Test 2

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1. Assume, you ran a classification exercise and you determined the accuracy over training set to be TE, and the accuracy on test set to be ET. Under what condition

will you use boosting to improve the performance?

will you use bagging to improve the performance? 40 minutes

2. How is bagging different from cross validation? 20 minutes

3. Repeat bagging and CV over heart, ecoli, and icu datasets and generate a performance (accuracy, AUC) matrix by class. (4 Hours)

Question 1

The Bagging and Boosting ensemble methods fixes different problems of the same domain. Imagine We have a model, that has very high accuracy on the training dataset, but fitting the data, it was not trained on returns poor accuracy. Verdict: model is overfitted, so it has very high variance. Overfitting can happen because of fitting a lot of features, that have no significant impact on the resulting value. So the model finds some random patterns in this data, that actually are just noise and define no tendency. In this case We should use Bagging. It is useful for unstable models. It splits dataset into m subsets of n observations with repetitions (so one observation can happen more than once in one sample), fits m different models and estimates their accuracy on the same testing dataset. This process repeats a few times and as a result, bagging returns the best model.

Another scenario is when we fit a model, that has low both TE and ET. Perhaps we chose not enough features, or we use highly linear model, such as OLS on non-linear data. In this case we should use Boosting. It will also train m models, but the difference is every wrongly predicted observation will be fitted again and again. After the process, method chooses the best model and returns it.

Question 2

First of all Bagging is an ensemble model, that can apply changes on your model (particularly decreasing variance, preventing overfitting). We use it when improving flexible models.

Cross validation is kind of evaluation method, that can be useful while fitting small datasets, or in case ob absence testing data. You can split dataset into training and testing samples with relation 80% to 20%, but it does not guarantee, that all the outliers didn’t happen to be in testing sample. In this case test error will be huge. As an example I can provide data from our Test 1. We got only 36 observations and a lot of outliers, so changing the seed could have cause decreasing of accuracy up to 30%.

So cross validation is just shuffling the training and testing data samples and provides insights about goodness of fit. While Bagging is a technique that improves the model.

Question 3

Heart Data

```
library(mltest)
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
library(e1071)
library(caret)
```

```
## Loading required package: ggplot2
```

```
## Loading required package: lattice
```

```
library(rpart)
library(ipred)
library(tidyverse)
```

```
## ── Attaching packages
## ───────────────────────────────────────
## tidyverse 1.3.2 ──
```

```
## ✔ tibble  3.1.8     ✔ purrr   0.3.4
## ✔ tidyr   1.2.0     ✔ stringr 1.4.0
## ✔ readr   2.1.2     ✔ forcats 0.5.1
## ── Conflicts ────────────────────────────────────────── tidyverse_conflicts() ──
## ✖ dplyr::filter() masks stats::filter()
## ✖ dplyr::lag()    masks stats::lag()
## ✖ purrr::lift()   masks caret::lift()
```

```
library(Metrics)
```

```
##
## Attaching package: 'Metrics'
##
## The following objects are masked from 'package:caret':
##
##     precision, recall
```

```
library(ggplot2)
library(cvms)
library(ggcorrplot)
library(GGally)
```

```
## Registered S3 method overwritten by 'GGally':
##   method from
##   +.gg   ggplot2
```

```
library(pROC)
```

```
## Type 'citation("pROC")' for a citation.
##
## Attaching package: 'pROC'
##
## The following object is masked from 'package:Metrics':
##
##     auc
##
## The following objects are masked from 'package:stats':
##
##     cov, smooth, var
```

```
heart <- read.csv("data/heart.csv")
ecoli <- read.csv("data/ecoli.csv")
options(warn=-1)
```

```
head(heart)
```

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang
	<int>	<int>	<int>	<int>	<int>	<int>	<int>	<int>	<int>
1	63	1	3	145	233	1	0	150	0
2	37	1	2	130	250	0	1	187	0
3	41	0	1	130	204	0	0	172	0
4	56	1	1	120	236	0	1	178	0
5	57	0	0	120	354	0	1	163	1

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang ▸
	<int>	<int>	<int>	<int>	<int>	<int>	<int>	<int>	<int>
6	57	1	0	140	192	0	1	148	0

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```
heart$target <- as.factor(heart$target)
```

```
set.seed(1)
sample <- sample(c(TRUE, FALSE), nrow(heart), replace=TRUE, prob=c(0.8,0.2))
train <- heart[sample, ]
test <- heart[!sample, ]

test.X <- test[1:13]
test.Y <- test[14]

train.X<-train[1:13]
train.Y<-train[14]
```

```
logit.fit <- glm(train$target ~ ., data=train, family = binomial)

logit.train <- predict(logit.fit, train.X, type="response")
logit.train <- ifelse(test=logit.train>0.5, yes=1, no=0)

logit.pred <- predict(logit.fit, test.X, type="response")
logit.pred <- ifelse(test=logit.pred>0.5, yes=1, no=0)

message("Train Error is ", round(mean(logit.train != train.Y$target),2)*100, "%")
```

```
## Train Error is 13%
```

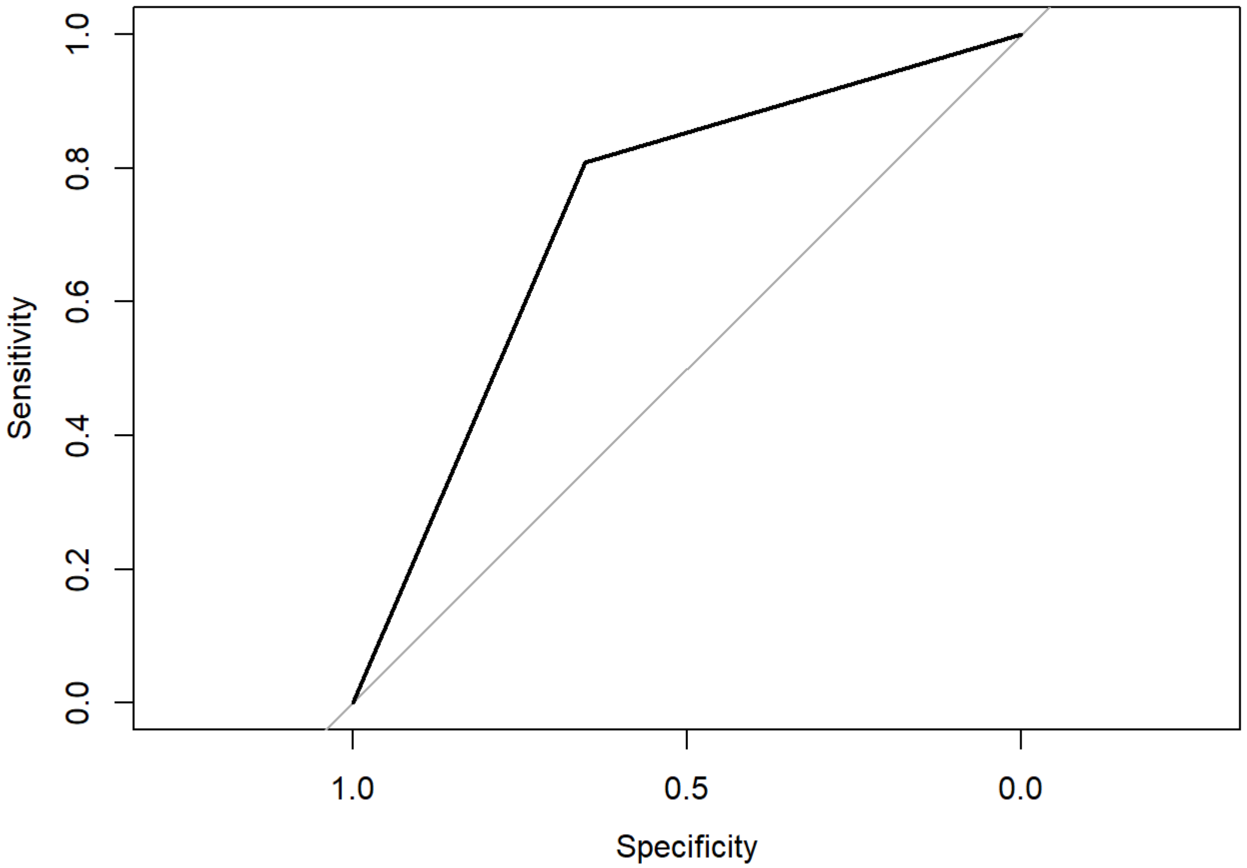
```
message("Test Error is ", round(mean(logit.pred != test.Y$target),2)*100, "%")
```

```
## Test Error is 27%
```

```
roc(test.Y$target, logit.pred, plot=TRUE)
```

```
## Setting levels: control = 0, case = 1
```

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



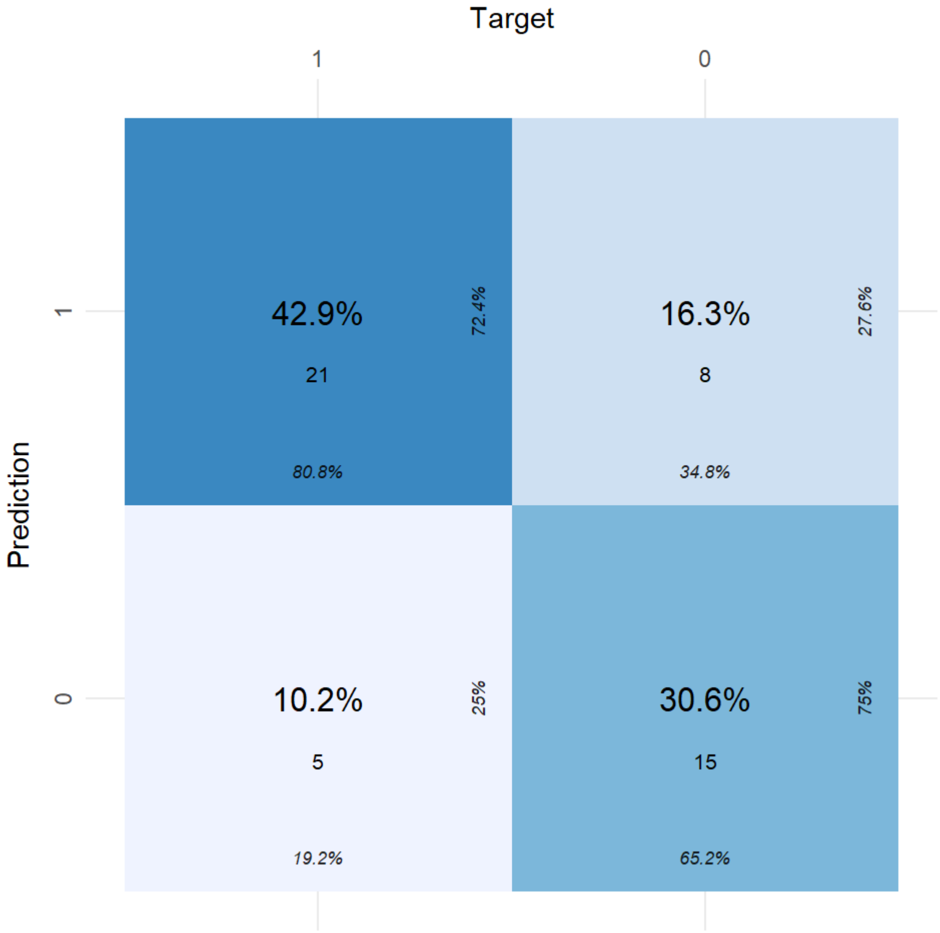
```
##
## Call:
## roc.default(response = test.Y$target, predictor = logit.pred,     plot = TRUE)
##
## Data: logit.pred in 23 controls (test.Y$target 0) < 26 cases (test.Y$target 1).
## Area under the curve: 0.7299
```

```
message("AUC: ", auc(test.Y$target, logit.pred))
```

```
## Setting levels: control = 0, case = 1
## Setting direction: controls < cases
```

```
## AUC: 0.729933110367893
```

```
plot_confusion_matrix(confusion_matrix(test.Y$target, logit.pred))
```



```
bag.fit <- bagging(formula = target ~ ., data = train, nbagg = 160, coob = TRUE,
  control = rpart.control(minsplit = 2, cp = 0)
)

bag.pred <- predict(bag.fit, newdata = test.X)
```

```
VI <- data.frame(var=names(heart[,-1]), imp=varImp(bag.fit))
VI_plot <- VI[order(VI$Overall, decreasing=TRUE),]
VI_plot
```

	var <chr>	Overall <dbl>
oldpeak	thalach	59.299643
thalach	thal	56.635545
cp	chol	53.686558
ca	cp	52.204492
thal	ca	43.421150
exang	fbs	42.446108
age	sex	32.725445

	var <chr>	Overall <dbl>
trestbps	target	30.041658
chol	trestbps	26.762765
slope	slope	17.193574

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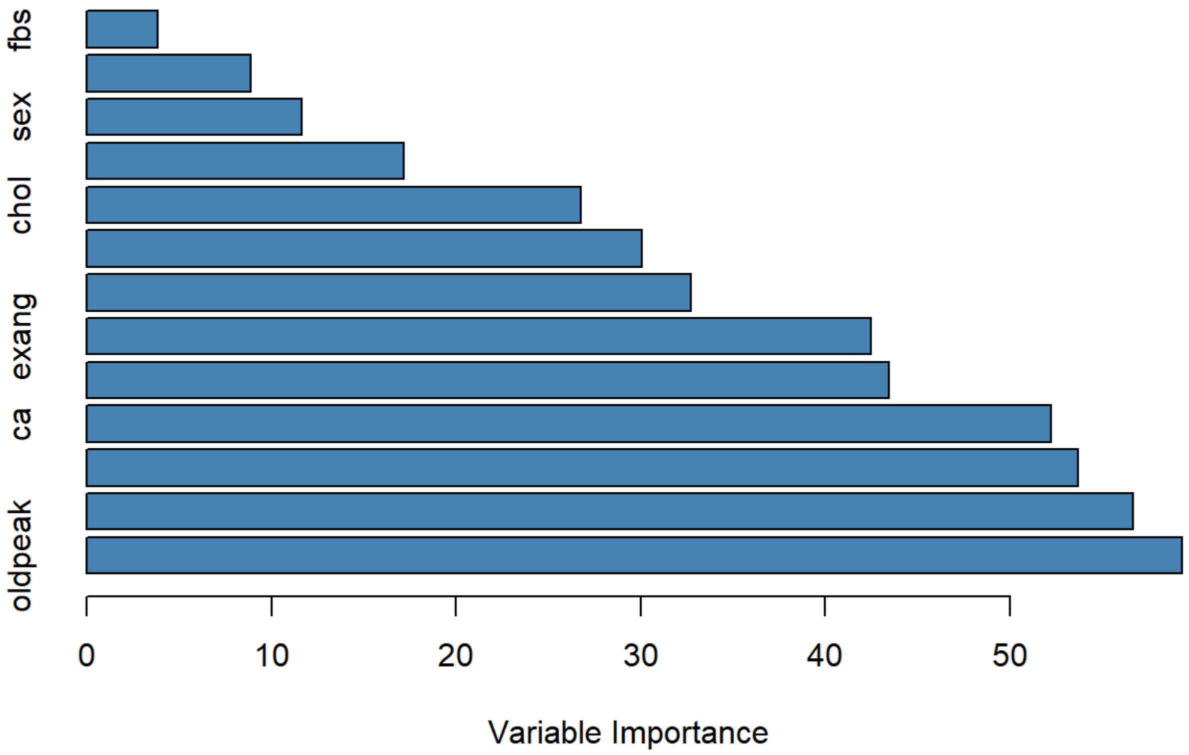
```
barplot(VI_plot$Overall,
        names.arg=rownames(VI_plot),
        horiz=TRUE,
        col='steelblue',
        xlab='Variable Importance')
```



```
heart <- heart[,c("target", "oldpeak", "thalach", "cp", "ca", "thal", "exang")]
sample <- sample(c(TRUE, FALSE), nrow(heart), replace=TRUE, prob=c(0.8,0.2))
train <- heart[sample, ]
test <- heart[!sample, ]

test.X <- test[2:7]
test.Y <- test[1]

train.X<-train[2:7]
train.Y<-train[1]
```

```
logit.fit <- glm(train$target ~ ., data=train, family = binomial)

logit.train <- predict(logit.fit, train.X, type="response")
logit.train <- ifelse(test=logit.train>0.5, yes=1, no=0)

logit.pred <- predict(logit.fit, test.X, type="response")
logit.pred <- ifelse(test=logit.pred>0.5, yes=1, no=0)

message("Train Error is ", round(mean(logit.train != train.Y$target),2)*100, "%")
```

```
## Train Error is 16%
```

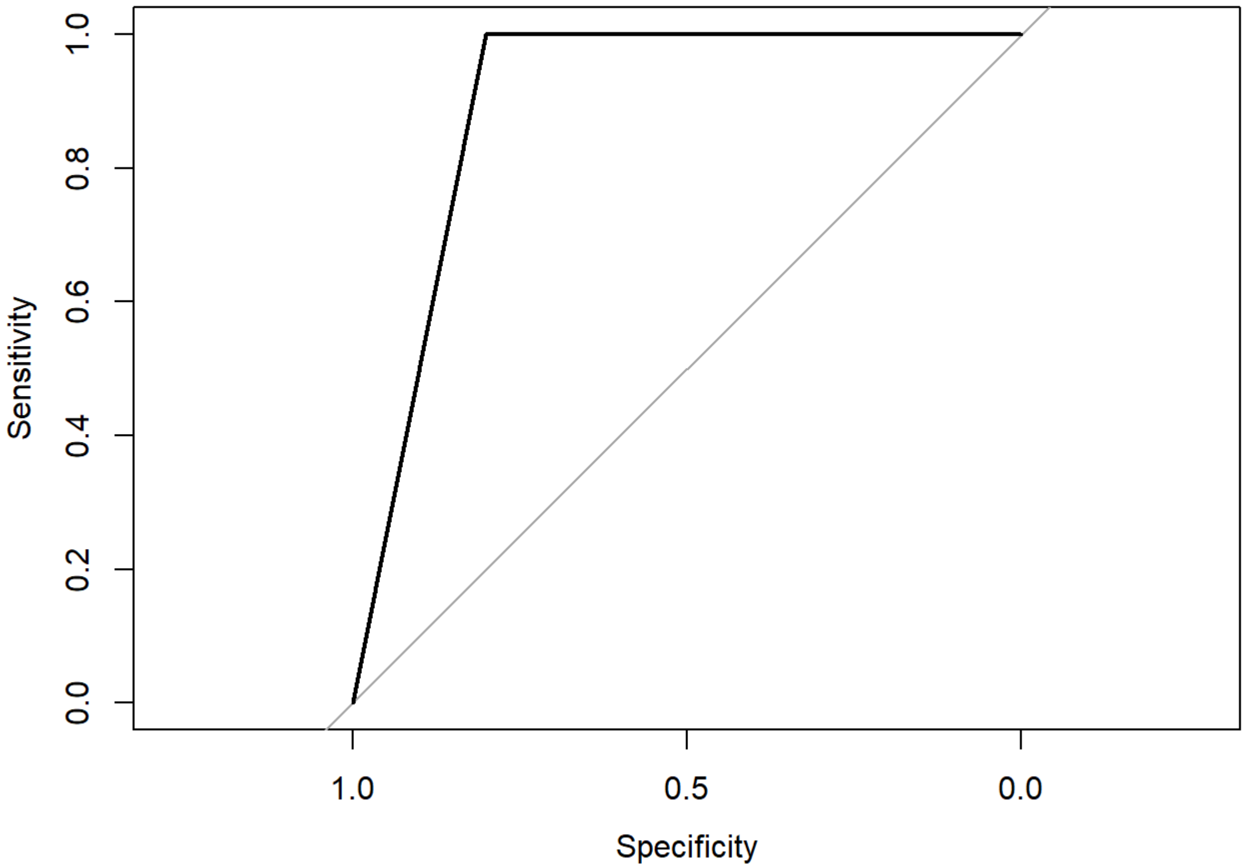
```
message("Test Error is ", round(mean(logit.pred != test.Y$target),2)*100, "%")
```

```
## Test Error is 10%
```

```
roc(test.Y$target, logit.pred, plot=TRUE)
```

```
## Setting levels: control = 0, case = 1
```

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



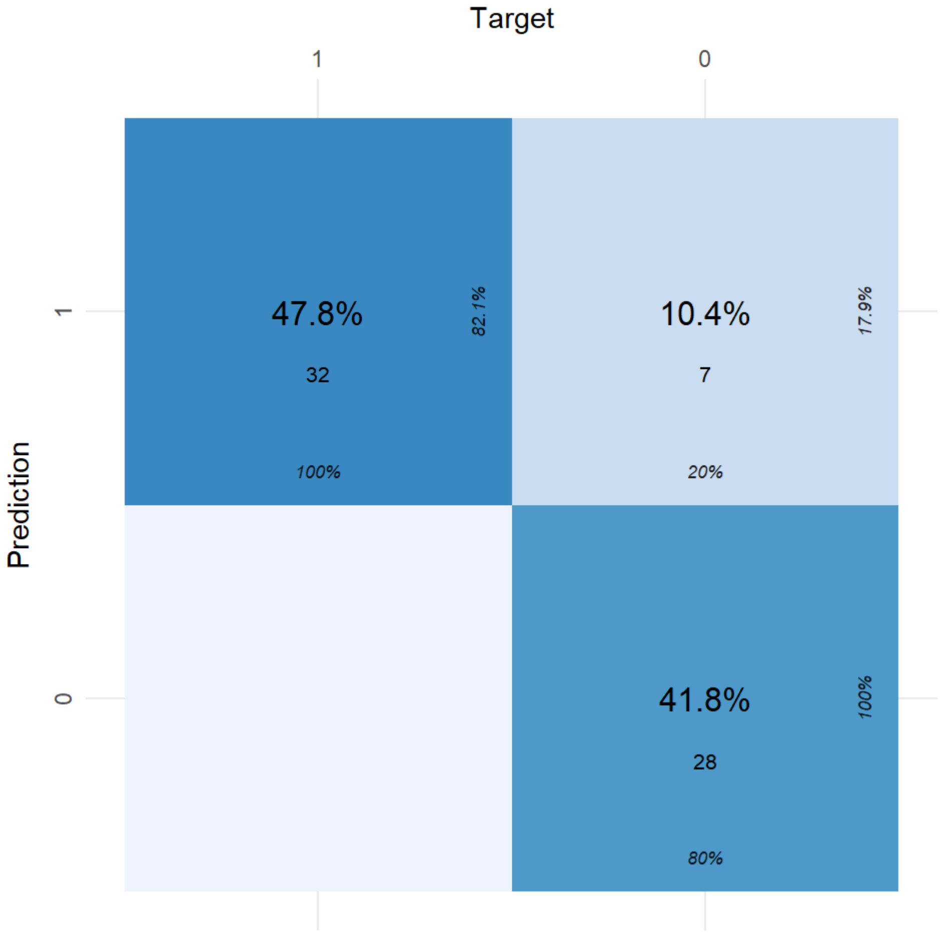
```
##
## Call:
## roc.default(response = test.Y$target, predictor = logit.pred,     plot = TRUE)
##
## Data: logit.pred in 35 controls (test.Y$target 0) < 32 cases (test.Y$target 1).
## Area under the curve: 0.9
```

```
message("AUC: ", auc(test.Y$target, logit.pred))
```

```
## Setting levels: control = 0, case = 1
## Setting direction: controls < cases
```

```
## AUC: 0.9
```

```
plot_confusion_matrix(confusion_matrix(test.Y$target, logit.pred))
```



Ecoli Data

```
head(ecoli)
```

	mcg <dbl>	gvh <dbl>	lip <dbl>	chg <dbl>	aac <dbl>	alm1 <dbl>	alm2 <dbl>	class <chr>
1	0.07	0.40	0.48	0.5	0.54	0.35	0.44	cp
2	0.56	0.40	0.48	0.5	0.49	0.37	0.46	cp
3	0.59	0.49	0.48	0.5	0.52	0.45	0.36	cp
4	0.23	0.32	0.48	0.5	0.55	0.25	0.35	cp
5	0.67	0.39	0.48	0.5	0.36	0.38	0.46	cp
6	0.29	0.28	0.48	0.5	0.44	0.23	0.34	cp

6 rows

```
unique(ecoli$class)
```

```
## [1] "cp"  "im"  "imS" "imL" "imU" "om"  "omL" "pp"
```

Unfortunately I don’t have time for this dataset, especially plotting every ROC curve. I’m really sorry.

Icu Data

```
icu <- read.csv("data/icu.csv")
head(icu)
```

	ID <int>	STA <int>	AGE <int>	SEX <int>	RACE <int>	SER <int>	CAN <int>	CRN <int>	INF <int>
1	8	0	27	1	1	0	0	0	1
2	12	0	59	0	1	0	0	0	0
3	14	0	77	0	1	1	0	0	0
4	28	0	54	0	1	0	0	0	1
5	32	0	87	1	1	1	0	0	1
6	38	0	69	0	1	0	0	0	1

6 rows | 1-10 of 22 columns

```
summary(icu)
```

```
##        ID             STA           AGE             SEX            RACE      
##  Min.   :  4.0   Min.   :0.0   Min.   :16.00   Min.   :0.00   Min.   :1.000  
##  1st Qu.:210.2   1st Qu.:0.0   1st Qu.:46.75   1st Qu.:0.00   1st Qu.:1.000  
##  Median :412.5   Median :0.0   Median :63.00   Median :0.00   Median :1.000  
##  Mean   :444.8   Mean   :0.2   Mean   :57.55   Mean   :0.38   Mean   :1.175  
##  3rd Qu.:671.8   3rd Qu.:0.0   3rd Qu.:72.00   3rd Qu.:1.00   3rd Qu.:1.000  
##  Max.   :929.0   Max.   :1.0   Max.   :92.00   Max.   :1.00   Max.   :3.000  
##       SER             CAN           CRN             INF            CPR       
##  Min.   :0.000   Min.   :0.0   Min.   :0.000   Min.   :0.00   Min.   :0.000  
##  1st Qu.:0.000   1st Qu.:0.0   1st Qu.:0.000   1st Qu.:0.00   1st Qu.:0.000  
##  Median :1.000   Median :0.0   Median :0.000   Median :0.00   Median :0.000  
##  Mean   :0.535   Mean   :0.1   Mean   :0.095   Mean   :0.42   Mean   :0.065  
##  3rd Qu.:1.000   3rd Qu.:0.0   3rd Qu.:0.000   3rd Qu.:1.00   3rd Qu.:0.000  
##  Max.   :1.000   Max.   :1.0   Max.   :1.000   Max.   :1.00   Max.   :1.000  
##       SYS             HRA              PRE            TYP       
##  Min.   : 36.0   Min.   : 39.00   Min.   :0.00   Min.   :0.000  
##  1st Qu.:110.0   1st Qu.: 80.00   1st Qu.:0.00   1st Qu.:0.000  
##  Median :130.0   Median : 96.00   Median :0.00   Median :1.000  
##  Mean   :132.3   Mean   : 98.92   Mean   :0.15   Mean   :0.735  
##  3rd Qu.:150.0   3rd Qu.:118.25   3rd Qu.:0.00   3rd Qu.:1.000  
##  Max.   :256.0   Max.   :192.00   Max.   :1.00   Max.   :1.000  
##       FRA             PO2             PH             PCO           BIC       
##  Min.   :0.000   Min.   :0.00   Min.   :0.000   Min.   :0.0   Min.   :0.000  
##  1st Qu.:0.000   1st Qu.:0.00   1st Qu.:0.000   1st Qu.:0.0   1st Qu.:0.000  
##  Median :0.000   Median :0.00   Median :0.000   Median :0.0   Median :0.000  
##  Mean   :0.075   Mean   :0.08   Mean   :0.065   Mean   :0.1   Mean   :0.075  
##  3rd Qu.:0.000   3rd Qu.:0.00   3rd Qu.:0.000   3rd Qu.:0.0   3rd Qu.:0.000  
##  Max.   :1.000   Max.   :1.00   Max.   :1.000   Max.   :1.0   Max.   :1.000  
##       CRE            LOC       
##  Min.   :0.00   Min.   :0.000  
##  1st Qu.:0.00   1st Qu.:0.000  
##  Median :0.00   Median :0.000  
##  Mean   :0.05   Mean   :0.125  
##  3rd Qu.:0.00   3rd Qu.:0.000  
##  Max.   :1.00   Max.   :2.000  
```

```
icu$STA <- as.factor(icu$STA)
icu$SEX <- as.factor(icu$SEX)
icu$RACE <- as.factor(icu$RACE)
icu$SER <- as.factor(icu$SER)
icu$CAN <- as.factor(icu$CAN)
icu$CRN <- as.factor(icu$CRN)
icu$INF <- as.factor(icu$INF)
icu$CPR <- as.factor(icu$CPR)
icu$PRE <- as.factor(icu$PRE)
icu$TYP <- as.factor(icu$TYP)
icu$FRA <- as.factor(icu$FRA)
icu$PO2 <- as.factor(icu$PO2)
icu$PH <- as.factor(icu$PH)
icu$PCO <- as.factor(icu$PCO)
icu$BIC <- as.factor(icu$BIC)
icu$CRE <- as.factor(icu$CRE)
icu$LOC <- as.factor(icu$LOC)
```

```
set.seed(4)
sample <- sample(c(TRUE, FALSE), nrow(icu), replace=TRUE, prob=c(0.8,0.2))
train <- icu[sample, ]
test <- icu[!sample, ]

test.X <- select(test, -STA)
test.Y <- test[2]

train.X<-select(train, -STA)
train.Y<-train[2]
```

```
logit.fit <- glm(train$STA ~ ., data=train, family = binomial)

logit.train <- predict(logit.fit, train.X, type="response")
logit.train <- ifelse(test=logit.train>0.5, yes=1, no=0)

logit.pred <- predict(logit.fit, test.X, type="response")
logit.pred <- ifelse(test=logit.pred>0.5, yes=1, no=0)

message("Train Error is ", round(mean(logit.train != train.Y$STA),2)*100, "%")
```

```
## Train Error is 14%
```

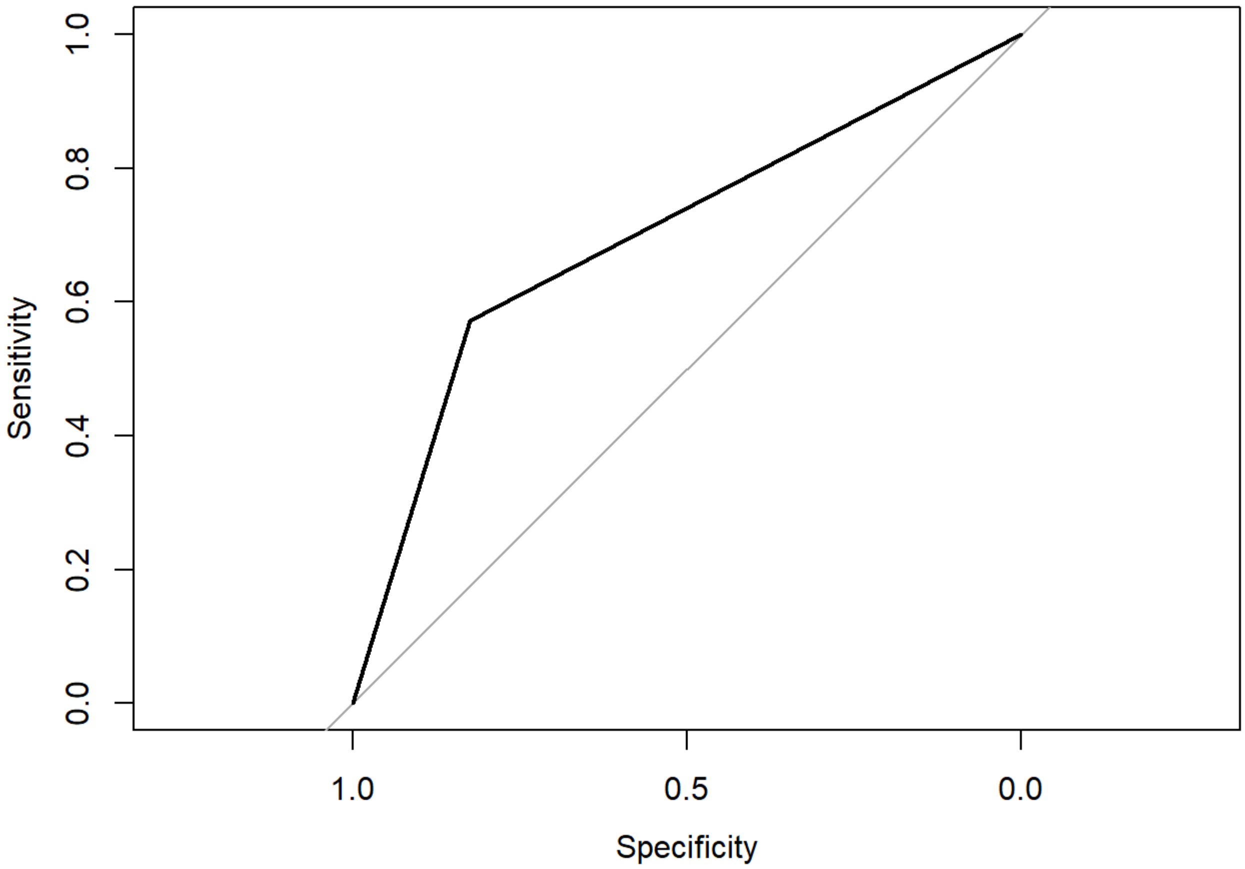
```
message("Test Error is ", round(mean(logit.pred != test.Y$STA),2)*100, "%")
```

```
## Test Error is 21%
```

```
roc(test.Y$STA, logit.pred, plot=TRUE)
```

```
## Setting levels: control = 0, case = 1
```

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



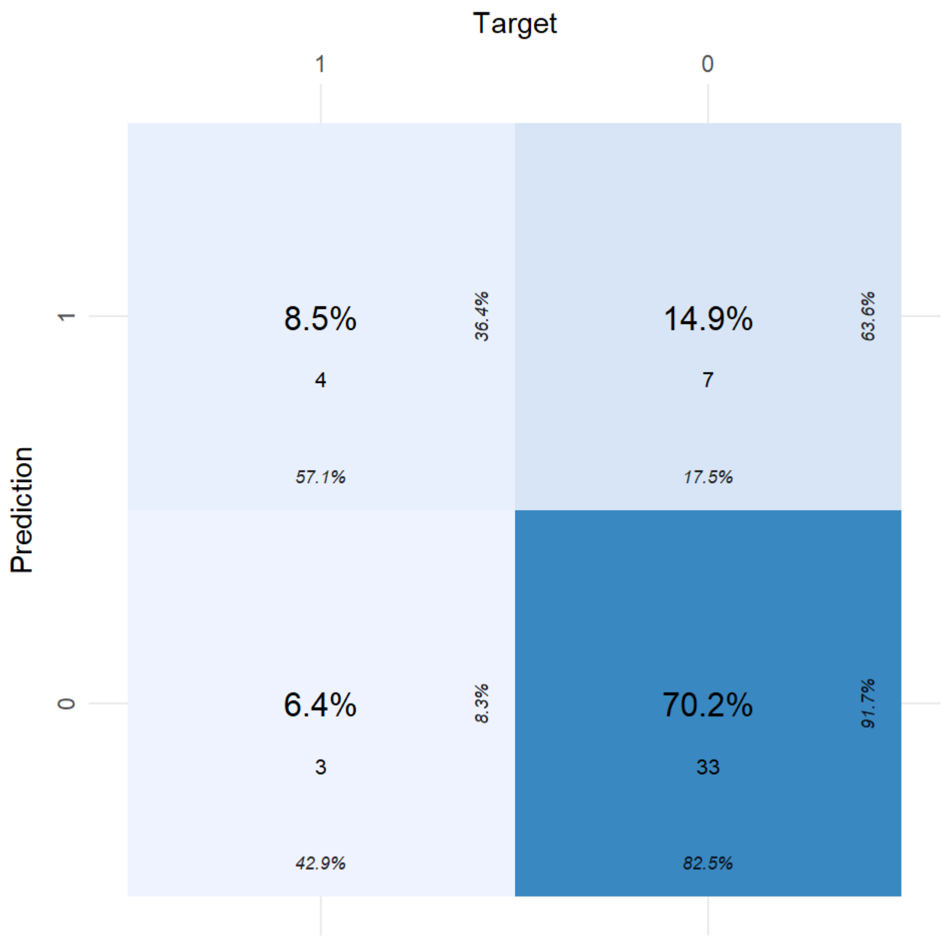
```
##
## Call:
## roc.default(response = test.Y$STA, predictor = logit.pred, plot = TRUE)
##
## Data: logit.pred in 40 controls (test.Y$STA 0) < 7 cases (test.Y$STA 1).
## Area under the curve: 0.6982
```

```
message("AUC: ", auc(test.Y$STA, logit.pred))
```

```
## Setting levels: control = 0, case = 1
## Setting direction: controls < cases
```

```
## AUC: 0.698214285714286
```

```
plot_confusion_matrix(confusion_matrix(test.Y$STA, logit.pred))
```



```
bag.fit <- bagging(formula = STA ~ ., data = train, nbagg = 160, coob = TRUE,
  control = rpart.control(minsplit = 2, cp = 0)
)

bag.pred <- predict(bag.fit, newdata = test.X)
```

```
VI <- data.frame(var=names(icu[,-1]), imp=varImp(bag.fit))
VI_plot <- VI[order(VI$Overall, decreasing=TRUE),]
VI_plot
```

	var <chr>	**Overall** <dbl>
ID	CPR	25.7476454
SYS	CRE	24.5015218
AGE	STA	22.3588908
HRA	INF	17.5158010
LOC	HRA	13.7341788
TYP	LOC	8.8356303
CRN	CAN	6.9789915

	var	Overall
	<chr>	<dbl>
SER	PCO	6.5927578
SEX	BIC	4.1431219
INF	SYS	3.9297404

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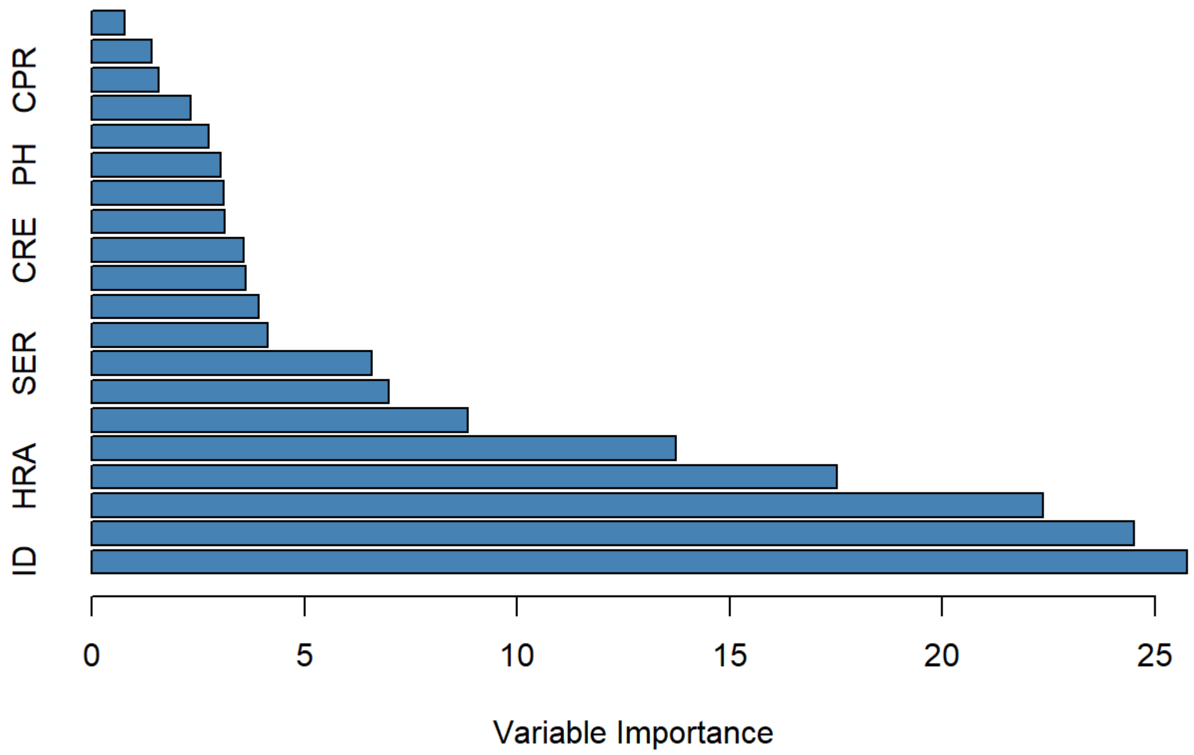
```
barplot(VI_plot$Overall,
        names.arg=rownames(VI_plot),
        horiz=TRUE,
        col='steelblue',
        xlab='Variable Importance')
```



```
set.seed(4)
icu <- icu[,c("STA", "SYS", "AGE", "ID", "HRA", "LOC", "TYP", "SER")]
sample <- sample(c(TRUE, FALSE), nrow(icu), replace=TRUE, prob=c(0.8,0.2))
train <- icu[sample, ]
test <- icu[!sample, ]

test.X <- test[2:8]
test.Y <- test[1]

train.X<-train[2:8]
train.Y<-train[1]
```

```
logit.fit <- glm(train$STA ~ ., data=train, family = binomial)

logit.train <- predict(logit.fit, train.X, type="response")
logit.train <- ifelse(test=logit.train>0.5, yes=1, no=0)

logit.pred <- predict(logit.fit, test.X, type="response")
logit.pred <- ifelse(test=logit.pred>0.5, yes=1, no=0)

message("Train Error is ", round(mean(logit.train != train.Y$STA),2)*100, "%")
```

```
## Train Error is 13%
```

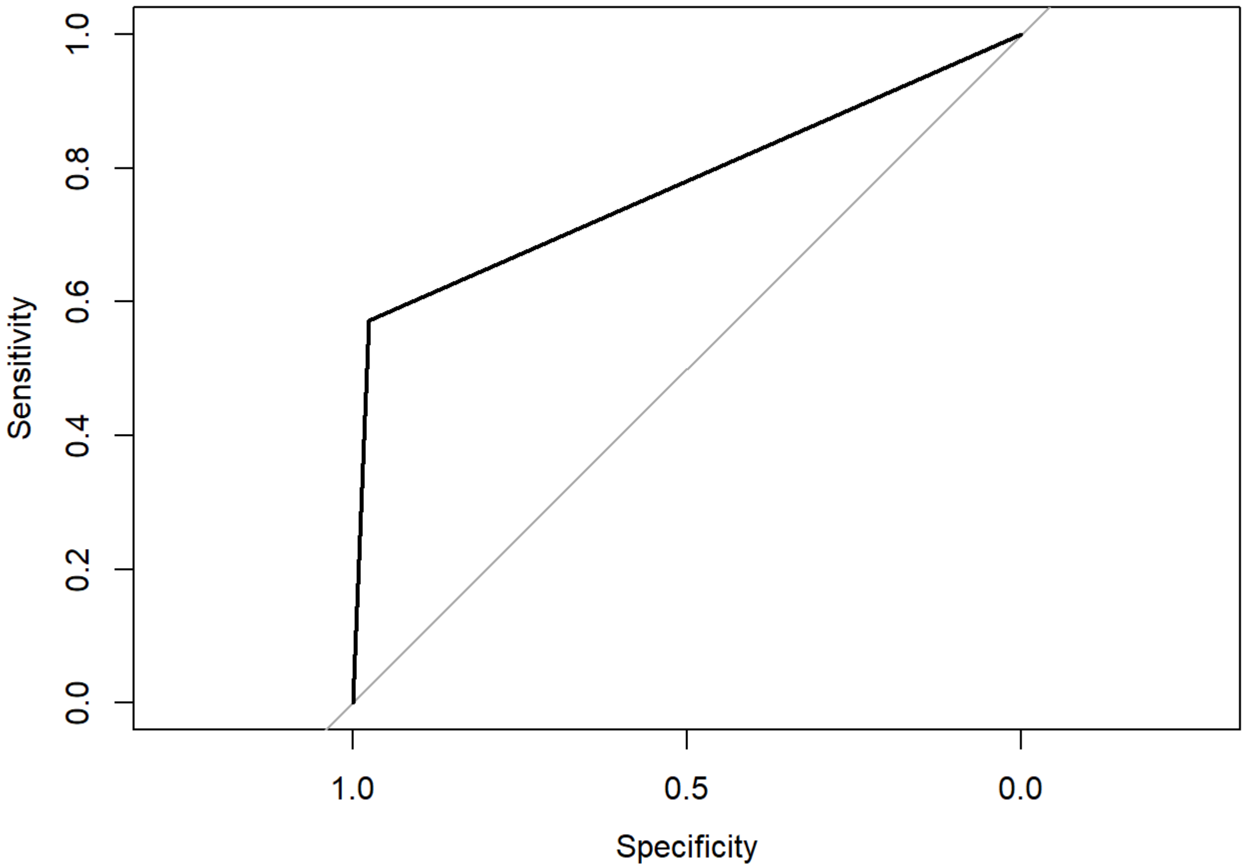
```
message("Test Error is ", round(mean(logit.pred != test.Y$STA),2)*100, "%")
```

```
## Test Error is 9%
```

```
roc(test.Y$STA, logit.pred, plot=TRUE)
```

```
## Setting levels: control = 0, case = 1
```

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



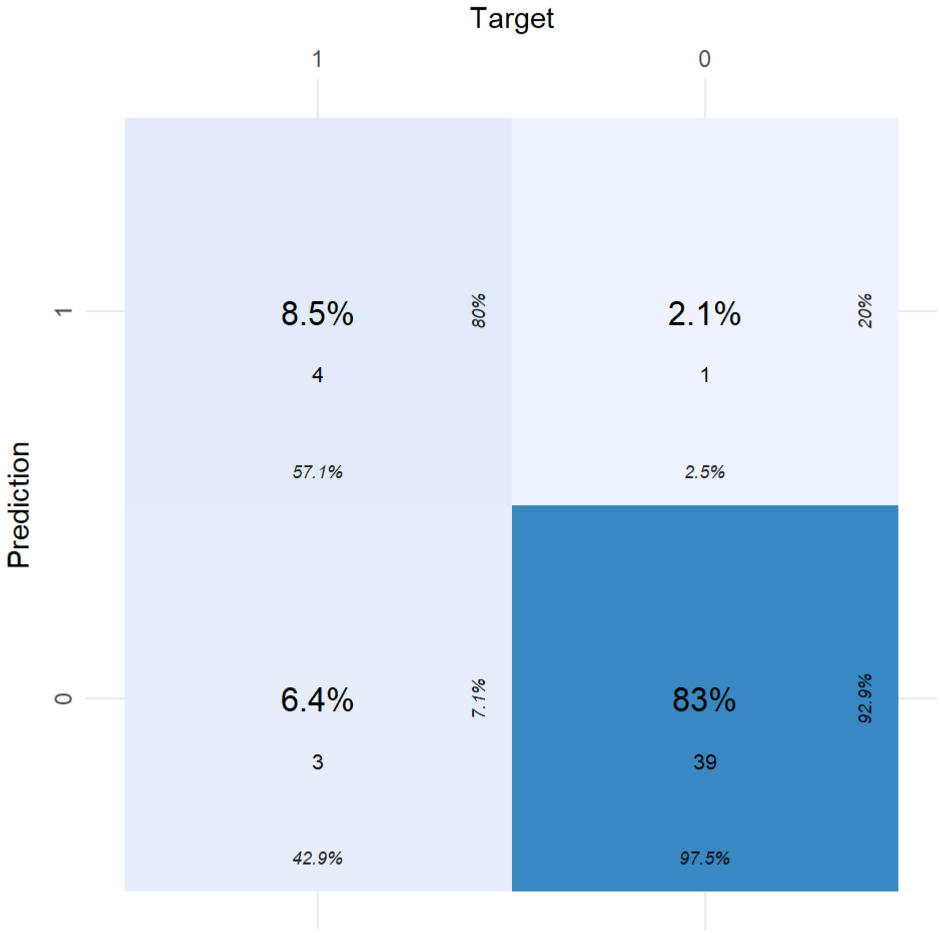
```
##
## Call:
## roc.default(response = test.Y$STA, predictor = logit.pred, plot = TRUE)
##
## Data: logit.pred in 40 controls (test.Y$STA 0) < 7 cases (test.Y$STA 1).
## Area under the curve: 0.7732
```

```
message("AUC: ", auc(test.Y$STA, logit.pred))
```

```
## Setting levels: control = 0, case = 1
## Setting direction: controls < cases
```

```
## AUC: 0.773214285714286
```

```
plot_confusion_matrix(confusion_matrix(test.Y$STA, logit.pred))
```



Results

So in both cases we used bagging in order to find the most important features and prevent overfitting (before bagging, there was low training error, but high test error).