RENNES SCHOOL OF BUSINESS

Exploring the Titanic Dataset

Vignesh Hariharan

Introduction

I chose to take up the Titanic dataset to do our R programming in Data Analysis project . I tried illustrative data visualizations to show analysis part. The tragic incident of Titanic is Ill known to everybody. I tried to create a Survival model to predict the survival of passenger on the Titanic.

There are three parts to script as follows

Representation: Featuring the Data
Imputation: Cleaning and inserting Missing Values
Prediction: Predicting a model Passenger

Feature Engineering

The **passenger name** variable can be broken down into additional meaningful variables. These variables can be broken used for predictions or additional new variables can be created for our use.

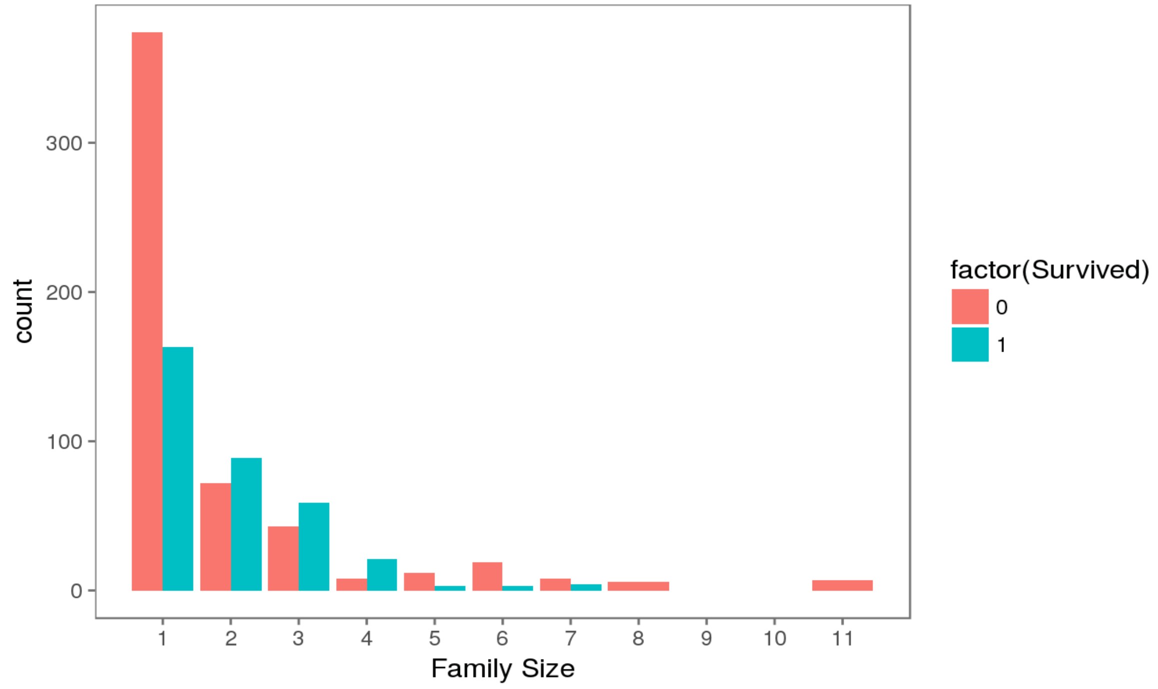
As I have used in the code, for example, the passenger name variable contains the **passenger title** and I can use **surname** to represent families. Lets do some representation using **feature engineering**!

```
# Grab title from passenger names
full$Title <- gsub('(.*, )|(\\..*)', '', full$Name)
```

Families : Survival probability as whole?

I spit passenger name into new variables. With the help of this new variable I create new family variables. At the begining?, I made a **family size** variable based on number of siblings/spouse(s) (I assumed that someone might have more than one spouse?) and number of children/parents.

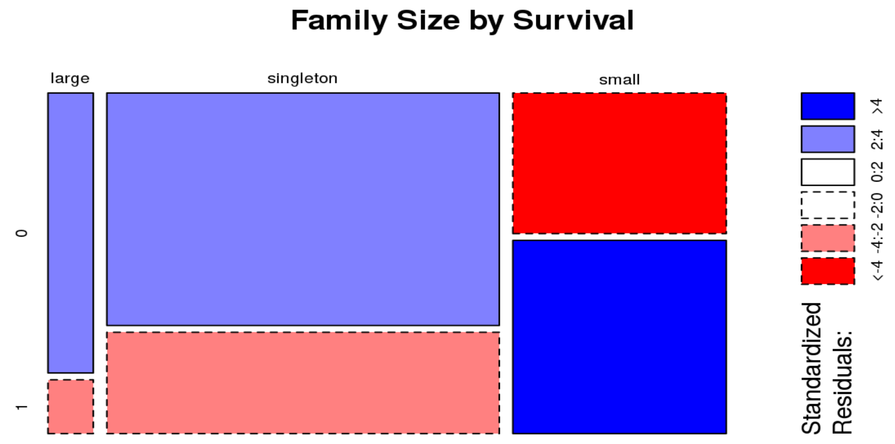
```
# Create a family size variable including the passenger themselves
full$Fsize <- full$SibSp + full$Parch + 1

# Create a family variable
full$Family <- paste(full$Surname, full$Fsize, sep='_')
```



For purpose of understanding relation betIen survival and how our family size variable looks like let’s plot it among the training data.

```
# Use ggplot2 to visualize the relationship betIen family size & survival
ggplot(full[1:891,], aes(x = Fsize, fill = factor(Survived))) +
  geom_bar(stat='count', position='dodge') +
  scale_x_continuous(breaks=c(1:11)) +
  labs(x = 'Family Size') +
  theme_few()
```

As per our observation there is a survival penalty to singles and t family sizes that are more than 4. I collapsed family size to survival variable into three levels which will be helpful since there are less large families compared overly. I created a **discretized family size** variable



The mosaic plot shows that I preserve our rule that there's a survival penalty among singletons and large families, but a benefit for passengers in small families.

Treat a few more variables

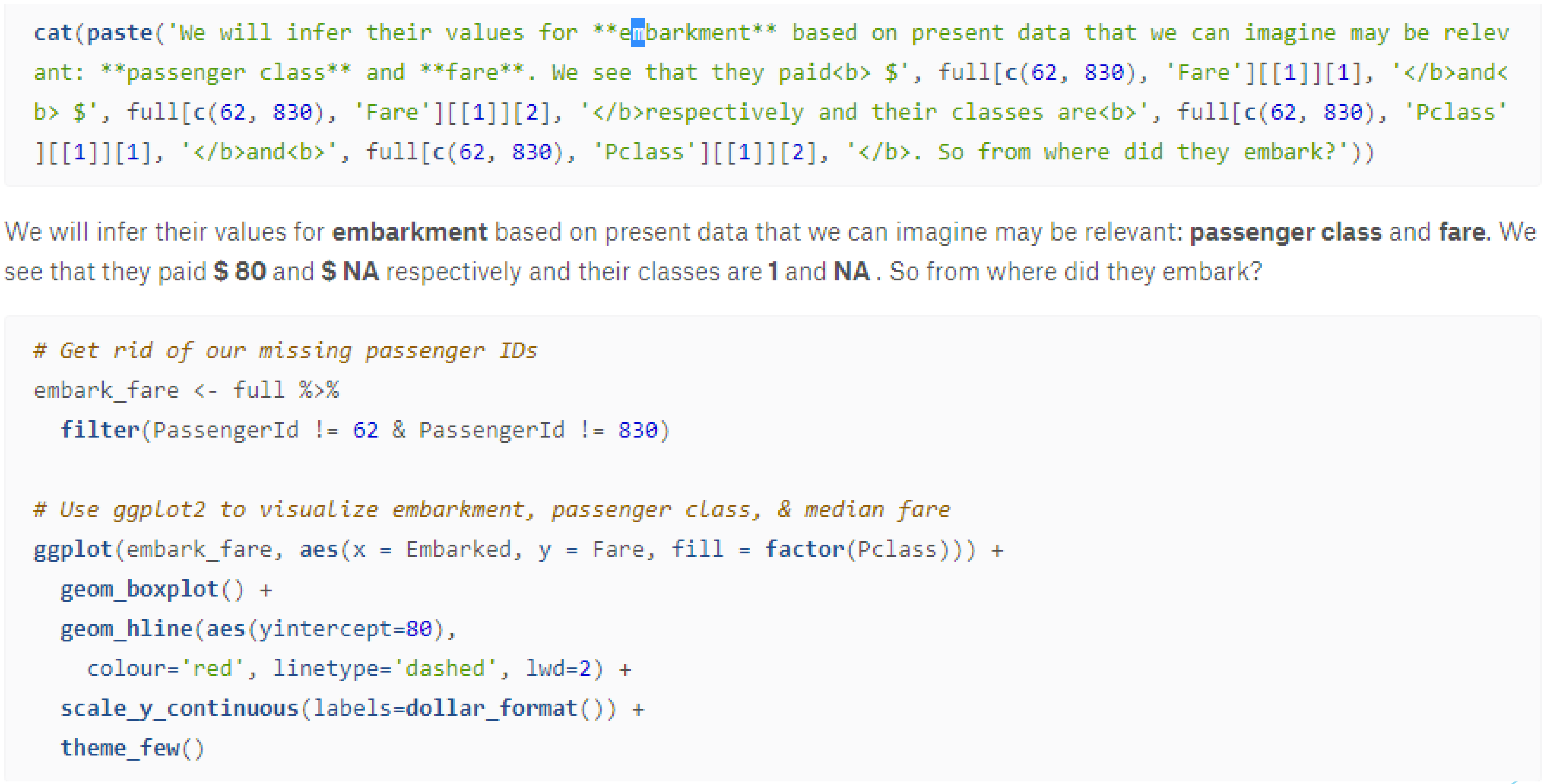
There is information that I can extract from **passenger cabin** variable including about their **deck**.

```
# This variable appears to have a lot of missing values
full$Cabin[1:28]


##  [1] ""          "C85"       ""          "C123"      ""
##  [6] ""          "E46"       ""          ""          ""
## [11] "G6"        "C103"      ""          ""          ""
## [16] ""          ""          ""          ""          ""
## [21] ""          "D56"       ""          "A6"        ""
## [26] ""          ""          "C23 C25 C27“

# The first character is the deck. For example:
strsplit(full$Cabin[2], NULL)[[1]]
```

Missingness

I had to discover missing data and rectify it through imputation. I had different options to do it but considering the small size of the dataset, I opted out of deleting either entire observations (rows) or variables (columns) containing missing values. So I decided to go forward with either replacing missing values with a sensible values as per the distribution of the data, e.g., the mean, median or mode. After this step I Int ahead with prediction.

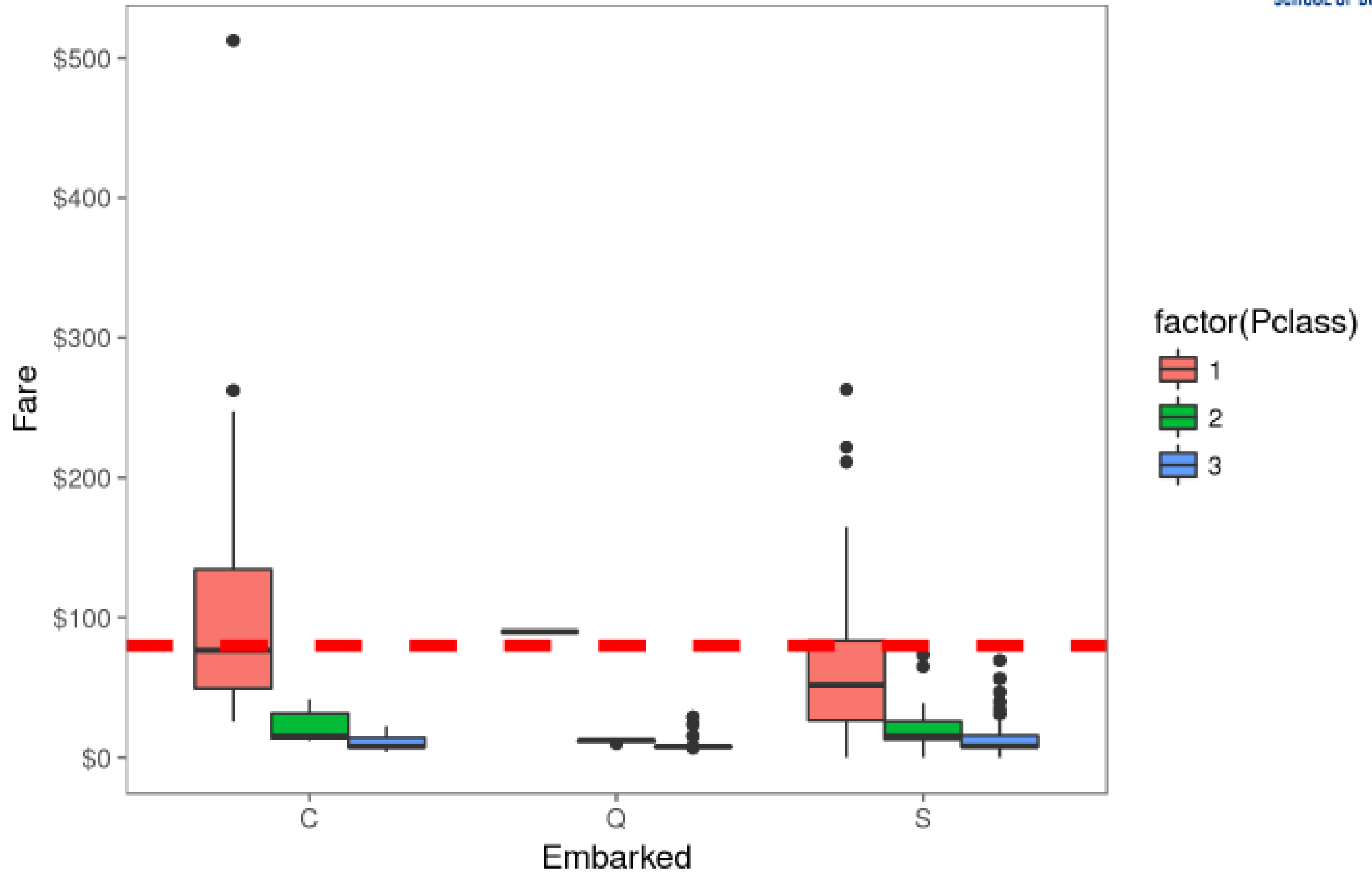
Sensible value imputation



```
cat(paste('We will infer their values for **embarkment** based on present data that we can imagine may be relev
ant: **passenger class** and **fare**. We see that they paid<b> $', full[c(62, 830), 'Fare'][[1]][1], '</b>and<
b> $', full[c(62, 830), 'Fare'][[1]][2], '</b>respectively and their classes are<b>', full[c(62, 830), 'Pclass'
][[1]][1], '</b>and<b>', full[c(62, 830), 'Pclass'][[1]][2], '</b>. So from where did they embark?'))
```

We will infer their values for **embarkment** based on present data that we can imagine may be relevant: **passenger class** and **fare**. We see that they paid **$ 80** and **$ NA** respectively and their classes are **1** and **NA** . So from where did they embark?

```
# Get rid of our missing passenger IDs
embark_fare <- full %>%
  filter(PassengerId != 62 & PassengerId != 830)

# Use ggplot2 to visualize embarkment, passenger class, & median fare
ggplot(embark_fare, aes(x = Embarked, y = Fare, fill = factor(Pclass))) +
  geom_boxplot() +
  geom_hline(aes(yintercept=80),
    colour='red', linetype='dashed', lwd=2) +
  scale_y_continuous(labels=dollar_format()) +
  theme_few()
```


$500
$400
$300
$200
$100
$0
Fare
C
Q
S
Embarked
factor(Pclass)
1
2
3

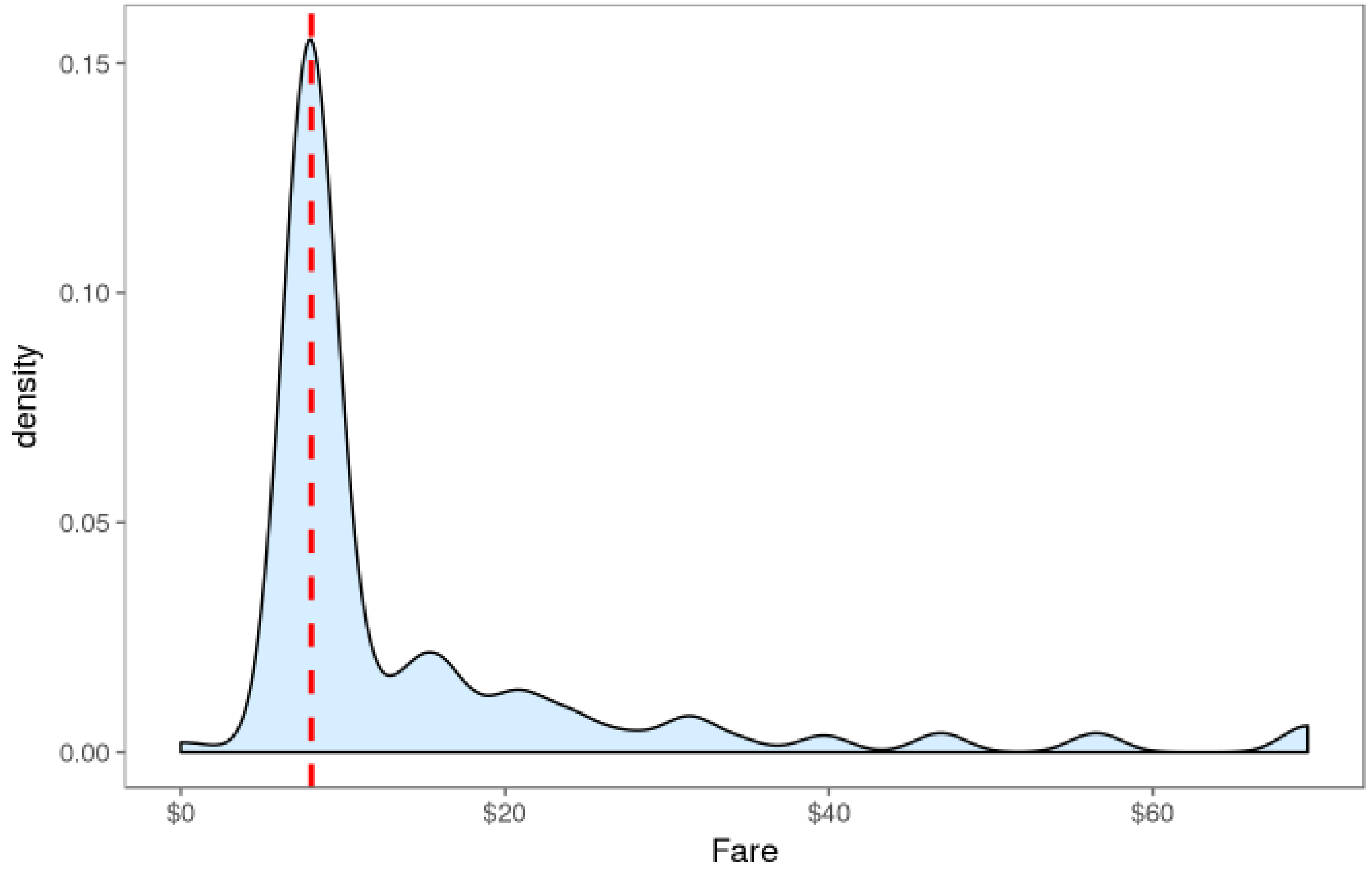
We're close to fixing the handful of NA values here and there. Passenger on row 1044 has an NA Fare value.

```
# Show row 1044
full[1044, ]
```

```
##      PassengerId Survived Pclass               Name  Sex  Age SibSp Parch
## 1044        1044       NA      3 Storey, Mr. Thomas male 60.5     0     0
##      Ticket Fare Cabin Embarked Title Surname Fsize   Family    FsizeD
## 1044   3701   NA              S    Mr  Storey     1 Storey_1 singleton
##      Deck
## 1044 <NA>
```

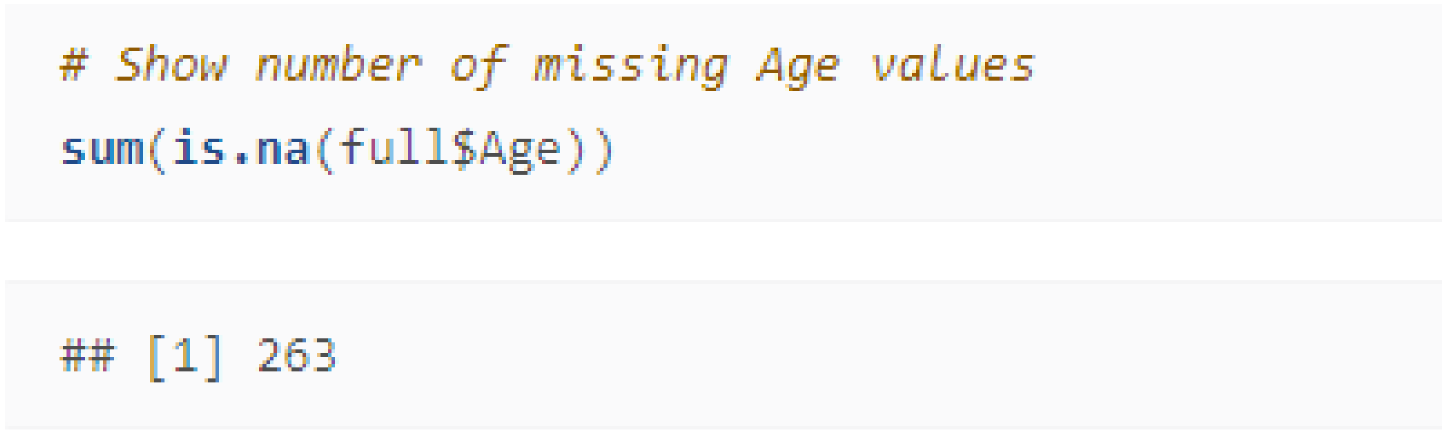
This is a third class passenger who departed from Southampton ('S'). Let's visualize Fares among all others sharing their class and embarkment (n = 494).

```
ggplot(full[full$Pclass == '3' & full$Embarked == 'S', ],
  aes(x = Fare)) +
  geom_density(fill = '#99d6ff', alpha=0.4) +
  geom_vline(aes(xintercept=median(Fare, na.rm=T)),
    colour='red', linetype='dashed', lwd=1) +
  scale_x_continuous(labels=dollar_format()) +
  theme_few()
```


0.15
0.10
0.05
0.00
density
$0
$20
$40
$60
Fare

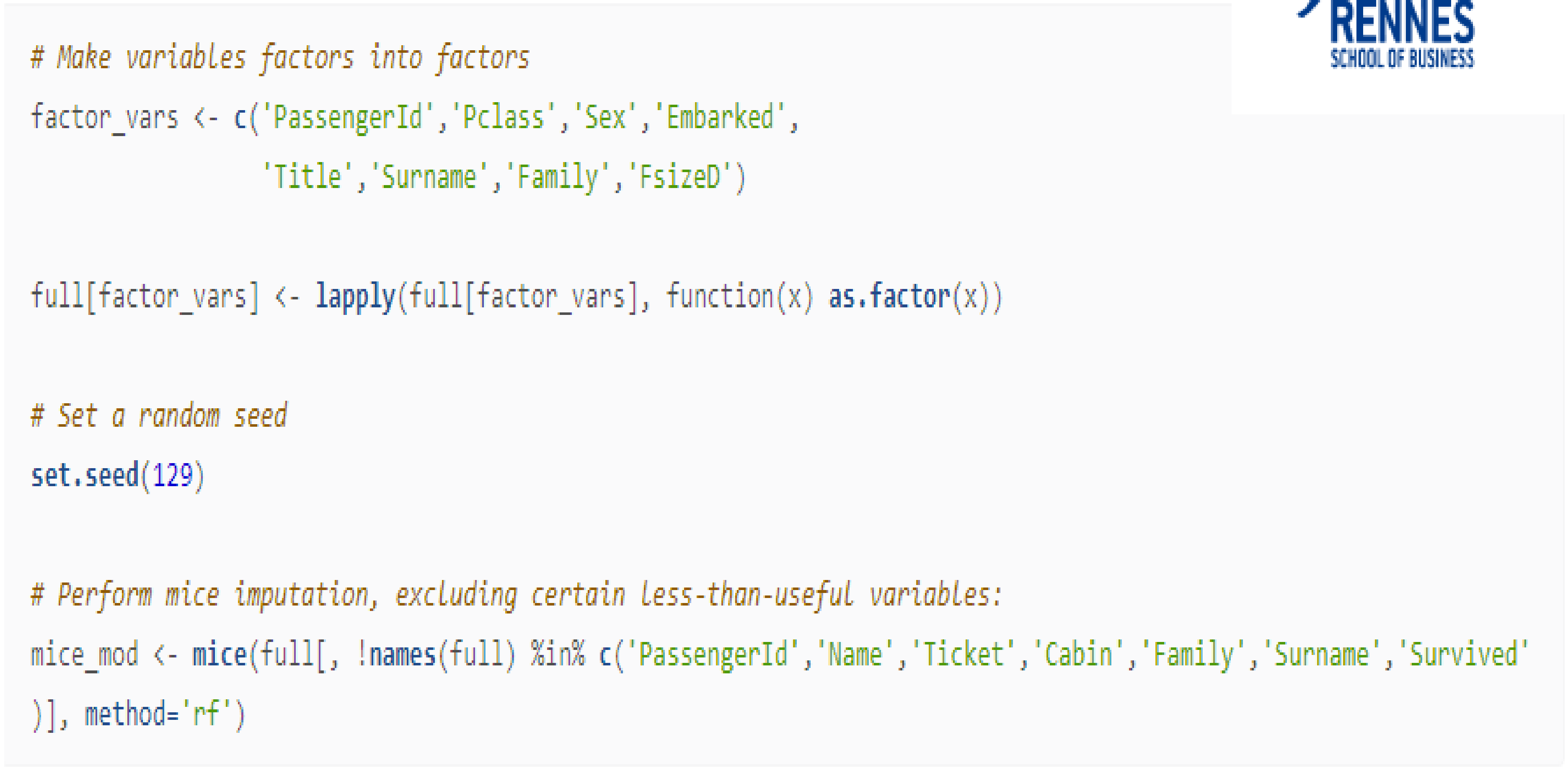
Predictive imputation

As per our former observation I encountered few missing **Age** values in our data. This I resolved by various intricate tricks of imputing missing age values. I will create a model predicting ages based on other variables.

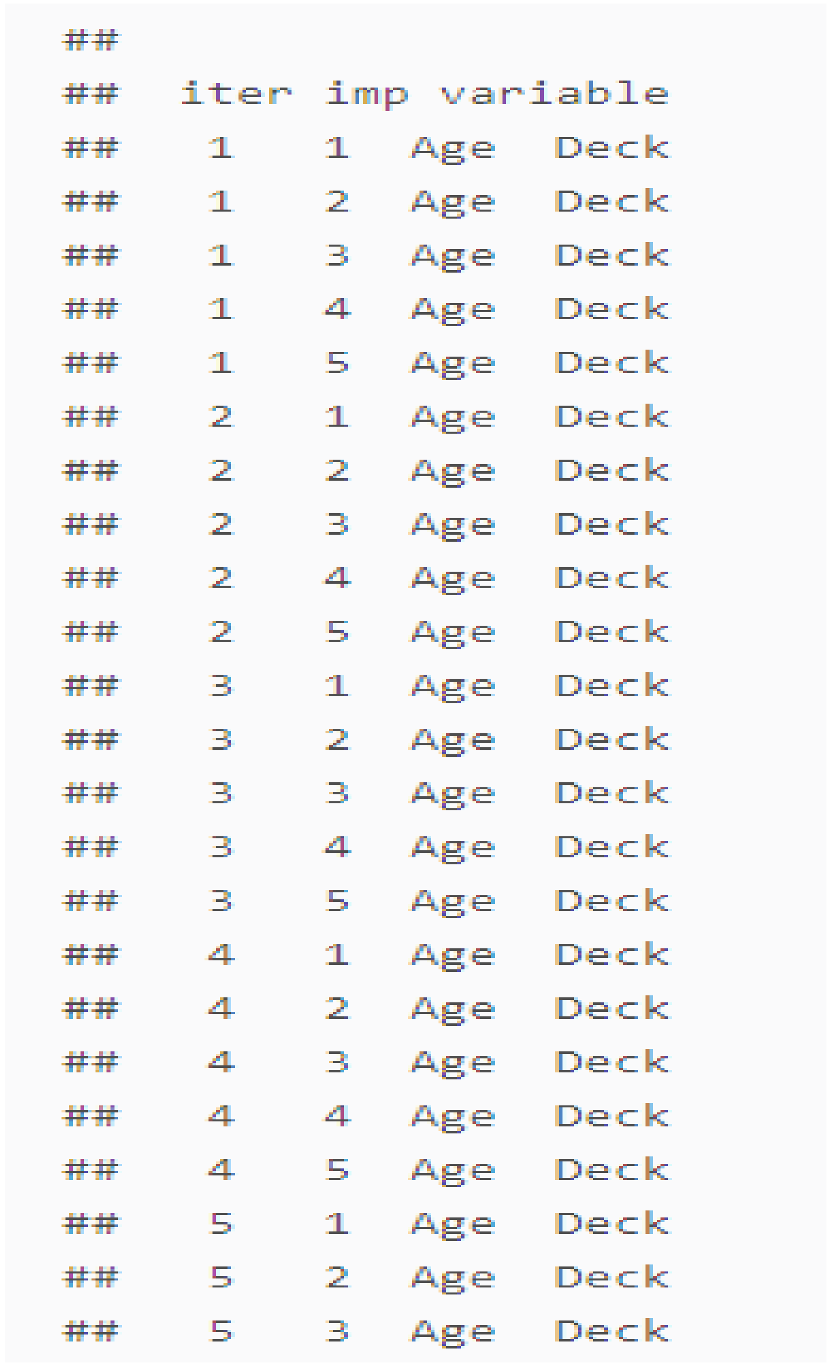


```
# Show number of missing Age values
sum(is.na(full$Age))
```

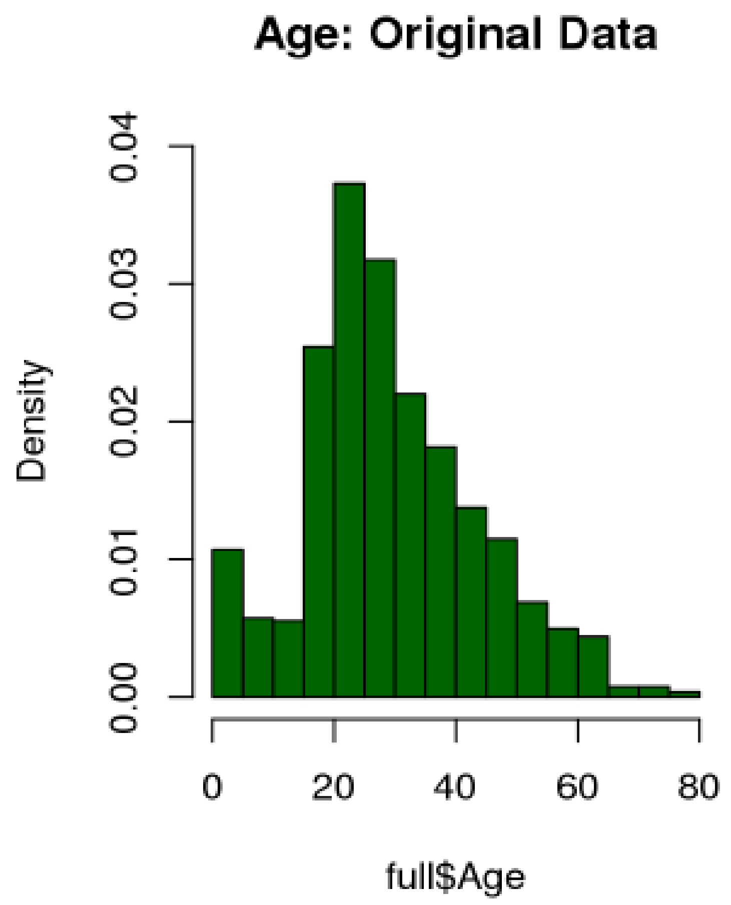
```
## [1] 263
```

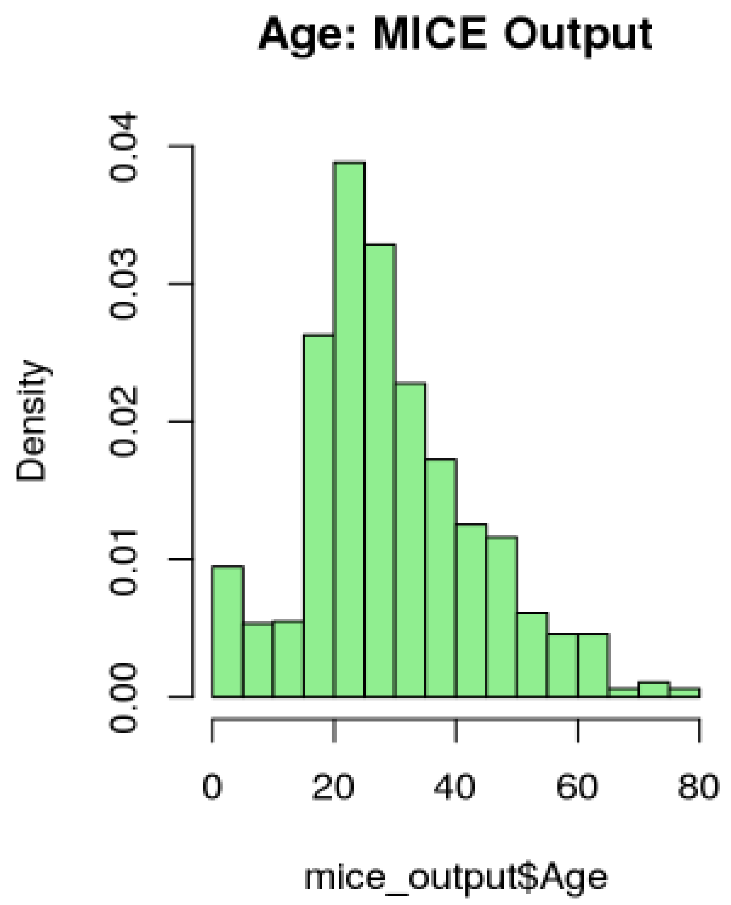


```r
# Make variables factors into factors
factor_vars <- c('PassengerId','Pclass','Sex','Embarked',
                 'Title','Surname','Family','FsizeD')

full[factor_vars] <- lapply(full[factor_vars], function(x) as.factor(x))

# Set a random seed
set.seed(129)

# Perform mice imputation, excluding certain less-than-useful variables:
mice_mod <- mice(full[, !names(full) %in% c('PassengerId','Name','Ticket','Cabin','Family','Surname','Survived'
)], method='rf')
```



```
##
##   iter imp variable
##    1    1   Age   Deck
##    1    2   Age   Deck
##    1    3   Age   Deck
##    1    4   Age   Deck
##    1    5   Age   Deck
##    2    1   Age   Deck
##    2    2   Age   Deck
##    2    3   Age   Deck
##    2    4   Age   Deck
##    2    5   Age   Deck
##    3    1   Age   Deck
##    3    2   Age   Deck
##    3    3   Age   Deck
##    3    4   Age   Deck
##    3    5   Age   Deck
##    4    1   Age   Deck
##    4    2   Age   Deck
##    4    3   Age   Deck
##    4    4   Age   Deck
##    4    5   Age   Deck
##    5    1   Age   Deck
##    5    2   Age   Deck
##    5    3   Age   Deck
```

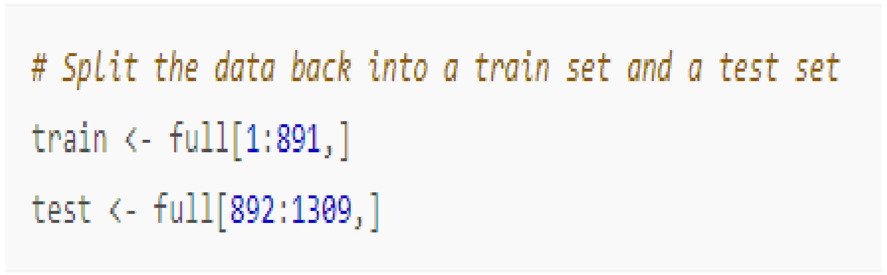

Age: Original Data
Density
0.00
0.01
0.02
0.03
0.04
0
20
40
60
80
full$Age


Age: MICE Output
Density
0.00
0.01
0.02
0.03
0.04
0
20
40
60
80
mice_output$Age

Prediction

Split into training & test sets

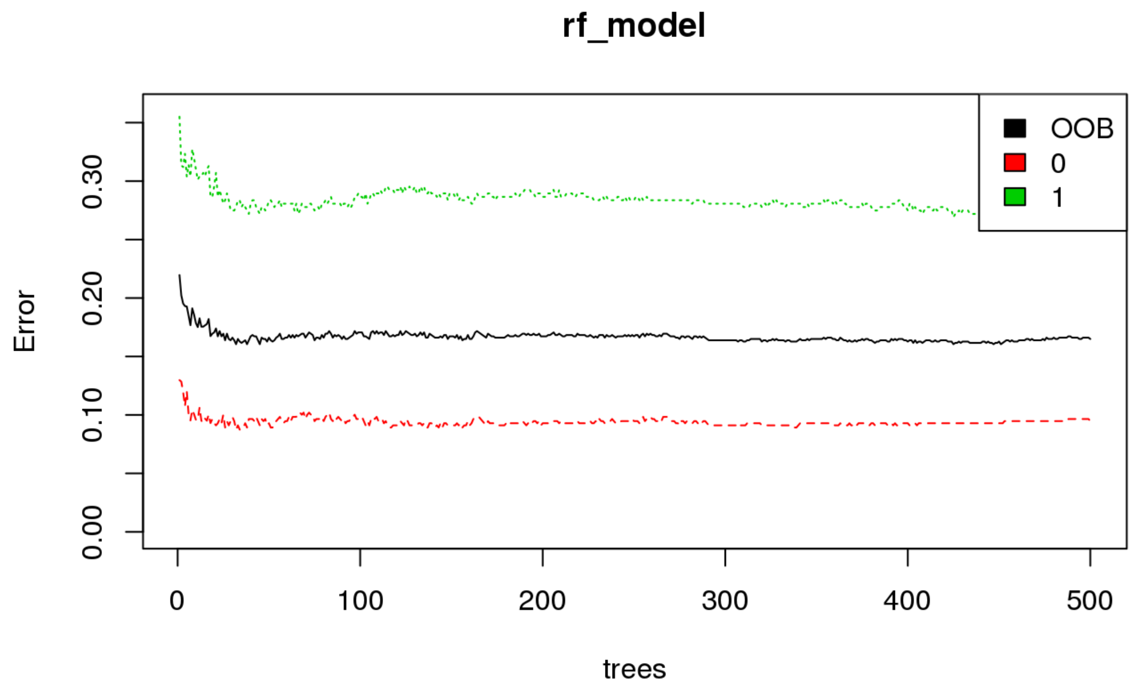
split the data back into the original test and training sets.



```r
# Split the data back into a train set and a test set
train <- full[1:891,]
test <- full[892:1309,]
```

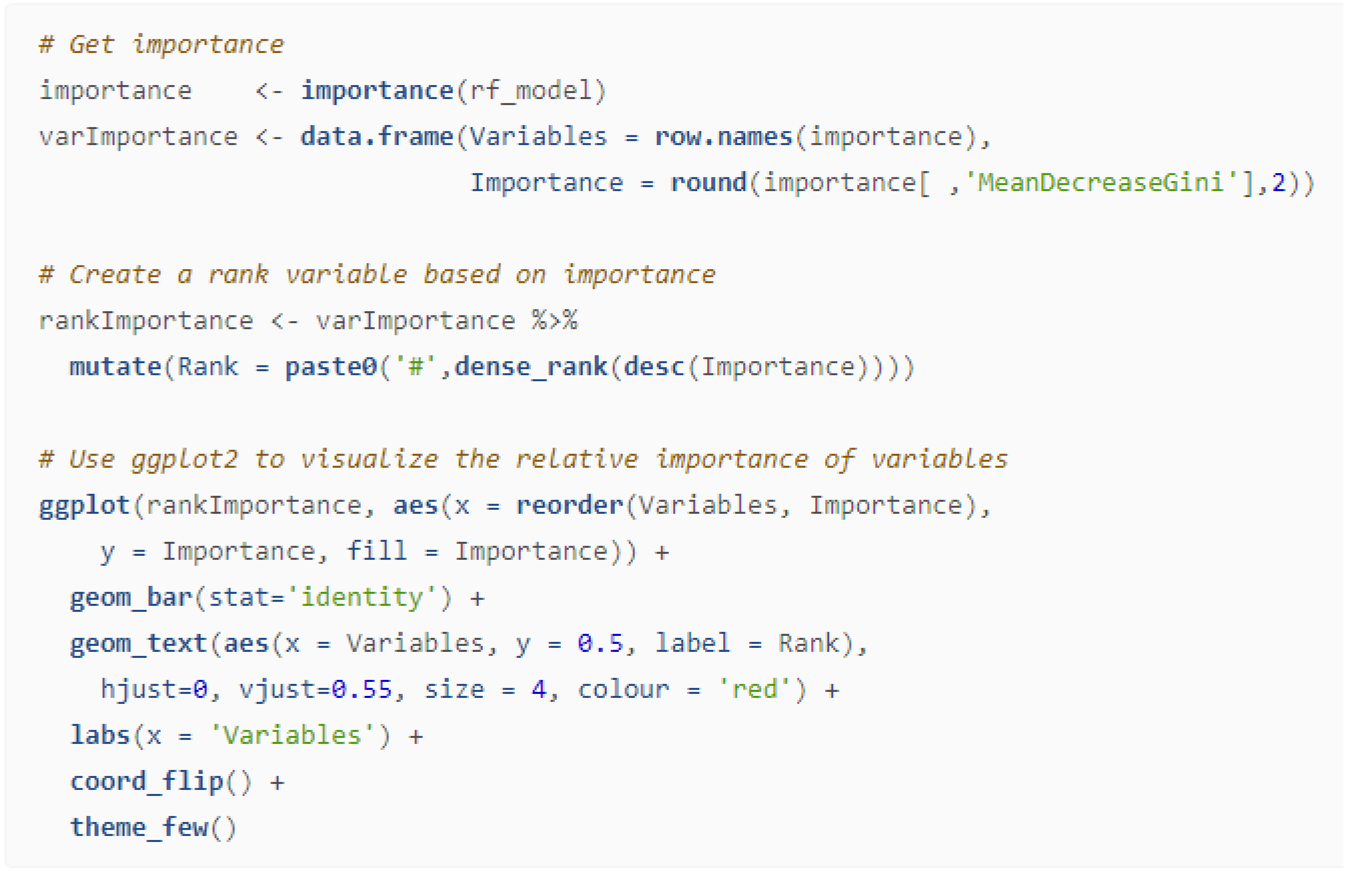
Building the model

```r
# Set a random seed
set.seed(754)

# Build the model (note: not all possible variables are used)
rf_model <- randomForest(factor(Survived) ~ Pclass + Sex + Age + SibSp + Parch +
                                             Fare + Embarked + Title +
                                             FsizeD + Child + Mother,
                                             data = train)

# Show model error
plot(rf_model, ylim=c(0,0.36))
legend('topright', colnames(rf_model$err.rate), col=1:3, fill=1:3)
```

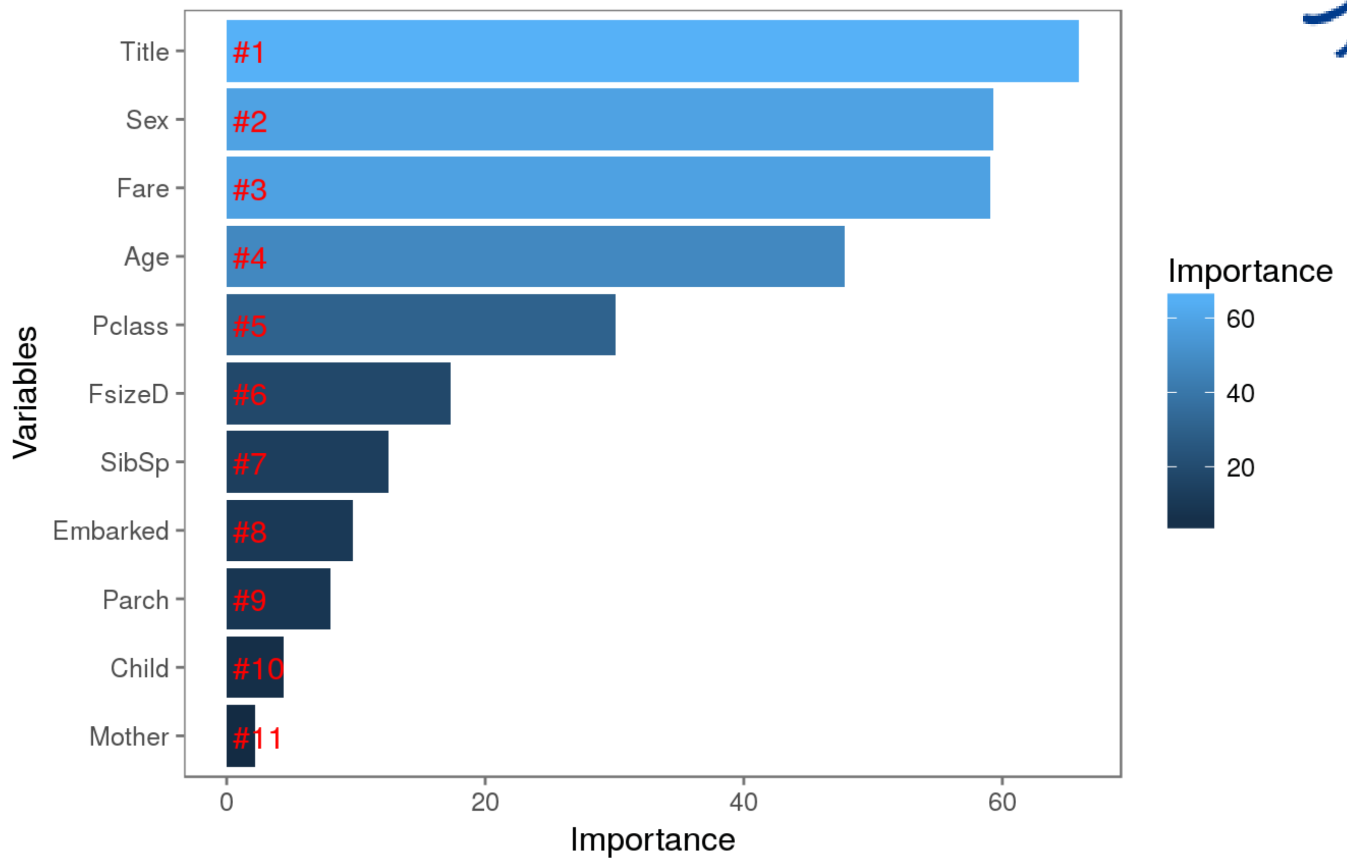


The black line shows the overall error rate which falls below 20%. The red lines show the error rate for 'died' and green lines show the error rate for 'survived' . Now I am efficient in predicting death than predicting the survival.

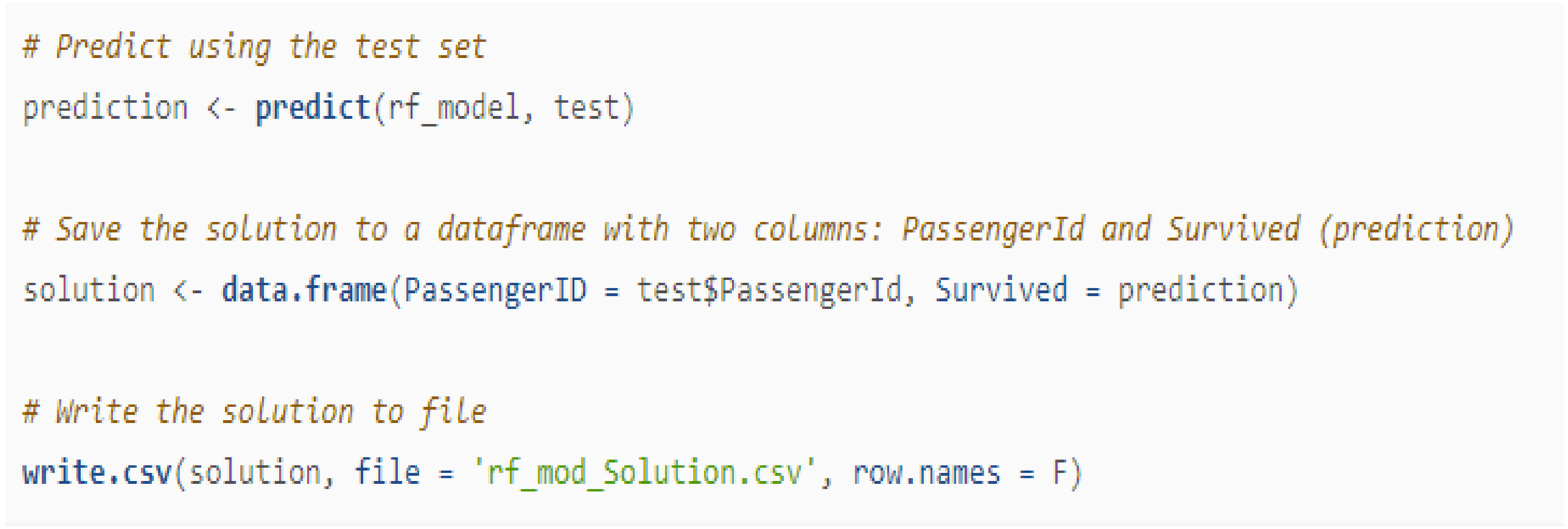
Variable importance



```r
# Get importance
importance    <- importance(rf_model)
varImportance <- data.frame(Variables = row.names(importance),
                            Importance = round(importance[ ,'MeanDecreaseGini'],2))

# Create a rank variable based on importance
rankImportance <- varImportance %>%
  mutate(Rank = paste0('#',dense_rank(desc(Importance))))

# Use ggplot2 to visualize the relative importance of variables
ggplot(rankImportance, aes(x = reorder(Variables, Importance),
    y = Importance, fill = Importance)) +
  geom_bar(stat='identity') +
  geom_text(aes(x = Variables, y = 0.5, label = Rank),
    hjust=0, vjust=0.55, size = 4, colour = 'red') +
  labs(x = 'Variables') +
  coord_flip() +
  theme_few()
```


Variables
Title
Sex
Fare
Age
Pclass
FsizeD
SibSp
Embarked
Parch
Child
Mother
#1
#2
#3
#4
#5
#6
#7
#8
#9
#10
#11
0
20
40
60
Importance
Importance
60
40
20

Conclusion



```
# Predict using the test set
prediction <- predict(rf_model, test)

# Save the solution to a dataframe with two columns: PassengerId and Survived (prediction)
solution <- data.frame(PassengerID = test$PassengerId, Survived = prediction)

# Write the solution to file
write.csv(solution, file = 'rf_mod_Solution.csv', row.names = F)
```