Machine Learning from Titanic Disaster

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Contents

Objective

This dataset contain the data related to the passengers of the Titanic. The goal is to see if we are able to build a model that can predict whether or not a passenger would survive. The `Survived` column of this dataset reflects if they really survived or not (`1`: survived, and `0`: didn't survive).

1. Load the attached csv file into your Markdown accounting for the missing values.
2. Preprocess the data.

- Check for the missing values for each variable.
- Use `missmap()` to visualize the missing values.
- Reasonably ignore variables that probably do not affect the predictions.
- Impute the missing values in the numeric (continuous) variables. Only `Age` here.
- Remove any of the rows with `NA` in their categorical variables (any categorical variable that is left in your data after leaving the unnecessary ones out).

3. Split the data up into the training and test set. (`set.seed = 1`).

- Sample 100 rows from the data and use as your test set. Use the rest as your training set.

4. Fit a logistic regression model onto the training set

- Fit and summarize the model to predict `Survived` as a function of all other remaining variables.
- Use `anova()` to see the effect of each variable on the residual deviance.
- Obtain pseudo-R2 of the model, e.g., McFadden R2.

5. Evaluate your model on the test set.

- Calculate the misclassification error on your test set with `threshold = 0.5`
- the accuracy result your obtained depends on the test set – so, now re-estimate the accuracy with a 10-fold CV
- Compute the confusion matrix for the model with the test set.
- Use library `ROCR` to plot ROC curve and also obtain the AUC of your model.

6. Redo the last two steps with only `Pclass` and `Age`.

- At last, plot the ROC curve from the two models on the same figure. What do you conclude?

Import Required Libraries and Tools

```r
library(caret)
```

```
## Loading required package: ggplot2

## Loading required package: lattice
```

```r
library(Amelia)
```

```
## Loading required package: Rcpp

## ##
## ## Amelia II: Multiple Imputation
## ## (Version 1.8.1, built: 2022-11-18)
## ## Copyright (C) 2005-2023 James Honaker, Gary King and Matthew Blackwell
## ## Refer to http://gking.harvard.edu/amelia/ for more information
## ##
```

```r
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
```

```r
library(boot)
```

```
##
## Attaching package: 'boot'

## The following object is masked from 'package:lattice':
##
##     melanoma
```

```r
library(ROCR)
library(pscl)
```

```
## Classes and Methods for R developed in the
## Political Science Computational Laboratory
## Department of Political Science
## Stanford University
## Simon Jackman
## hurdle and zeroinfl functions by Achim Zeileis
```

1. Import/read the data.

Load the attached csv file into your Markdown accounting for the missing values.

Import the csv file

Let's import the training data here:

```
training.data.raw <- read.csv('Titanic.csv', na.strings=c(""))
# training.data.raw <- read.csv('Titanic.csv')

head(training.data.raw)
```

```
##   PassengerId Survived Pclass
## 1           1        0      3
## 2           2        1      1
## 3           3        1      3
## 4           4        1      1
## 5           5        0      3
## 6           6        0      3
##                                                  Name    Sex Age SibSp Parch
## 1                             Braund, Mr. Owen Harris   male  22     1     0
## 2 Cumings, Mrs. John Bradley (Florence Briggs Thayer) female  38     1     0
## 3                              Heikkinen, Miss. Laina female  26     0     0
## 4        Futrelle, Mrs. Jacques Heath (Lily May Peel) female  35     1     0
## 5                            Allen, Mr. William Henry   male  35     0     0
## 6                                    Moran, Mr. James   male  NA     0     0
##             Ticket    Fare Cabin Embarked
## 1        A/5 21171  7.2500  <NA>        S
## 2         PC 17599 71.2833   C85        C
## 3 STON/O2. 3101282  7.9250  <NA>        S
## 4           113803 53.1000  C123        S
## 5           373450  8.0500  <NA>        S
## 6           330877  8.4583  <NA>        Q
```

2. Preprocess the data.

Missing values

- Check for the missing values for each variable.

Now we need to check for missing values and look how many unique values there are for each variable using the `sapply()` function to apply `is.na()` on to all variables in the data.

```
# sapply(data, function(x){})
```

```
sapply(training.data.raw,function(x) sum(is.na(x)))
```

```
## PassengerId    Survived      Pclass        Name         Sex         Age
##           0           0           0           0           0         177
##       SibSp       Parch      Ticket        Fare       Cabin    Embarked
##           0           0           0           0         687           2
```

```r
sapply(training.data.raw, function(x) length(unique(x)))
```

```
## PassengerId    Survived      Pclass        Name         Sex         Age
##         891           2           3         891           2          89
##       SibSp       Parch      Ticket        Fare       Cabin    Embarked
##           7           7         681         248         148           4
```

Leave out irrelevant variables

- Ignore/leave out the variables `PassengerID`, `Cabin`, `Ticket`, and `Name`.

```r
names(training.data.raw)
```

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

```r
# data <- subset(training.data.raw,select=c(2,3,5,6,7,8,10,12))
data <- training.data.raw %>%
  select(-c("PassengerId", "Cabin", "Ticket", "Name"))

head(data)
```

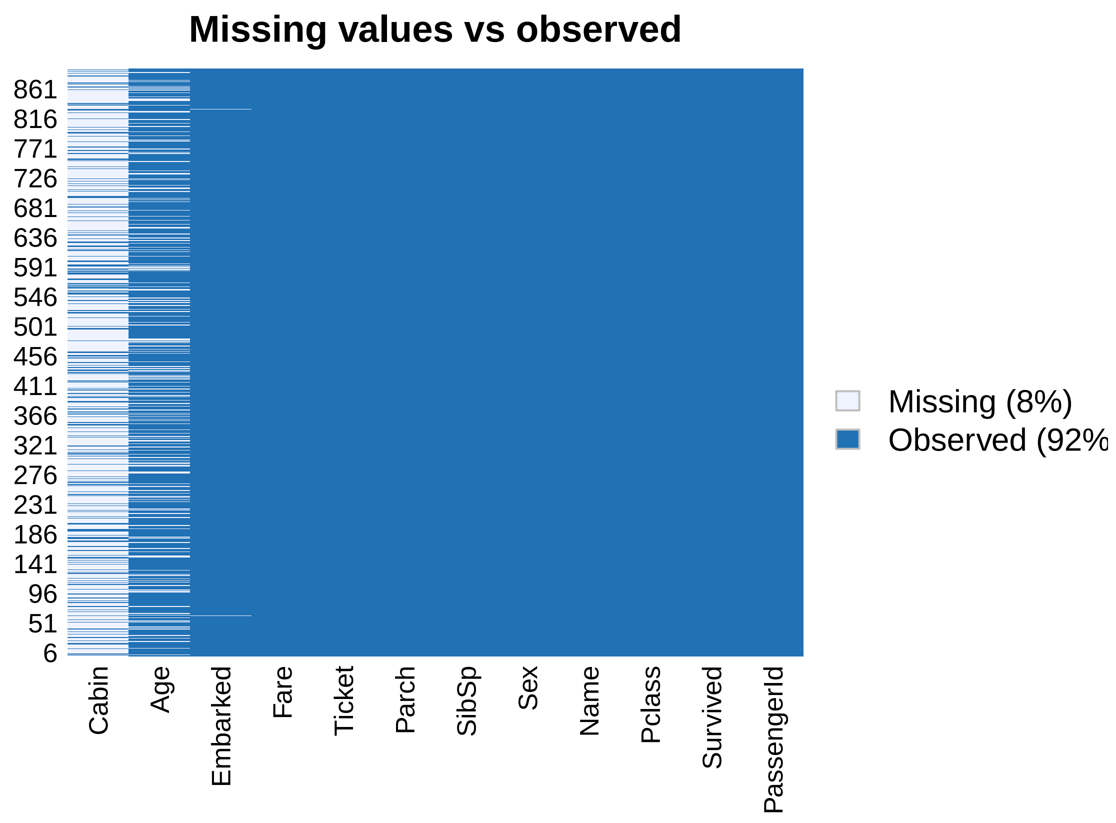
```
##   Survived Pclass    Sex Age SibSp Parch    Fare Embarked
## 1        0      3   male  22     1     0  7.2500        S
## 2        1      1 female  38     1     0 71.2833        C
## 3        1      3 female  26     0     0  7.9250        S
## 4        1      1 female  35     1     0 53.1000        S
## 5        0      3   male  35     0     0  8.0500        S
## 6        0      3   male  NA     0     0  8.4583        Q
```

Visualize missing values

- Use `missmap()` to visualize the missing values.

We can also visualize the missing values using the function `missmap()`.

```r
missmap(training.data.raw, main = "Missing values vs observed")
```



Impute the missing values

- Only keep those rows that are not `NA` in `Embarked`
- Then, impute the missing values in `Age` with mean value.

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

data$Age[is.na(data$Age)] <- mean(data$Age,na.rm=T)

head(data)
```

```
##   Survived Pclass    Sex      Age SibSp Parch    Fare Embarked
## 1        0      3   male 22.00000     1     0  7.2500        S
## 2        1      1 female 38.00000     1     0 71.2833        C
## 3        1      3 female 26.00000     0     0  7.9250        S
## 4        1      1 female 35.00000     1     0 53.1000        S
## 5        0      3   male 35.00000     0     0  8.0500        S
## 6        0      3   male 29.64209     0     0  8.4583        Q
```

3. Split the data

Split the data up into the training and test set. (`set.seed = 1`).

Split the data

- Sample 100 rows from the data and use as your test set. Use the rest as your training set.

```r
set.seed(1)
test.ID <- sample(dim(data)[1], 100)
train <- data[-test.ID,]
test <- data[test.ID,]
```

4. Logistic Regression

Fit a logistic regression model onto the training set

Fit and summarize

- Fit and summarize the model to predict `Survived` as a function of all other remaining variables.

```r
model <- glm(Survived ~ ., family=binomial(link="logit"), data = train)
summary(model)
```

```
##
## Call:
## glm(formula = Survived ~ ., family = binomial(link = "logit"),
##     data = train)
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  5.246098   0.601126   8.727  < 2e-16 ***
## Pclass      -1.047623   0.152370  -6.876 6.18e-12 ***
## Sexmale     -2.717508   0.212350 -12.797  < 2e-16 ***
## Age         -0.041380   0.008403  -4.925 8.45e-07 ***
## SibSp       -0.298049   0.110674  -2.693  0.00708 **
## Parch       -0.125844   0.124312  -1.012  0.31138
## Fare         0.001772   0.002772   0.639  0.52263
## EmbarkedQ   -0.146313   0.403005  -0.363  0.71656
## EmbarkedS   -0.428994   0.247267  -1.735  0.08275 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 1049.04  on 788  degrees of freedom
## Residual deviance:  706.49  on 780  degrees of freedom
## AIC: 724.49
##
## Number of Fisher Scoring iterations: 5
```

Use `anova()`

- Use `anova()` to see the effect of each variable on the residual deviance.

```r
anova(model, 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                       788    1049.04
## Pclass    1   82.196       787     966.85 < 2.2e-16 ***
## Sex       1  221.992       786     744.85 < 2.2e-16 ***
## Age       1   20.725       785     724.13 5.302e-06 ***
## SibSp     1   12.431       784     711.70 0.0004223 ***
## Parch     1    0.857       783     710.84 0.3544538
## Fare      1    0.974       782     709.87 0.3236963
## Embarked  2    3.376       780     706.49 0.1848942
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Pseudo-R2

- Obtain pseudo-R2 of the model, e.g., McFadden R2.

```r
pR2(model)
```

```
## fitting null model for pseudo-r2
```

```
##          llh      llhNull           G2     McFadden         r2ML         r2CU
## -353.2453603 -524.5205194  342.5503183    0.3265366    0.3521898    0.4789011
```

5. Evaluate your model on the test set.

Misclassification error

- Use your model on the test set to make predictions of `Survived`.
- Calculate the misclassification error on your test set with threshold = `0.5`.

```r
pred.results <- predict(model, newdata=subset(test, select=-1), type = "response")

pred.results <- ifelse(pred.results > .5, 1, 0)


misClassificationError <- mean(pred.results!= test$Survived)
print(paste("Accuracy = ", 1-misClassificationError))
```

```
## [1] "Accuracy =  0.83"
```

Confusion Matrix

- Compute the confusion matrix for the model with the test set.

You may use either `table()` or `confusionMatrix()` to obtain the confusion matrix.

```r
confusionMatrix(factor(test$Survived), factor(pred.results))
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  0  1
##          0 52  9
##          1  8 31
##
##                Accuracy : 0.83
##                  95% CI : (0.7418, 0.8977)
##     No Information Rate : 0.6
##     P-Value [Acc > NIR] : 6.256e-07
##
##                   Kappa : 0.6444
##
##  Mcnemar's Test P-Value : 1
##
##             Sensitivity : 0.8667
##             Specificity : 0.7750
##          Pos Pred Value : 0.8525
##          Neg Pred Value : 0.7949
##              Prevalence : 0.6000
##          Detection Rate : 0.5200
##    Detection Prevalence : 0.6100
##       Balanced Accuracy : 0.8208
##
##        'Positive' Class : 0
##
```

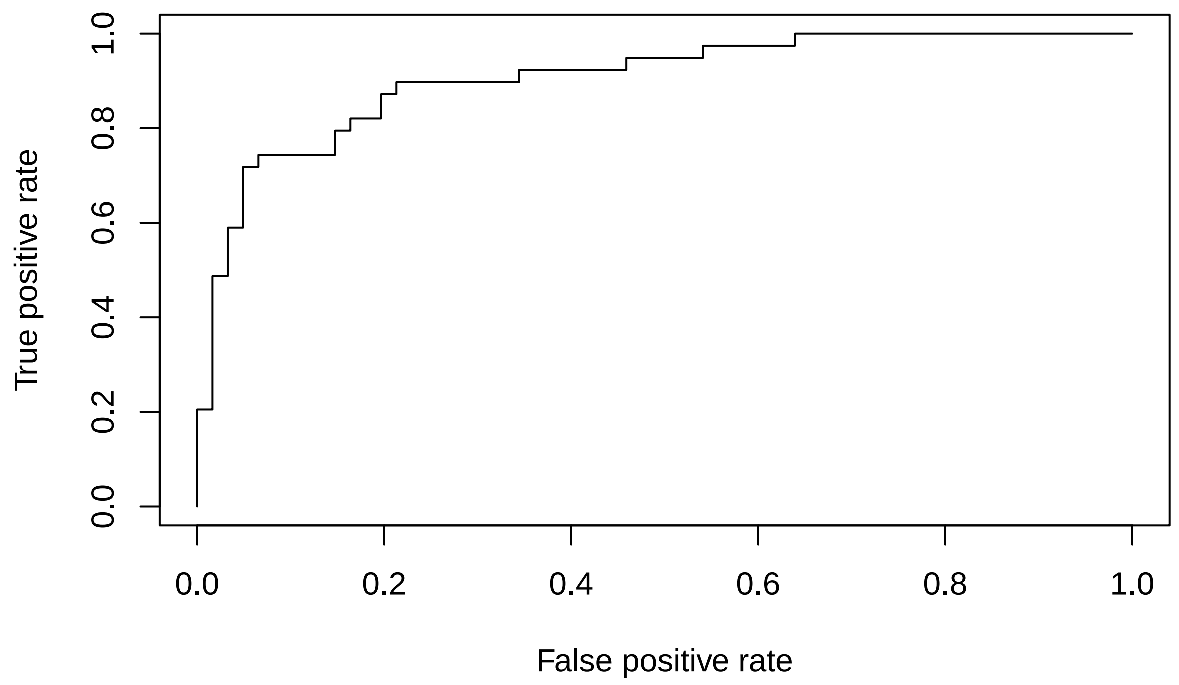
```r
# table(test$Survived, pred.results)
```

Plot ROC

- Use library **ROCR** to plot ROC curve.

Use `prediction()` and then pass its output to `performance()` to obtain the true positive rate (`"tpr"`) and false positive rate (`"fpr"`) values for different thresholds. Notice that you will not have to worry about setting thresholds. `performance()` will automatically try different thresholds and accordingly return the rate values in two arrays that are accessible by `@` (instead of `$`).

```r
pred <- predict(model, newdata=subset(test, select=-1), type = "response")
pr <- prediction(pred, test$Survived)
prf <- performance(pr, measure = "tpr", x.measure = "fpr")
plot(prf)
```



Obtain AUC

- Your measure in `performance()` will be `"auc"` this time.

```
auc <- performance(pr, measure = "auc")
auc <- auc@y.values[[1]]
auc
```

```
## [1] 0.9058428
```

Calculate the accuracy using CV error

- the accuracy result your obtained depends on the test set – so, now re-estimate the accuracy with a 10-fold CV

```
model.full <- glm(Survived ~ ., family=binomial(link="logit"), data = data)
cv.error <- cv.glm(data, model.full, K=10)$delta[1]
accuracy <- 1 - cv.error
accuracy
```

```
## [1] 0.8566667
```

6. Fit a new model

- Redo the last two steps with only `Pclass` and `Age`.

Implement a new fit with `Pclass` and `Age`

Do the fit again with only `Pclass` and `Age`;

```
model2 <- glm(Survived ~ Pclass + Age, family=binomial(link="logit"), data = train)
summary(model2)
```

```
##
## Call:
## glm(formula = Survived ~ Pclass + Age, family = binomial(link = "logit"),
##     data = train)
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  2.92568    0.37483   7.805 5.94e-15 ***
## Pclass      -1.03179    0.10490  -9.836  < 2e-16 ***
## Age         -0.03666    0.00678  -5.408 6.38e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 1049.04  on 788  degrees of freedom
## Residual deviance:  935.76  on 786  degrees of freedom
## AIC: 941.76
##
## Number of Fisher Scoring iterations: 4
```

Anova

```
anova(model, model2)
```

```
## Analysis of Deviance Table
##
## Model 1: Survived ~ Pclass + Sex + Age + SibSp + Parch + Fare + Embarked
## Model 2: Survived ~ Pclass + Age
##   Resid. Df Resid. Dev Df Deviance
## 1       780     706.49
## 2       786     935.76 -6  -229.27
```

Estimate the accuracy with 10-fold CV.

```r
model2.cv <- glm(Survived ~ Pclass + Age, family=binomial(link="logit"), data = data)
cv.error2 <- cv.glm(data, model2.cv, K=10)$delta[1]
accuracy <- 1 - cv.error2
accuracy
```

```
## [1] 0.7985145
```

Misclassification on test set

- Make predictions on the test set and calculate misclassification

```r
pred.results2 <- predict(model2, newdata=subset(test, select=-1))
pred.results2 <- ifelse(pred.results > .5, 1, 0)

misClassificationError <- mean(pred.results!= test$Survived)
print(paste("Accuracy = ", 1-misClassificationError))
```

```
## [1] "Accuracy =  0.83"
```

Confusion Matrix

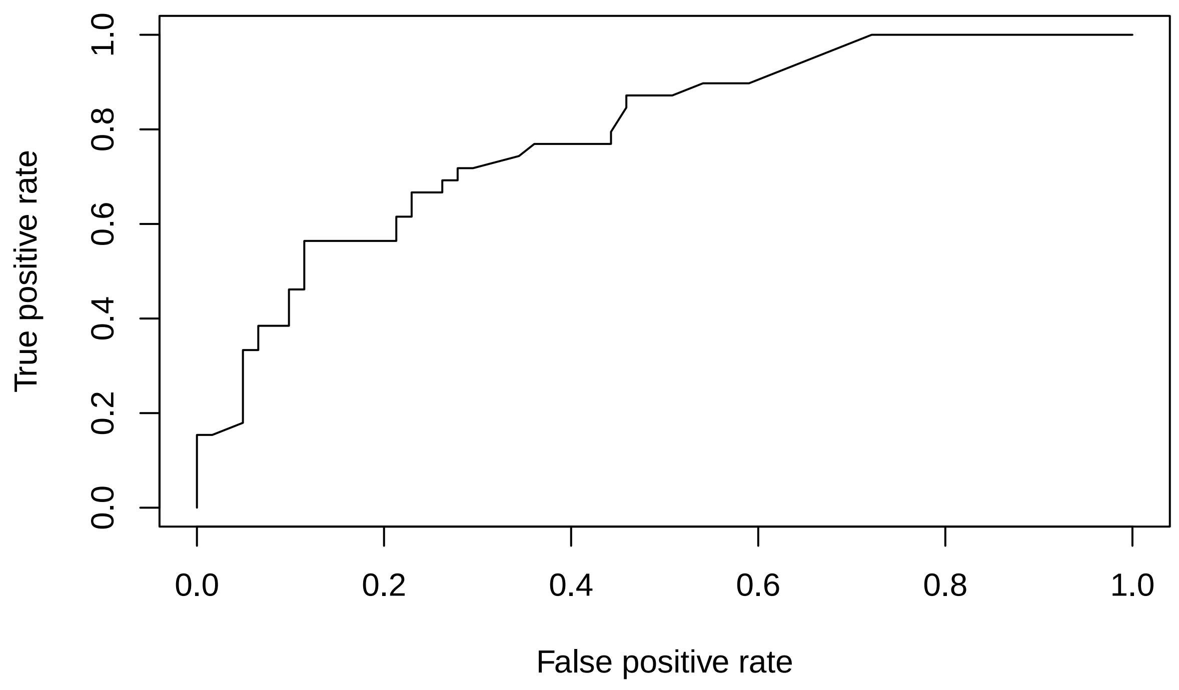
```r
confusionMatrix(factor(test$Survived), factor(pred.results2))
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  0  1
##          0 52  9
##          1  8 31
##
##                Accuracy : 0.83
##                  95% CI : (0.7418, 0.8977)
##     No Information Rate : 0.6
##     P-Value [Acc > NIR] : 6.256e-07
##
##                   Kappa : 0.6444
##
##  Mcnemar's Test P-Value : 1
##
##             Sensitivity : 0.8667
##             Specificity : 0.7750
##          Pos Pred Value : 0.8525
##          Neg Pred Value : 0.7949
##              Prevalence : 0.6000
##          Detection Rate : 0.5200
##    Detection Prevalence : 0.6100
##       Balanced Accuracy : 0.8208
##
##        'Positive' Class : 0
##
```

ROC Curve

Plot ROC for this new model on top of the ROC curve for the full model - what do you conclude?

```r
pred2 <- predict(model2, newdata=subset(test, select=-1), type = "response")
pr2 <- prediction(pred2, test$Survived)
prf2 <- performance(pr2, measure = "tpr", x.measure = "fpr")
plot(prf2)
```



```r
auc2 <- performance(pr2, measure = "auc")
auc2 <- auc2@y.values[[1]]
auc2
```

```
## [1] 0.7881463
```

Both ROC Curves

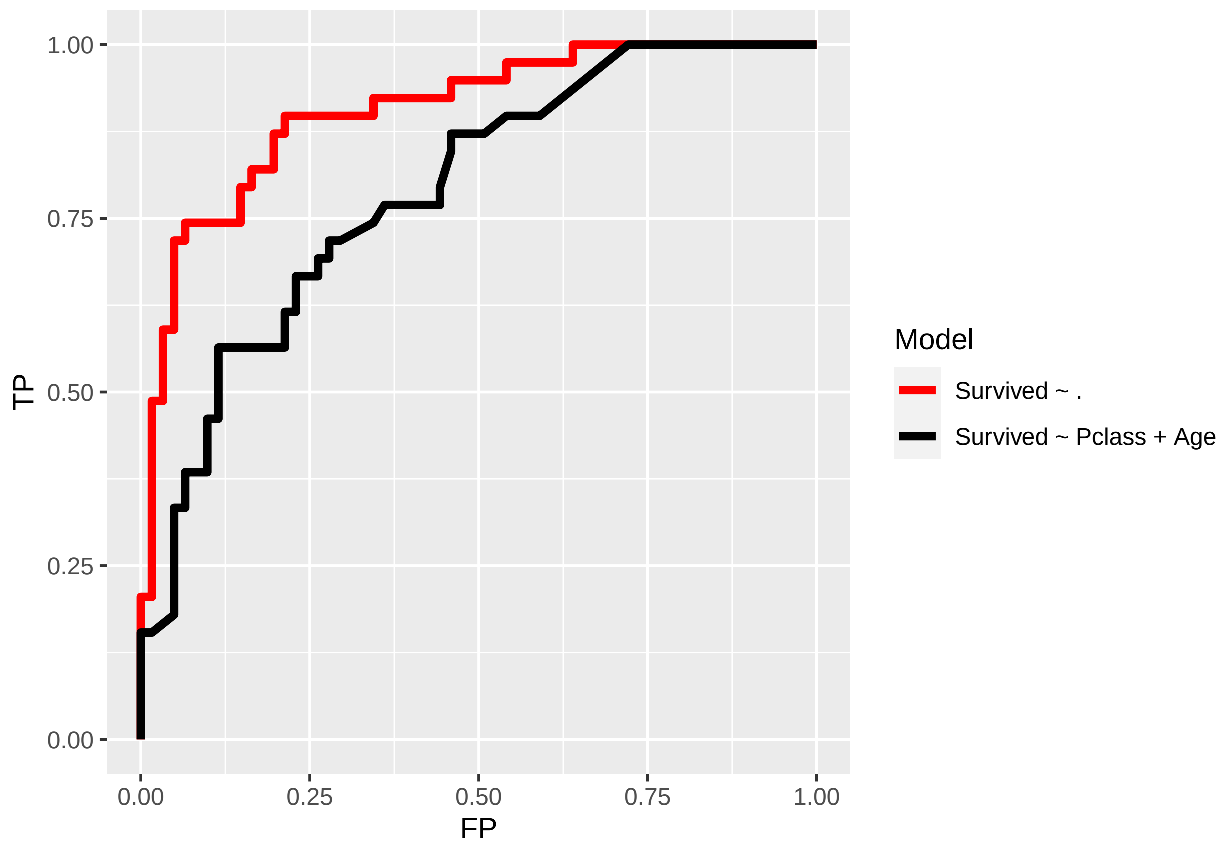
```r
df1 <- data.frame(prf@y.values, prf@x.values) %>%
  mutate(Model = "Survived ~ .") %>%
  `colnames<-`(c("TP", "FP", "Model"))

df2 <- data.frame(prf2@y.values, prf2@x.values) %>%
  mutate("Model" = "Survived ~ Pclass + Age") %>%
  `colnames<-`(c("TP", "FP", "Model"))

df <- rbind(df1, df2)
```

```
ggplot(df) +
  geom_line(aes(x = FP, y = TP, col = Model), size = 1.5) +
  scale_color_manual(values = c("red", "black"))
```

```
## Warning: Using ‘size‘ aesthetic for lines was deprecated in ggplot2 3.4.0.
## i Please use ‘linewidth‘ instead.
## This warning is displayed once every 8 hours.
## Call ‘lifecycle::last_lifecycle_warnings()‘ to see where this warning was
## generated.
```


TP
FP
Model
Survived ~ .
Survived ~ Pclass + Age