Who survived the Titanic disaster? Exploring data with Multinomial Logistic Regression

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# Abstract

Below paper was prepared for the needs of the final project for Advanced Econometrics at the University of Warsaw. By using Multinomial Logit Model on the data of Titanic survivors we wanted to verify whether the socio-economic status or paying higher fare impacted passenger’s probability of survival. The data is originally available on the Kaggle competition website “Titanic: Machine Learning from Disaster” and contains data for 1.309 passengers indicating whether they survive, what was their material status, what gender they were, what age they were etc. As our explanatory variables are individual specific (they do not change across alternatives) we decided to use Multinomial Logit Model. In this paper, dependent variable Survival was explained with different independent variables that were selected using multinomial logit model and verified by statistical tests. The econometric model was built in R with the use of mlogit, survival, stargazer packages. The end result is a final model with significant variables that best explains survival rate.

**Keywords:** Titanic, Survival Rate, Multinomial Logit Model, Kaggle Titanic Dataset, Data pre-processing.

# 1. Introduction

The sinking of the Titanic is one of the most infamous shipwrecks in history. On April 15, 1912, during her maiden voyage, the widely considered “unsinkable” RMS Titanic sank after colliding with an iceberg. Unfortunately, there were not enough lifeboats for everyone onboard,resulting in the death of 1502 out of 2224 passengers and crew. While there was some element of luck involved in surviving, it seems some groups of people were more likely to survive than others. Therefore this topic seems interesting for further investigation to see which variables influenced survival rate the most.

We will verify the following hypothesis using multinomial logit model:

**Hypothesis 1:**

H0: Having a seat in higher class significantly increases the chance of passenger to survive.

H1: Having a seat in higher class did not increases the chance of passenger to survive.

**Hypothesis 2:**

H0: Paying a higher fare/having a family member on board increases the chance of passenger to survive.

H1: Paying a higher fare/having a family member on board does not increase the chance of passenger survival.

# 2. Literature review

The Titanic disaster resulting in the sinking of the British passenger ship with the loss of 722 passengers and crew occurred in the North Atlantic on April 15, 1912. Although it has been many years since this maritime disaster took place, research on understanding what impacts individual’s survival or death has been attracting researchers’ attention. It appears that this is somewhat of a common problem to work on especially that data set is publicly available. Many researchers were exploring this data with different predictive models. For example scientists from Kansas State University applied CART methodology as well as bagging and random forests that provide quite good prediction accuracy at the level of 77%[[1]](#footnote-23). Using Logistic Regression also provides satisfactory results, accuracy i.e. almost of about 95%[[2]](#footnote-24) which was obtained by researchers from University of San Francisco. They concluded that the model predicted better with binary dependent variables which means the variable has a binary value as its output. Applying other methods, like random forest model predicts even better than previous models giving 93% of accuracy[[3]](#footnote-25).

# 3.Dataset and preprocessing

## 3.1.Dataset

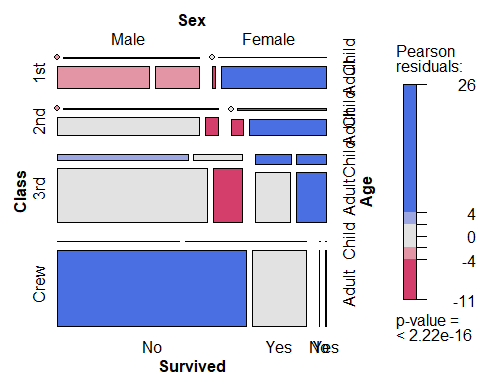
The Titanic passenger data consists of a training set, a test set and a gender\_submission set all are .csv files. The training set includes the response variable Survived and 11 other descriptive variables pertaining to 891 passengers. The test set does not include the response variable, but does contain the 11 other variables for 418 passengers. Additionally, gender submission includes only response variables for test set, that’s why we started our data preprocessing by merging them.

From a sample of the RMS Titanic data, we can see the various features present for each passenger on the ship: **“Survived”**: Outcome of survival (0 = No; 1 = Yes) **“Pclass”**: Socio-economic class (1 = Upper class; 2 = Middle class; 3 = Lower class) **“Name”**: Name of passenger **“Sex”**: Sex of the passenger **“Age”**: Age of the passenger (Some entries contain NaN) **“SibSp”**: Number of siblings and spouses of the passenger aboard **“Parch”**: Number of parents and children of the passenger aboard **“Ticket”**: Ticket number of the passenger **“Fare”**: Fare paid by the passenger **“Cabin”**: Cabin number of the passenger (Some entries contain NaN) **“Embarked”**: Port of embarkation of the passenger (C = Cherbourg; Q = Queenstown; S = Southampton)

library(vcd)

## Loading required package: grid

mosaic(~Class+Sex+Age+Survived, data=Titanic, shade=TRUE, legend=TRUE)



## 3.2.Preprocessing

library("sandwich")  
library("zoo")  
library("lmtest")  
library("MASS")  
library("aod")  
library("nnet")  
library("Formula")  
library("miscTools")  
library("maxLik")  
library("mlogit")  
library("car")  
library("survival")  
library("AER")  
library("stargazer")

As previously mentioned we started our data preprocessing with merging respectively datasets to get complete data for further transformations.

# Loading Dataset  
setwd(dirname(rstudioapi::getSourceEditorContext()$path))  
dfx <- read.csv("train.csv")  
df1 <- read.csv("test.csv")  
df2 <- read.csv("gender\_submission.csv")  
dfy <- merge(df1, df2)  
df <- rbind(dfx, dfy)  
head(df)

## 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 S  
## 2 PC 17599 71.2833 C85 C  
## 3 STON/O2. 3101282 7.9250 S  
## 4 113803 53.1000 C123 S  
## 5 373450 8.0500 S  
## 6 330877 8.4583 Q

# EDA  
summary(df)

## PassengerId Survived Pclass Name   
## Min. : 1 Min. :0.0000 Min. :1.000 Length:1309   
## 1st Qu.: 328 1st Qu.:0.0000 1st Qu.:2.000 Class :character   
## Median : 655 Median :0.0000 Median :3.000 Mode :character   
## Mean : 655 Mean :0.3774 Mean :2.295   
## 3rd Qu.: 982 3rd Qu.:1.0000 3rd Qu.:3.000   
## Max. :1309 Max. :1.0000 Max. :3.000   
##   
## Sex Age SibSp Parch   
## Length:1309 Min. : 0.17 Min. :0.0000 Min. :0.000   
## Class :character 1st Qu.:21.00 1st Qu.:0.0000 1st Qu.:0.000   
## Mode :character Median :28.00 Median :0.0000 Median :0.000   
## Mean :29.88 Mean :0.4989 Mean :0.385   
## 3rd Qu.:39.00 3rd Qu.:1.0000 3rd Qu.:0.000   
## Max. :80.00 Max. :8.0000 Max. :9.000   
## NA's :263   
## Ticket Fare Cabin Embarked   
## Length:1309 Min. : 0.000 Length:1309 Length:1309   
## Class :character 1st Qu.: 7.896 Class :character Class :character   
## Mode :character Median : 14.454 Mode :character Mode :character   
## Mean : 33.295   
## 3rd Qu.: 31.275   
## Max. :512.329   
## NA's :1

Since the data can have missing fields, incomplete fields, or fields containing hidden or useless information, a crucial step is to remove them in order not to complicate the further analysis. Variables Fare and Embarked will not be used, so we decided to remove them. Especially embarked variable will not be used as is not individual specific.

Our second hypothesis has to verify whether having a family on board has increased the chance of passenger to survive, therefore a new variable Family has been created as a sum of already existing variables SibSp - number of siblings and spouses of the passenger aboard and Parch- number of parents and children of the passenger aboard.

# Processing & Cleaning Data set  
fdf <- subset(df, df$Embarked != "")  
fdf <- subset(fdf, fdf$Fare != "")  
fdf <- subset(fdf, fdf$Age != "")  
fdf$Family <- fdf$SibSp + fdf$Parch  
fdf$Survived <- ifelse(fdf$Survived == 0, "No", "Yes")  
fdf$Pclass <- as.factor(fdf$Pclass)  
fdf$Embarked <- as.factor(fdf$Embarked)  
fdf$Survived <- as.factor(fdf$Survived)  
fdf$Sex <- as.factor(fdf$Sex)  
head(fdf)

## PassengerId Survived Pclass  
## 1 1 No 3  
## 2 2 Yes 1  
## 3 3 Yes 3  
## 4 4 Yes 1  
## 5 5 No 3  
## 7 7 No 1  
## 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  
## 7 McCarthy, Mr. Timothy J male 54 0 0  
## Ticket Fare Cabin Embarked Family  
## 1 A/5 21171 7.2500 S 1  
## 2 PC 17599 71.2833 C85 C 1  
## 3 STON/O2. 3101282 7.9250 S 0  
## 4 113803 53.1000 C123 S 1  
## 5 373450 8.0500 S 0  
## 7 17463 51.8625 E46 S 0

# 4. Application of Econometric Models

# Filtering Data   
fdf <- fdf[,c("Sex", "Pclass", "SibSp", "Parch", "Family", "Embarked", "Survived", "Fare", "Age")]  
fdf$Farepp <- fdf$Fare/(fdf$Family + 1)

# Exploring and Test Multinom Models

# Modeling  
model1 <- multinom(Survived ~ ., data = fdf)

## # weights: 13 (12 variable)  
## initial value 722.952509   
## iter 10 value 418.303559  
## iter 20 value 391.968038  
## iter 20 value 391.968037  
## iter 20 value 391.968037  
## final value 391.968037   
## converged

model2 <- multinom(Survived ~ .-Fare - Farepp, data = fdf)

## # weights: 11 (10 variable)  
## initial value 722.952509   
## iter 10 value 429.162839  
## final value 392.309873   
## converged

model3 <- multinom(Survived ~ .-Fare - Farepp-Embarked, fdf)

## # weights: 9 (8 variable)  
## initial value 722.952509   
## iter 10 value 392.953976  
## final value 392.735365   
## converged

model4 <- multinom(Survived ~ .-Fare - Farepp-Embarked-SibSp-Parch, fdf)

## # weights: 7 (6 variable)  
## initial value 722.952509   
## iter 10 value 393.518417  
## final value 393.495630   
## converged

#summary(model1)  
#summary(model2)  
#summary(model3)  
#summary(model4)

# statistical significance  
z1 <- summary(model1)$coefficients/summary(model1)$standard.errors  
z2 <- summary(model2)$coefficients/summary(model2)$standard.errors  
z3 <- summary(model3)$coefficients/summary(model3)$standard.errors  
z4 <- summary(model4)$coefficients/summary(model4)$standard.errors  
stargazer(z1,z2,z3,z4, type = "text")

##   
## ===============================================================================================  
## (Intercept) Sexmale Pclass2 Pclass3 SibSp Parch Family EmbarkedQ EmbarkedS Fare Age Farepp  
## -----------------------------------------------------------------------------------------------  
## 9.180 -17.459 -3.826 -6.720 -1.797 0.357 -2.499 -0.554 -0.711 0.209 -4.809 0.271   
## -----------------------------------------------------------------------------------------------  
##   
## ==================================================================================  
## (Intercept) Sexmale Pclass2 Pclass3 SibSp Parch Family EmbarkedQ EmbarkedS Age   
## ----------------------------------------------------------------------------------  
## 10.603 -17.535 -4.497 -8.092 -1.831 0.431 -2.936 -0.623 -0.878 -4.859  
## ----------------------------------------------------------------------------------  
##   
## ==============================================================  
## (Intercept) Sexmale Pclass2 Pclass3 SibSp Parch Family Age   
## --------------------------------------------------------------  
## 10.747 -17.700 -5.084 -8.879 -1.888 0.475 -2.978 -4.964  
## --------------------------------------------------------------  
##   
## =================================================  
## (Intercept) Sexmale Pclass2 Pclass3 Family Age   
## -------------------------------------------------  
## 10.718 -17.817 -5.045 -8.845 -2.934 -4.870  
## -------------------------------------------------

# 2-tailed z test  
p1 <- (1 - pnorm(abs(z1), 0, 1)) \* 2  
p2 <- (1 - pnorm(abs(z2), 0, 1)) \* 2  
p3 <- (1 - pnorm(abs(z3), 0, 1)) \* 2  
p4 <- (1 - pnorm(abs(z4), 0, 1)) \* 2  
stargazer(p1,p2,p3,p4, type = "text")

##   
## ===============================================================================================  
## (Intercept) Sexmale Pclass2 Pclass3 SibSp Parch Family EmbarkedQ EmbarkedS Fare Age Farepp  
## -----------------------------------------------------------------------------------------------  
## 0 0 0.0001 0 0.072 0.721 0.012 0.580 0.477 0.834 0.00000 0.786   
## -----------------------------------------------------------------------------------------------  
##   
## ==================================================================================  
## (Intercept) Sexmale Pclass2 Pclass3 SibSp Parch Family EmbarkedQ EmbarkedS Age   
## ----------------------------------------------------------------------------------  
## 0 0 0.00001 0 0.067 0.667 0.003 0.533 0.380 0.00000  
## ----------------------------------------------------------------------------------  
##   
## ==============================================================  
## (Intercept) Sexmale Pclass2 Pclass3 SibSp Parch Family Age   
## --------------------------------------------------------------  
## 0 0 0.00000 0 0.059 0.635 0.003 0.00000  
## --------------------------------------------------------------  
##   
## ==================================================  
## (Intercept) Sexmale Pclass2 Pclass3 Family Age   
## --------------------------------------------------  
## 0 0 0.00000 0 0.003 0.00000  
## --------------------------------------------------

# Comparing all Models  
stargazer(model1, model2, model3, model4, type = "text")

##   
## =========================================================  
## Dependent variable:   
## ---------------------------------------  
## Survived   
## (1) (2) (3) (4)   
## ---------------------------------------------------------  
## Sexmale -3.686\*\*\* -3.693\*\*\* -3.691\*\*\* -3.703\*\*\*  
## (0.211) (0.211) (0.209) (0.208)   
##   
## Pclass2 -1.150\*\*\* -1.241\*\*\* -1.322\*\*\* -1.306\*\*\*  
## (0.301) (0.276) (0.260) (0.259)   
##   
## Pclass3 -2.089\*\*\* -2.202\*\*\* -2.285\*\*\* -2.271\*\*\*  
## (0.311) (0.272) (0.257) (0.257)   
##   
## SibSp -0.172\* -0.175\* -0.179\*   
## (0.095) (0.095) (0.095)   
##   
## Parch 0.034 0.040 0.044   
## (0.095) (0.092) (0.092)   
##   
## Family -0.138\*\* -0.135\*\*\* -0.135\*\*\* -0.199\*\*\*  
## (0.055) (0.046) (0.045) (0.068)   
##   
## EmbarkedQ -0.275 -0.308   
## (0.496) (0.494)   
##   
## EmbarkedS -0.175 -0.212   
## (0.247) (0.242)   
##   
## Fare 0.001   
## (0.004)   
##   
## Age -0.036\*\*\* -0.036\*\*\* -0.037\*\*\* -0.036\*\*\*  
## (0.007) (0.007) (0.007) (0.007)   
##   
## Farepp 0.001   
## (0.005)   
##   
## Constant 4.371\*\*\* 4.544\*\*\* 4.447\*\*\* 4.411\*\*\*   
## (0.476) (0.429) (0.414) (0.412)   
##   
## ---------------------------------------------------------  
## Akaike Inf. Crit. 805.936 802.620 799.471 798.991   
## =========================================================  
## Note: \*p<0.1; \*\*p<0.05; \*\*\*p<0.01

# Exploring MLogit Data and Model

mldf <- mlogit.data(fdf, shape = "wide", choice= "Survived")  
mldf

## ~~~~~~~  
## first 10 observations out of 2086   
## ~~~~~~~  
## Sex Pclass SibSp Parch Family Embarked Survived Fare Age Farepp chid  
## 1 male 3 1 0 1 S TRUE 7.2500 22 3.62500 1  
## 2 male 3 1 0 1 S FALSE 7.2500 22 3.62500 1  
## 3 female 1 1 0 1 C FALSE 71.2833 38 35.64165 2  
## 4 female 1 1 0 1 C TRUE 71.2833 38 35.64165 2  
## 5 female 3 0 0 0 S FALSE 7.9250 26 7.92500 3  
## 6 female 3 0 0 0 S TRUE 7.9250 26 7.92500 3  
## 7 female 1 1 0 1 S FALSE 53.1000 35 26.55000 4  
## 8 female 1 1 0 1 S TRUE 53.1000 35 26.55000 4  
## 9 male 3 0 0 0 S TRUE 8.0500 35 8.05000 5  
## 10 male 3 0 0 0 S FALSE 8.0500 35 8.05000 5  
## alt idx  
## 1 No 1:No  
## 2 Yes 1:Yes  
## 3 No 2:No  
## 4 Yes 2:Yes  
## 5 No 3:No  
## 6 Yes 3:Yes  
## 7 No 4:No  
## 8 Yes 4:Yes  
## 9 No 5:No  
## 10 Yes 5:Yes  
##   
## ~~~ indexes ~~~~  
## chid alt  
## 1 1 No  
## 2 1 Yes  
## 3 2 No  
## 4 2 Yes  
## 5 3 No  
## 6 3 Yes  
## 7 4 No  
## 8 4 Yes  
## 9 5 No  
## 10 5 Yes  
## indexes: 1, 2

model <- mlogit(Survived~ 0| Sex + Family + Pclass + Age, data = mldf)  
model

##   
## Call:  
## mlogit(formula = Survived ~ 0 | Sex + Family + Pclass + Age, data = mldf, method = "nr")  
##   
## Coefficients:  
## (Intercept):Yes Sexmale:Yes Family:Yes Pclass2:Yes   
## 4.411308 -3.703381 -0.199020 -1.306308   
## Pclass3:Yes Age:Yes   
## -2.271218 -0.035976

summary(model)

##   
## Call:  
## mlogit(formula = Survived ~ 0 | Sex + Family + Pclass + Age,   
## data = mldf, method = "nr")  
##   
## Frequencies of alternatives:choice  
## No Yes   
## 0.60211 0.39789   
##   
## nr method  
## 6 iterations, 0h:0m:0s   
## g'(-H)^-1g = 1.91E-06   
## successive function values within tolerance limits   
##   
## Coefficients :  
## Estimate Std. Error z-value Pr(>|z|)   
## (Intercept):Yes 4.4113075 0.4115900 10.7177 < 2.2e-16 \*\*\*  
## Sexmale:Yes -3.7033811 0.2078565 -17.8170 < 2.2e-16 \*\*\*  
## Family:Yes -0.1990198 0.0678444 -2.9335 0.003352 \*\*   
## Pclass2:Yes -1.3063077 0.2589408 -5.0448 4.54e-07 \*\*\*  
## Pclass3:Yes -2.2712179 0.2567849 -8.8448 < 2.2e-16 \*\*\*  
## Age:Yes -0.0359755 0.0073881 -4.8694 1.12e-06 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Log-Likelihood: -393.5  
## McFadden R^2: 0.4387   
## Likelihood ratio test : chisq = 615.11 (p.value = < 2.22e-16)

# Part A

We compare the restricted model to the unrestricted model to obtain the joint significance test. Number of restrictions are 4. We compare the restricted model to the constant model using likelihood ratio test.

p-value = 2.2 e-16 and LR test = 615.11

Null hypothesis: Pclass = 0, Sex = 0, Family = 0 and Age = 0

The p-value is lower than the significance level of 0.05. Therefore, we have to reject the null hypothesis which states parameters are jointly insignificant. **The parameters are jointly significant.**

# General-to-specific method for variables selection  
x <- multinom(Survived~ Pclass + Sex + Family + Age, data = fdf)

## # weights: 7 (6 variable)  
## initial value 722.952509   
## iter 10 value 393.518417  
## final value 393.495630   
## converged

y <- multinom(Survived~1, data=fdf)

## # weights: 2 (1 variable)  
## initial value 722.952509   
## final value 701.049473   
## converged

lrtest(x, y)

## Likelihood ratio test  
##   
## Model 1: Survived ~ Pclass + Sex + Family + Age  
## Model 2: Survived ~ 1  
## #Df LogLik Df Chisq Pr(>Chisq)   
## 1 6 -393.50   
## 2 1 -701.05 -5 615.11 < 2.2e-16 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

# Part B

The model is created with non linear relation (square of Fare) and interactions between Age:Pclass & Sex:Pclass. The Fare and Fare^2 both have a p-value < 0.05. Similarly, for Pclass2:Age, Sexmale:Pclass2 and Sexmale:Pclass3 have p-value < 0.05. This means, we reject the null hypothesis. The parameters add meaningful addition to model. Pclass:Age interaction is insignificant.

# One nonlinear relationship and interaction between variables  
  
fdf$Fare2 <- fdf$Fare^2  
fdf$Farepp2 <- fdf$Farepp^2  
nlr\_model <- multinom(Survived ~ Fare + Fare2 + Sex + Pclass + Age+ Age\*Pclass + Sex \* Pclass, data = fdf)

## # weights: 12 (11 variable)  
## initial value 722.952509   
## iter 10 value 398.759983  
## iter 20 value 373.133076  
## final value 373.132688   
## converged

stargazer(nlr\_model, type = "text")

##   
## =============================================  
## Dependent variable:   
## ---------------------------  
## Survived   
## ---------------------------------------------  
## Fare -0.015\*\*\*   
## (0.004)   
##   
## Fare2 0.00004\*\*\*   
## (0.00001)   
##   
## Sexmale -5.104\*\*\*   
## (0.0001)   
##   
## Pclass2 0.357\*\*\*   
## (0.0003)   
##   
## Pclass3 -4.525\*\*\*   
## (0.0003)   
##   
## Age -0.029\*\*\*   
## (0.006)   
##   
## Pclass2:Age -0.064\*\*\*   
## (0.009)   
##   
## Pclass3:Age 0.003   
## (0.007)   
##   
## Sexmale:Pclass2 -0.799\*\*\*   
## (0.0002)   
##   
## Sexmale:Pclass3 2.453\*\*\*   
## (0.0001)   
##   
## Constant 5.900\*\*\*   
## (0.0002)   
##   
## ---------------------------------------------  
## Akaike Inf. Crit. 768.265   
## =============================================  
## Note: \*p<0.1; \*\*p<0.05; \*\*\*p<0.01

# Part C

Marginal effects are used to quantify the incremental risk associated with each factor.We start by creating a vector z which contains average characterstics.

# Calculation and interpretation of marginal effects for the model (from the general-tospecific approach)  
  
model <- mlogit(Survived~ 0| Fare + Family +Age, data = mldf)  
z <- with(mldf, data.frame(Fare = tapply(Fare, index(model)$alt, mean), Family = tapply(Family, index(model)$alt, mean), Age = tapply(Age, index(model)$alt, mean)))

The effect of Fare on Survival for each increment is by 0.3%. More the fare, more chances of survival.

# Marginal effects for Fare  
x <- effects(model, covariate = "Fare", data = z)  
stargazer(x, type = "text")

##   
## ============  
## No Yes   
## ------------  
## -0.003 0.003  
## ------------

The effect of Family size on Survival for each increment in Family members is by -0.7%. More the family, lesser the chances of survival.

# Marginal effects for Family  
y <- effects(model, covariate = "Family", data = z)  
stargazer(y, type = "text")

##   
## ============  
## No Yes   
## ------------  
## 0.007 -0.007  
## ------------

The effect of Age on Survival for each increment in Age is by -0.4%. Older the person, lesser the chances of survival.

# Marginal effects for Age  
z <- effects(model, covariate = "Age", data = z)  
stargazer(z, type = "text")

##   
## ============  
## No Yes   
## ------------  
## 0.004 -0.004  
## ------------

# Part D

The final model is (3) in the table which can be represented by the formula:

log(P(Survived=Yes)/P(Survived=No)) = 4.411 + (-3.703 \* Sexmale) + (-1.306 \* Pclass2) + (-2.271 \* Pclass3) + (-0.199 \* Family) + (-0.036 \* Age)

#present models in one quality table  
  
inter <- multinom(Survived~ Sex + Family + Pclass + Age + Sex\*Age, data = fdf)

## # weights: 8 (7 variable)  
## initial value 722.952509   
## iter 10 value 388.410789  
## final value 386.513555   
## converged

stargazer(model1, inter, model4, type="text")

##   
## ===============================================  
## Dependent variable:   
## -----------------------------  
## Survived   
## (1) (2) (3)   
## -----------------------------------------------  
## Sexmale -3.686\*\*\* -2.314\*\*\* -3.703\*\*\*  
## (0.211) (0.415) (0.208)   
##   
## Pclass2 -1.150\*\*\* -1.480\*\*\* -1.306\*\*\*  
## (0.301) (0.278) (0.259)   
##   
## Pclass3 -2.089\*\*\* -2.377\*\*\* -2.271\*\*\*  
## (0.311) (0.267) (0.257)   
##   
## SibSp -0.172\*   
## (0.095)   
##   
## Parch 0.034   
## (0.095)   
##   
## Family -0.138\*\* -0.211\*\*\* -0.199\*\*\*  
## (0.055) (0.066) (0.068)   
##   
## EmbarkedQ -0.275   
## (0.496)   
##   
## EmbarkedS -0.175   
## (0.247)   
##   
## Fare 0.001   
## (0.004)   
##   
## Age -0.036\*\*\* -0.008 -0.036\*\*\*  
## (0.007) (0.011) (0.007)   
##   
## Farepp 0.001   
## (0.005)   
##   
## Sexmale:Age -0.051\*\*\*   
## (0.014)   
##   
## Constant 4.371\*\*\* 3.787\*\*\* 4.411\*\*\*   
## (0.476) (0.441) (0.412)   
##   
## -----------------------------------------------  
## Akaike Inf. Crit. 805.936 787.027 798.991   
## ===============================================  
## Note: \*p<0.1; \*\*p<0.05; \*\*\*p<0.01

# Part E

The linktest is used to check the appropriate form of the model. The condition for linktest is to have yhat as significant and  
yhat^2 as insgnificant.

Ho: The model has appropriate form

In the below model, we have yhat and yhat2 as significant. Therefore, we reject the null hypothesis. The model has an inapproprate form.

# perform the linktest and interpret the result  
  
linktest = function(model)   
{  
 y = as.numeric(fdf$Survived) -1  
 yhat = log(model$fitted.values/(1-model$fitted.values))  
 yhat2 = yhat^2  
 # auxiliary regression  
 aux.reg = multinom(y~yhat+yhat2)  
 show(summary(aux.reg))  
 return(aux.reg)  
}  
  
mylogit <- multinom(Survived~ Sex + Pclass + Age + Family, data=fdf)

## # weights: 7 (6 variable)  
## initial value 722.952509   
## iter 10 value 393.518417  
## final value 393.495630   
## converged

lt <- linktest(mylogit)

## # weights: 4 (3 variable)  
## initial value 722.952509   
## iter 10 value 389.738500  
## final value 389.072894   
## converged  
## Call:  
## multinom(formula = y ~ yhat + yhat2)  
##   
## Coefficients:  
## Values Std. Err.  
## (Intercept) -0.2902284 0.13709556  
## yhat 1.0639517 0.06340950  
## yhat2 0.1066136 0.03661831  
##   
## Residual Deviance: 778.1458   
## AIC: 784.1458

stargazer(lt, type="text")

##   
## =============================================  
## Dependent variable:   
## ---------------------------  
## y   
## ---------------------------------------------  
## yhat 1.064\*\*\*   
## (0.063)   
##   
## yhat2 0.107\*\*\*   
## (0.037)   
##   
## Constant -0.290\*\*   
## (0.137)   
##   
## ---------------------------------------------  
## Akaike Inf. Crit. 784.146   
## =============================================  
## Note: \*p<0.1; \*\*p<0.05; \*\*\*p<0.01

# Hypothesis Testing

**Hypothesis 1**

H0: Having a seat in higher class insignificant to survive.

H1: Having a seat in higher class is significant to survive.

**Result 1**

The parameters Pclass2 and Pclass3 are significant as their p-value is < 0.05. Having a seat in class 2 and class 3 is significant to survival but as the coefficient is negative it decreases the probability of survival.The rate of survival is class 2 is more than in class 3. The rate of survival in class 1 is the most as pclass 2 = 0 and pclass 3 = 0.

Therefore, we reject the null hypothesis. Having a seat in higher class indeed increases the chance of passenger to survive.

**Hypothesis 2**

H0: Paying a higher fare/having a family member on board is insignificant to survive.

H1: Paying a higher fare/having a family member on board is significant survival.

**Result 2**

Fare is insignificant as the p-value is greater than 0.05. We fail to reject the null hypothesis. Paying a higher fare is insignificant to survive.

However, having a family member on board is significant as the p-value is less than 0.05. We reject the null hypothesis. Having a family member on board is significant for survival. As the coefficient is negative, it is in fact reducing the probability to survive significantly.

hypothesis <- multinom(Survived ~ Pclass + Age + Sex + Family + Fare, data = fdf)

## # weights: 8 (7 variable)  
## initial value 722.952509   
## iter 10 value 393.222368  
## final value 392.965611   
## converged

stargazer(hypothesis, type = "text")

##   
## =============================================  
## Dependent variable:   
## ---------------------------  
## Survived   
## ---------------------------------------------  
## Pclass2 -1.173\*\*\*   
## (0.290)   
##   
## Pclass3 -2.109\*\*\*   
## (0.302)   
##   
## Age -0.036\*\*\*   
## (0.007)   
##   
## Sexmale -3.697\*\*\*   
## (0.208)   
##   
## Family -0.219\*\*\*   
## (0.071)   
##   
## Fare 0.002   
## (0.002)   
##   
## Constant 4.232\*\*\*   
## (0.447)   
##   
## ---------------------------------------------  
## Akaike Inf. Crit. 799.931   
## =============================================  
## Note: \*p<0.1; \*\*p<0.05; \*\*\*p<0.01

# References

1. Whitley M., “Using statistical learning to predict survival of passengers on the RMS Titanic” K-State Research Exchange, (1), 2015, pp. 32 [↑](#footnote-ref-23)
2. Kshirsagar V., Phalke N., “Titanic Survival Analysis using Logistic Regression” International Research Journal of Engineering and Technology (IRJET), (2), 2019, pp. 90 [↑](#footnote-ref-24)
3. Donges N., “Predicting the Survival of Titanic Passengers” towardsdatascience.com, (3), 2018 [↑](#footnote-ref-25)