heart_Classfication_rerun.R

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```
##            A script for exploratory data analysis, and            -
##             classification training four classifiers             -
##   to diagnose heart disease based on the Heart Disease Data Set   -
```

```
#####################################################################
##                    Author: Abhinav Mishra                       ##
#####################################################################
```

```
##              Loading/Installing packages required              -
```

```
#install.packages(c("MLeval", caret", "ggvis","skimr",
#"tidyverse","ggvis", "e1071", "mice", "RColorBrewer"))

library(tidyverse)
```

```
## -- Attaching packages --------------------------------------- tidyverse 1.3.2 --
## v ggplot2 3.4.0      v purrr   0.3.5
## v tibble  3.1.8      v dplyr   1.0.10
## v tidyr   1.2.1      v stringr 1.4.1
## v readr   2.1.3      v forcats 0.5.2
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
library(skimr)
library(ggvis)
```

```
##
## Attaching package: 'ggvis'
##
## The following object is masked from 'package:ggplot2':
##
##     resolution
```

```
library(caret)
```

```
## Loading required package: lattice
##
## Attaching package: 'caret'
##
## The following object is masked from 'package:purrr':
##
##     lift
```

```
library(MLeval)
library(mice)
```

```
##
## Attaching package: 'mice'
##
## The following object is masked from 'package:stats':
##
##     filter
##
## The following objects are masked from 'package:base':
##
##     cbind, rbind
```

```
library(RColorBrewer)
```

```
##                   Loading data from the file                    -
```

```
processedWithHeader_cleveland <- read_csv("~/Documents/Freie/IFA/WiSe 22-23/Data Science/Week 4/processe
                                          show_col_types = FALSE, na = "?")


heart_data <- data.frame(processedWithHeader_cleveland)
heart_data$ID <- seq.int(nrow(heart_data))
```

```
##                       Passing as factors                        -
```

```
#
heart_data$fbs <- as.factor(heart_data$fbs)
heart_data$restecg <- as.factor(heart_data$restecg)
heart_data$exang <- as.factor(heart_data$exang)
heart_data$slope <- as.factor(heart_data$slope)
#heart_data$cp <- as.factor(heart_data$cp)
```

```
##                 Data wrangling with preparation                 -
```

```
heart_data[heart_data$sex == 0, ]$sex <- "F"
heart_data[heart_data$sex == 1, ]$sex <- "M"
heart_data$sex <- as.factor(heart_data$sex)


heart_data[heart_data$goal == 0, ]$goal <- "healthy"
heart_data[heart_data$goal == 1, ]$goal <- "unhealthy"
heart_data[heart_data$goal == 2, ]$goal <- "unhealthy"
heart_data[heart_data$goal == 3, ]$goal <- "unhealthy"
heart_data[heart_data$goal == 4, ]$goal <- "unhealthy"


write.table(heart_data, file = 'heart_data')
table(heart_data$goal)
```

```
##
##   healthy unhealthy
##       164       139
```

```
##             Descriptive Statistics + NA values omit             -
```

```
str(heart_data)
```

```
## 'data.frame':    303 obs. of  15 variables:
##  $ age     : num  63 67 67 37 41 56 62 57 63 53 ...
##  $ sex     : Factor w/ 2 levels "F","M": 2 2 2 2 1 2 1 1 2 2 ...
##  $ cp      : num  1 4 4 3 2 2 4 4 4 4 ...
##  $ trestbps: num  145 160 120 130 130 120 140 120 130 140 ...
##  $ chol    : num  233 286 229 250 204 236 268 354 254 203 ...
##  $ fbs     : Factor w/ 2 levels "0","1": 2 1 1 1 1 1 1 1 1 2 ...
##  $ restecg : Factor w/ 3 levels "0","1","2": 3 3 3 1 3 1 3 1 3 3 ...
##  $ thalach : num  150 108 129 187 172 178 160 163 147 155 ...
##  $ exang   : Factor w/ 2 levels "0","1": 1 2 2 1 1 1 1 2 1 2 ...
##  $ oldpeak : num  2.3 1.5 2.6 3.5 1.4 0.8 3.6 0.6 1.4 3.1 ...
##  $ slope   : Factor w/ 3 levels "1","2","3": 3 2 2 3 1 1 3 1 2 3 ...
##  $ ca      : num  0 3 2 0 0 0 2 0 1 0 ...
##  $ thal    : num  6 3 7 3 3 3 3 3 7 7 ...
##  $ goal    : chr  "healthy" "unhealthy" "unhealthy" "healthy" ...
##  $ ID      : int  1 2 3 4 5 6 7 8 9 10 ...
```

```
summary(heart_data)
```

```
##       age        sex           cp           trestbps          chol
##  Min.   :29.00   F: 97   Min.   :1.000   Min.   : 94.0   Min.   :126.0
##  1st Qu.:48.00   M:206   1st Qu.:3.000   1st Qu.:120.0   1st Qu.:211.0
##  Median :56.00           Median :3.000   Median :130.0   Median :241.0
##  Mean   :54.44           Mean   :3.158   Mean   :131.7   Mean   :246.7
##  3rd Qu.:61.00           3rd Qu.:4.000   3rd Qu.:140.0   3rd Qu.:275.0
##  Max.   :77.00           Max.   :4.000   Max.   :200.0   Max.   :564.0
##
##  fbs     restecg    thalach      exang      oldpeak     slope
##  0:258   0:151   Min.   : 71.0   0:204   Min.   :0.00   1:142
##  1: 45   1:  4   1st Qu.:133.5   1: 99   1st Qu.:0.00   2:140
##          2:148   Median :153.0           Median :0.80   3: 21
##                  Mean   :149.6           Mean   :1.04
##                  3rd Qu.:166.0           3rd Qu.:1.60
##                  Max.   :202.0           Max.   :6.20
##
##        ca              thal           goal                 ID
##  Min.   :0.0000   Min.   :3.000   Length:303         Min.   :  1.0
##  1st Qu.:0.0000   1st Qu.:3.000   Class :character   1st Qu.: 76.5
##  Median :0.0000   Median :3.000   Mode  :character   Median :152.0
##  Mean   :0.6722   Mean   :4.734                      Mean   :152.0
##  3rd Qu.:1.0000   3rd Qu.:7.000                      3rd Qu.:227.5
##  Max.   :3.0000   Max.   :7.000                      Max.   :303.0
##  NA's   :4        NA's   :2
```

```
sum(is.na(heart_data))
```

```
## [1] 6
```

```
##                    Missing Value: Impute                      -
```

```
colnames(heart_data)[apply(heart_data, 2, anyNA)]
```

```
## [1] "ca"   "thal"
```

```
###  ca: number of major vessels (0-3) colored by flourosopy
###  thal: 3 = normal; 6 = fixed defect; 7 = reversable defect
```

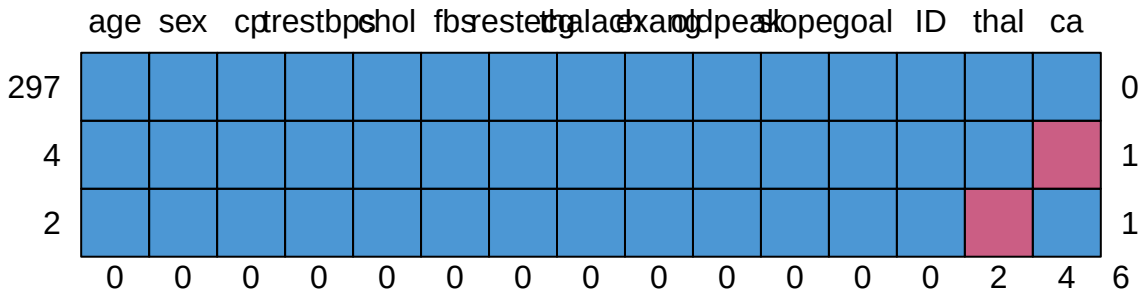
```
summary(heart_data$ca)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##  0.0000  0.0000  0.0000  0.6722  1.0000  3.0000       4
```

```
summary(heart_data$thal)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##   3.000   3.000   3.000   4.734   7.000   7.000       2
```

```
###  missing block
md.pattern(heart_data)
```




```
##     age sex cp trestbps chol fbs restecg thalach exang oldpeak slope goal ID
## 297   1   1  1        1    1   1       1       1     1       1     1    1  1
## 4     1   1  1        1    1   1       1       1     1       1     1    1  1
## 2     1   1  1        1    1   1       1       1     1       1     1    1  1
##       0   0  0        0    0   0       0       0     0       0     0    0  0
##     thal ca
## 297    1  1 0
## 4      1  0 1
## 2      0  1 1
##        2  4 6
```

```
###  imputation
###  m = 5 (iteration models)
impute <- mice(heart_data, m = 5, maxit = 50, method = "pmm",
               seed = 112, printFlag = FALSE)
```

```
## Warning: Number of logged events: 1
```

```
###  5 imputed dataset values
impute$imp$ca
```

```
##     1 2 3 4 5
## 167 0 0 0 0 2
## 193 1 0 0 0 0
## 288 1 0 1 1 0
## 303 0 0 0 0 0
```

```
impute$imp$thal
```

```
##     1 2 3 4 5
## 88  3 3 3 3 3
## 267 7 7 7 7 7
```

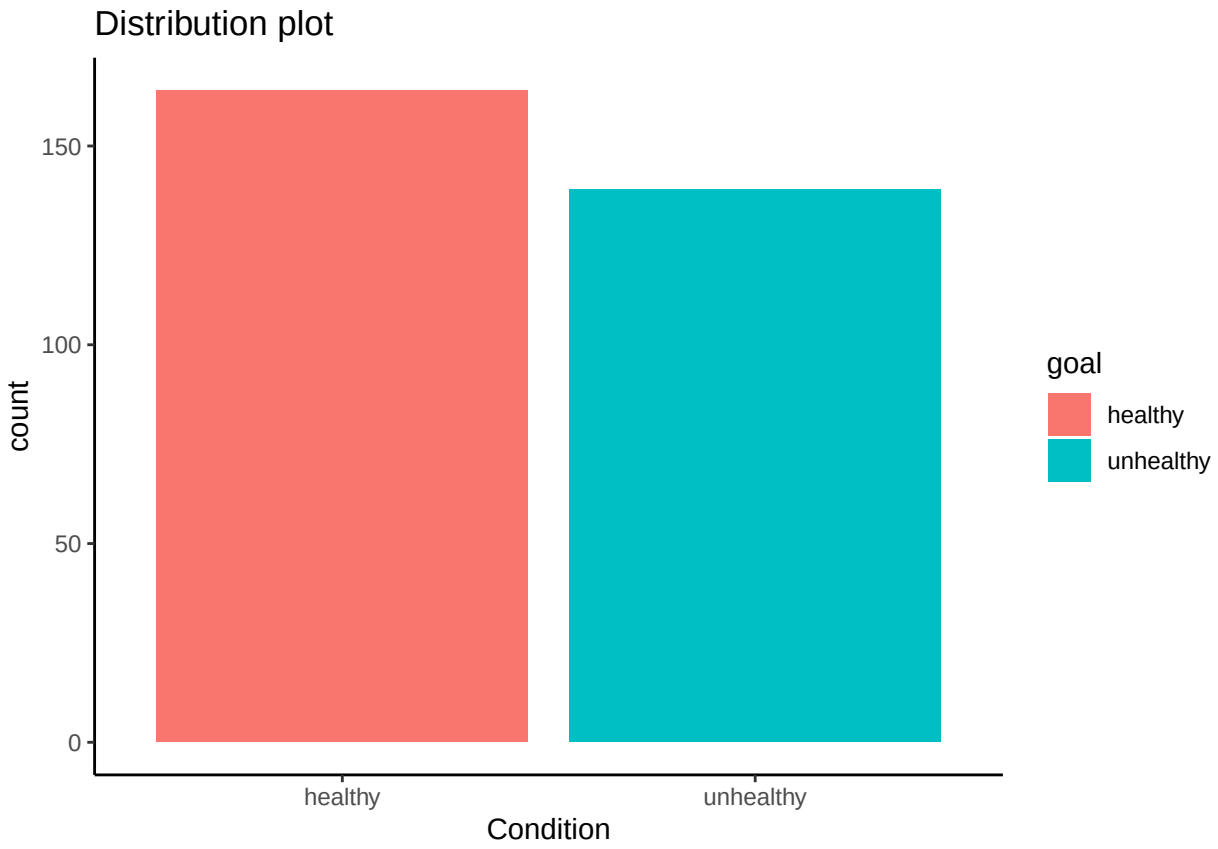
```
###  appending the imputed values (second out of five)
heart_data <- complete(impute, 2)
###  no missing values now
sum(is.na(heart_data))
```

```
## [1] 0
```

```
#########################################################################
##      No evidence of imbalanced classes (both datasets),      ##
##     hence, no change the composition of the training set     ##
#########################################################################
```

```
##                       Descriptive plots                       -
```

```
ggplot(heart_data, aes(x = goal, fill = goal)) +
  geom_bar() + theme_classic() +
  labs(title='Distribution plot') +
  xlab("Condition")
```




```
table(heart_data$goal)
```

```
##
##   healthy unhealthy
##       164       139
```

```
round(prop.table(table(heart_data$goal)) * 100, digits = 1)
```

```
##
##   healthy unhealthy
##      54.1      45.9
```

```
##                  Scatter plots by condition                    -
```

```
#heart_data %>% ggvis(~age, ~trestbps, fill = ~goal) %>% layer_points()

#heart_data %>% ggvis(~age, ~trestbps, fill = ~sex) %>% layer_points()

#heart_data %>% ggvis(~age, ~trestbps, fill = ~ cp) %>% layer_points()
```

```
##                         Data partition                          -
```

```
test_index <- createDataPartition(y = heart_data$goal, times = 1,
                                  p = 0.2, list= FALSE)
heart_data$goal <- as.factor(heart_data$goal)
train_data <- heart_data[-test_index, ]
test_data <- heart_data[test_index, ]
```

```
##                          Classifiers                          -
```

```
##        1. Logistic regression: Fit the logistic regression model,        -
##   that is a GLM using a binomial link using the caret function train()   -
```

```
set.seed(112)
log_fit <- train(goal ~.-ID ,
                 data = train_data,
                 method = "glm",
                 family = "binomial")
```

```
## Warning in predict.lm(object, newdata, se.fit, scale = 1, type = if (type == :
## prediction from a rank-deficient fit may be misleading
```

```
log_pred <- predict(log_fit, test_data)
confusionMatrix(log_pred, test_data$goal)
```

```
## Confusion Matrix and Statistics
##
##            Reference
## Prediction  healthy unhealthy
##   healthy        26         5
##   unhealthy       7        23
##
##                Accuracy : 0.8033
##                  95% CI : (0.6816, 0.894)
##     No Information Rate : 0.541
##     P-Value [Acc > NIR] : 1.767e-05
##
##                   Kappa : 0.606
##
##  Mcnemar's Test P-Value : 0.7728
##
##             Sensitivity : 0.7879
##             Specificity : 0.8214
##          Pos Pred Value : 0.8387
##          Neg Pred Value : 0.7667
##              Prevalence : 0.5410
##          Detection Rate : 0.4262
##    Detection Prevalence : 0.5082
##       Balanced Accuracy : 0.8047
##
##        'Positive' Class : healthy
##
```

```
##                        2. Random forest                         -
```

```
set.seed(112)
rf_fit <- train(goal ~.-ID ,
                   data = train_data,
                   method = "rf")

rf_pred <- predict(rf_fit, test_data)
confusionMatrix(rf_pred, test_data$goal)
```

```
## Confusion Matrix and Statistics
```

```
##
##            Reference
## Prediction  healthy unhealthy
##   healthy        27         5
##   unhealthy       6        23
##
##                Accuracy : 0.8197
##                  95% CI : (0.7002, 0.9064)
##     No Information Rate : 0.541
##     P-Value [Acc > NIR] : 4.82e-06
##
##                   Kappa : 0.6379
##
##  Mcnemar's Test P-Value : 1
##
##             Sensitivity : 0.8182
##             Specificity : 0.8214
##          Pos Pred Value : 0.8438
##          Neg Pred Value : 0.7931
##              Prevalence : 0.5410
##          Detection Rate : 0.4426
##    Detection Prevalence : 0.5246
##       Balanced Accuracy : 0.8198
##
##        'Positive' Class : healthy
##
```

```
##  3. Boosted logistic regression: using decision stumps (one node decision trees)    -
##           as weak learners. It implements a internal version of decision            -
##                           stump classifier instead of using                         -
##               calls to rpart. Also, training and testing phases of the              -
##              classification process are split into separate functions.              -
```

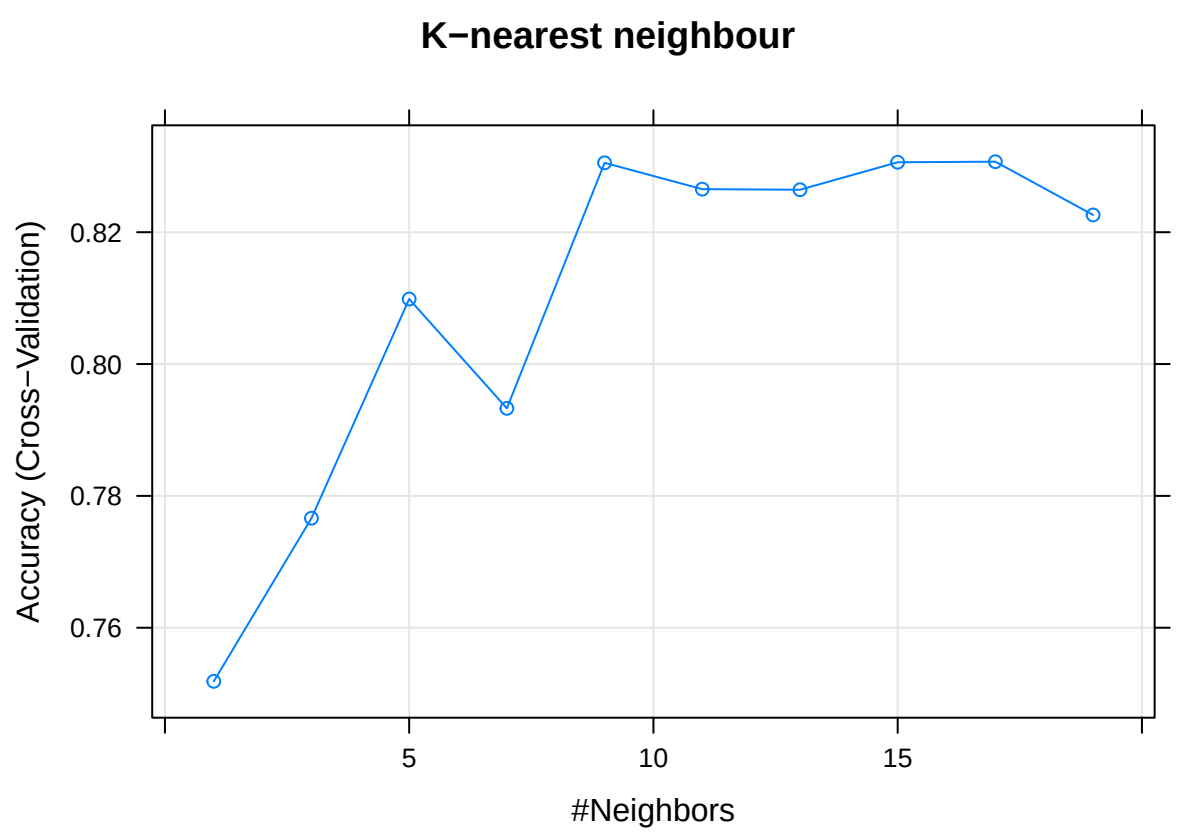
```
set.seed(112)
blog_fit <- train(goal ~.-ID,
                  data = train_data,
                  method = "LogitBoost")
blog_pred <- predict(blog_fit, test_data)
confusionMatrix(blog_pred, test_data$goal)
```

```
## Confusion Matrix and Statistics
##
##            Reference
## Prediction  healthy unhealthy
##   healthy        25         6
##   unhealthy       8        22
##
##                Accuracy : 0.7705
##                  95% CI : (0.645, 0.8685)
##     No Information Rate : 0.541
##     P-Value [Acc > NIR] : 0.0001784
##
##                   Kappa : 0.5404
##
##  Mcnemar's Test P-Value : 0.7892680
```

```
##
##             Sensitivity : 0.7576
##             Specificity : 0.7857
##          Pos Pred Value : 0.8065
##          Neg Pred Value : 0.7333
##              Prevalence : 0.5410
##          Detection Rate : 0.4098
##    Detection Prevalence : 0.5082
##       Balanced Accuracy : 0.7716
##
##        'Positive' Class : healthy
##
```

```
##                              4. KNN                                -
```

```
ctrl <- trainControl(method = "cv", verboseIter = FALSE, number = 5)

knn_fit <- train(goal ~. -ID , data = train_data,
                 method = "knn", preProcess = c("center","scale"),
                 trControl = ctrl , tuneGrid = expand.grid(k = seq(1, 20, 2)))

plot(knn_fit, main = "K-nearest neighbour")
```




```
knn_pred <- predict(knn_fit, test_data)
confusionMatrix(knn_pred, test_data$goal)
```

```
## Confusion Matrix and Statistics
##
```

```
##            Reference
## Prediction  healthy unhealthy
##   healthy        26         5
##   unhealthy       7        23
##
##                Accuracy : 0.8033
##                  95% CI : (0.6816, 0.894)
##     No Information Rate : 0.541
##     P-Value [Acc > NIR] : 1.767e-05
##
##                   Kappa : 0.606
##
##  Mcnemar's Test P-Value : 0.7728
##
##             Sensitivity : 0.7879
##             Specificity : 0.8214
##          Pos Pred Value : 0.8387
##          Neg Pred Value : 0.7667
##              Prevalence : 0.5410
##          Detection Rate : 0.4262
##    Detection Prevalence : 0.5082
##       Balanced Accuracy : 0.8047
##
##        'Positive' Class : healthy
##
```

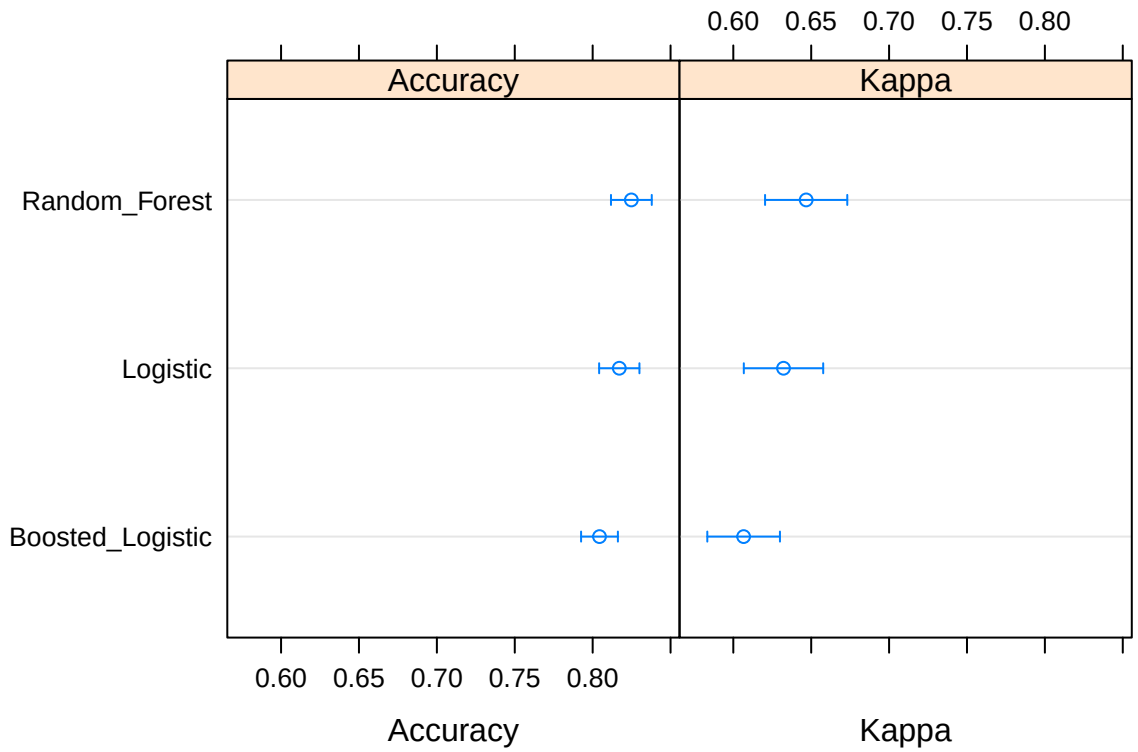
```
## ------------------- Performance Comparison -------------------
```

```
results <- resamples(list(Logistic = log_fit,
                          Random_Forest = rf_fit,
                          Boosted_Logistic = blog_fit))
summary(results)
```

```
##
## Call:
## summary.resamples(object = results)
##
## Models: Logistic, Random_Forest, Boosted_Logistic
## Number of resamples: 25
##
## Accuracy
##                      Min.   1st Qu.    Median      Mean   3rd Qu.      Max.
## Logistic         0.7727273 0.7857143 0.8222222 0.8171039 0.8352941 0.8901099
## Random_Forest    0.7710843 0.7978723 0.8250000 0.8248519 0.8409091 0.9000000
## Boosted_Logistic 0.7553191 0.7826087 0.8064516 0.8043928 0.8235294 0.8695652
##                  NA's
## Logistic            0
## Random_Forest       0
## Boosted_Logistic    0
##
## Kappa
##                      Min.   1st Qu.    Median      Mean   3rd Qu.      Max.
## Logistic         0.5463918 0.5723982 0.6401799 0.6322267 0.6701774 0.7799807
## Random_Forest    0.5419692 0.5887829 0.6454721 0.6467726 0.6831276 0.7982063
## Boosted_Logistic 0.5158979 0.5619048 0.6094260 0.6066206 0.6468330 0.7287469
```

```
##                  NA's
## Logistic            0
## Random_Forest       0
## Boosted_Logistic    0
```

```
dotplot(results)
```



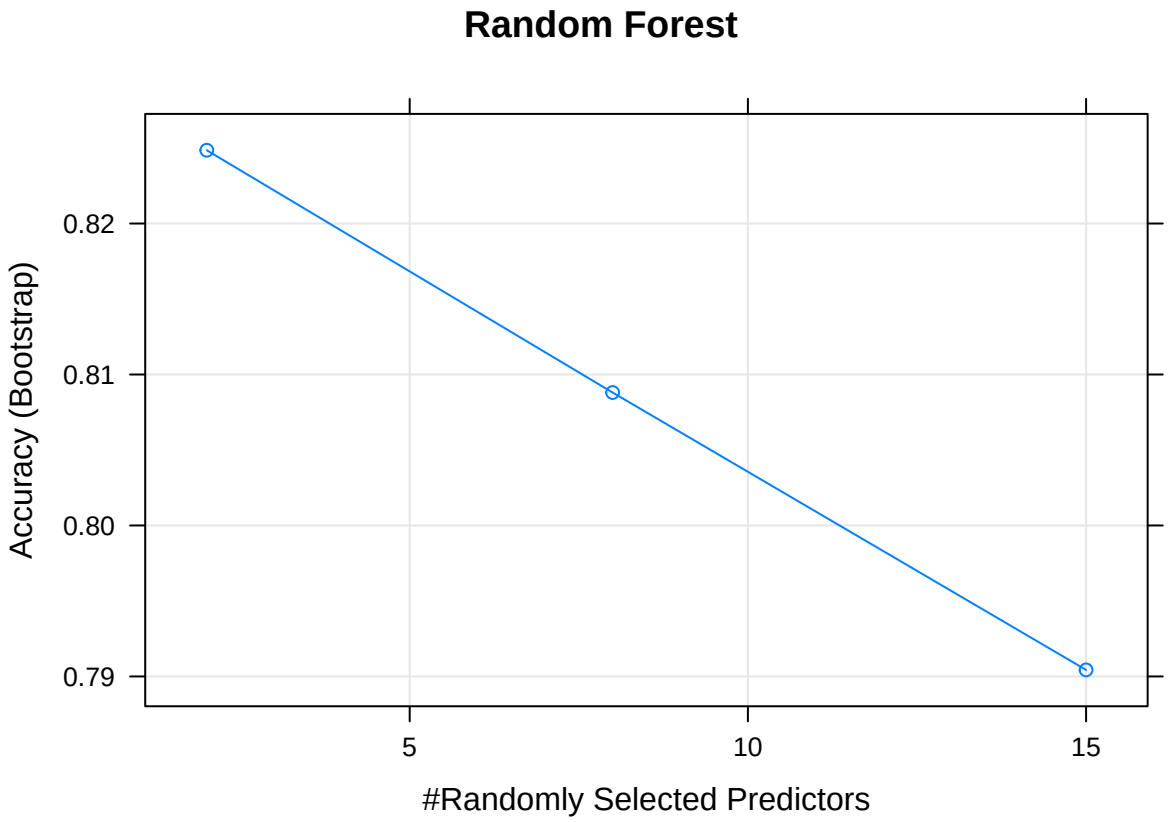
Confidence Level: 0.95

```
cf_rf <- confusionMatrix(rf_pred, test_data$goal)
cf_log <- confusionMatrix(log_pred, test_data$goal)
cf_blog <- confusionMatrix(log_pred, test_data$goal)
cf_knn <- confusionMatrix(knn_pred, test_data$goal)

Accuracy <- 100*rbind(cf_log[["overall"]][["Accuracy"]],
              cf_rf[["overall"]][["Accuracy"]],
              cf_blog[["overall"]][["Accuracy"]],
              cf_knn[["overall"]][["Accuracy"]])

Specificity <- 100*rbind(cf_log[["byClass"]][["Specificity"]],
               cf_rf[["byClass"]][["Specificity"]],
               cf_blog[["byClass"]][["Specificity"]],
               cf_knn[["byClass"]][["Specificity"]])

Sensitivity <- 100*rbind(cf_log[["byClass"]][["Sensitivity"]],
               cf_rf[["byClass"]][["Sensitivity"]],
               cf_blog[["byClass"]][["Sensitivity"]],
               cf_knn[["byClass"]][["Sensitivity"]])
```

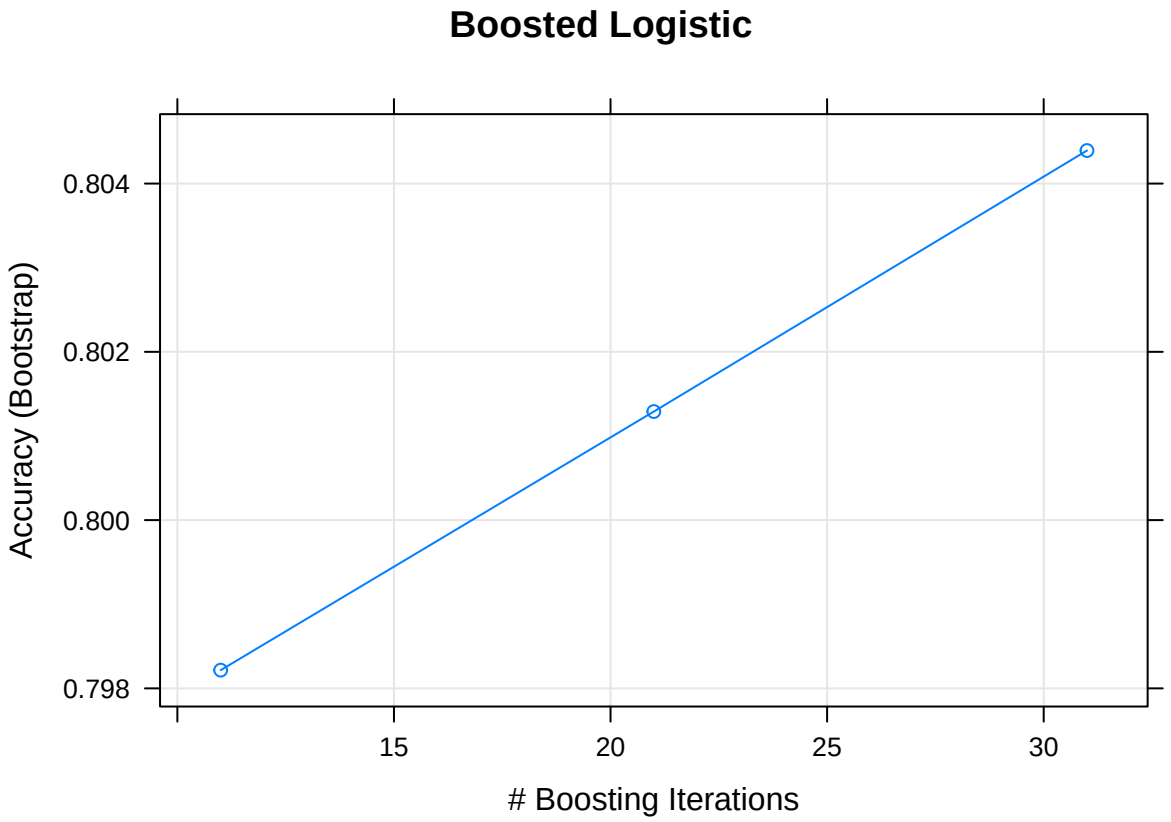
```r
pf_result <- t(data.frame(Accuracy, Specificity, Sensitivity))
colnames(pf_result) <- c("Log", "RF", "LogitB", "KNN")
pf_result <- as.matrix(pf_result)

pf_result
```

```
##                  Log       RF   LogitB      KNN
## Accuracy    80.32787 81.96721 80.32787 80.32787
## Specificity 82.14286 82.14286 82.14286 82.14286
## Sensitivity 78.78788 81.81818 78.78788 78.78788
```

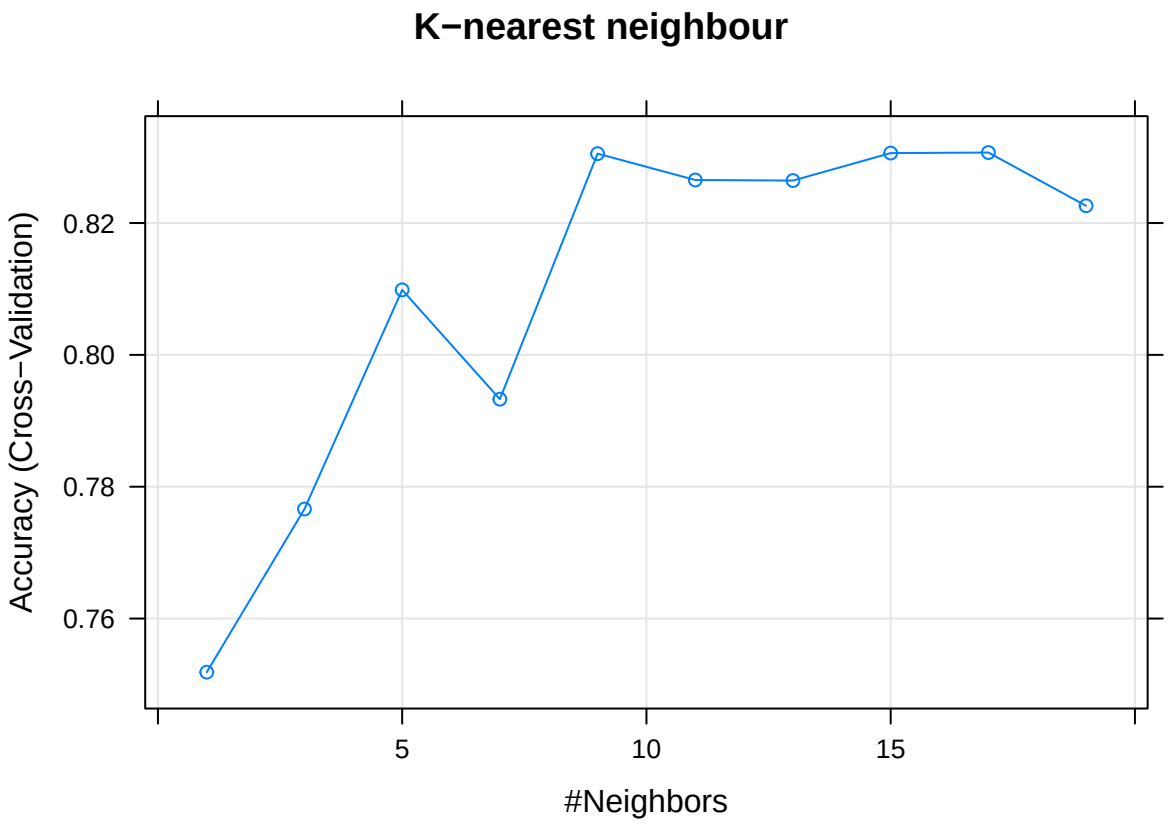
```r
plot(rf_fit, main = "Random Forest")
```



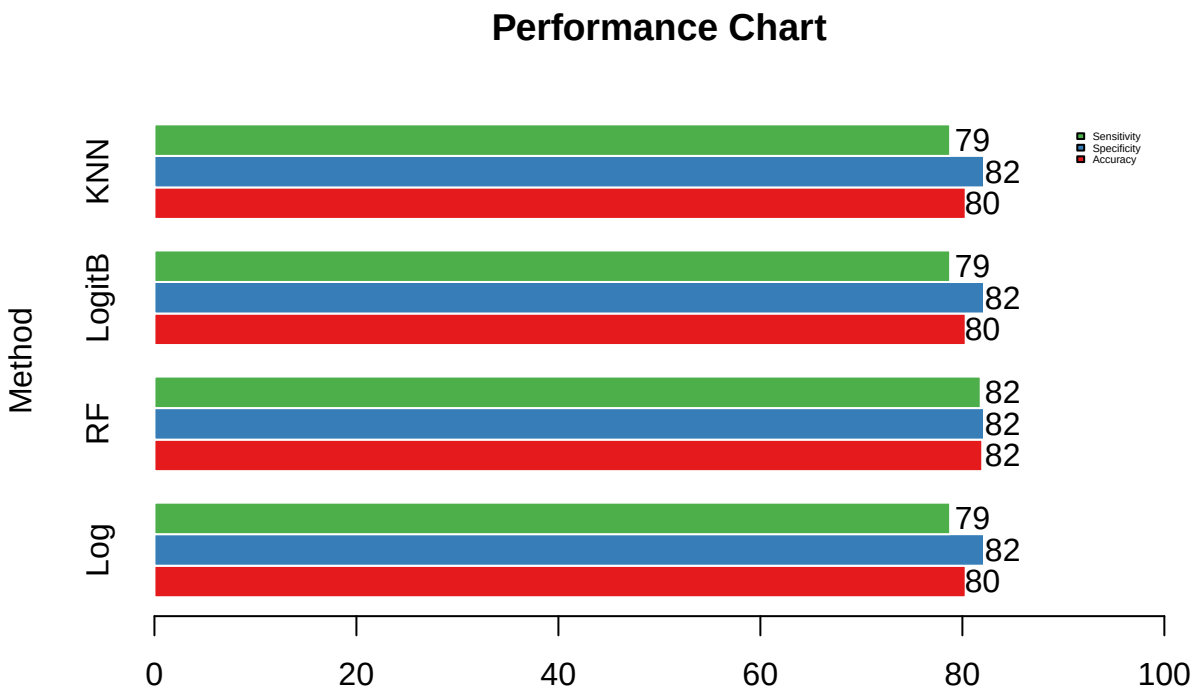

```r
plot(blog_fit, main = "Boosted Logistic")
```




```
plot(knn_fit, main = "K-nearest neighbour")
```

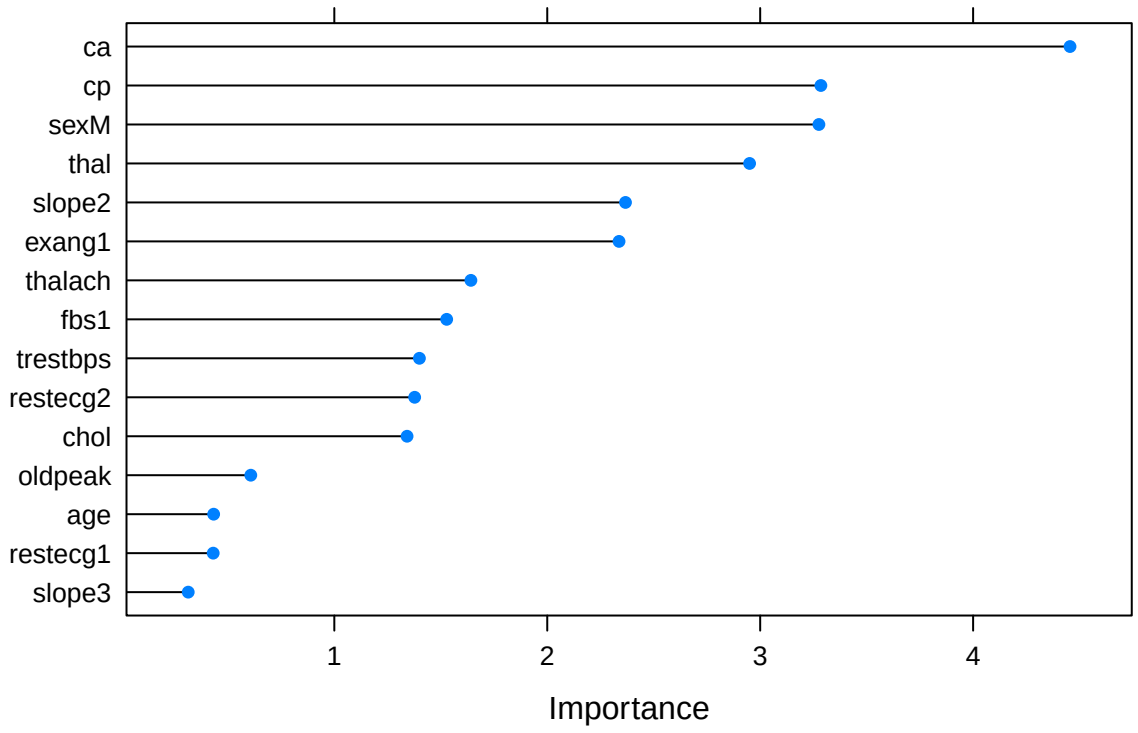



```
y <- barplot(pf_result, beside = TRUE, horiz = TRUE,
             col=brewer.pal(3,"Set1"),border="white",
             legend.text = c("Accuracy", "Specificity", "Sensitivity"),
             args.legend = list(bty = "n", cex = 0.3), xlim=c(0,100),
             main = "Performance Chart", ylab = "Method")

x <- round(pf_result)

text(x+2,y,labels=as.character(x))
```

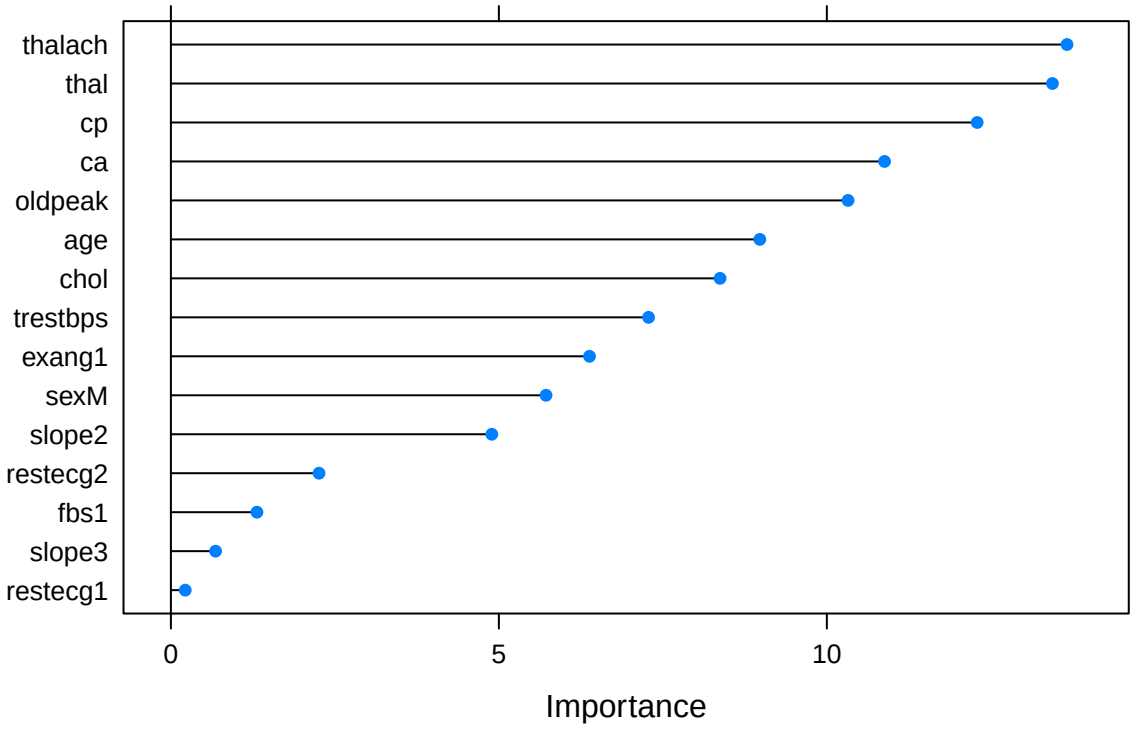



```
##                          Feature extraction                          -
```

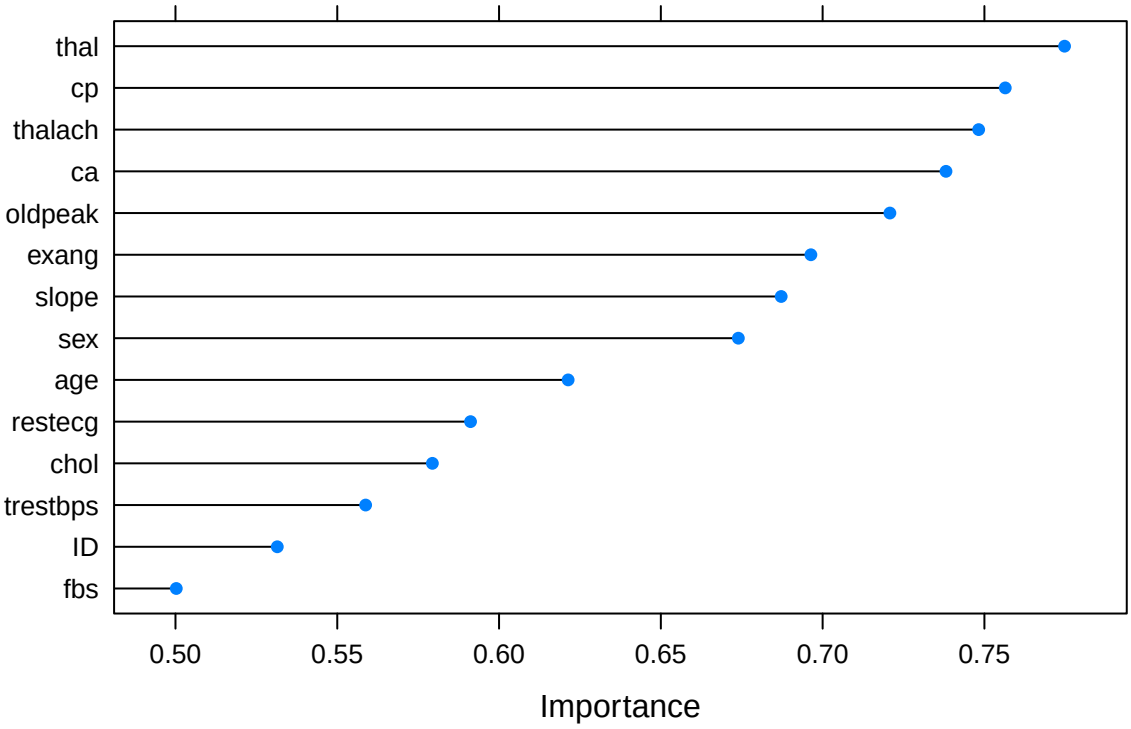
```
feat_log <- varImp(log_fit, scale = FALSE)
feat_rf <- varImp(rf_fit, scale = FALSE)
feat_blog <- varImp(blog_fit, scale = FALSE)
feat_knn <- varImp(knn_fit, scale = FALSE)

plot(feat_log, main = "Logistic regression: features")
```



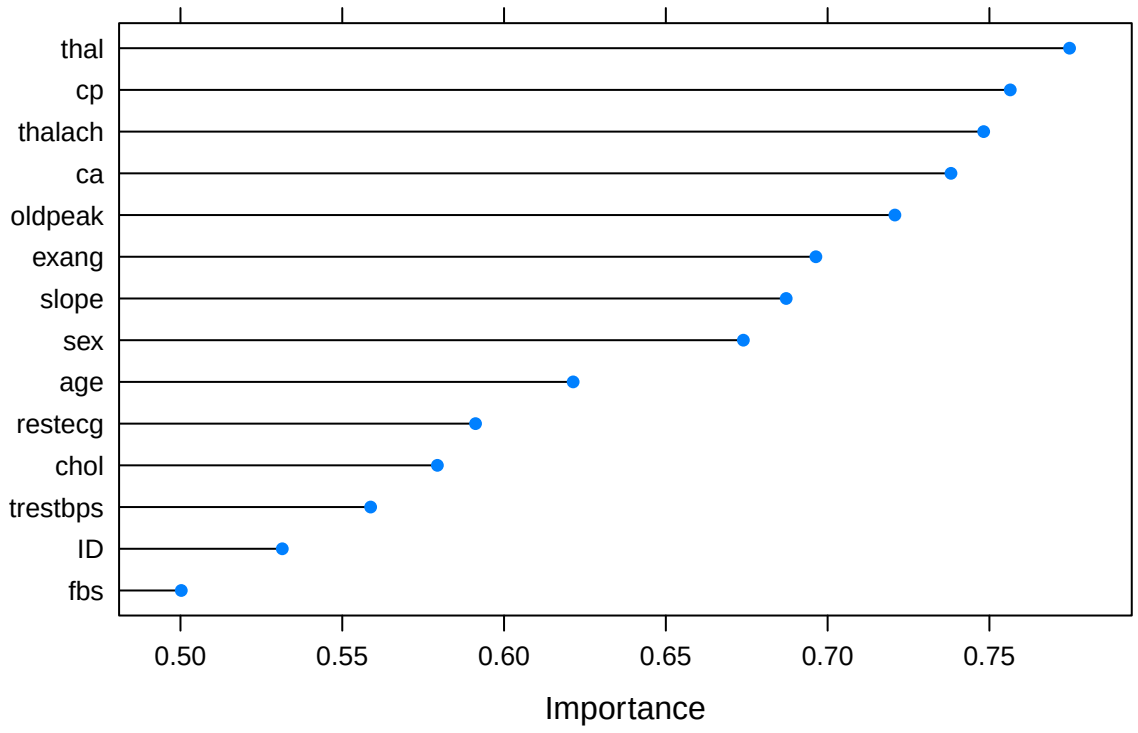

```
plot(feat_rf, main = "Random forest: features")
```




```
plot(feat_blog, main = "Boosted Logistic regression: features")
```




```
plot(feat_knn, main = "KNN: features")
```




```
##      Model Evaluation with ROC, calibration, precision        -
##       recall gain, and Obs vs. Pred probabilities curve       -
```

```
cont <- trainControl(method="cv",
                     summaryFunction=twoClassSummary,
                     classProbs=T,
                     savePredictions = T)

log <- train(goal ~.-ID ,
                 data = train_data,
                 method = "glm", preProc=c("center", "scale"),
                 family = "binomial", trControl=cont)
```

```
## Warning in train.default(x, y, weights = w, ...): The metric "Accuracy" was not
## in the result set. ROC will be used instead.
```

```
rf <- train(goal ~.-ID ,
                data = train_data, preProc=c("center", "scale"),
                method = "rf", trControl=cont)
```

```
## Warning in train.default(x, y, weights = w, ...): The metric "Accuracy" was not
## in the result set. ROC will be used instead.
```

```
blog <- train(goal ~.-ID,
              data = train_data, preProc=c("center", "scale"),
              method = "LogitBoost", trControl=cont)
```

```
## Warning in train.default(x, y, weights = w, ...): The metric "Accuracy" was not
```

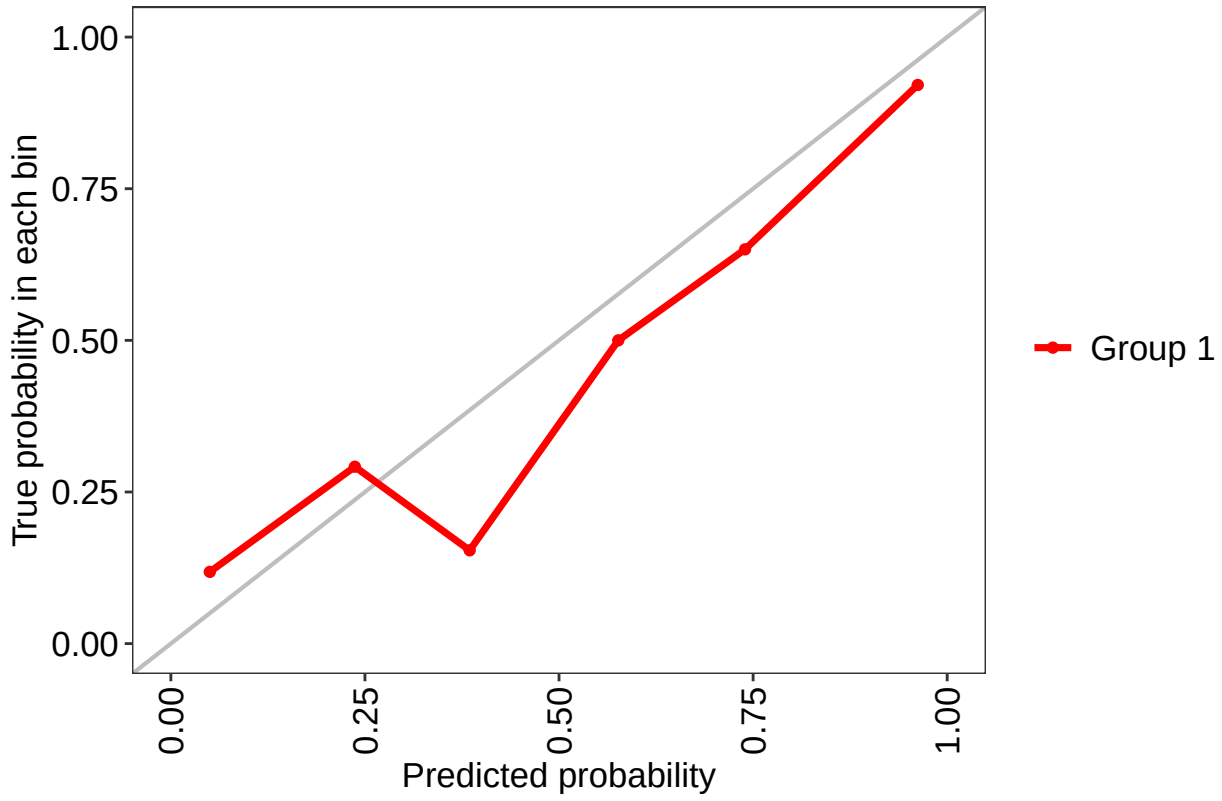
```
## in the result set. ROC will be used instead.
```

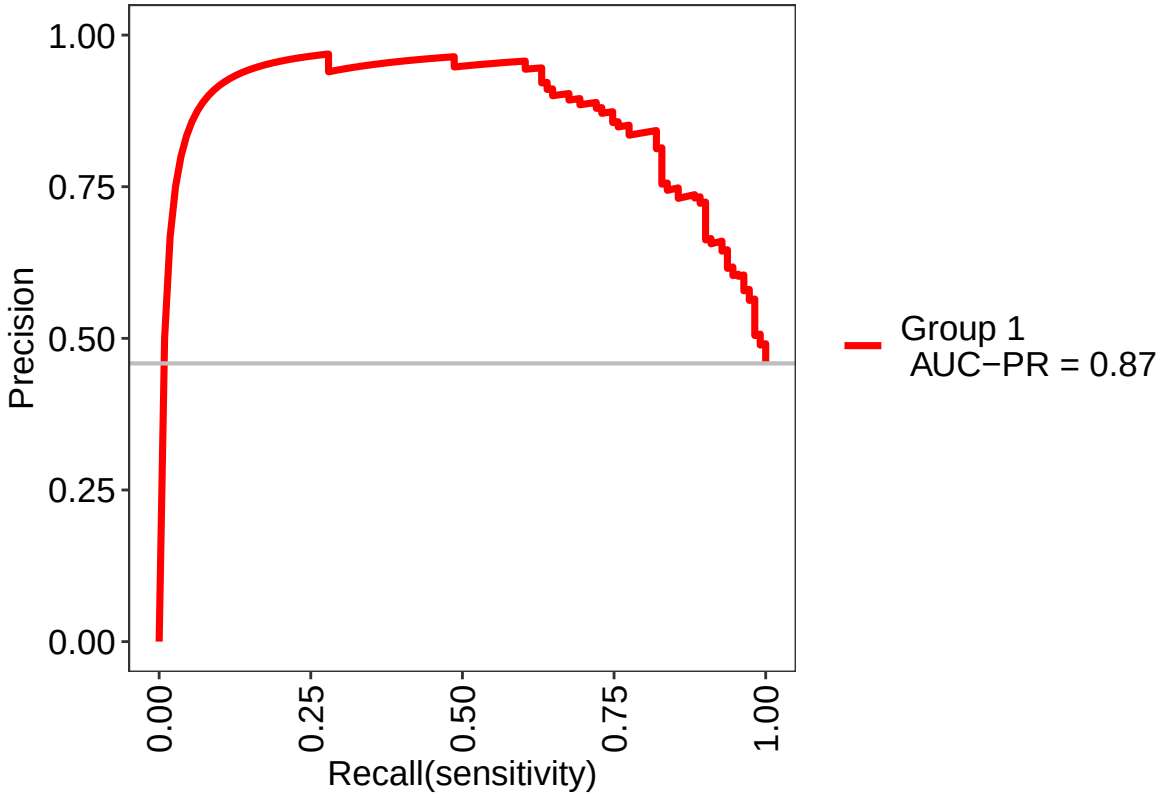
```
knn <- train(goal ~. -ID , data = train_data,
             method = "knn", preProcess = c("center","scale"),
             trControl = cont , tuneGrid = expand.grid(k = seq(1, 20, 2)))
```

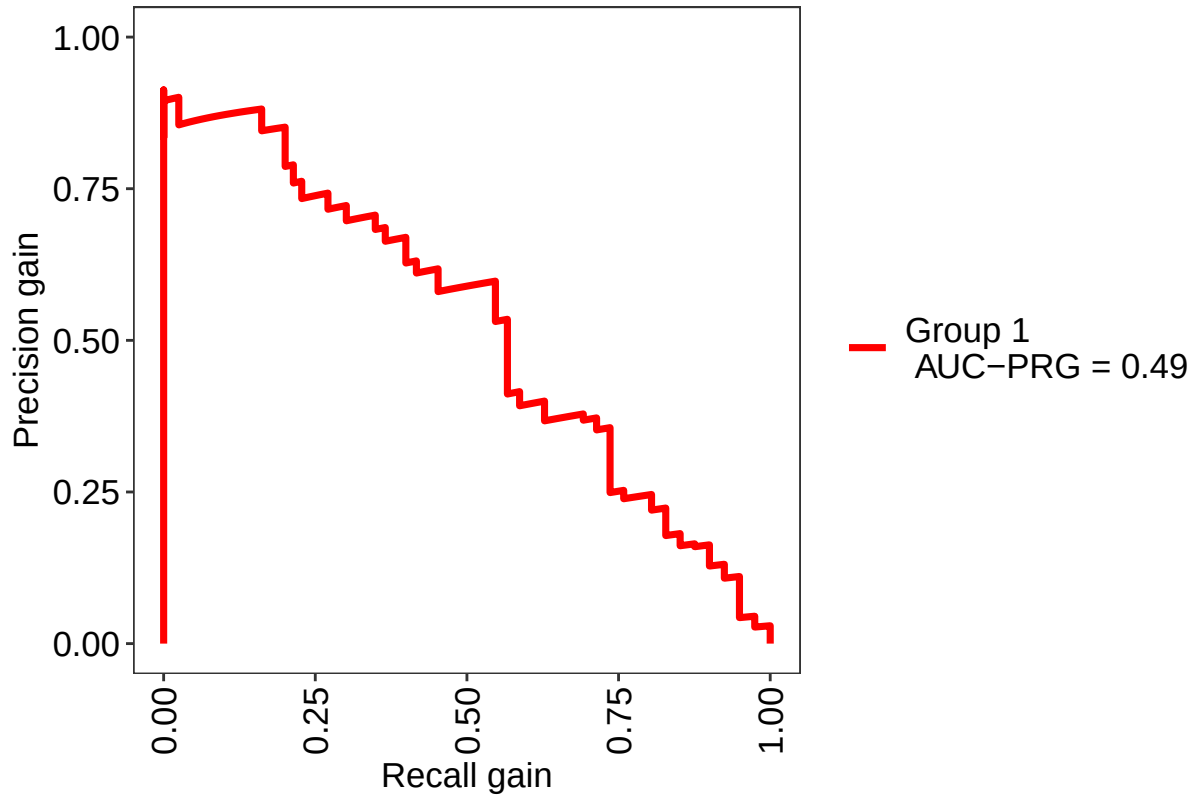
```
## Warning in train.default(x, y, weights = w, ...): The metric "Accuracy" was not
## in the result set. ROC will be used instead.
```

```
#####################################################################
##            Logistic Classifier: Performance Plots             ##
#####################################################################
res.log <- evalm(log)
```

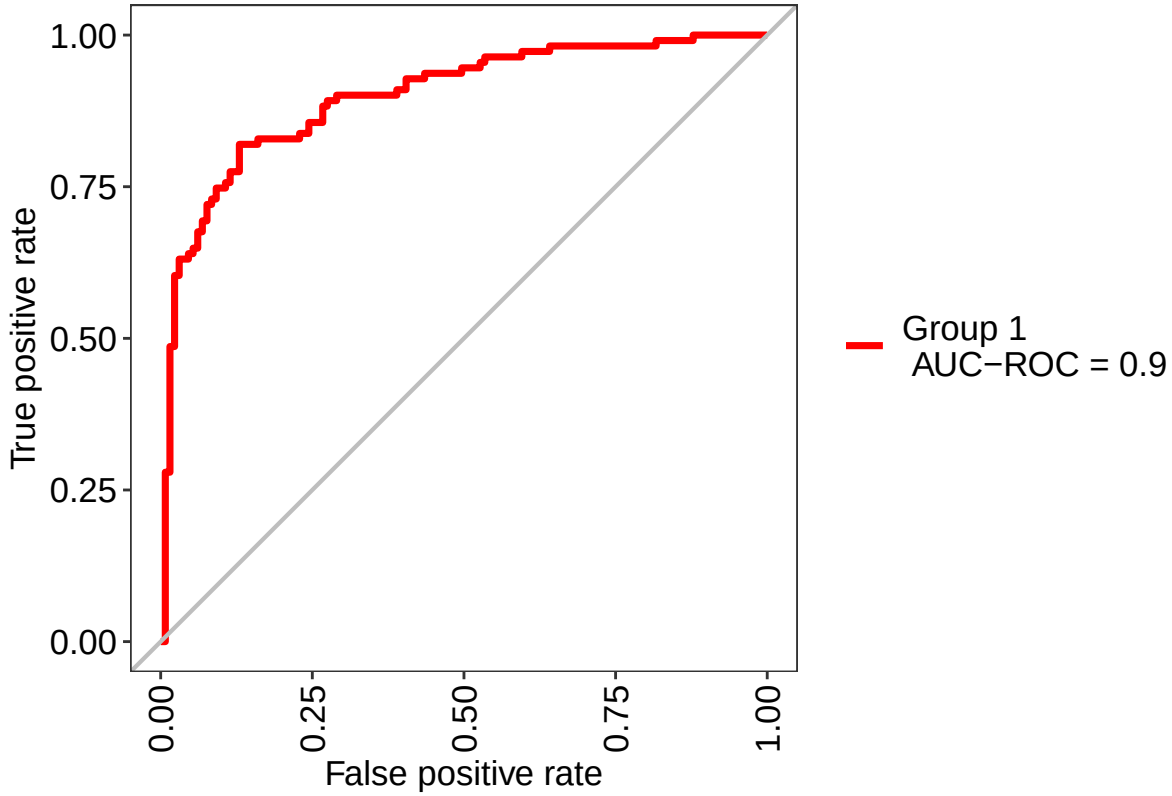
```
## ***MLeval: Machine Learning Model Evaluation***

## Input: caret train function object

## Not averaging probs.

## Group 1 type: cv

## Observations: 242

## Number of groups: 1

## Observations per group: 242

## Positive: unhealthy

## Negative: healthy

## Group: Group 1

## Positive: 111

## Negative: 131

## ***Performance Metrics***
```


1.00
0.75
0.50
0.25
0.00
True probability in each bin
0.00
0.25
0.50
0.75
1.00
Predicted probability
Group 1


1.00
0.75
0.50
0.25
0.00
Precision
0.00
0.25
0.50
0.75
1.00
Recall(sensitivity)
Group 1
AUC−PR = 0.87

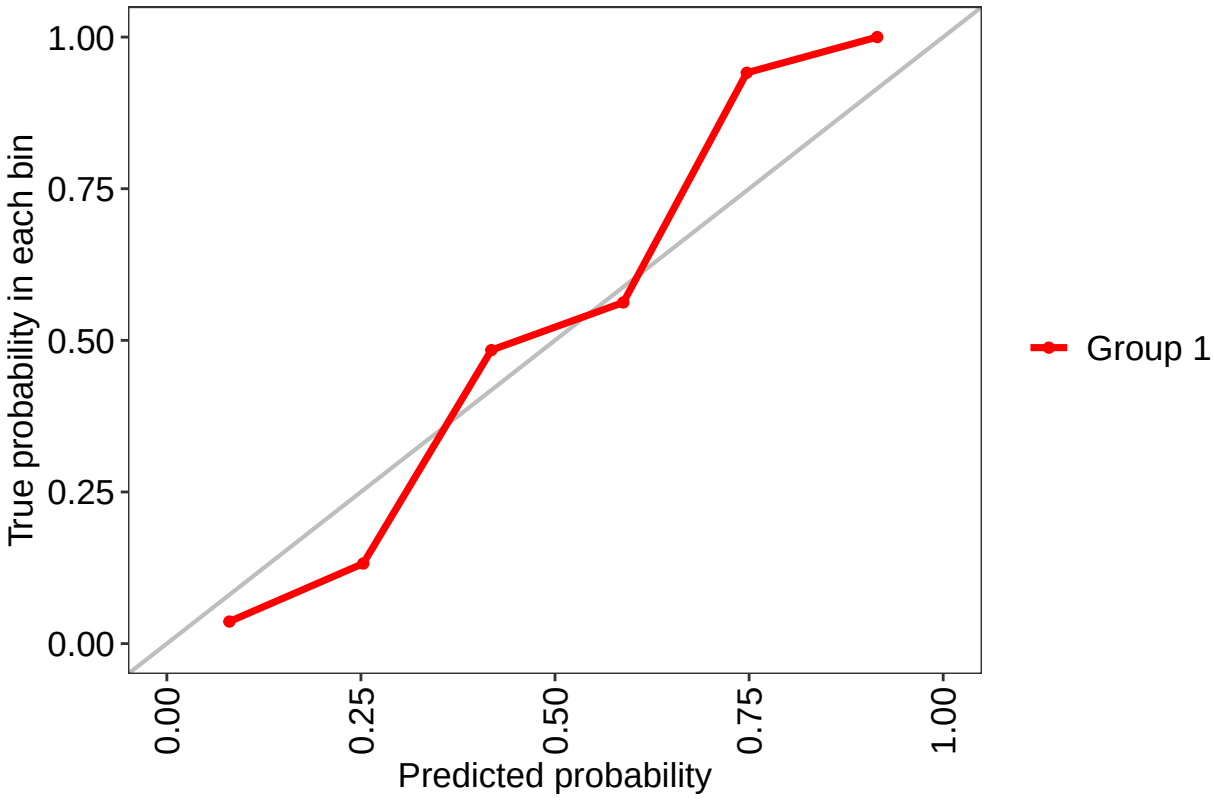


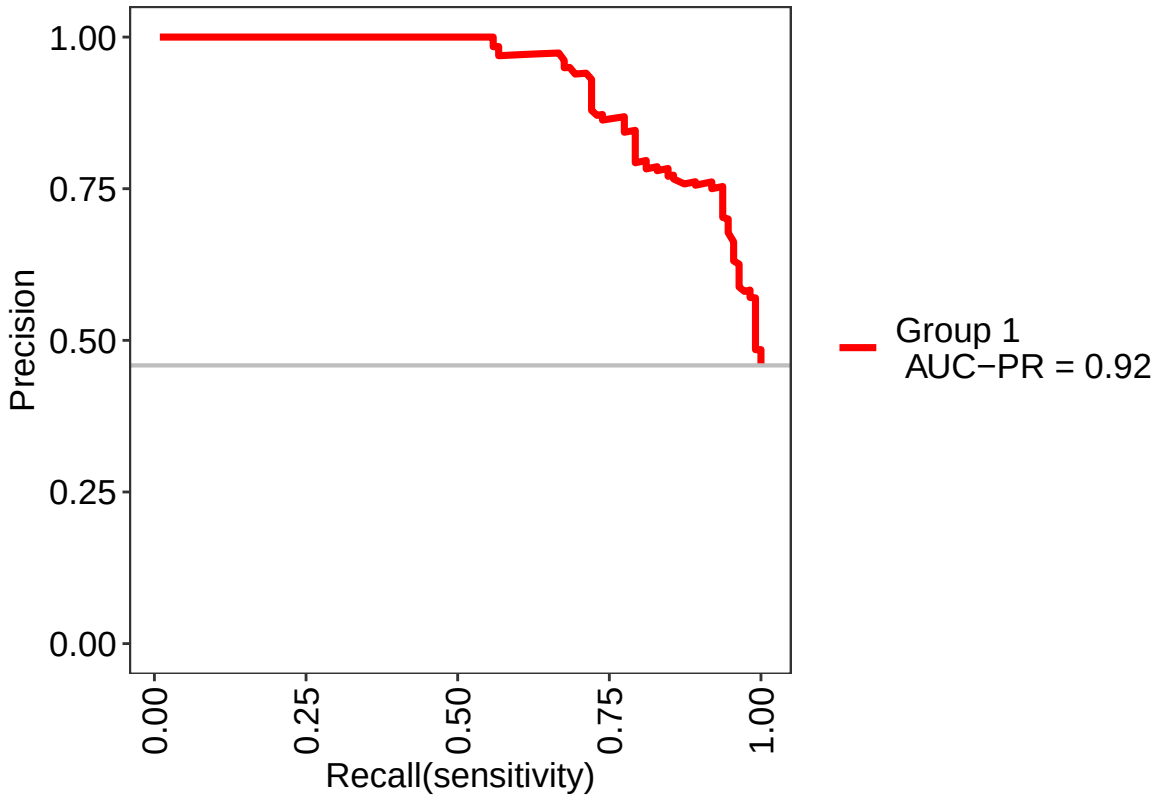

```
## Group 1 Optimal Informedness = 0.690048827453408
## Group 1 AUC-ROC = 0.9
```

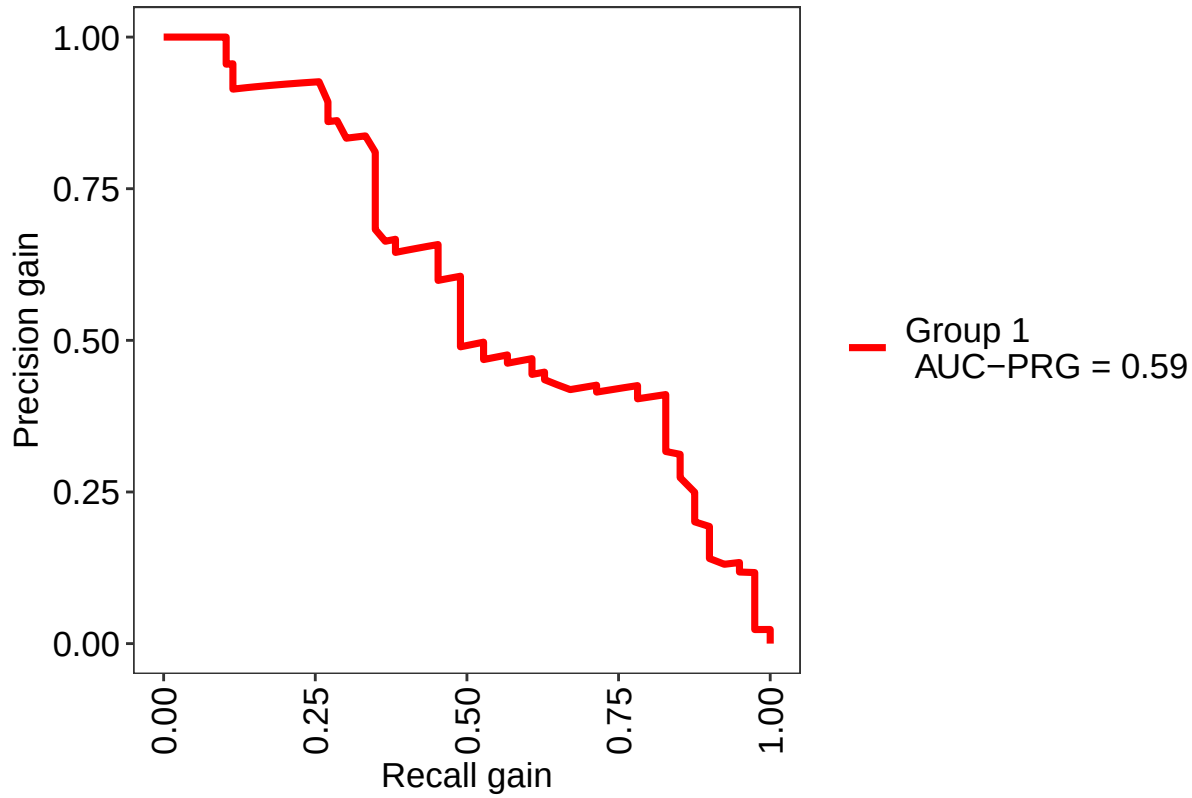



```
#####################################################################
##          Random Forest Classifier: Performance Plots          ##
#####################################################################
res.rf <- evalm(rf)
```

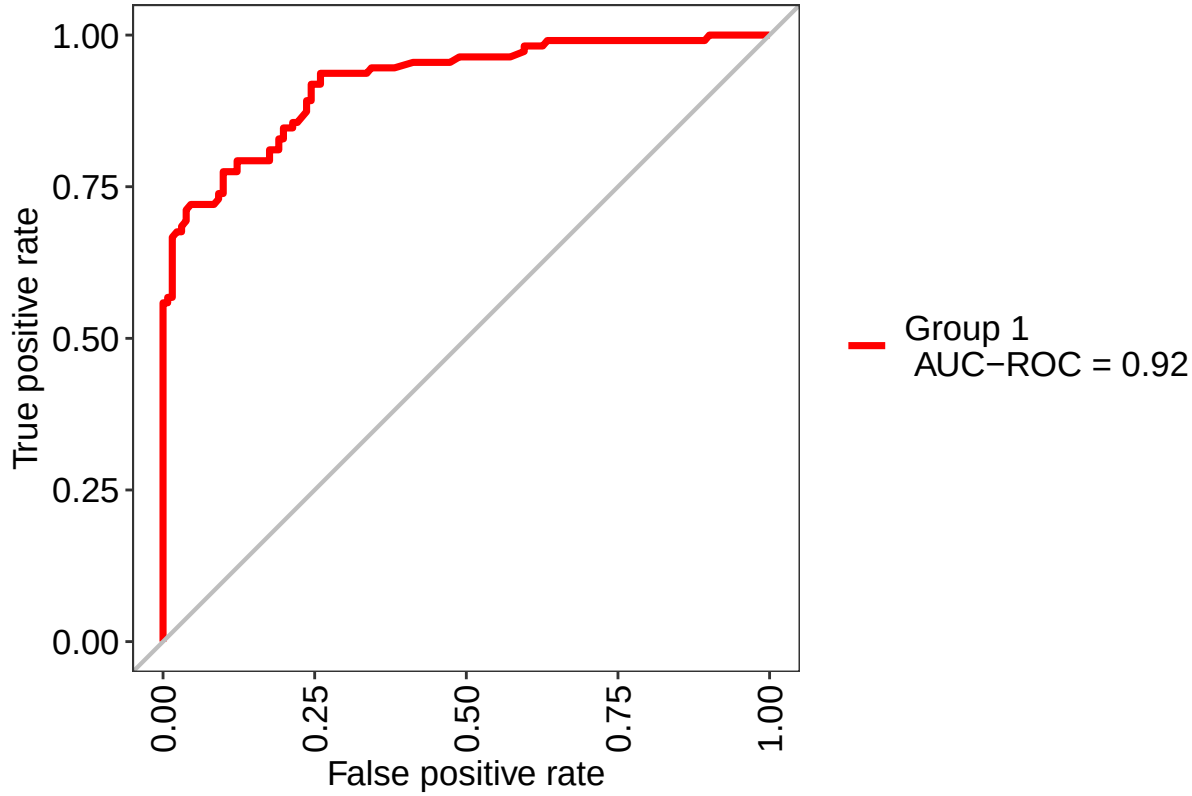
```
## ***MLeval: Machine Learning Model Evaluation***
## Input: caret train function object
## Not averaging probs.
## Group 1 type: cv
## Observations: 242
## Number of groups: 1
## Observations per group: 242
## Positive: unhealthy
## Negative: healthy
## Group: Group 1
## Positive: 111
## Negative: 131
## ***Performance Metrics***
```


1.00
0.75
0.50
0.25
0.00
True probability in each bin
0.00
0.25
0.50
0.75
1.00
Predicted probability
Group 1


1.00
0.75
0.50
0.25
0.00
Precision
0.00
0.25
0.50
0.75
1.00
Recall(sensitivity)
Group 1
AUC−PR = 0.92

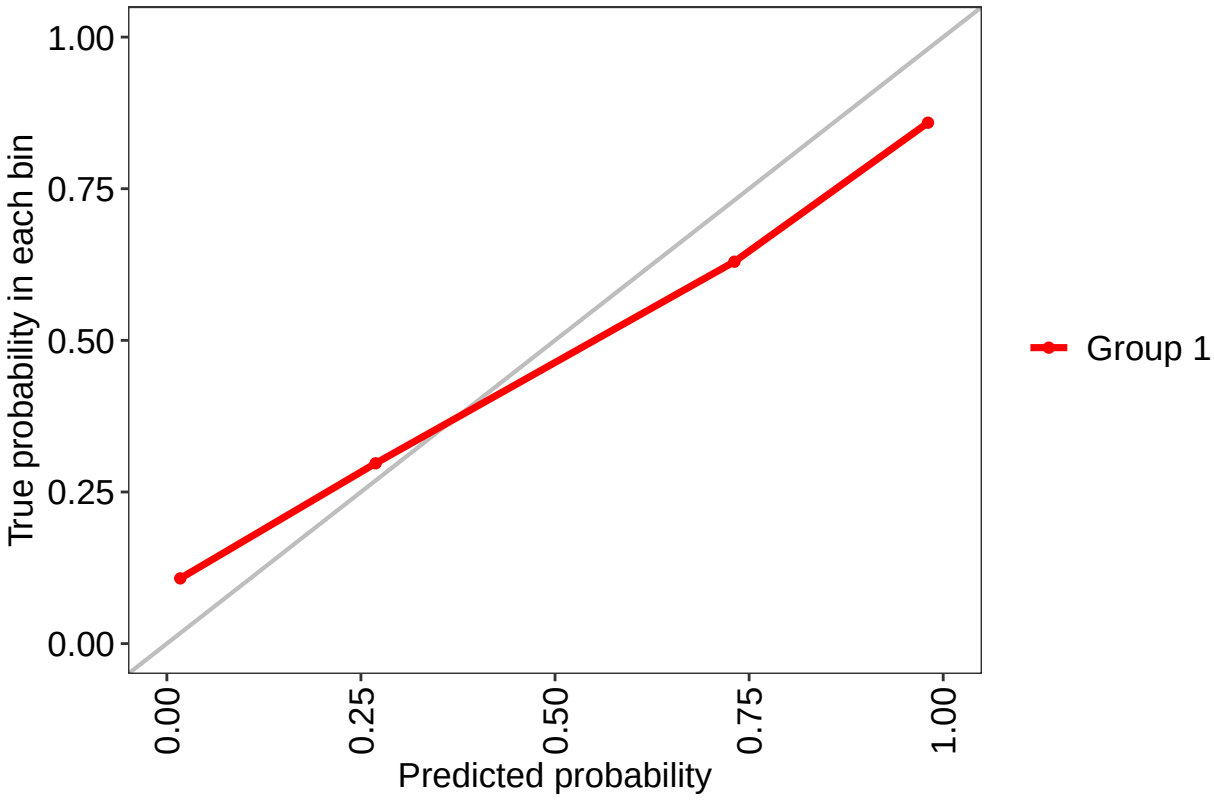


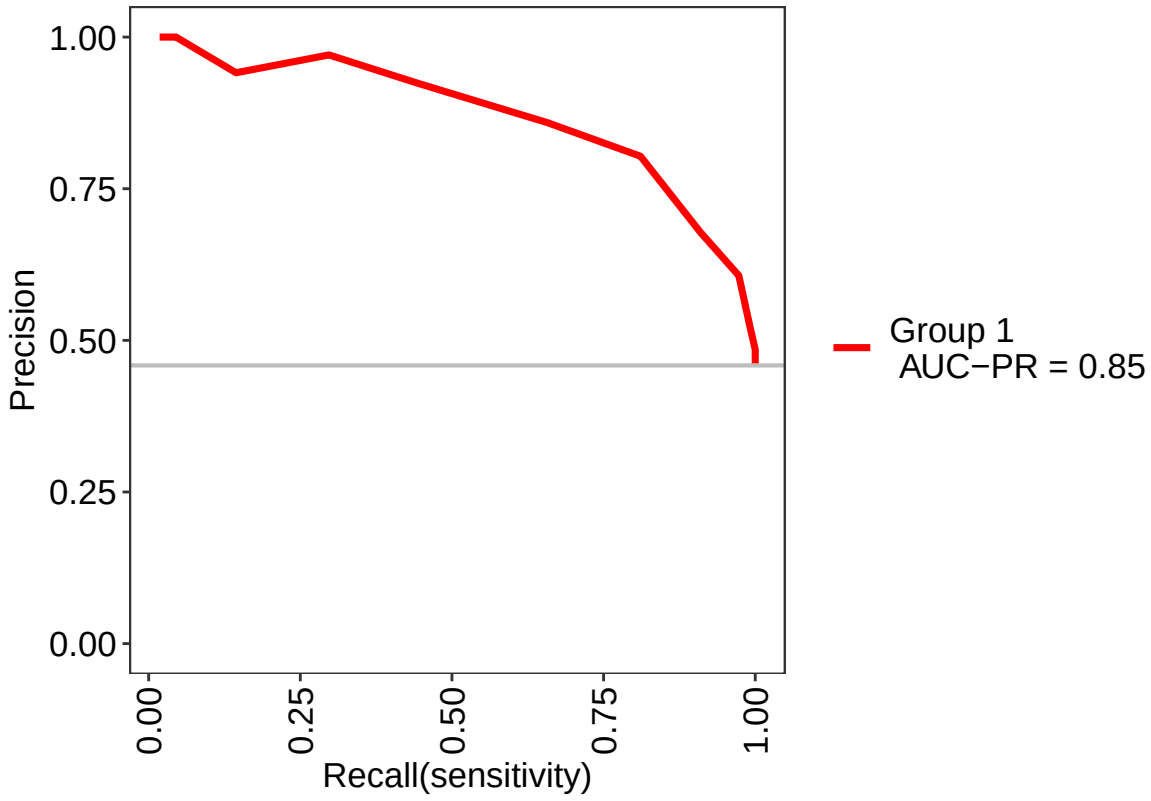

```
## Group 1 Optimal Informedness = 0.677394952204112
## Group 1 AUC-ROC = 0.92
```

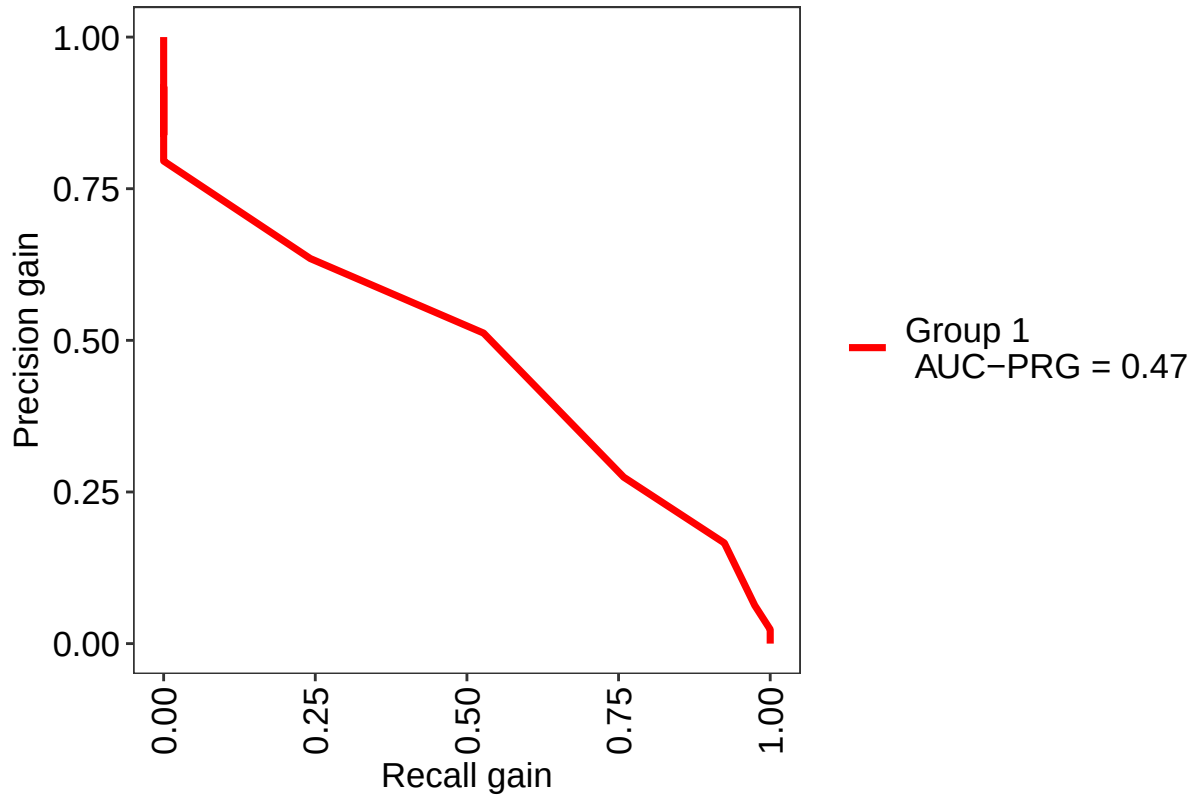



```
######################################################################
##          Boosted logit Classifier: Performance Plots             ##
######################################################################
res.blog <- evalm(blog)
```

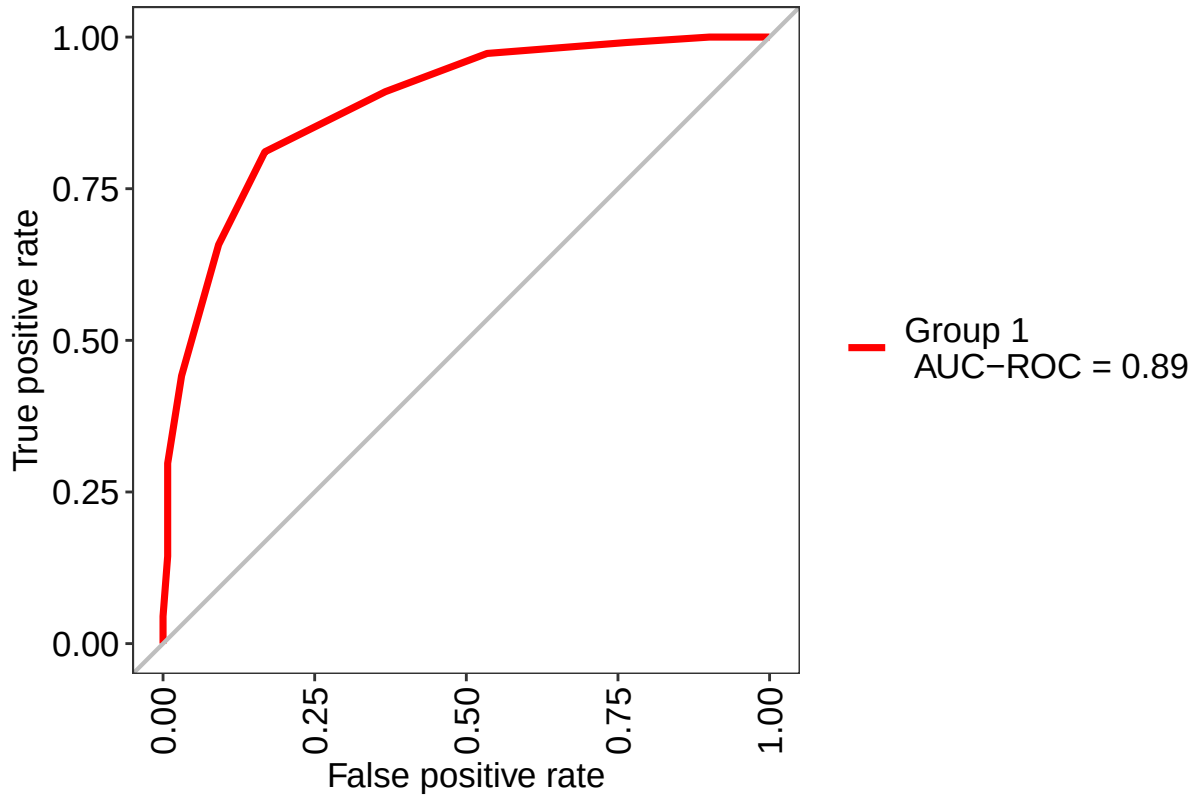
```
## ***MLeval: Machine Learning Model Evaluation***
## Input: caret train function object
## Not averaging probs.
## Group 1 type: cv
## Observations: 242
## Number of groups: 1
## Observations per group: 242
## Positive: unhealthy
## Negative: healthy
## Group: Group 1
## Positive: 111
## Negative: 131
## ***Performance Metrics***
```


1.00
0.75
0.50
0.25
0.00
True probability in each bin
0.00
0.25
0.50
0.75
1.00
Predicted probability
Group 1


1.00
0.75
0.50
0.25
0.00
Precision
0.00
0.25
0.50
0.75
1.00
Recall(sensitivity)
Group 1
AUC−PR = 0.85

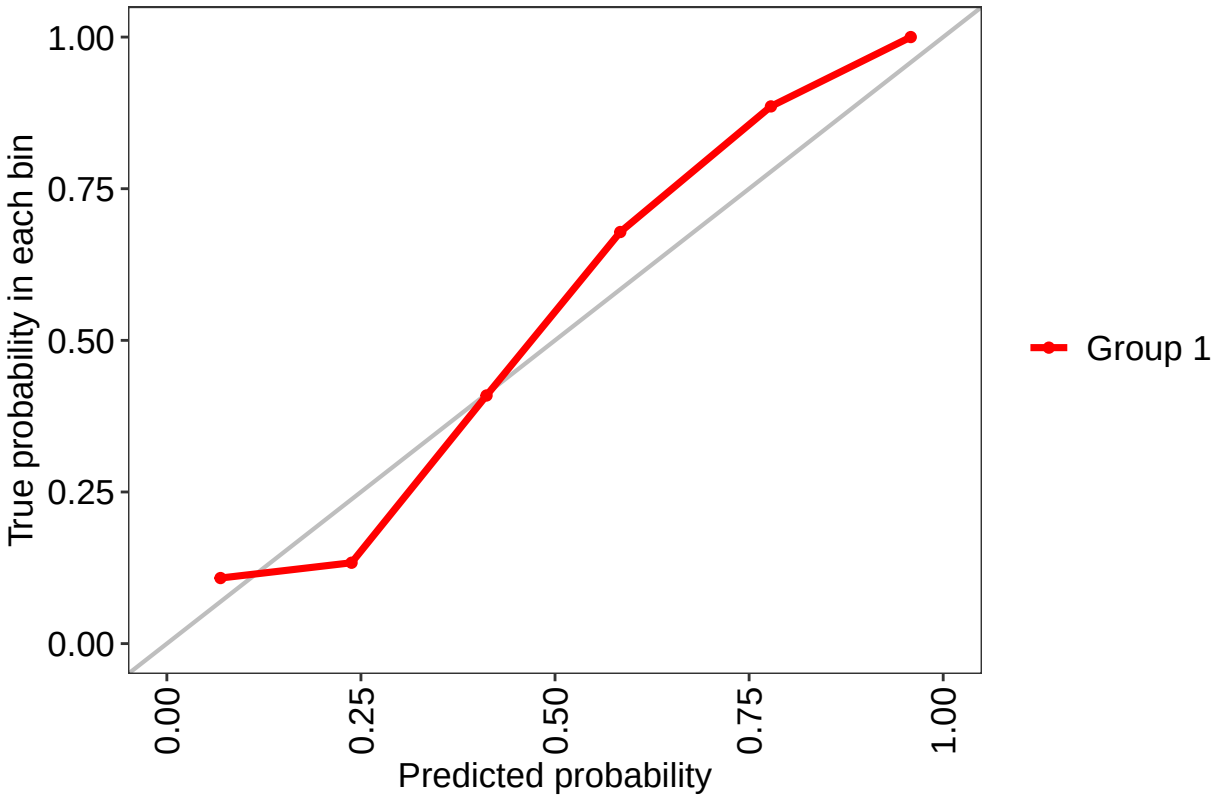


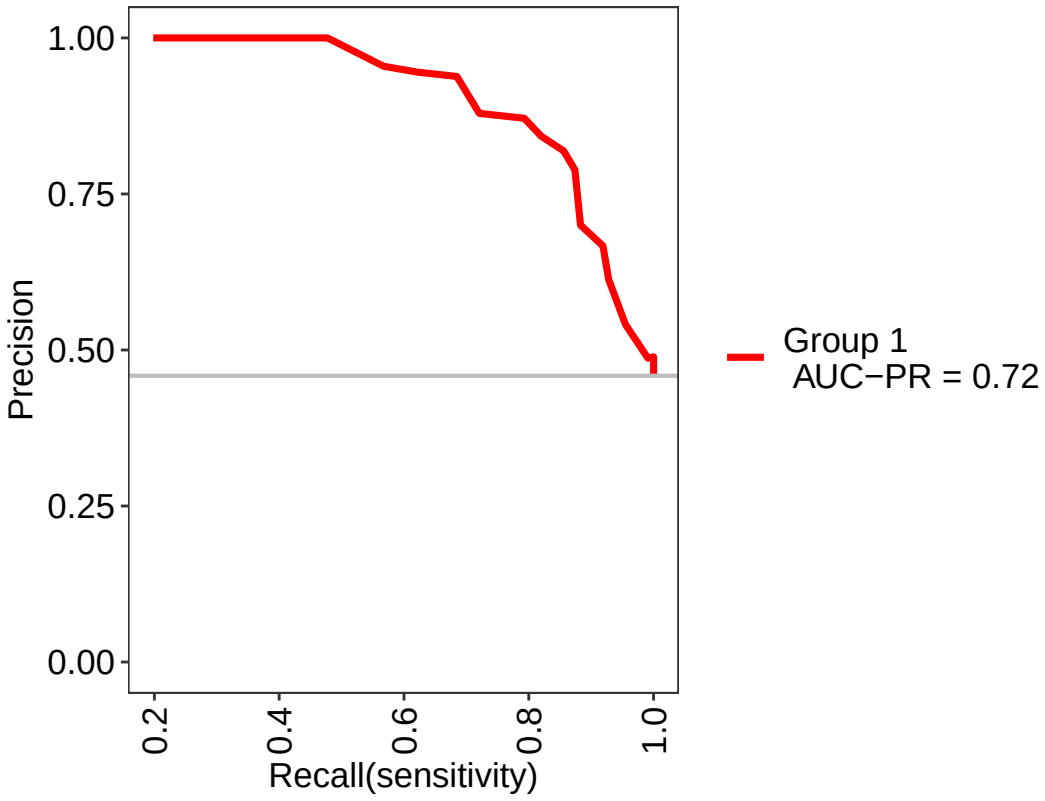

```
## Group 1 Optimal Informedness = 0.642871879513101
## Group 1 AUC-ROC = 0.89
```

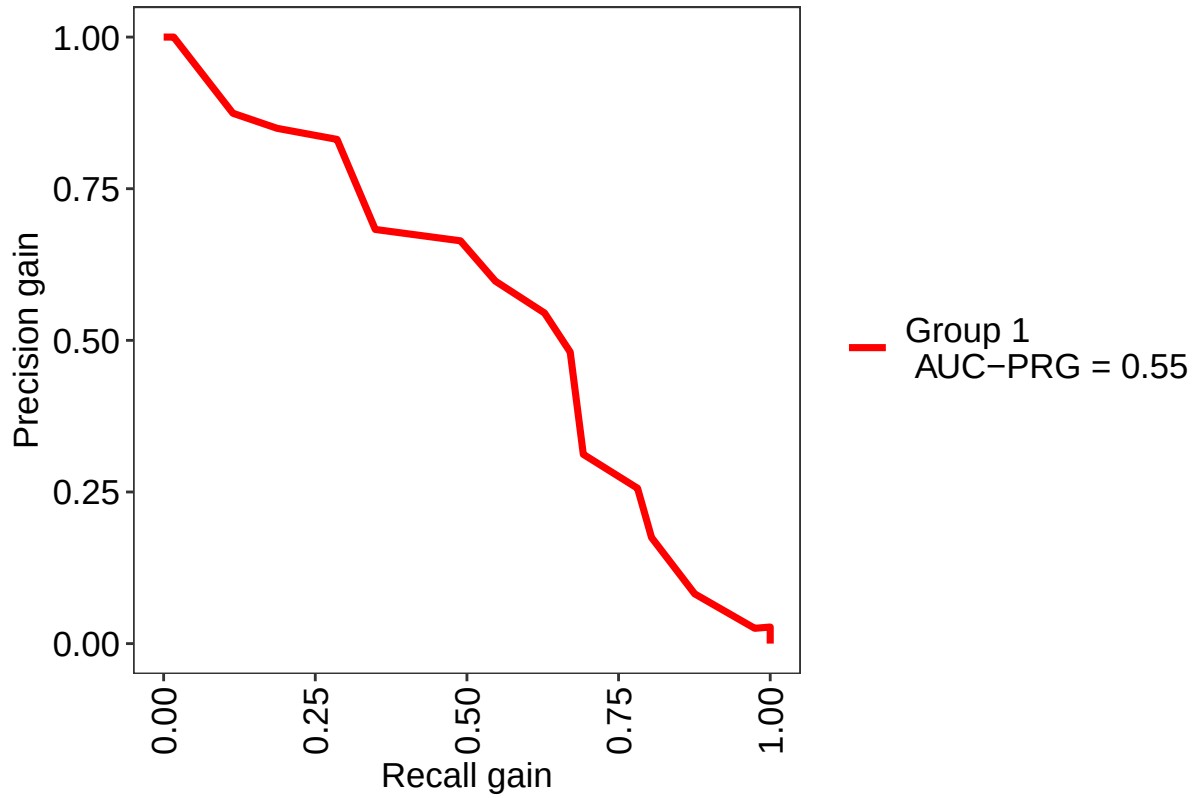



```
######################################################################
##              k-NN Classifier: Performance Plots                  ##
######################################################################
res.knn <- evalm(knn)
```

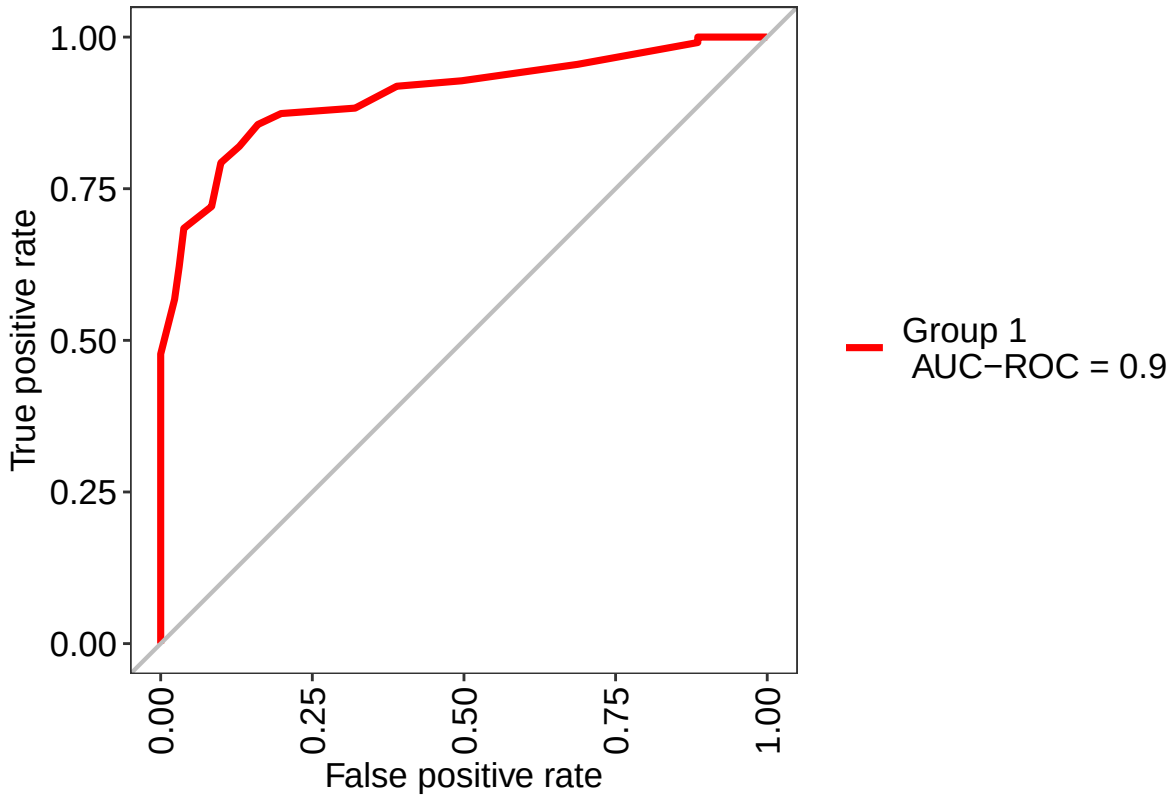
```
## ***MLeval: Machine Learning Model Evaluation***
## Input: caret train function object
## Not averaging probs.
## Group 1 type: cv
## Observations: 242
## Number of groups: 1
## Observations per group: 242
## Positive: unhealthy
## Negative: healthy
## Group: Group 1
## Positive: 111
## Negative: 131
## ***Performance Metrics***
```


1.00
0.75
0.50
0.25
0.00
True probability in each bin
0.00
0.25
0.50
0.75
1.00
Predicted probability
Group 1


1.00
0.75
0.50
0.25
0.00
Precision
0.2
0.4
0.6
0.8
1.0
Recall(sensitivity)
Group 1
AUC−PR = 0.72




```
## Group 1 Optimal Informedness = 0.695550512344405
## Group 1 AUC-ROC = 0.9
```


1.00
0.75
0.50
0.25
0.00
True positive rate
0.00
0.25
0.50
0.75
1.00
False positive rate
Group 1
AUC−ROC = 0.9