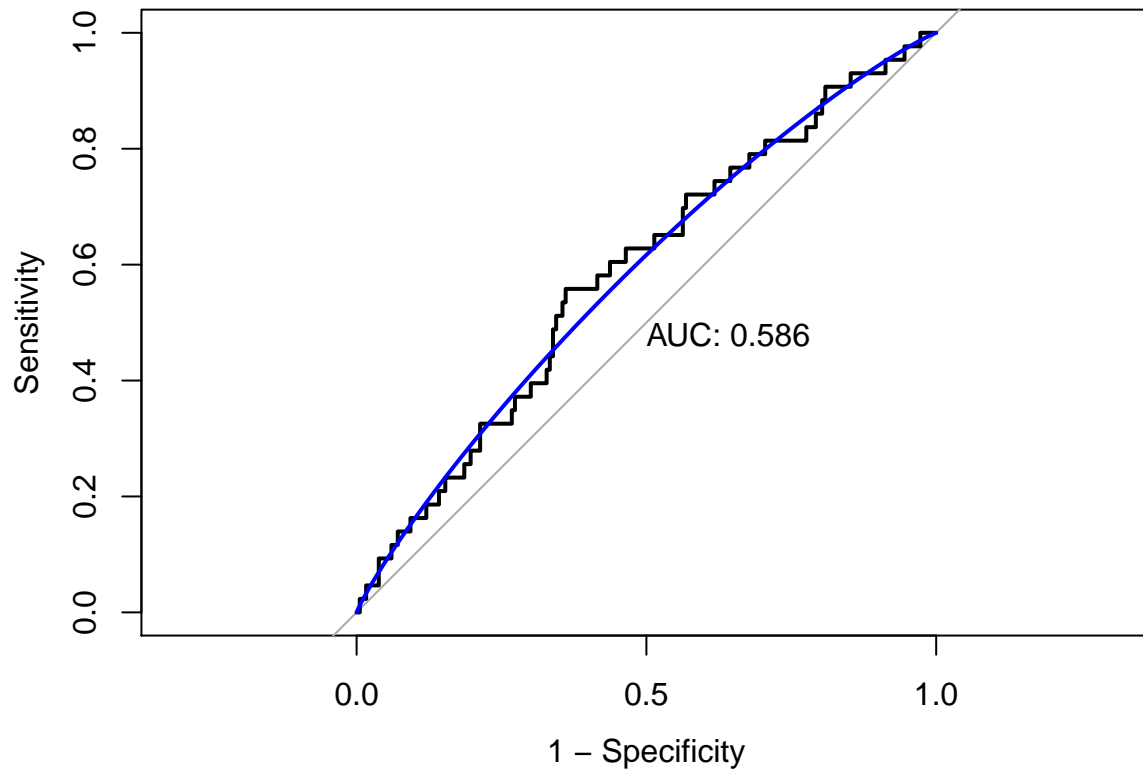
```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  N    Y
##           N 182  43
##           Y   1   0
##
##           Accuracy : 0.8053
##           95% CI : (0.7476, 0.8548)
##           No Information Rate : 0.8097
##           P-Value [Acc > NIR] : 0.6066
##
##           Kappa : -0.0087
##
## Mcnemar's Test P-Value : 6.37e-10
##
##           Sensitivity : 0.000000
##           Specificity : 0.994536
##           Pos Pred Value : 0.000000
##           Neg Pred Value : 0.808889
##           Prevalence : 0.190265
##           Detection Rate : 0.000000
##           Detection Prevalence : 0.004425
##           Balanced Accuracy : 0.497268
##
##           'Positive' Class : Y
##
```

```
roc.glm <- roc(dat$false_positive[-rowTrain],test_pred_prob)
```

```
## Setting levels: control = N, case = Y
```

```
## Setting direction: controls < cases
```

```
plot(roc.glm,legacy.axes=TRUE,print.auc=TRUE)
plot(smooth(roc.glm),col=4,add=TRUE)
```

```
ctrl1 <- trainControl(method = "repeatedcv",
                      repeats = 5,
                      summaryFunction = twoClassSummary,
                      classProbs = TRUE)

dat <- as.data.frame(dat)

set.seed(2)
model.glm <- train(x = dat[rowTrain,1:10],
                  y = dat$false_positive[rowTrain],
                  method = "glm",
                  metric = "ROC",
                  trControl = ctrl1)

model.glm$results

##   parameter      ROC      Sens      Spec      ROCSD      SensSD
## 1      none 0.5512064 0.9761261 0.01361111 0.09833474 0.02488757
##      SpecSD
## 1 0.03727731

glmGrid <- expand.grid(.alpha = seq(0,1,length = 6),
                      .lambda = exp(seq(-10,5,length = 40)))

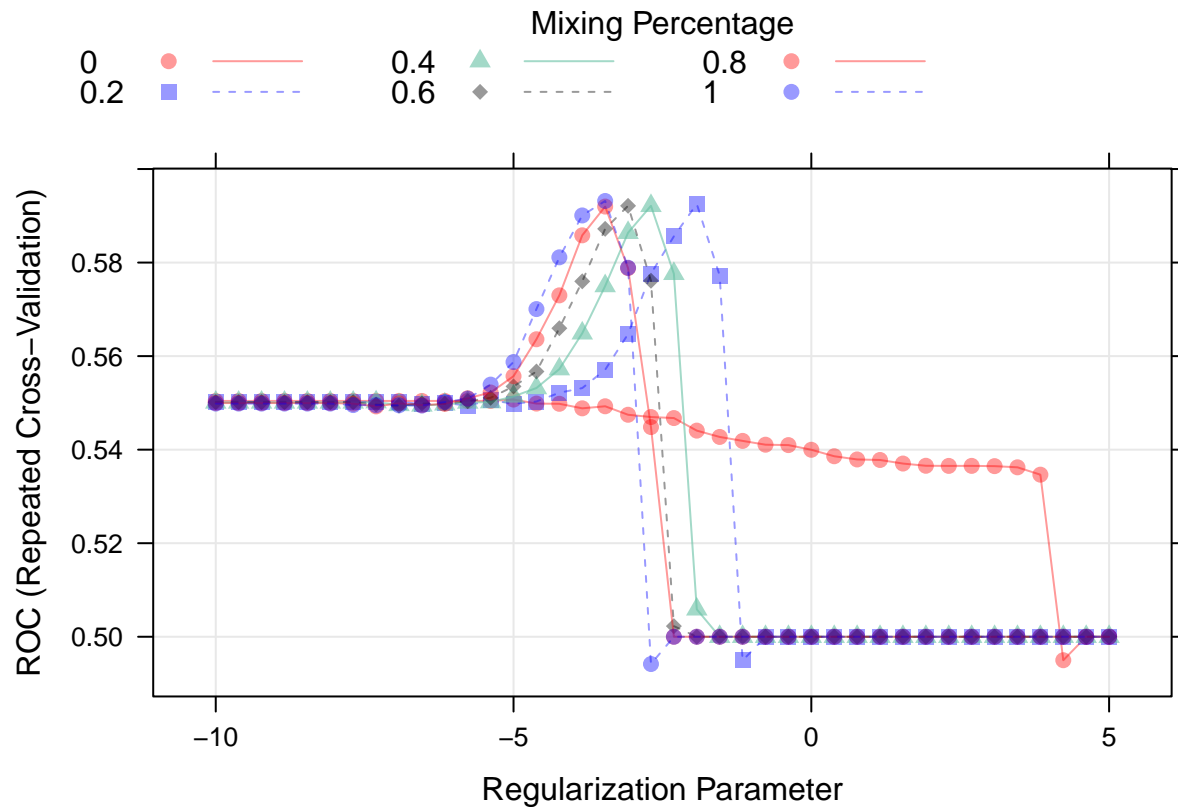
set.seed(2)
```

```

model.glmn <- train(x=x[rowTrain,],
  y=y[rowTrain],
  method = "glmnet",
  tuneGrid = glmnGrid,
  metric = "ROC",
  trControl = ctrl1)

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

```



```

model.glmn$bestTune

```

```

##      alpha      lambda
## 218      1 0.03138145

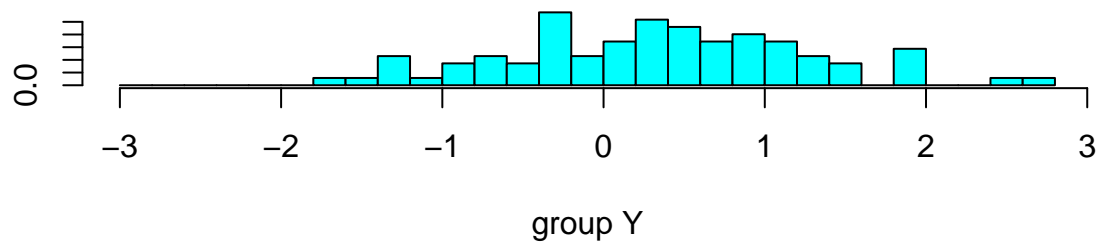
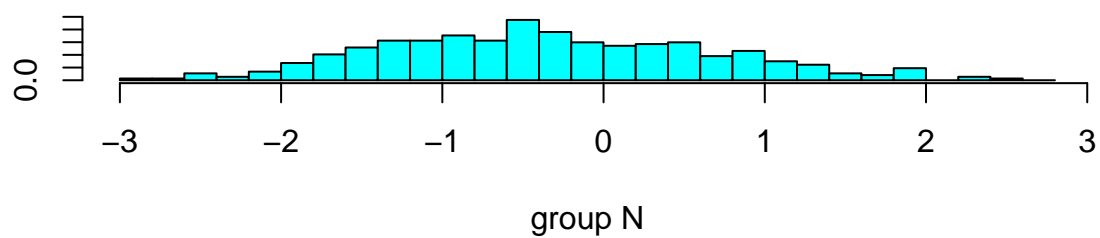
```

```

# use MASS
lda.fit <- lda(false_positive~.,data=dat,
  subset = rowTrain)

plot(lda.fit)

```



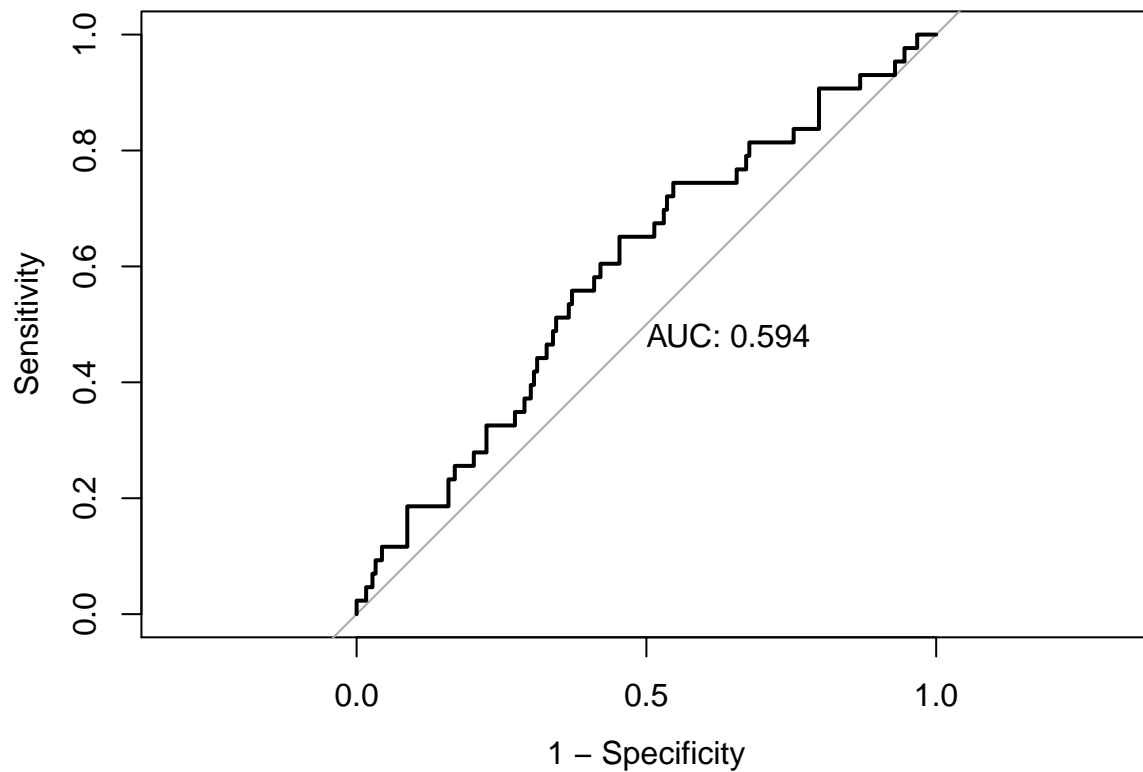
```
lda.pred <- predict(lda.fit,newdata = dat[-rowTrain,])
head(lda.pred$posterior)
```

```
##           N           Y
## 2  0.8674905 0.13250952
## 3  0.8843941 0.11560590
## 5  0.6450966 0.35490335
## 11 0.9460330 0.05396703
## 15 0.8536691 0.14633090
## 17 0.9328468 0.06715319
```

```
roc.lda <- roc(dat$false_positive[-rowTrain],lda.pred$posterior[,2],
              levels = c("N","Y"))
```

```
## Setting direction: controls < cases
```

```
plot(roc.lda,legacy.axes=TRUE,print.auc=TRUE)
```



```
# Use caret
set.seed(2)
model.lda <- train(x=x[rowTrain,],
                  y=y[rowTrain],
                  method = "lda",
                  metric = "ROC",
                  trControl = ctrl1)
```

```
model.lda$results
```

```
## parameter      ROC      Sens      Spec      ROCSD      SensSD
## 1      none 0.5576858 0.9712312 0.01583333 0.09679923 0.02709565
##      SpecSD
## 1 0.03968353
```

```
set.seed(2)
model.qda <- train(x = x[rowTrain,],
                  y = y[rowTrain],
                  method = "qda",
                  metric = "ROC",
                  trControl = ctrl1)
```

```
model.qda$results
```

```
##      parameter      ROC      Sens Spec      ROCSD      SensSD      SpecSD
## 1      none 0.5141066 0.8397898 0.165 0.1099408 0.06442617 0.1264136
```

```
# use MASS
```

```
qda.fit <- qda(false_positive~.,data=dat,
               subset = rowTrain)
```

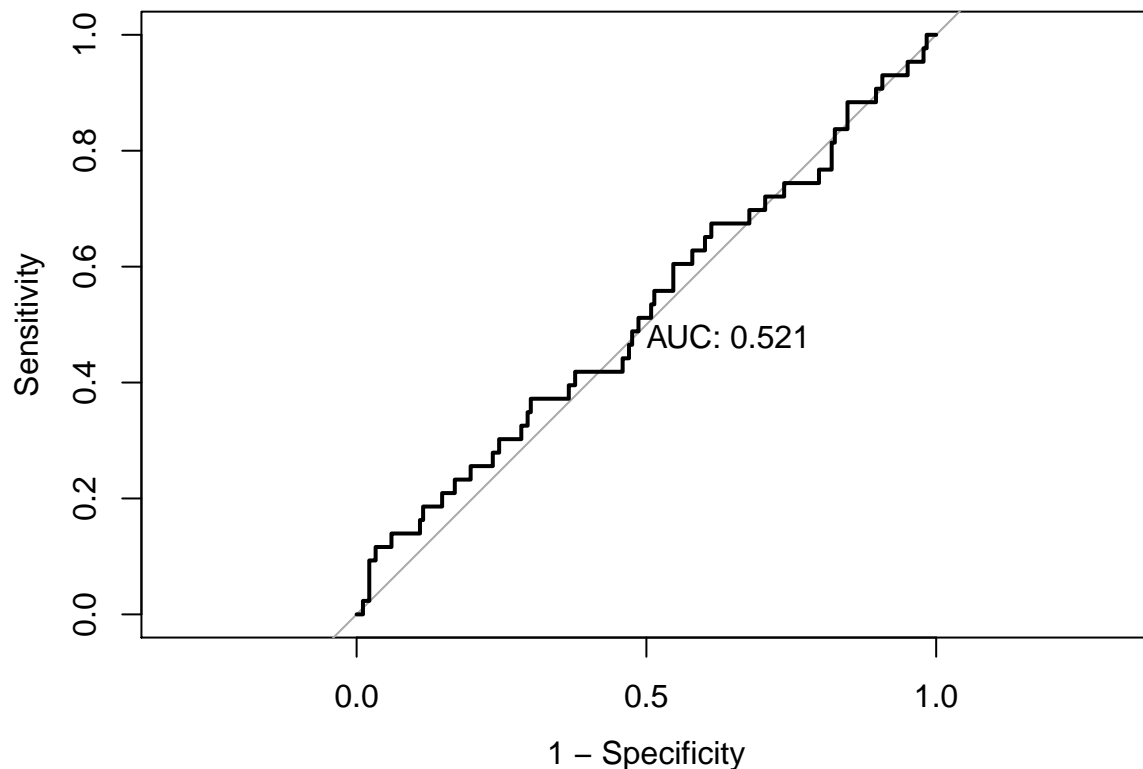
```
qda.pred <- predict(qda.fit,newdata = dat[-rowTrain,])
head(qda.pred$posterior)
```

```
##      N      Y
## 2 0.9999986 1.366513e-06
## 3 0.9957406 4.259354e-03
## 5 0.9850572 1.494279e-02
## 11 0.9999997 3.154563e-07
## 15 0.8523819 1.476181e-01
## 17 0.9839995 1.600050e-02
```

```
roc.qda <- roc(dat$false_positive[-rowTrain],qda.pred$posterior[,2],
               levels = c("N","Y"))
```

```
## Setting direction: controls > cases
```

```
plot(roc.qda,legacy.axes=TRUE,print.auc=TRUE)
```



```

set.seed(2)
nbGrid <- expand.grid(usekernel=c(FALSE,TRUE),
                      fL=1,
                      adjust=seq(0.2,8,by=0.2))

model.nb <- train(x=dat[rowTrain,1:10],
                  y=dat$false_positive[rowTrain],
                  method = "nb",
                  tuneGrid = nbGrid,
                  metric = "ROC",
                  trControl = ctrl1)

```

```

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 23

```

```

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 27

```

```

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 23

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```

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 27

```

```

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 34

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```

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
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[illegible]


```

## observation 34

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
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```

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 15

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
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## observation 37

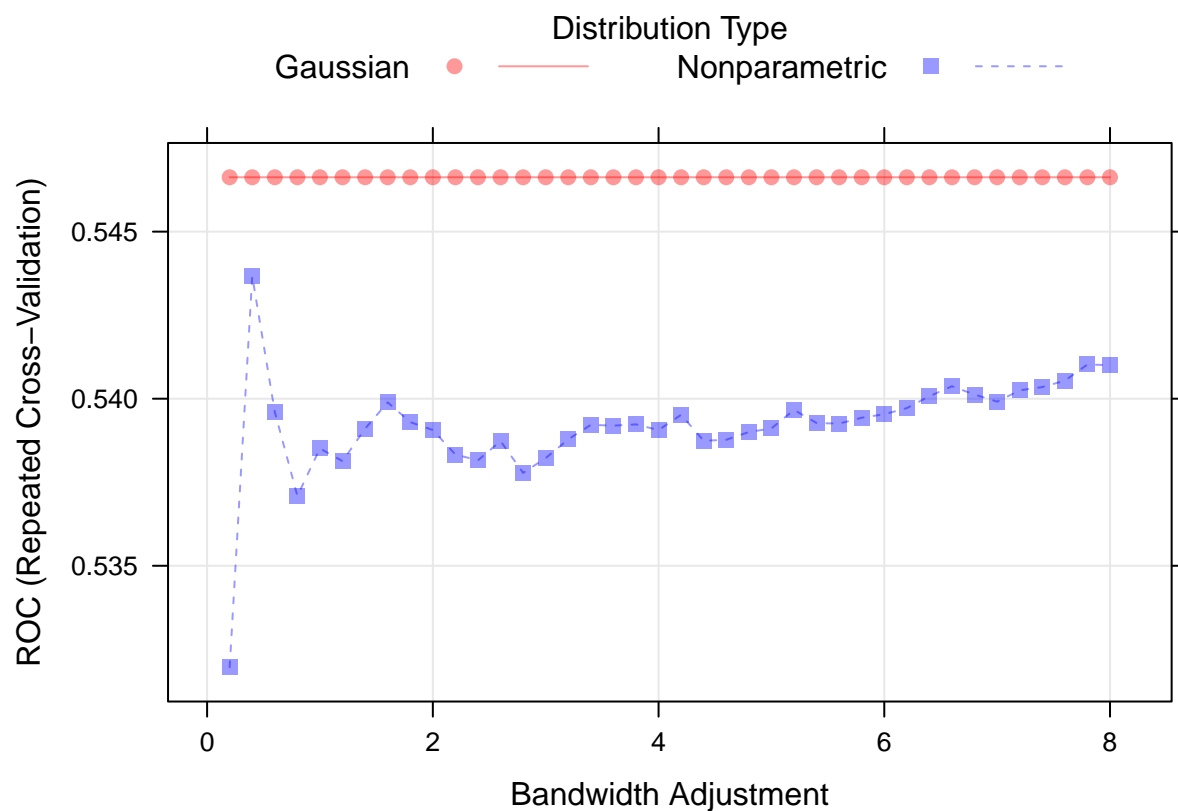
## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 37

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 37

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 37

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 37
```

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



```
model.nb$bestTune
```

```
## fL usekernel adjust
## 1 1 FALSE 0.2
```

```
res <- resamples(list(GLM = model.glm, GLMN = model.glmn,
                      LDA = model.lda, QDA = model.qda,
                      NB = model.nb))
```

```
summary(res)
```

```
##
## Call:
## summary.resamples(object = res)
##
## Models: GLM, GLMN, LDA, QDA, NB
## Number of resamples: 50
##
## ROC
##      Min.   1st Qu.   Median     Mean   3rd Qu.     Max. NA's
## GLM  0.3310811 0.5034409 0.5611862 0.5512064 0.6099850 0.8209877    0
## GLMN 0.3802083 0.5266517 0.5990991 0.5931703 0.6545712 0.8288288    0
## LDA  0.3445946 0.5034722 0.5643769 0.5576858 0.6099850 0.8024691    0
## QDA  0.2500000 0.4470721 0.5245871 0.5141066 0.5709459 0.7901235    0
## NB   0.3753754 0.4634947 0.5516975 0.5466273 0.6275338 0.8240741    0
```



```
##
## Sens
##      Min.    1st Qu.    Median      Mean    3rd Qu.  Max. NA's
## GLM  0.9189189 0.9722222 0.9729730 0.9761261 1.0000000    1    0
## GLMN 1.0000000 1.0000000 1.0000000 1.0000000 1.0000000    1    0
## LDA  0.9166667 0.9459459 0.9729730 0.9712312 1.0000000    1    0
## QDA  0.6756757 0.7905405 0.8494745 0.8397898 0.8888889    1    0
## NB   0.9189189 0.9729730 1.0000000 0.9837237 1.0000000    1    0
##
## Spec
##      Min.    1st Qu.    Median      Mean    3rd Qu.  Max. NA's
## GLM    0 0.0000000 0.000 0.013611111 0.0000000 0.1250000    0
## GLMN    0 0.0000000 0.000 0.000000000 0.0000000 0.0000000    0
## LDA    0 0.0000000 0.000 0.015833333 0.0000000 0.1250000    0
## QDA    0 0.1111111 0.125 0.165000000 0.2222222 0.5000000    0
## NB    0 0.0000000 0.000 0.004444444 0.0000000 0.1111111    0
```

```
glm_pred <- predict(model.glm,newdata = dat[-rowTrain,],
                    type="prob")[,2]
glmn_pred <- predict(model.glmn,newdata = x[-rowTrain,],
                    type = "prob")[,2]
lda_pred <- predict(model.lda,newdata = x[-rowTrain,],
                    type = "prob")[,2]
qda_pred <- predict(model.qda,newdata = x[-rowTrain,],
                    type = "prob")[,2]
nb_pred <- predict(model.nb, newdata = dat[-rowTrain,],
                    type = "prob")[,2]

roc_glm <- roc(dat$false_positive[-rowTrain],glm_pred)
```

```
## Setting levels: control = N, case = Y
```

```
## Setting direction: controls < cases
```

```
roc_glmn <- roc(y[-rowTrain],glmn_pred)
```

```
## Setting levels: control = N, case = Y
```

```
## Setting direction: controls < cases
```

```
roc_lda <- roc(y[-rowTrain],lda_pred)
```

```
## Setting levels: control = N, case = Y
```

```
## Setting direction: controls < cases
```

```
roc_qda <- roc(y[-rowTrain],qda_pred)
```

```
## Setting levels: control = N, case = Y
```

```
## Setting direction: controls > cases
```

```

roc_nb <- roc(dat$false_positive[-rowTrain],nb_pred)

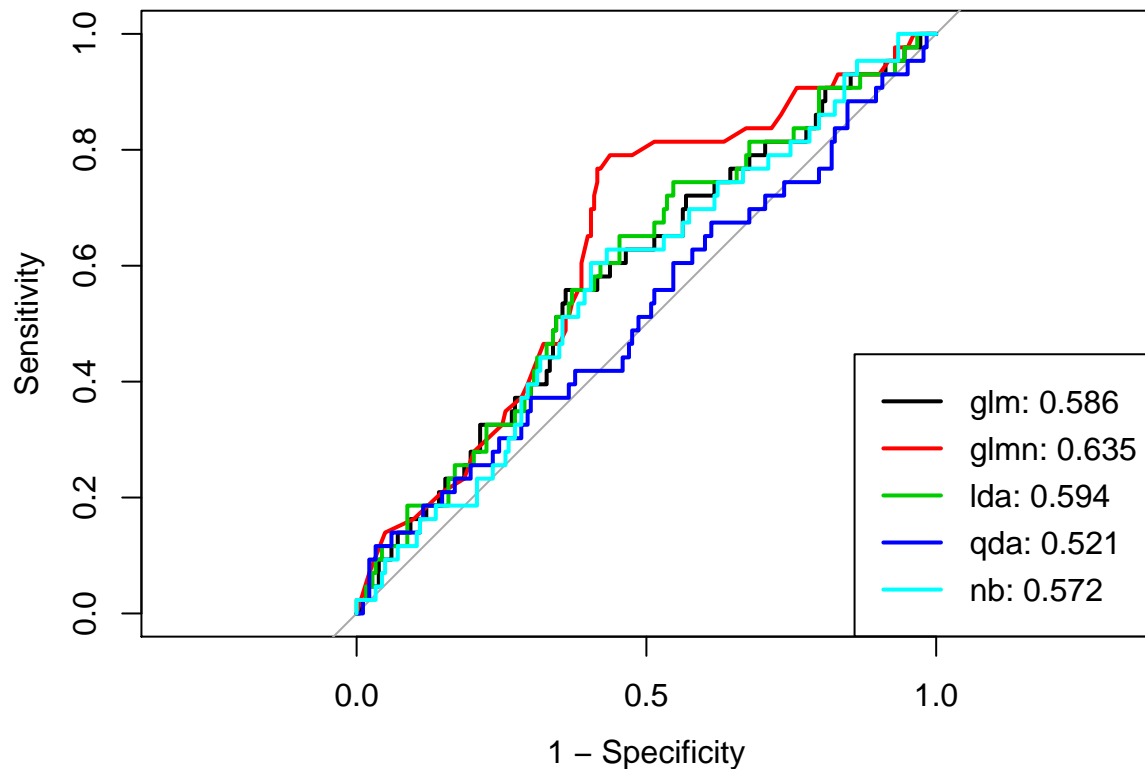
## Setting levels: control = N, case = Y

## Setting direction: controls < cases

auc <- c(roc_glm$auc[1],roc_glmn$auc[1],roc_lda$auc[1],
         roc_qda$auc[1],roc_nb$auc[1])

plot(roc_glm,legacy.axes=TRUE)
plot(roc_glmn,col=2,add=TRUE)
plot(roc_lda,col=3,add=TRUE)
plot(roc_qda,col=4,add=TRUE)
plot(roc_nb,col=5,add=TRUE)
modelNames <- c("glm","glmn","lda","qda","nb")
legend("bottomright",legend = paste0(modelNames,": ",round(auc,3)),
      col = 1:5,lwd = 2)

```



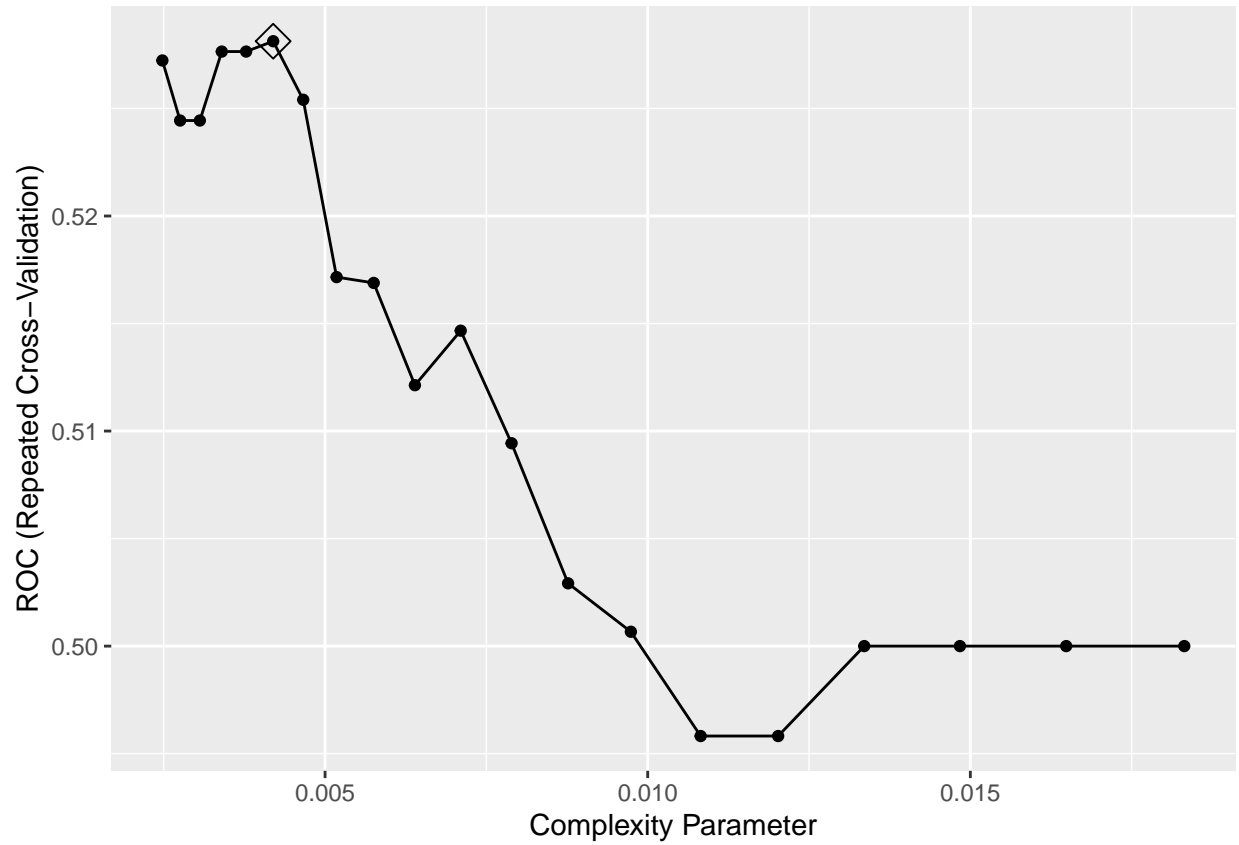
```

# CART
set.seed(2)
rpart.fit <- train(false_positive~.,dat,
                  subset = rowTrain,
                  method="rpart",
                  tuneGrid = data.frame(cp=exp(seq(-6,-4,len=20))),

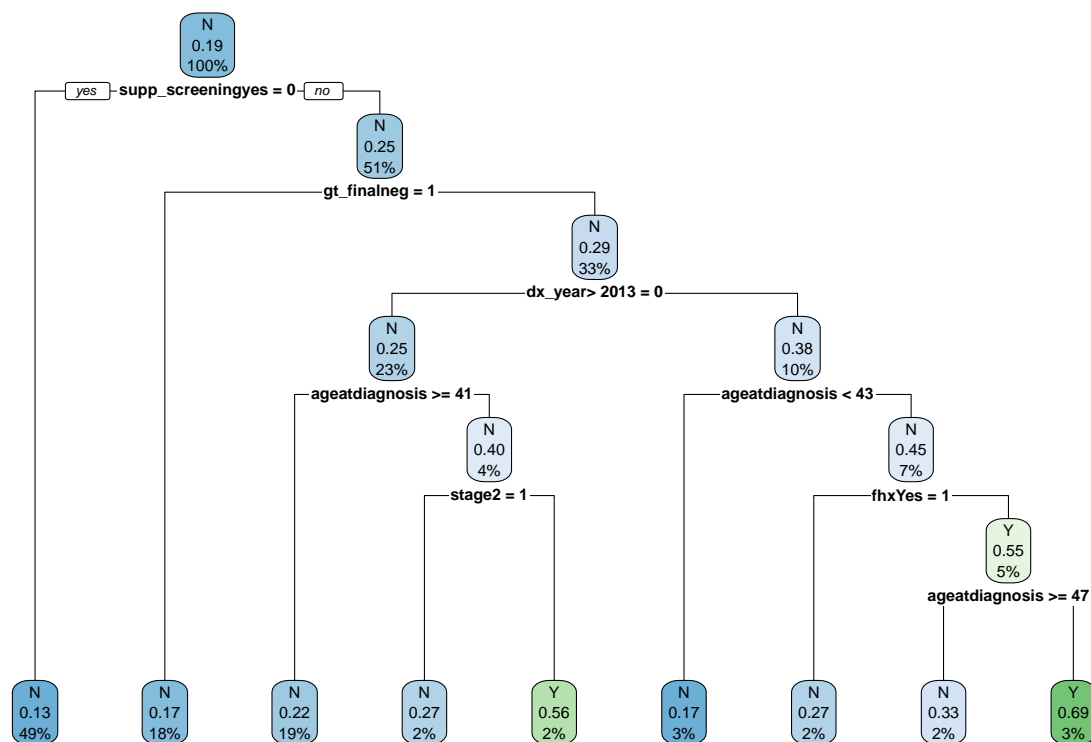
```

```
trControl=ctrl1,
metric="ROC")

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



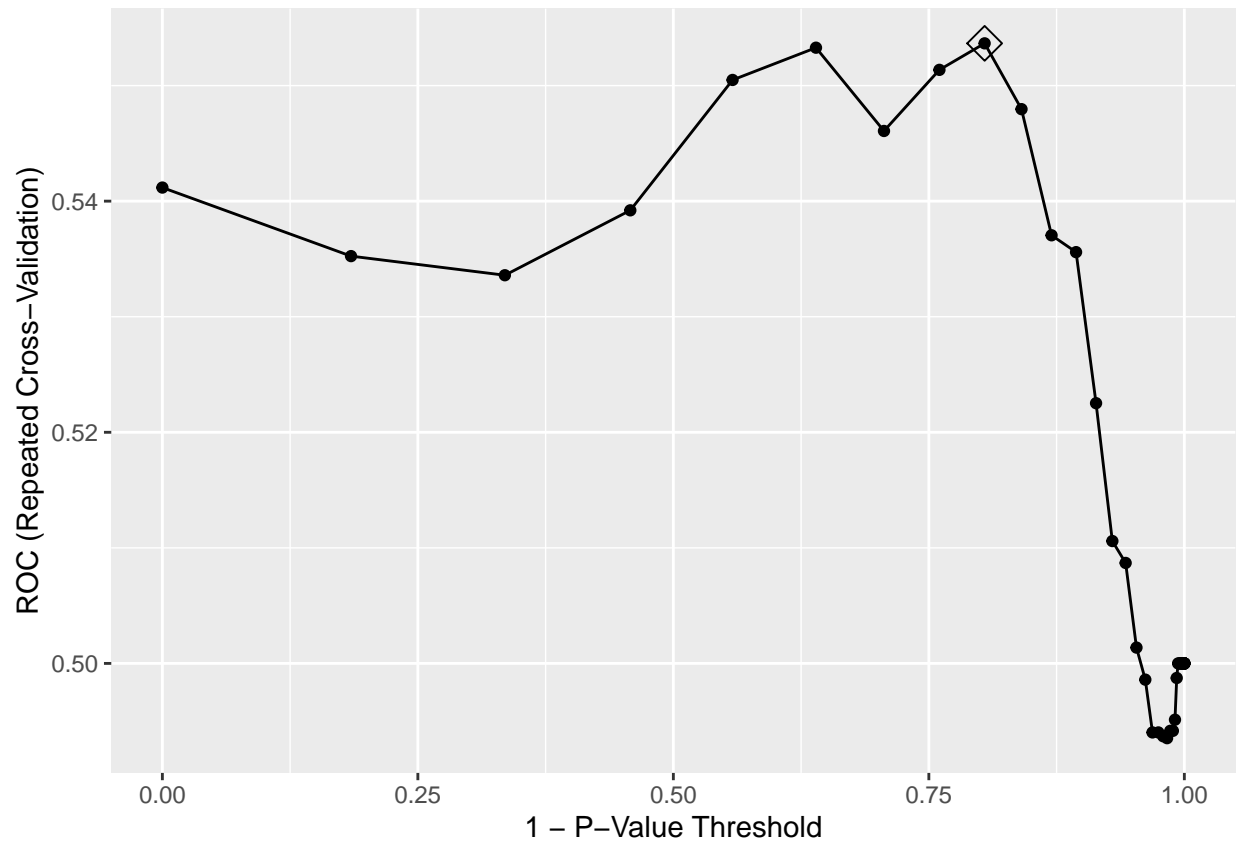
```
rpart.plot(rpart.fit$finalModel)
```



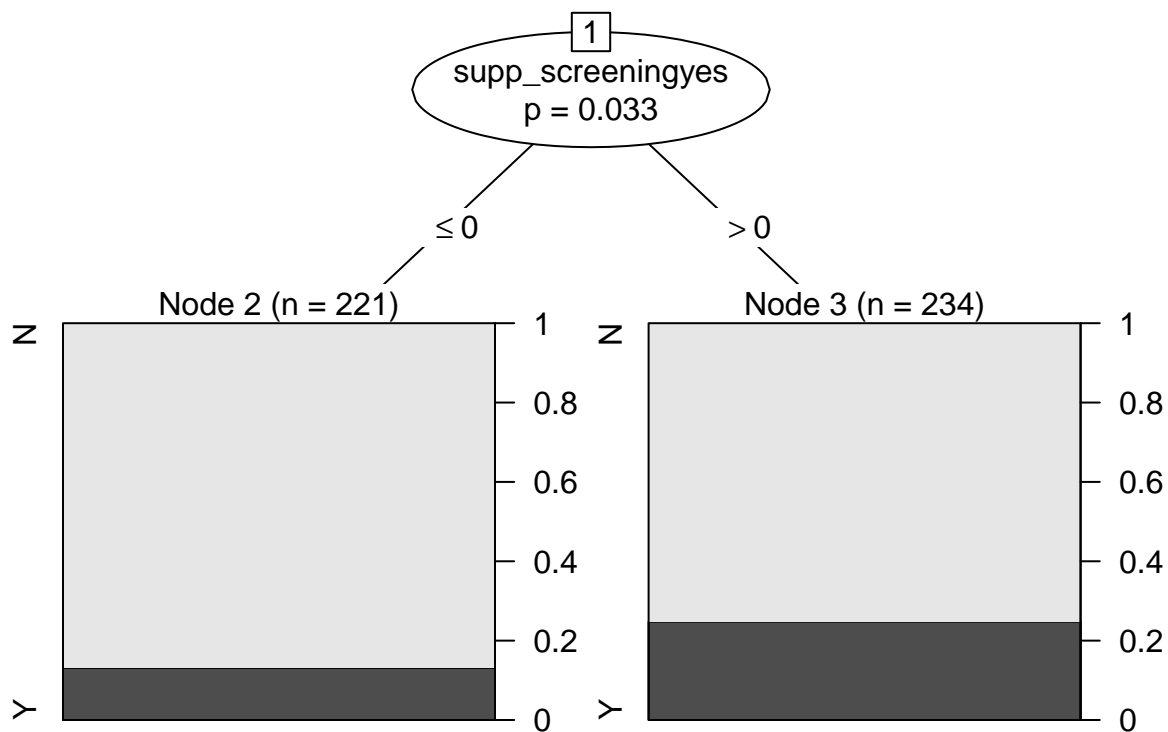
```
rpart.pred <- predict(rpart.fit,newdata = dat[-rowTrain,],
  type = "prob")[,1]
```

```
# CIT
set.seed(2)
ctree.fit <- train(false_positive~.,dat,
  subset = rowTrain,
  method = "ctree",
  tuneGrid = data.frame(mincriterion = 1-exp(seq(-10,0,length=50))),
  metric = "ROC",
  trControl = ctrl1)

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



```
plot(ctree.fit$finalModel)
```

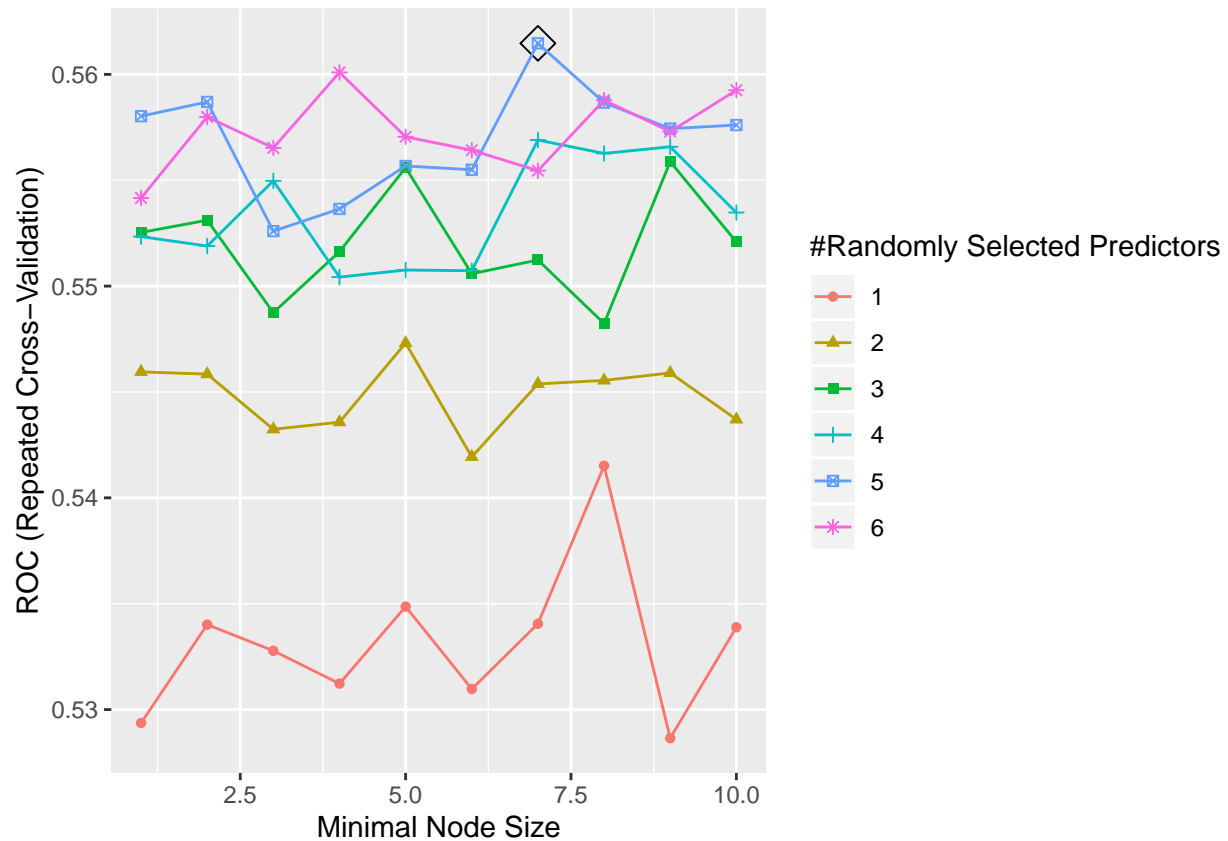


```
ctree.pred <- predict(ctree.fit,newdata = dat[-rowTrain,],
                      type = "prob")[,1]
```

```
rf.grid <- expand.grid(mtry=1:6,
                      splitrule="gini",
                      min.node.size=1:10)
```

```
set.seed(2)
rf.fit <- train(false_positive~.,dat,
                subset=rowTrain,
                method="ranger",
                tuneGrid=rf.grid,
                metric="ROC",
                trControl=ctrl1)
```

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

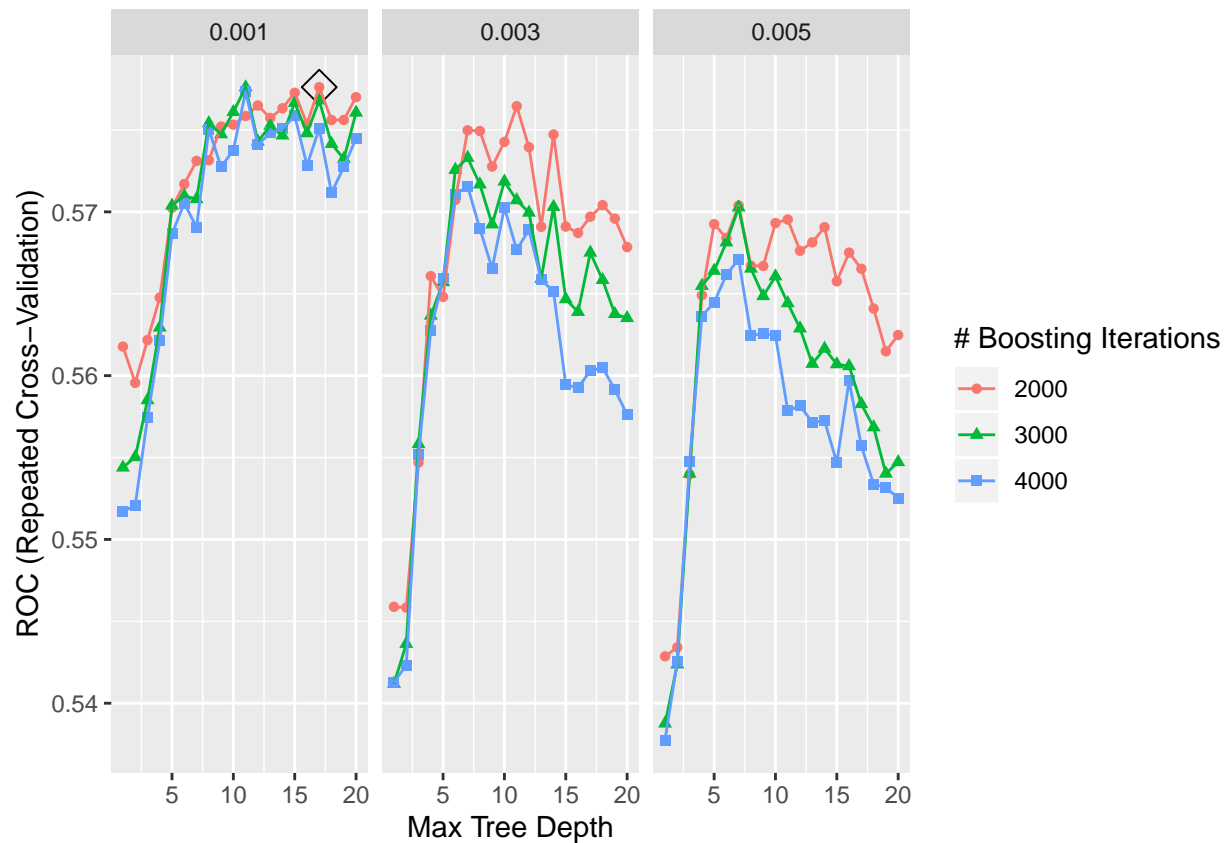


```
rf.pred <- predict(rf.fit,newdata = dat[-rowTrain,],type = "prob")[,1]
```

```
gbmB.grid <- expand.grid(n.trees=c(2000,3000,4000),
  interaction.depth = 1:20,
  shrinkage = c(0.001,0.003,0.005),
  n.minobsinnode = 1)
```

```
set.seed(2)
gbmB.fit <- train(false_positive~.,dat,
  subset=rowTrain,
  tuneGrid = gbmB.grid,
  trControl = ctrl1,
  method = "gbm",
  distribution="bernoulli",
  metric = "ROC",
  verbose = FALSE)
```

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

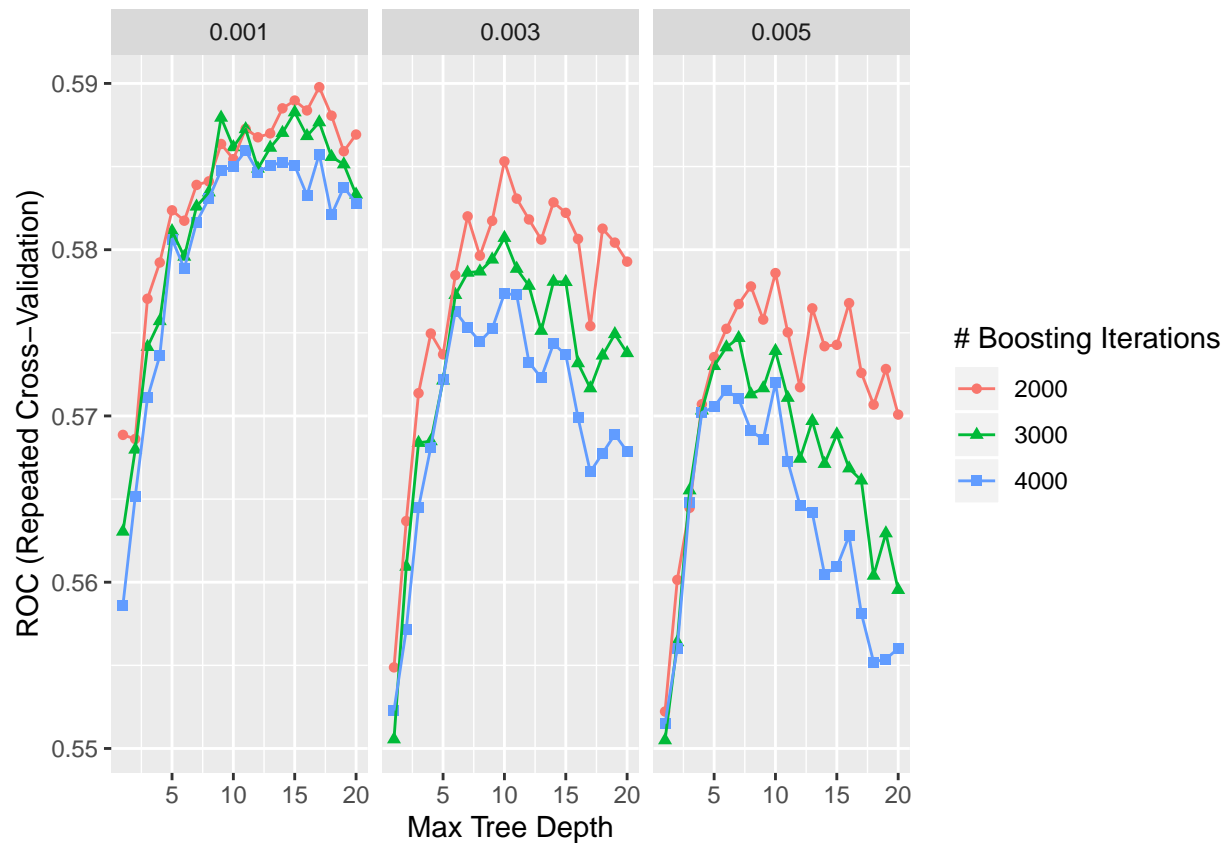


```
gbmB_pred <- predict(gbmB.fit, newdata = dat[-rowTrain,], type = "prob")[,1]
```

```
gbmA.grid <- expand.grid(n.trees = c(2000, 3000, 4000),
  interaction.depth = 1:20,
  shrinkage = c(0.001, 0.003, 0.005),
  n.minobsinnode = 1)
```

```
set.seed(2)
gbmA.fit <- train(false_positive ~ ., dat,
  subset = rowTrain,
  tuneGrid = gbmA.grid,
  trControl = ctrl1,
  method = "gbm",
  distribution = "adaboost",
  metric = "ROC",
  verbose = FALSE)
```

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

```
gbmA_pred <- predict(gbmA.fit,newdata = dat[-rowTrain,],type = "prob")[,1]
```

```
resamp <- resamples(list(rf=rf.fit,
                        gbmA=gbmA.fit,
                        gbmB=gbmB.fit,
                        rpart=rpart.fit,
                        ctree=ctree.fit))
```

```
summary(resamp)
```

```
##
## Call:
## summary.resamples(object = resamp)
##
## Models: rf, gbmA, gbmB, rpart, ctree
## Number of resamples: 50
##
## ROC
```

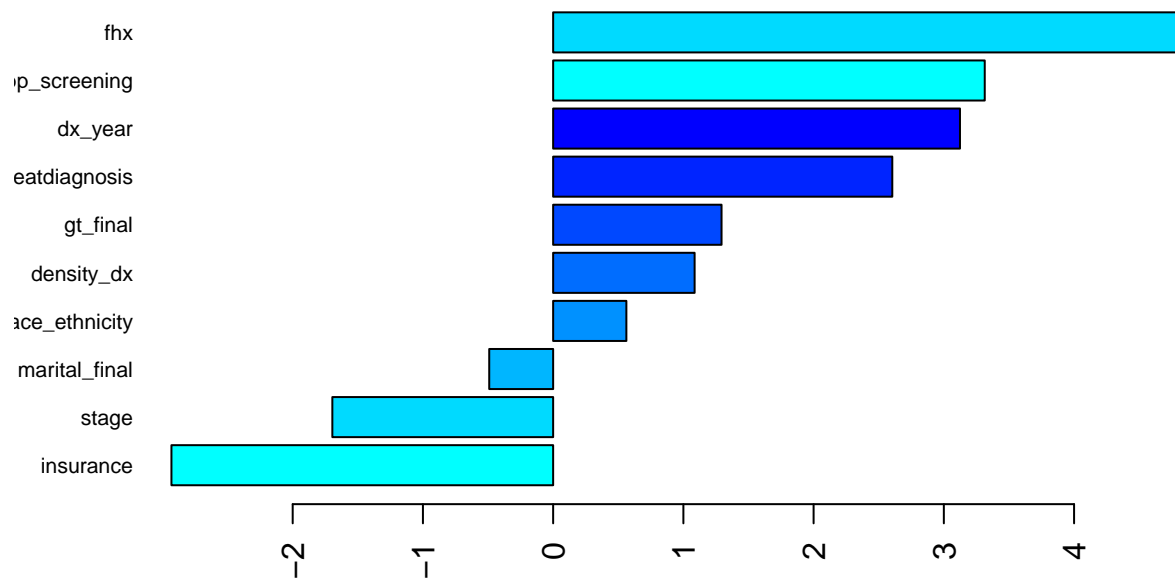
	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
rf	0.3854167	0.4973932	0.5533033	0.5614646	0.6238739	0.8006757	0
gbmA	0.4087838	0.5223348	0.5930931	0.5897762	0.6388889	0.7837838	0
gbmB	0.3923611	0.5174550	0.5720721	0.5776149	0.6281907	0.7777778	0
rpart	0.2824074	0.4680931	0.5179242	0.5281270	0.6052459	0.7608025	0
ctree	0.3750000	0.4954955	0.5615616	0.5536551	0.6185248	0.7083333	0

```
##
```

```
## Sens
##      Min.   1st Qu.   Median     Mean   3rd Qu.  Max. NA's
## rf      0.8918919 0.9729730 1.0000000 0.9864565 1.0000000    1    0
## gbmA     0.9729730 1.0000000 1.0000000 0.9994595 1.0000000    1    0
## gbmB     0.8918919 0.9729730 0.9729730 0.9809760 1.0000000    1    0
## rpart    0.8108108 0.9166667 0.9459459 0.9413664 0.9932432    1    0
## ctree    1.0000000 1.0000000 1.0000000 1.0000000 1.0000000    1    0
##
## Spec
##      Min. 1st Qu. Median      Mean   3rd Qu.      Max. NA's
## rf        0      0      0 0.006944444 0.0000000 0.1250000    0
## gbmA       0      0      0 0.000000000 0.0000000 0.0000000    0
## gbmB       0      0      0 0.011388889 0.0000000 0.1250000    0
## rpart      0      0      0 0.038333333 0.1111111 0.2222222    0
## ctree      0      0      0 0.000000000 0.0000000 0.0000000    0
```

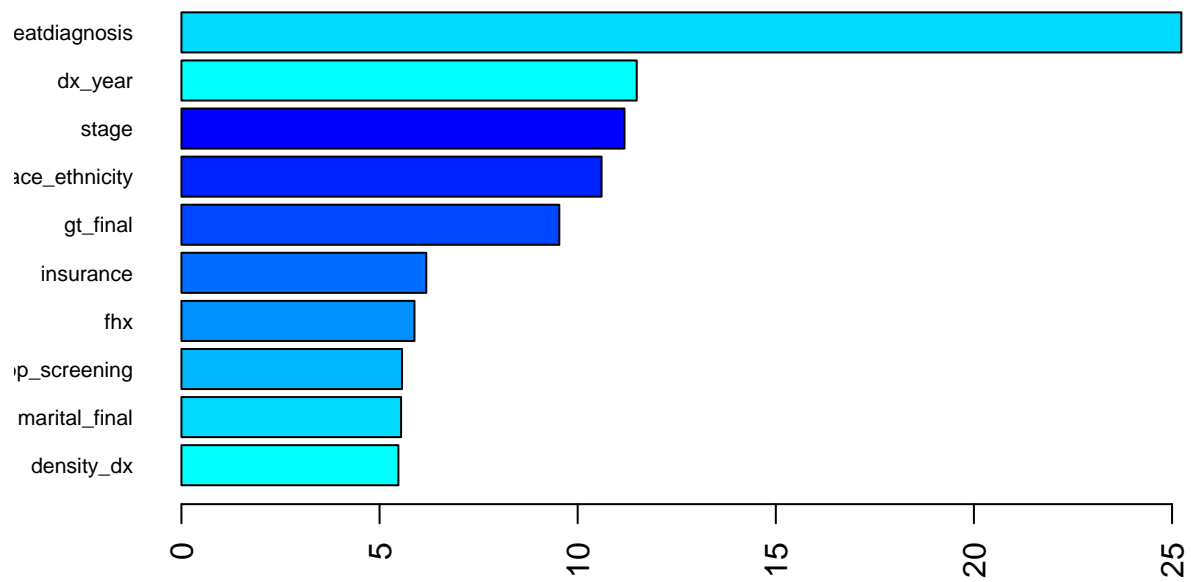
```
set.seed(2)
rf2.final.per <- ranger(false_positive~.,dat[rowTrain,],
                        mtry=3,
                        min.node.size=5,
                        splitrule = "gini",
                        importance = "permutation",
                        scale.permutation.importance = TRUE)

barplot(sort(ranger::importance(rf2.final.per),decreasing = FALSE),
        las = 2, horiz = TRUE,cex.names = 0.7,
        col=colorRampPalette(colors = c("cyan","blue"))(8))
```

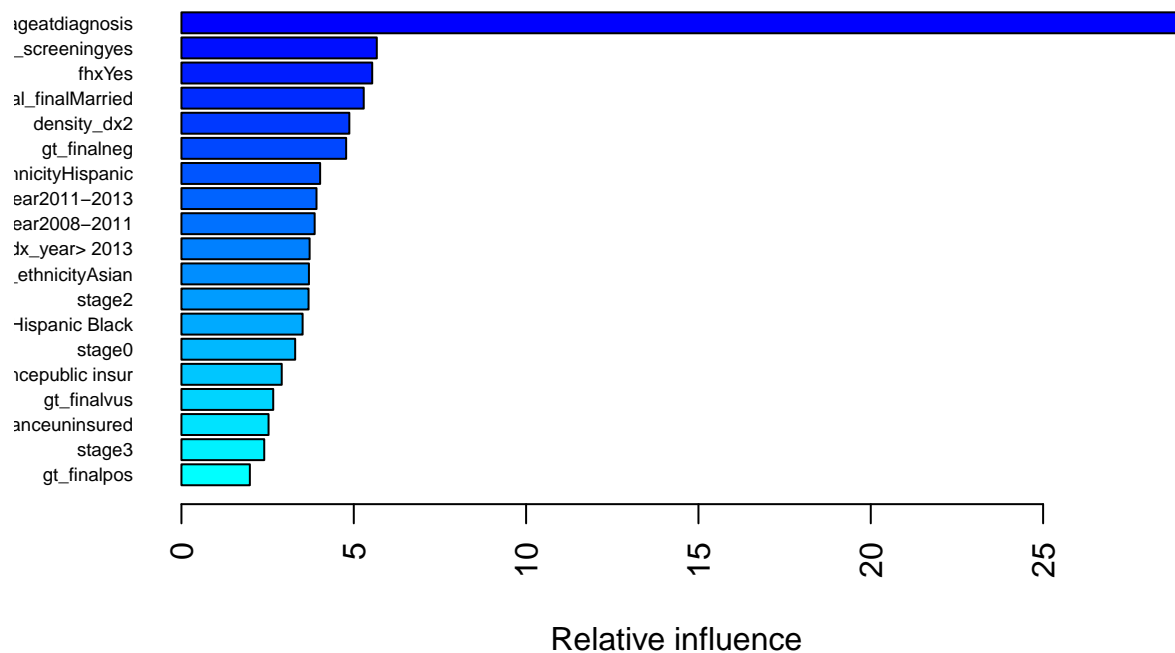


```
set.seed(2)
rf2.final.imp <- ranger(false_positive~.,dat[rowTrain,],
                        mtry = 3,splitrule = "gini",
                        min.node.size = 5,
                        importance = "impurity")

barplot(sort(ranger::importance(rf2.final.imp),decreasing = FALSE),
        las=2,horiz=TRUE,cex.names = 0.7,
        col = colorRampPalette(colors = c("cyan","blue"))(8))
```



```
summary(gbmA.fit$finalModel, las=2, cBars=19, cex.names=0.6)
```



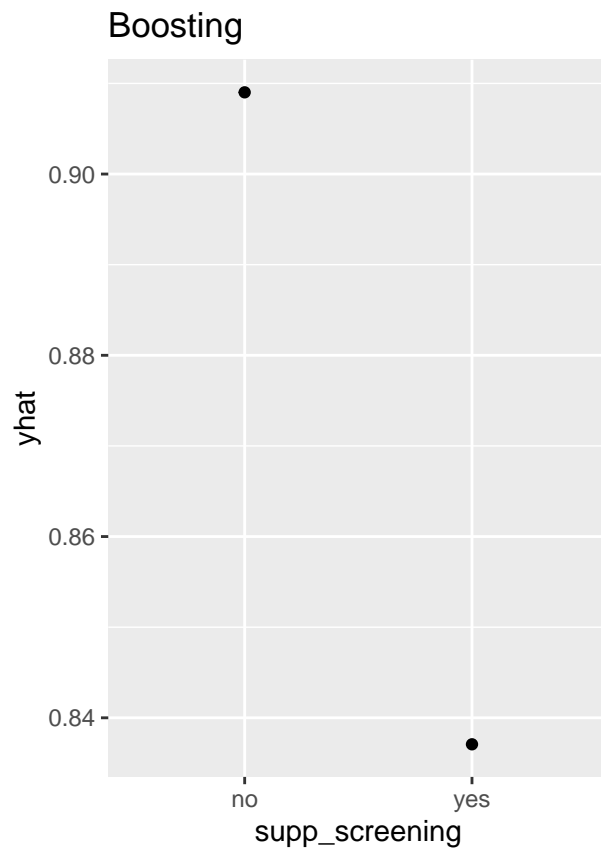
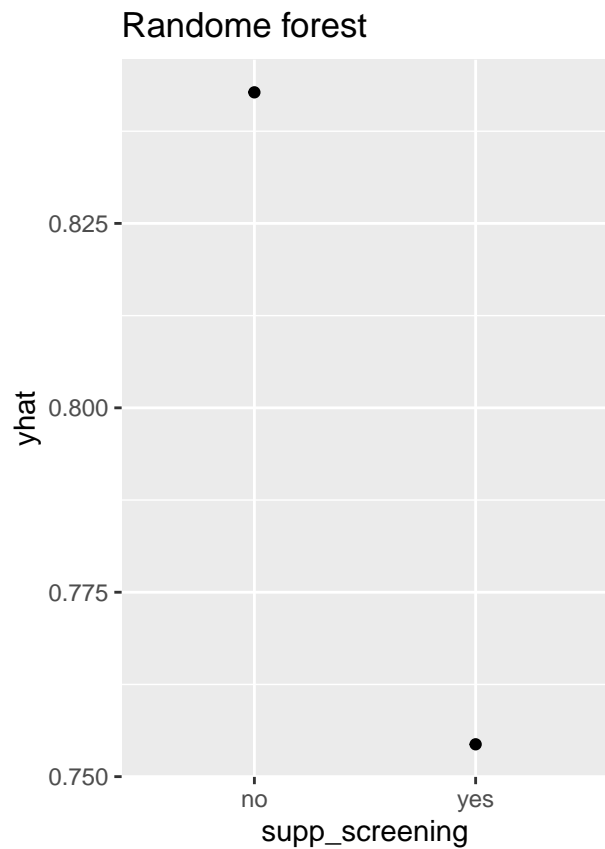
##	var
## ageatdiagnosis	ageatdiagnosis
## supp_screeningyes	supp_screeningyes
## fhxYes	fhxYes
## marital_finalMarried	marital_finalMarried
## density_dx2	density_dx2
## gt_finalneg	gt_finalneg
## race_ethnicityHispanic	race_ethnicityHispanic
## dx_year2011-2013	dx_year2011-2013
## dx_year2008-2011	dx_year2008-2011
## dx_year> 2013	dx_year> 2013
## race_ethnicityAsian	race_ethnicityAsian
## stage2	stage2
## race_ethnicityNon-Hispanic Black	race_ethnicityNon-Hispanic Black
## stage0	stage0
## insurancepublic insur	insurancepublic insur
## gt_finalvus	gt_finalvus
## insuranceuninsured	insuranceuninsured
## stage3	stage3
## gt_finalpos	gt_finalpos
## race_ethnicityOther or unknown	race_ethnicityOther or unknown
## stage9	stage9
##	rel.inf
## ageatdiagnosis	29.0107084
## supp_screeningyes	5.6677960
## fhxYes	5.5349737

```
## marital_finalMarried          5.2890871
## density_dx2                   4.8708923
## gt_finalneg                   4.7787158
## race_ethnicityHispanic        4.0240053
## dx_year2011-2013              3.9188835
## dx_year2008-2011              3.8650580
## dx_year> 2013                 3.7192815
## race_ethnicityAsian           3.6990427
## stage2                       3.6879024
## race_ethnicityNon-Hispanic Black 3.5156419
## stage0                       3.2998870
## insurancepublic insur         2.9100340
## gt_finalvus                   2.6633797
## insuranceuninsured            2.5273216
## stage3                       2.4025172
## gt_finalpos                   1.9854485
## race_ethnicityOther or unknown 1.8120582
## stage9                       0.8173651
```

```
# supp_screening
pdp.rf <- rf.fit %>%
  pdp::partial(pred.var = "supp_screening",
    grid.resolution = 100,
    prob = TRUE) %>%
  autoplot(rug = TRUE, train = dat[rowTrain,])+
  ggtitle("Random forest")

pdp.gbm <- gbmA.fit %>%
  pdp::partial(pred.var = "supp_screening",
    grid.resolution = 100,
    prob = "TRUE") %>%
  autoplot(rug = TRUE, train = dat[rowTrain,])+
  ggtitle("Boosting")

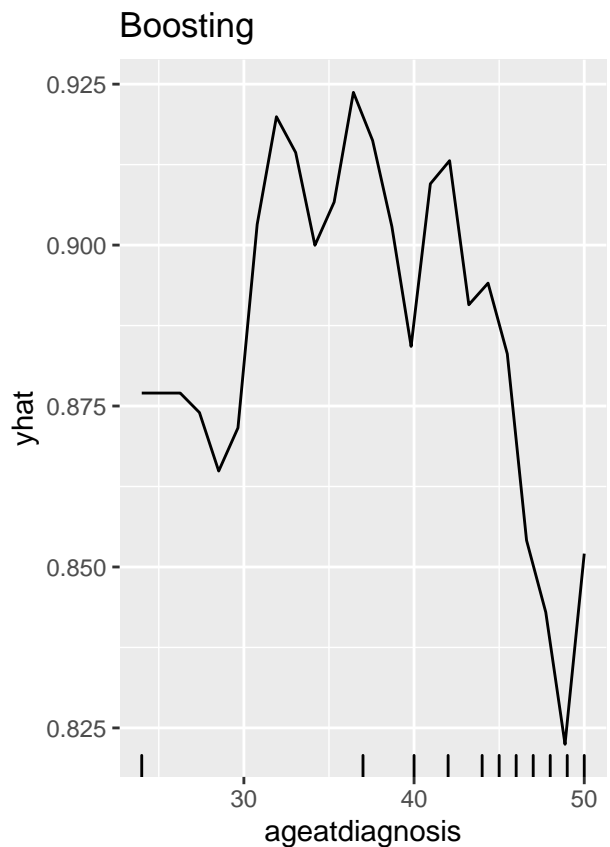
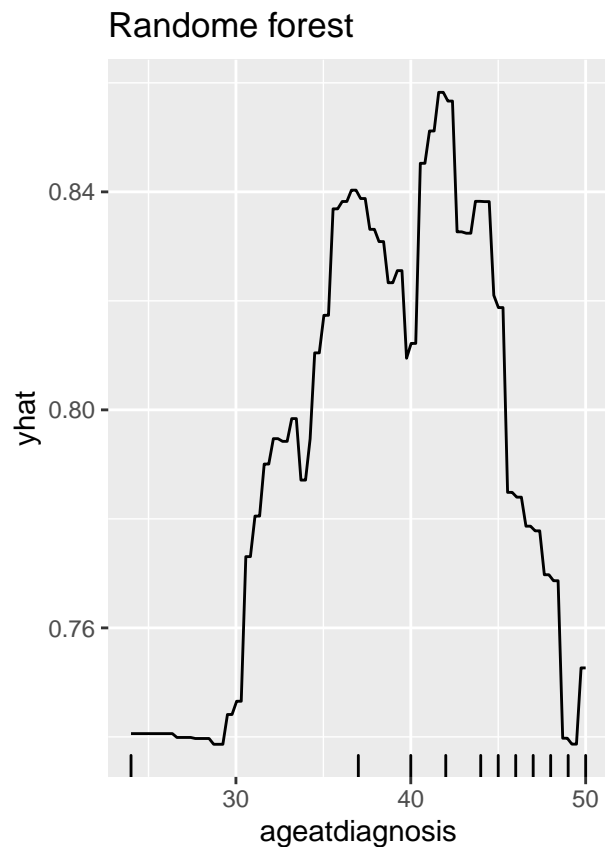
grid.arrange(pdp.rf, pdp.gbm, nrow=1)
```



```
# age at diagnosis
pdp_rf_age <- rf.fit %>%
  pdp::partial(pred.var = "ageatdiagnosis",
    grid.resolution = 100,
    prob = TRUE) %>%
  autoplot(rug = TRUE, train = dat[rowTrain,]) +
  ggtitle("Random forest")

pdp_gbm_age <- gbmA.fit %>%
  pdp::partial(pred.var = "ageatdiagnosis",
    grid.solution = 100,
    prob = "TRUE") %>%
  autoplot(rug = TRUE, train = dat[rowTrain,]) +
  ggtitle("Boosting")

grid.arrange(pdp_rf_age, pdp_gbm_age, nrow=1)
```



```
# supp_screening
ice1.rf <- rf.fit %>%
  pdp::partial(pred.var = "supp_screening",
    grid.resolution = 100,
    ice = TRUE,
    prob = TRUE) %>%
  autoplot(train = dat[rowTrain,], alpha=0.1)+
  ggtitle("Random forest, non-centered")

ice2.rf <- rf.fit %>%
  pdp::partial(pred.var = "supp_screening",
    grid.resolution = 100,
    ice = TRUE,
    prob = TRUE) %>%
  autoplot(train = dat[rowTrain,], alpha=0.1,
    center = TRUE)+
  ggtitle("Random forest, centered")

ice1.gbm <- gbmA.fit %>%
  pdp::partial(pred.var = "supp_screening",
    grid.resolution = 100,
    ice = TRUE,
    prob = TRUE) %>%
  autoplot(train = dat[rowTrain,], alpha = 0.1)+
  ggtitle("Boosting, non-centered")
```



```

ice2.gbm <- gbmA.fit%>%
  pdp::partial(pred.var = "supp_screening",
    grid.resolution = 100,
    ice = TRUE,
    prob = TRUE) %>%
  autoplot(train = dat[rowTrain,],alpha = 0.1,
    center = TRUE)+
  ggtitle("Boosting, centered")

# age at diagnosis
ice1_rf_age <- rf.fit %>%
  pdp::partial(pred.var = "ageatdiagnosis",
    grid.resolution = 100,
    ice = TRUE,
    prob = TRUE) %>%
  autoplot(train = dat[rowTrain,],alpha=0.1)+
  ggtitle("Random forest, non-centered")

ice2_rf_age <- rf.fit %>%
  pdp::partial(pred.var = "ageatdiagnosis",
    grid.resolution = 100,
    ice = TRUE,
    prob = TRUE) %>%
  autoplot(train = dat[rowTrain,],alpha=0.1,
    center = TRUE)+
  ggtitle("Random forest, centered")

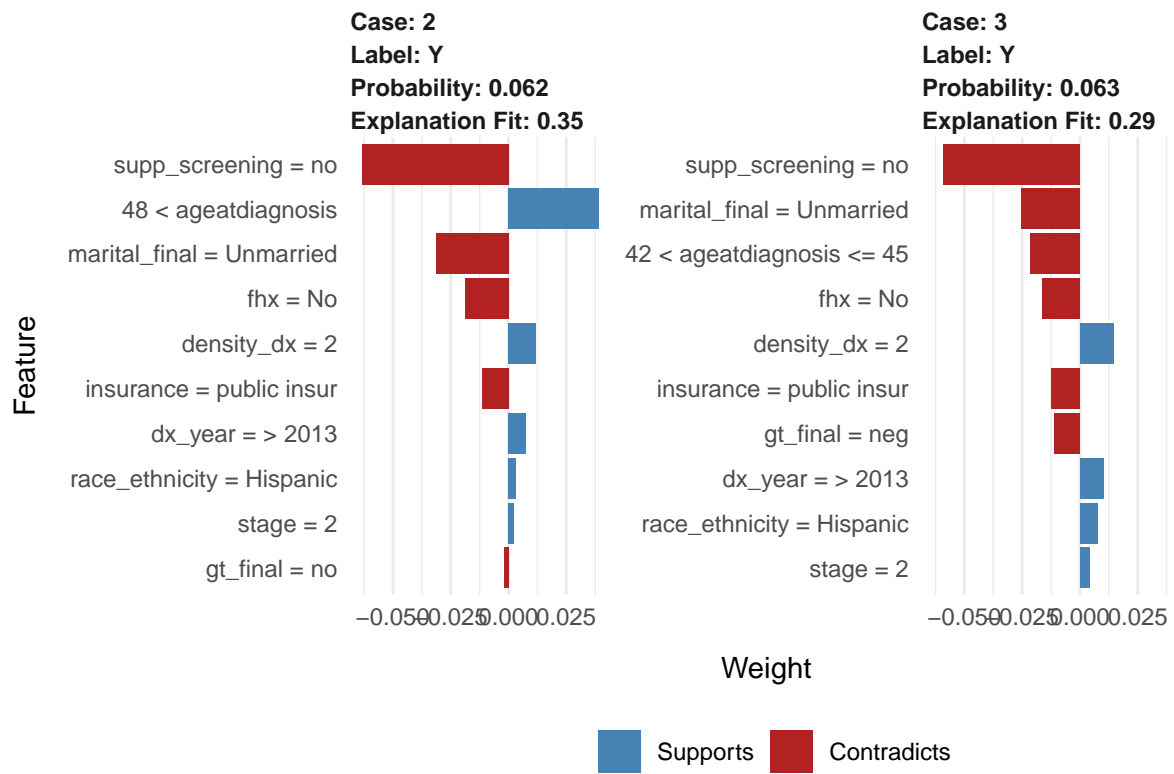
ice1_gbm_age <- gbmA.fit %>%
  pdp::partial(pred.var = "ageatdiagnosis",
    grid.resolution = 100,
    ice = TRUE,
    prob = TRUE) %>%
  autoplot(train = dat[rowTrain,],alpha = 0.1)+
  ggtitle("Boosting, non-centered")

ice2_gbm_age <- gbmA.fit%>%
  pdp::partial(pred.var = "ageatdiagnosis",
    grid.resolution = 100,
    ice = TRUE,
    prob = TRUE) %>%
  autoplot(train = dat[rowTrain,],alpha = 0.1,
    center = TRUE)+
  ggtitle("Boosting, centered")

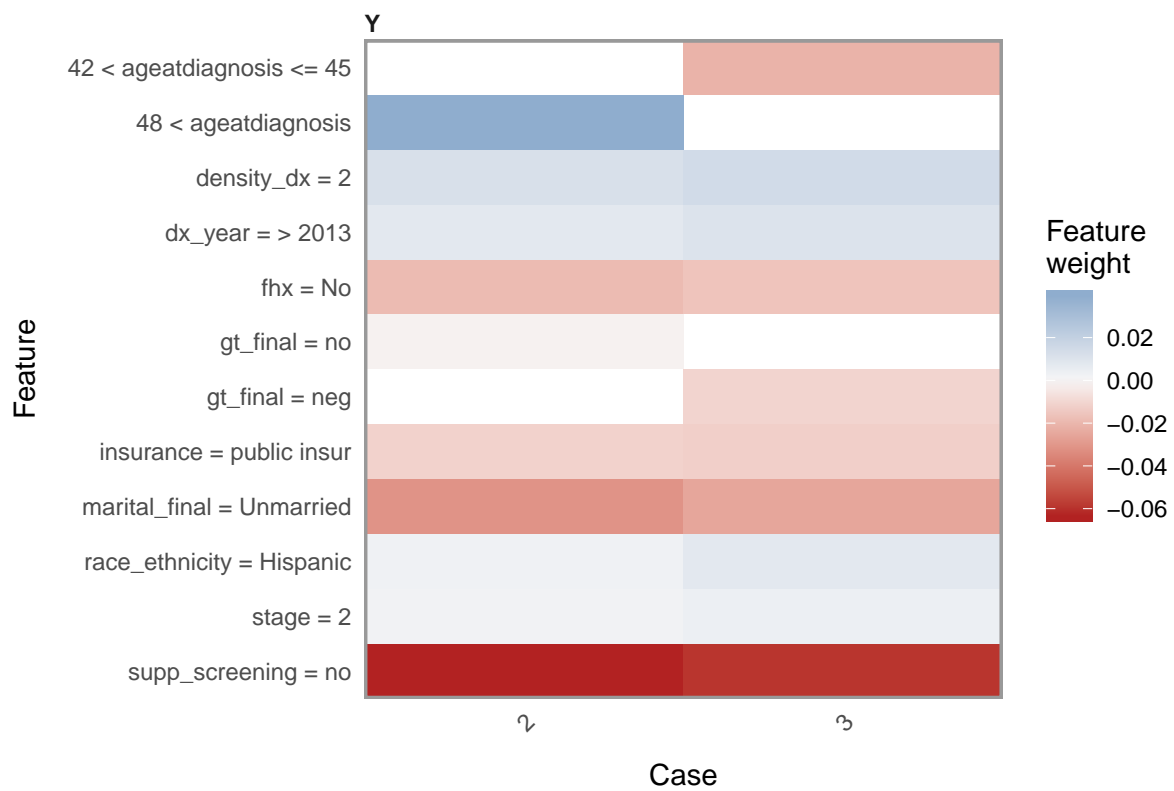
new_obs <- dat[-rowTrain,-11][1:2,]
explainer.gbm <- lime(dat[rowTrain,-11],gbmA.fit)
explanation.gbm <- explain(new_obs,explainer.gbm,n_features = 10,
  labels = "Y")

plot_features(explanation.gbm)

```

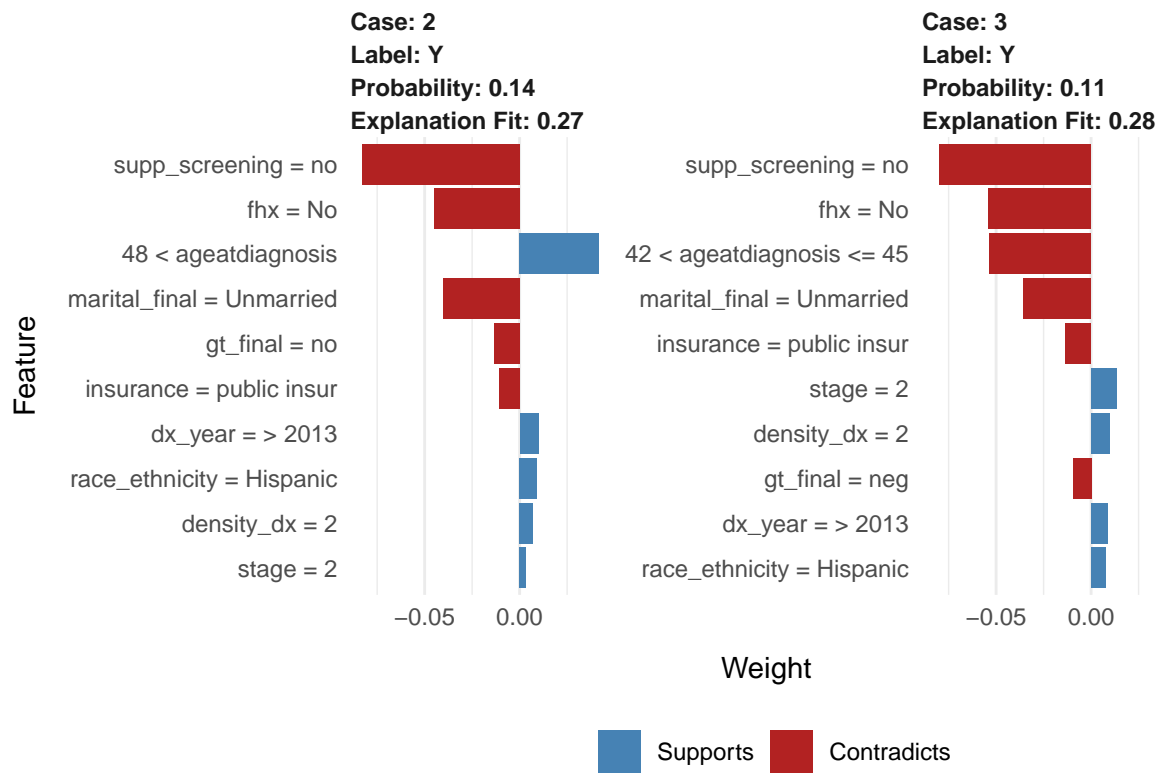


```
plot_explanations(explanation.gbm)
```

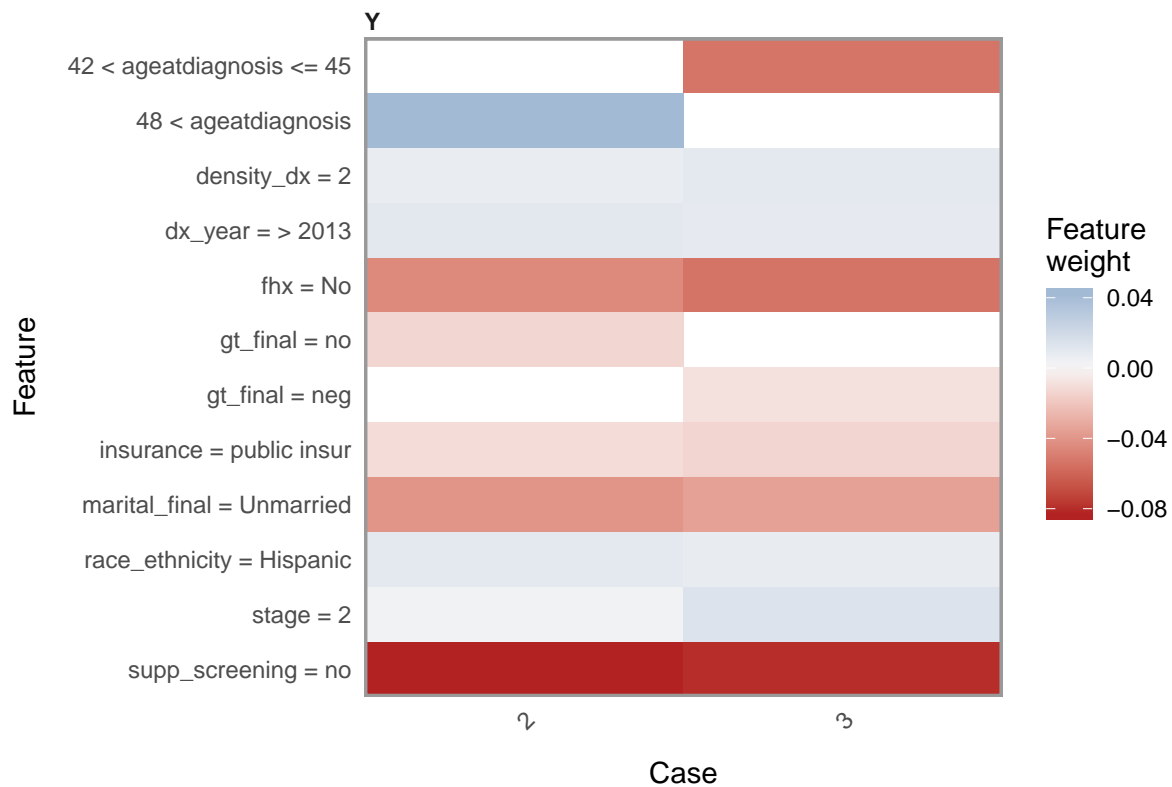


```
explainer.rf <- lime(dat[rowTrain,-11],rf.fit)
explanation.rf <- explain(new_obs,explainer.rf,n_features = 10,
                        labels = "Y")

plot_features(explanation.rf)
```



```
plot_explanations(explanation.rf)
```



```
roc.rpart <- roc(dat$false_positive[-rowTrain],rpart.pred)
```

```
## Setting levels: control = N, case = Y
```

```
## Setting direction: controls > cases
```

```
roc.ctree <- roc(dat$false_positive[-rowTrain],ctree.pred)
```

```
## Setting levels: control = N, case = Y
```

```
## Setting direction: controls > cases
```

```
roc.rf <- roc(dat$false_positive[-rowTrain],rf.pred)
```

```
## Setting levels: control = N, case = Y
```

```
## Setting direction: controls > cases
```

```
roc.gbma <- roc(dat$false_positive[-rowTrain],gbmA_pred)
```

```
## Setting levels: control = N, case = Y
```

```
## Setting direction: controls > cases
```

```

roc.gbmB <- roc(dat$false_positive[-rowTrain],gbmB_pred)

## Setting levels: control = N, case = Y
## Setting direction: controls > cases

auc1 <- c(roc.rpart$auc[1],roc.ctree$auc[1],roc.rf$auc[1],
          roc.gbmA$auc[1],roc.gbmB$auc[1])

modelNames1 <- c("rpart_caret", "ctree", "rf", "gbmA", "gbmB")

plot(roc.rpart)
plot(roc.ctree,add = TRUE,col = 2)
plot(roc.rf, add = TRUE, col = 3)
plot(roc.gbmA, add = TRUE, col = 4)
plot(roc.gbmB, add = TRUE, col = 5)
legend("bottomright",legend=paste0(modelNames1,": ", round(auc,3)),
      col = 1:5, lwd = 2)

```

