Doing Data Science in R

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INFORMS Code & Data Boot Camp

Intro

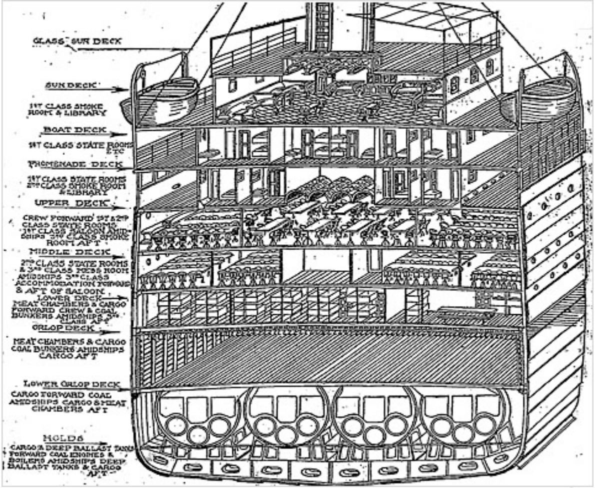
In this project we'll do a simple data science project based on the Kaggle Titanic Challenge.

Overview

- Data Exploration
- Data Cleaning
- Training a Model
- Fitting a Model

Disclaimer: Draws heavily from http://statsguys.wordpress.com/2014/01/03/first-post/ and https://github.com/wehrley/wehrley.github.io/blob/master/SOUPTONUTS.md.

Who survives the Titanic?



Getting started

- Download the CSV and R script file from http://bit.ly/USFCodeCamp2014
- Open the R script
- Set your working directory

The data

Loading the data

```
titanic <- read.csv('titanic.csv', header = TRUE,
                    na.strings=c('NA', ''))

titanic$Survived <- factor(titanic$Survived,
                           labels=c('No', 'Yes'))
titanic$Pclass <- factor(titanic$Pclass)
```

Quick look at the data

```
names(titanic)
```

```
##  [1] "PassengerId" "Survived"    "Pclass"      "Name"        "Sex"
##  [6] "Age"         "SibSp"       "Parch"       "Ticket"      "Fare"
## [11] "Cabin"       "Embarked"
```

Also look at:

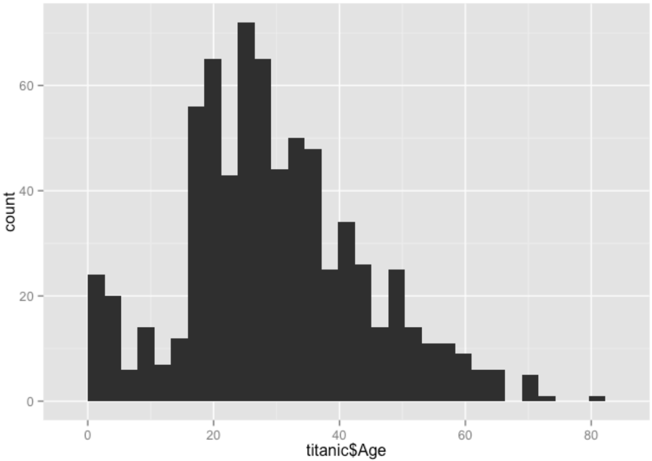
```
head(titanic)
summary(titanic)
str(titanic)
```

Variable Meanings

Variable	Meaning
survival	Survival
	(0 = No; 1 = Yes)
pclass	Passenger Class
	(1 = 1st; 2 = 2nd; 3 = 3rd)
name	Name
sex	Sex
age	Age
sibsp	Number of Siblings/Spouses Aboard
parch	Number of Parents/Children Aboard
ticket	Ticket Number
fare	Passenger Fare
cabin	Cabin
embarked	Port of Embarkation
	(C = Cherbourg; Q = Queenstown; S = Southampton)

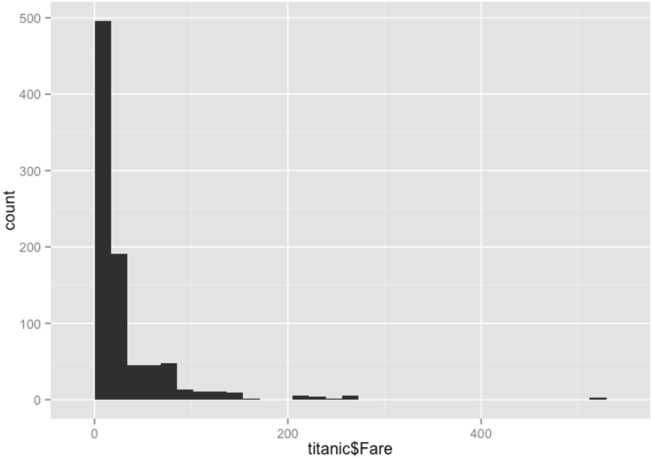
Plotting age

```
require(ggplot2)
qplot(titanic$Age, geom='histogram')
```



Plot Fare

```
qplot(titanic$Fare, geom='histogram')
```



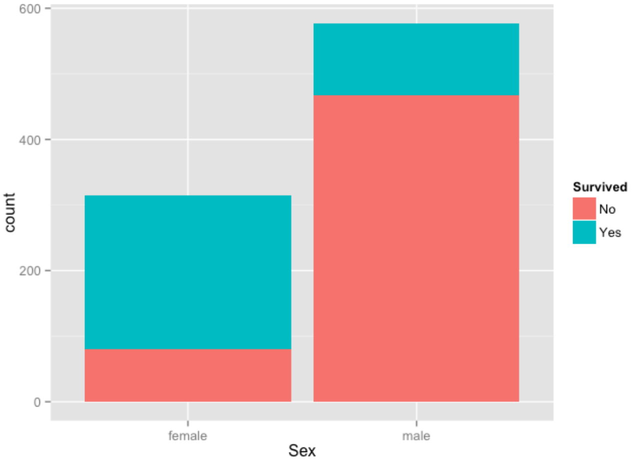
Survival by gender

```r
table(titanic$Survived, titanic$Sex)
```

```
##
##         female male
##   No        81  468
##   Yes      233  109
```

Survival by gender plot

```
ggplot(titanic, aes(x=Sex, fill=Survived))+geom_histogram()
```



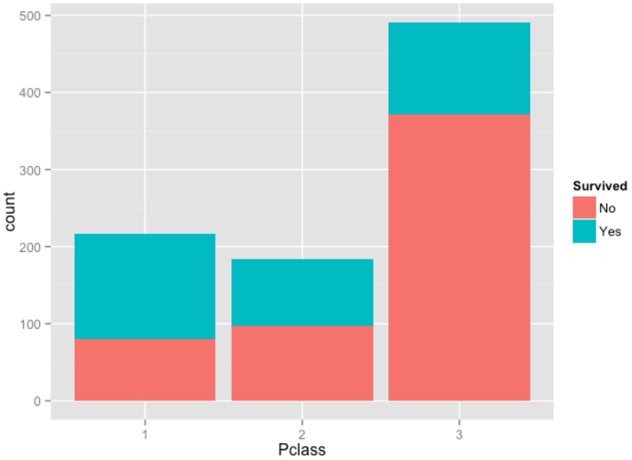
Survival by Passenger Class

```
table(titanic$Survived, titanic$Pclass)
```

```
##
##          1   2   3
##   No    80  97 372
##   Yes  136  87 119
```

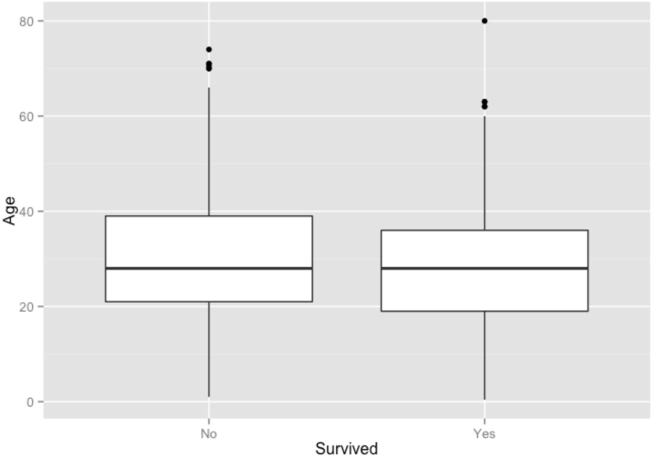
Survival by Passenger Class plot

```
ggplot(titanic, aes(x=Pclass, fill=Survived))+
  geom_histogram(binwidth=1)
```



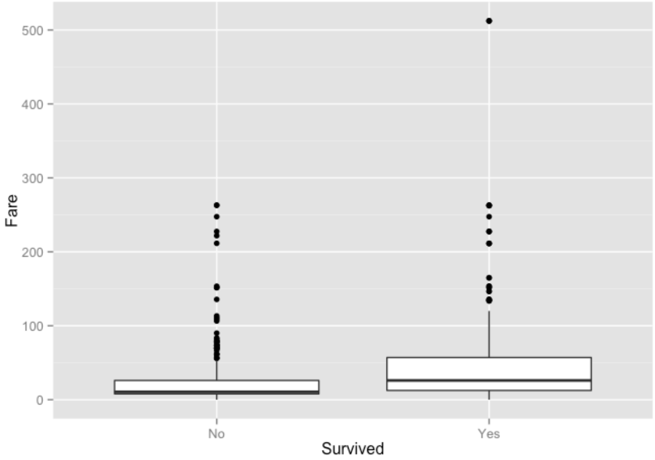
Survival by Age

```
ggplot(titanic, aes(x=Survived, y=Age))+geom_boxplot()
```



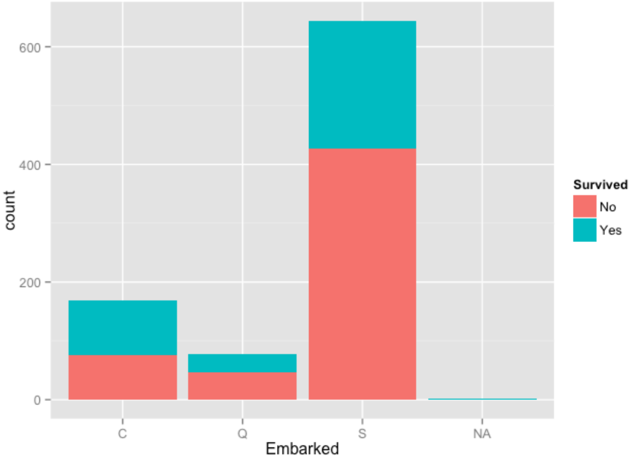
Survival by Fare

```r
ggplot(titanic, aes(x=Survived, y=Fare))+geom_boxplot()
```



Survival by Port

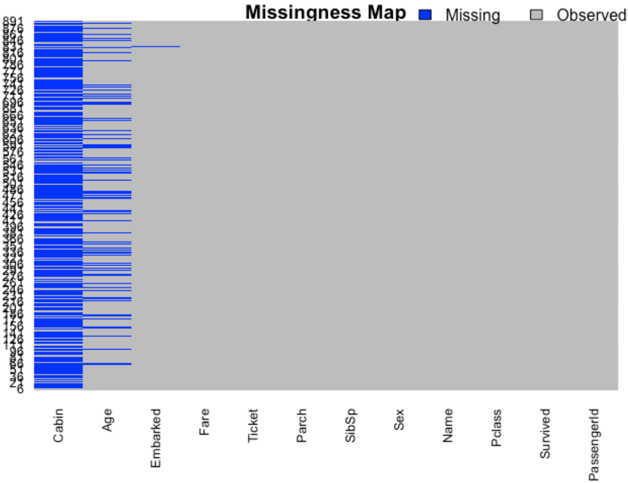
```
ggplot(titanic, aes(x=Embarked, fill=Survived))+geom_histogram()
```



Thoughts?

Thoughts?

```r
require(Amelia)
missmap(titanic, col=c('blue', 'grey'))
```



Cleaning the data

Missing values

Clearly we need to work on the missing values. Let's ignore `Cabin` and drop passengers missing `Embarked`.

```
names(titanic)
```

```
##  [1] "PassengerId" "Survived"    "Pclass"      "Name"        "Sex"
##  [6] "Age"         "SibSp"       "Parch"       "Ticket"      "Fare"
## [11] "Cabin"       "Embarked"
```

```
titanic <- titanic[, -11]
titanic <- titanic[!is.na(titanic$Embarked),]
```

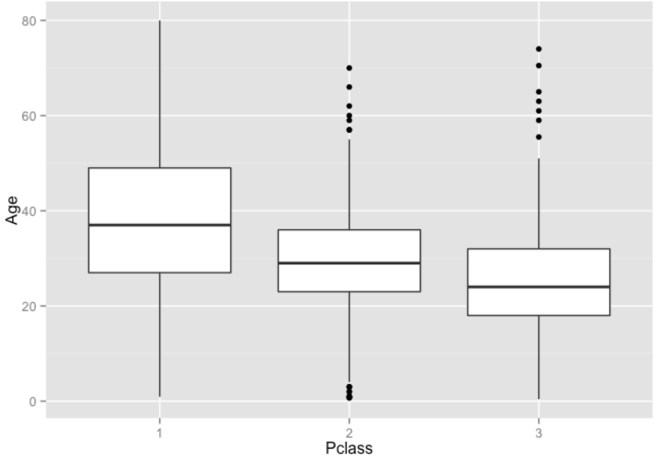
But we definitely need to fix `Age`

```
length(titanic[is.na(titanic$Age),'Age'])/dim(titanic)[1]
```

```
## [1] 0.199
```

Does Passenger Class Help?

```
ggplot(titanic, aes(x=Pclass, y=Age))+geom_boxplot()
```



maybe...

What about the passenger names?

```r
rrows <- c(766, 490, 509, 384, 34,
           126, 887, 815, 856, 851)
titanic[rrows, 'Name']
```

```
##  [1] Brewe, Dr. Arthur Jackson
##  [2] Hagland, Mr. Konrad Mathias Reiersen
##  [3] Lang, Mr. Fang
##  [4] Plotcharsky, Mr. Vasil
##  [5] Wheadon, Mr. Edward H
##  [6] McMahon, Mr. Martin
##  [7] Johnston, Miss. Catherine Helen "Carrie"
##  [8] Fry, Mr. Richard
##  [9] Daly, Mr. Peter Denis
## [10] Boulos, Miss. Nourelain
## 891 Levels: Abbing, Mr. Anthony ... Zimmerman, Mr. Leo
```

Passenger Titles

The following titles have at least one person missing `Age`

- Dr.
- Master.
- Miss.
- Mr.
- Mrs.

These titles are clearly correlated with passenger age.

How we're going to do this

- Find indexes of Names that contain `Dr.`

```
dr <- grep('Dr.', titanic$Name, fixed=TRUE); dr
```

```
## [1] 245 317 398 632 660 766 796
```

- Calculate median age for those passengers

```
m_age <- median(titanic[dr, 'Age'], na.rm=TRUE); m_age
```

```
## [1] 46.5
```

- Select indexes that are both missing and have `Dr.`

```
dr[dr %in% which(is.na(titanic$Age))]
```

```
## [1] 766
```

Impute Age with median age for titles

```r
titles <- c('Dr.', 'Master.', 'Miss.', 'Mr.', 'Mrs.')
```

```r
for(title in titles){
  passengers <- grep(title, titanic$Name, fixed=TRUE)
    median_age <- median(titanic[passengers, 'Age'], na.rm=TRUE)
    titanic[passengers[passengers %in% which(is.na(titanic$Age))],
          'Age'] <- median_age
}
```

Adding features: Child?

Add a feature to indicate if the passenger is a child (<12)

```
titanic$Child <- 'No'
titanic[titanic$Age <= 12, 'Child'] <- 'Yes'
titanic$Child <- factor(titanic$Child)
summary(titanic$Child)
```

```
##  No Yes
## 816  73
```

Adding features: Mother?

Add a feature to indicate if the passenger is a mother. Use the variable `Parch` and title `'Mrs.'`

Adding features: Mother?

Add a feature to indicate if the passenger is a mother. Use the variable `Parch` and title `'Mrs.'`

```
titanic$Mother <- 'No'
mrs <- grep('Mrs.', titanic$Name, fixed=TRUE)
parent <- which(titanic$Parch > 0)
titanic[mrs %in% parent, 'Mother'] <- 'Yes'
titanic$Mother <- factor(titanic$Mother)
summary(titanic$Mother)
```

```
##  No Yes
## 493 396
```

Divide the data

Divide the data into training and testing sets.

We'll use the `caret` package for this.

```
require(caret)
require(pROC)
require(e1071)
```

http://caret.r-forge.r-project.org/

Can be used as a power tool to test and train models.

Make a training and testing set

```r
train_index <- createDataPartition(y=titanic$Survived,
                                   p=0.80,
                                   list=FALSE)

train <- titanic[ train_index,]
test  <- titanic[-train_index,]

dim(train)
```

```
## [1] 712  13
```

```r
dim(test)
```

```
## [1] 177  13
```

Build some models!

Generalized Linear Model (logistic regression)

```
train.glm <- glm(Survived ~ Pclass + Sex + Age +
                   Child + Sex*Pclass + Mother +
                   Embarked + Fare,
                 family = binomial,
                 data = train)
```

Model summary

```
train.glm
```

```
##
## Call:  glm(formula = Survived ~ Pclass + Sex + Age + Child + Sex + Pclass +
##     Mother + Embarked + Fare, family = binomial, data = train)
##
## Coefficients:
## (Intercept)      Pclass2      Pclass3      Sexmale          Age     ChildYes
##    3.182712    -0.593098    -2.127109    -2.506753    -0.020691     0.965256
##   MotherYes    EmbarkedQ    EmbarkedS         Fare
##    0.093608     0.058169    -0.671614     0.000492
##
## Degrees of Freedom: 711 Total (i.e. Null);  702 Residual
## Null Deviance:       947
## Residual Deviance: 637   AIC: 657
```

Anova

```r
anova(train.glm, test='Chisq')
```

```
## Analysis of Deviance Table
##
## Model: binomial, link: logit
##
## Response: Survived
##
## Terms added sequentially (first to last)
##
##
##          Df Deviance Resid. Df Resid. Dev Pr(>Chi)
## NULL                       711        947
## Pclass    2     86.8       709        860  < 2e-16 ***
## Sex       1    188.9       708        671  < 2e-16 ***
## Age       1     19.6       707        652  9.5e-06 ***
## Child     1      4.9       706        647    0.026 *
## Mother    1      0.1       705        647    0.760
## Embarked  2      9.7       703        637    0.008 **
## Fare      1      0.1       702        637    0.822
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Set up caret to train models for us

This just reduces repeated typing later

```
cv.ctrl <- trainControl(method = 'repeatedcv',
                        repeats = 3,
                        summaryFunction = twoClassSummary,
                        classProbs = TRUE)
```

Train glm with caret

```
glm.train <- train(Survived ~ Pclass + Sex +
                     Age + Child + Embarked,
                   data = train,
                   method = 'glm',
                   metric = 'ROC',
                   trControl = cv.ctrl)
```

Check results

```
glm.train
```

```
## Generalized Linear Model
##
## 712 samples
##  12 predictors
##   2 classes: 'No', 'Yes'
##
## No pre-processing
## Resampling: Cross-Validated (10 fold, repeated 3 times)
##
## Summary of sample sizes: 641, 641, 640, 641, 640, 641, ...
##
## Resampling results
##
##   ROC  Sens  Spec  ROC SD  Sens SD  Spec SD
##   0.8  0.9   0.7   0.05    0.06     0.08
##
##
```

More details

```r
summary(glm.train)
```

```
##
## Call:
## NULL
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -2.671  -0.728  -0.362   0.641   2.475
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  3.27714    0.48035    6.82  9.0e-12 ***
## Pclass2     -0.62824    0.29361   -2.14    0.032 *
## Pclass3     -2.17345    0.28058   -7.75  9.5e-15 ***
## Sexmale     -2.51053    0.21020  -11.94  < 2e-16 ***
## Age         -0.02083    0.00975   -2.14    0.033 *
## ChildYes     0.97452    0.41203    2.37    0.018 *
## EmbarkedQ    0.05882    0.40999    0.14    0.886
## EmbarkedS   -0.67022    0.26379   -2.54    0.011 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 947.02  on 711  degrees of freedom
## Residual deviance: 637.24  on 704  degrees of freedom
## AIC: 653.2
##
## Number of Fisher Scoring iterations: 5
```

Random forest model

Let's try the method known as *random forests*.

```
set.seed(42)
rf.train <- train(Survived ~ Pclass + Sex +
                    Age + Child + Embarked,
                  data = train,
                  method = 'rf',
                  metric = 'ROC',
                  trControl = cv.ctrl)
```

Random forests results

```
rf.train
```

```
## Random Forest
##
## 712 samples
##  12 predictors
##   2 classes: 'No', 'Yes'
##
## No pre-processing
## Resampling: Cross-Validated (10 fold, repeated 3 times)
##
## Summary of sample sizes: 641, 641, 641, 641, 641, 641, ...
##
## Resampling results across tuning parameters:
##
##   mtry  ROC  Sens  Spec  ROC SD  Sens SD  Spec SD
##   2     0.9  1     0.6   0.04    0.03     0.09
##   4     0.9  0.9   0.6   0.05    0.03     0.09
##   7     0.8  0.9   0.7   0.06    0.05     0.1
##
## ROC was used to select the optimal model using  the largest value.
## The final value used for the model was mtry = 2.
```

Compare performance

Make our predictions

```r
glm.pred <- predict(glm.train, test)
rf.pred  <- predict(rf.train, test)

glm.prob <- predict(glm.train, test, type='prob')
rf.prob  <- predict(rf.train, test, type='prob')
```

glm prediction results

```r
confusionMatrix(glm.pred, test$Survived)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction No Yes
##        No  95  24
##        Yes 14  44
##
##                Accuracy : 0.785
##                  95% CI : (0.717, 0.843)
##     No Information Rate : 0.616
##     P-Value [Acc > NIR] : 1.07e-06
##
##                   Kappa : 0.533
##  Mcnemar's Test P-Value : 0.144
##
##             Sensitivity : 0.872
##             Specificity : 0.647
##          Pos Pred Value : 0.798
##          Neg Pred Value : 0.759
##              Prevalence : 0.616
##          Detection Rate : 0.537
##    Detection Prevalence : 0.672
##       Balanced Accuracy : 0.759
##
##        'Positive' Class : No
##
```

randomForest results

```r
confusionMatrix(rf.pred, test$Survived)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  No Yes
##        No  102  26
##        Yes   7  42
##
##                Accuracy : 0.814
##                  95% CI : (0.748, 0.868)
##     No Information Rate : 0.616
##     P-Value [Acc > NIR] : 1.06e-08
##
##                   Kappa : 0.584
##  Mcnemar's Test P-Value : 0.00173
##
##             Sensitivity : 0.936
##             Specificity : 0.618
##          Pos Pred Value : 0.797
##          Neg Pred Value : 0.857
##              Prevalence : 0.616
##          Detection Rate : 0.576
##    Detection Prevalence : 0.723
##       Balanced Accuracy : 0.777
##
##        'Positive' Class : No
##
```

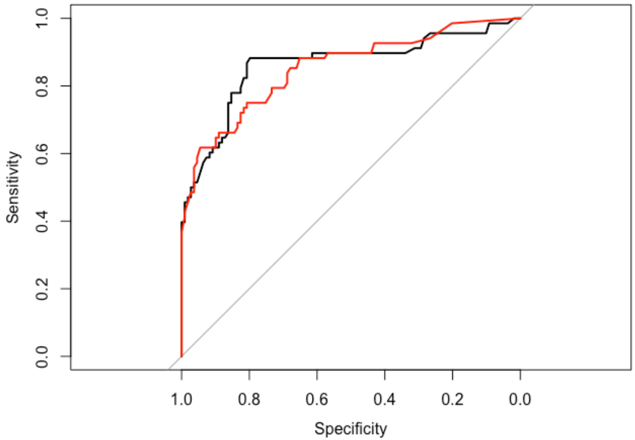
pROC objects for ROC curves

```
glm.ROC <- roc(response = test$Survived,
               predictor = glm.prob$Yes,
               levels = levels(test$Survived))

rf.ROC  <- roc(response = test$Survived,
               predictor = rf.prob$Yes,
               levels = levels(test$Survived))
```

ROC Plot

```
plot(glm.ROC)
plot(rf.ROC, add=TRUE, col="red")
```



Thanks!