# Titanic passenger survival prediction using classification models

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#### Table of contents

T	Project description	1
2	Titanic data analysis 2.1 Loading data and R packages	<b>2</b>
3	Exploratory data analysis	3
	3.1 Data overview	3
	3.2 Compute correlations	6
	3.3 Boxplots and bar plots	7
4	Logistic regression	13
	4.1 Initial model	13
	4.2 VIF and multicollinearity	
	4.3 Further improving our model	14
5	Model validation	16
	5.1 Prediction plot	16
	5.2 Model accuracy	19

#### 1 Project description

This project aims to develop a predictive model to estimate the survival chances of Titanic passengers and to identify the key factors that influenced their outcomes. Using logistic regression on a cleaned version of the Titanic dataset, we examined the relationship between survival and various passenger characteristics.

A correlation analysis of numerical variables revealed that survival was positively associated with ticket fare and the number of parents or children aboard, while it was negatively

associated with passenger class and age. Passenger ID and the number of siblings/spouses aboard showed little to no correlation with survival.

After stepwise feature selection, the final logistic regression model included four key predictors: passenger class (Pclass), sex (Sex), age (Age), and number of siblings/spouses aboard (SibSp). All were statistically significant, with males, older passengers, and those in lower classes having a significantly lower chance of survival. The model demonstrated good performance, achieving an accuracy of 80.9%.

Additionally, we simulated predictions for 12 of the most common passenger profiles. Results consistently showed that female passengers had a much higher survival probability, and survival likelihood decreased with increasing age. This model provides a clear and interpretable view of the main factors affecting survival on the Titanic.

#### 2 Titanic data analysis

library(car)

Our analysis is to develop a model to determine the survival chances of Titanic passengers and identify the key factors influecing their outcomes.

#### 2.1 Loading data and R packages

```
library(tidyverse)
-- Attaching core tidyverse packages --
                                                     ----- tidyverse 2.0.0 --
v dplyr
            1.1.4
                      v readr
                                  2.1.5
v forcats 1.0.0
                      v stringr
                                  1.5.1
v ggplot2
            3.5.2
                      v tibble
                                  3.2.1
v lubridate 1.9.4
                      v tidyr
                                   1.3.1
v purrr
            1.0.4
-- Conflicts ----- tidyverse conflicts() --
x dplyr::filter() masks stats::filter()
x dplyr::lag()
                  masks stats::lag()
i Use the conflicted package (<a href="http://conflicted.r-lib.org/">http://conflicted.r-lib.org/</a>) to force all conflicts to be
library(corrplot)
corrplot 0.95 loaded
```

```
Loading required package: carData

Attaching package: 'car'

The following object is masked from 'package:dplyr':
    recode

The following object is masked from 'package:purrr':
    some

data<- read.csv("titanic.csv")
```

#### 3 Exploratory data analysis

#### 3.1 Data overview

```
glimpse(data)
```

```
Rows: 891
Columns: 12
$ PassengerId <int> 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17,~
$ Survived
                                            <int> 0, 1, 1, 1, 0, 0, 0, 0, 1, 1, 1, 1, 0, 0, 0, 1, 0, 1, 0, 1~
                                            <int> 3, 1, 3, 1, 3, 3, 1, 3, 3, 2, 3, 1, 3, 3, 3, 2, 3, 2, 3, 3~
$ Pclass
                                            <chr> "Braund, Mr. Owen Harris", "Cumings, Mrs. John Bradley (Fl~
$ Name
                                            <chr> "male", "female", "female", "female", "male", "m
$ Sex
                                            <dbl> 22, 38, 26, 35, 35, NA, 54, 2, 27, 14, 4, 58, 20, 39, 14, ~
$ Age
$ SibSp
                                            <int> 1, 1, 0, 1, 0, 0, 0, 3, 0, 1, 1, 0, 0, 1, 0, 0, 4, 0, 1, 0~
                                            <int> 0, 0, 0, 0, 0, 0, 1, 2, 0, 1, 0, 0, 5, 0, 0, 1, 0, 0~
$ Parch
                                            <chr> "A/5 21171", "PC 17599", "STON/O2. 3101282", "113803", "37~
$ Ticket
                                            <dbl> 7.2500, 71.2833, 7.9250, 53.1000, 8.0500, 8.4583, 51.8625,~
$ Fare
                                            <chr> "", "C85", "", "C123", "", "E46", "", "", "", "G6", "C~
$ Cabin
                                            <chr> "S", "C", "S", "S", "S", "Q", "S", "S", "S", "C", "S", "S"~
$ Embarked
```

#### summary(data)

PassengerId	Survived	Pclass	Name
Min. : 1.0	Min. :0.0000	Min. :1.000	Length:891
1st Qu.:223.5	1st Qu.:0.0000	1st Qu.:2.000	Class :character
Median :446.0	Median :0.0000	Median :3.000	Mode :character

```
Mean :446.0 Mean :0.3838 Mean :2.309
3rd Qu.:668.5 3rd Qu.:1.0000 3rd Qu.:3.000
Max. :891.0 Max. :1.0000 Max. :3.000
```

Sex	Age	SibSp	Parch
Length:891	Min. : 0.42	Min. :0.000	Min. :0.0000
Class :character	1st Qu.:20.12	1st Qu.:0.000	1st Qu.:0.0000
Mode :character	Median :28.00	Median :0.000	Median :0.0000
	Mean :29.70	Mean :0.523	Mean :0.3816
	3rd Qu.:38.00	3rd Qu.:1.000	3rd Qu.:0.0000
	Max. :80.00	Max. :8.000	Max. :6.0000
	NA's :177		
Ticket	Fare	Cabin	Embarked
Length:891	Min. : 0.00	Length:891	Length:891
Class :character	1st Qu.: 7.91	Class :characte	r Class :character
Mode :character	Median : 14.45	Mode :characte	r Mode :character
	Mean : 32.20		
	3rd Qu.: 31.00		
	Max. :512.33		

Using count function to know the distribution of the character variables.

```
data|>
  count(Survived, name="count")
```

```
Survived count
1 0 549
2 1 342
```

In our dataset, we have 342 Survived cases, compared to 549 dead cases.

```
data|>
  count(Pclass, name="count")
```

In our data set, we have 216 passengers with class 1, 184 passengers with Class 2, 491 passengers with Class 3.

```
data|>
  count(Embarked, name="Count")
```

# Embarked Count 1 2 2 C 168 3 Q 77 4 S 644

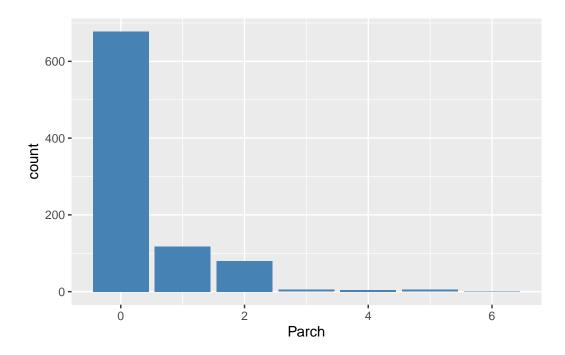
In the data set, there are 644 passengers boarded the ship at Southampton. 77 passengers board on the ship at Queenstown, 168 passengers boarded on the ship at Cherbourg.

```
data|>
  count(SibSp, name="count")
```

	SibSp	${\tt count}$
1	0	608
2	1	209
3	2	28
4	3	16
5	4	18
6	5	5
7	8	7

From the table, we can see 608 passengers on board have no siblings and spouse aboard, 209 passengers on board have one siblings or wife aboard. However, 5 passengers on board have 5 siblings or spouse aboard. 8 passengers on board have 7 siblings or spouse aboard.

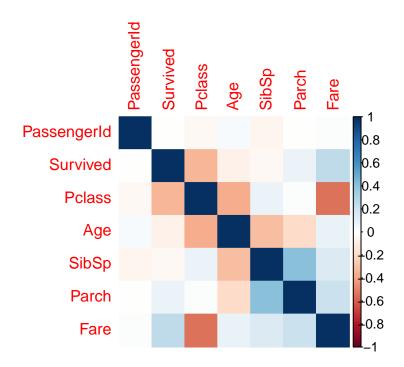
```
data%>%
   ggplot(aes(x=Parch))+
   geom_bar(fill="steelblue")
```



From the bar plot, we can see most passengers have no parents/children Aboard. Very few passengers have 3, 4 and 5 parents/Children Aboard.

#### 3.2 Compute correlations

```
data %>%
  select((where(is.numeric)))%>%
  cor(,use="pairwise.complete.obs")%>%
  corrplot(method="color")
```



From the correlation plot of numerical variable, we can see the survived rate has propositional relation to the ticket Fare, the number of parents/children aboard. and the survived chances has inverse propositional relation to the Passenger class and the age of passenger. It seems has no clear relation with the passenger ID and the number of siblings/spouses aboard.

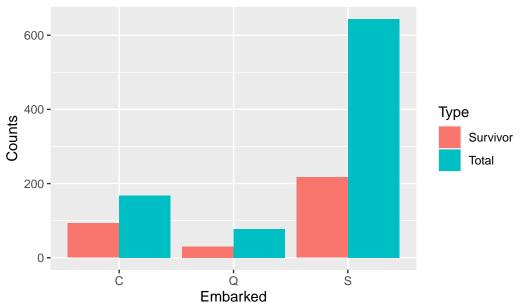
#### 3.3 Boxplots and bar plots

First convert the character variable to factor variable.

```
data%>%
  mutate(across(where(is.character), as.factor))
```

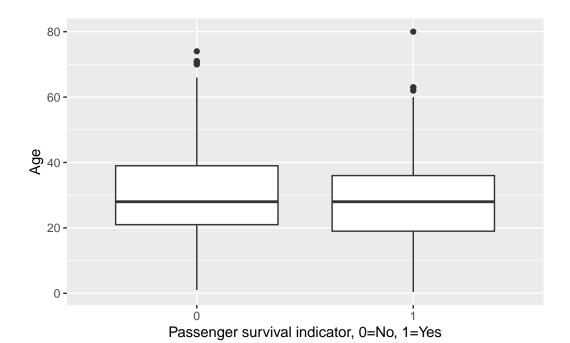
```
data%>%
  filter(Embarked !="")%>%
  group_by(Embarked) %>%
  summarise(Survivor=sum(Survived==1),Total=n(), Rate=Survivor/Total)%>%
  pivot_longer(cols=c(Survivor, Total), names_to = "Type", values_to="Counts")%>%
  ggplot(aes(x=Embarked, y=Counts, fill=Type))+
  geom_col(position="dodge")+
  labs(title= "Survivor numbers vs. total numbers at different embarking port")
```



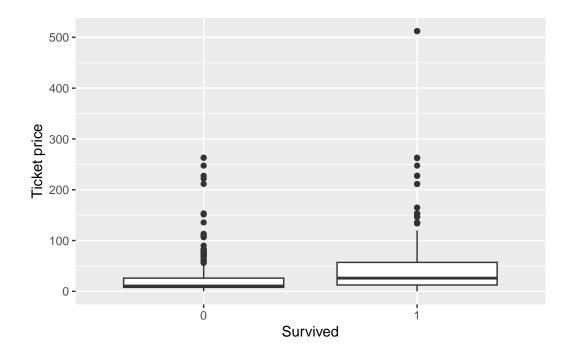


From the computation, we see the passengers from Embarked port at Cherbourg have Survivor Rate 55.4%, compared to 39.0% for Queenstown and 33.7% for Southampton.

```
ggplot(data, aes(x=as.character(Survived), y=Age))+
geom_boxplot(na.rm=TRUE)+
labs(x="Passenger survival indicator, 0=No, 1=Yes")
```

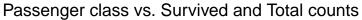


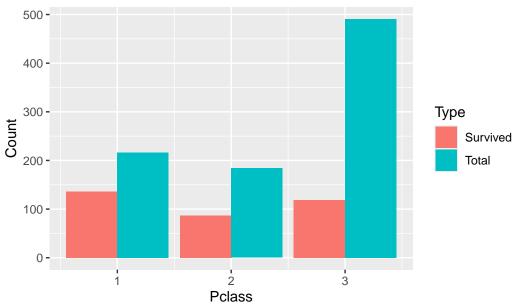
Fro the box plot, we see there is no big age mean difference for the survivors and dead people. Survivor ages are slightly younger than the dead group.



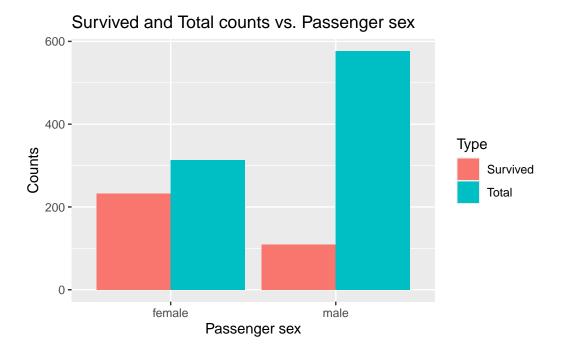
From the box plot, the Survived group has more expensive ticket than the death group.

```
data%>%
  group_by(Pclass)%>%
  summarise(Survived=sum(Survived==1), Total=n(), Rate=Survived/Total)%>%
  pivot_longer(cols=c(Survived, Total), names_to="Type", values_to="Count")%>%
  ggplot(aes(x=Pclass, y=Count, fill=Type))+
  geom_col(position="dodge")+
  labs(title="Passenger class vs. Survived and Total counts")
```

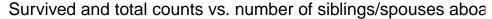


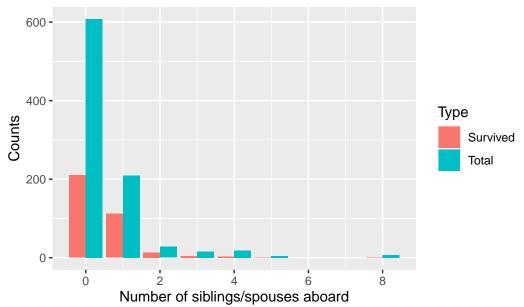


From the bar chart, the 1st passenger class has 63.0% survivor rate, compared to the 47.3% for 2nd class, 24.2% for 3rd class.



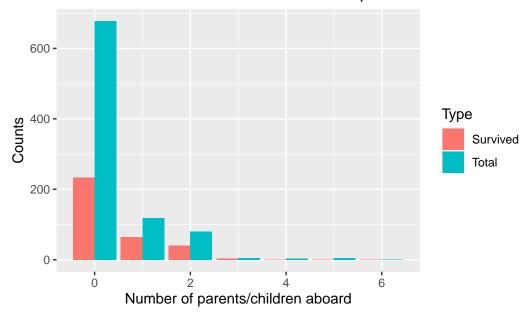
From the computation, the female survival rate is 74.2%, compared to 18.9% for males. This means women had four times the chance of being saved compared to men.





From the computation, the highest survivor rate is 53.6% for 1 siblings/spouses aboard, the second one is 46.4% for 2 siblings/spouses aboard, the third one is 34.5% for non siblings/spouses aboard, the fourth is 25% for 3 siblings/spouse aboard, the fifth is 16.7% for 4 siblings aboard. No survivor rate for 5 and 8 siblings/spouse group.

#### Survival and total counts vs. number of parents/children aboar



From the computation, the highest survived rate is 60% for 3 parents/children aboard. The second is 55.1% for 1 parents/children aboard. the third is 50% for 2 parents/children aboard. The fourth is 34.4% for non parents/children aboard. the fifth is 20% for 5 parents/children aboard. the other groups have 0% survived rate.

#### 4 Logistic regression

#### 4.1 Initial model

```
data_clean<-data%>%
  filter(Embarked!="")%>%
  select(-PassengerId, -Name, -Ticket, -Cabin)
model1<-glm(Survived~., data=data_clean, family=binomial)
summary(model1)</pre>
```

```
Sexmale
         Age
         SibSp
Parch
         -0.060270 0.123900 -0.486 0.62666
Fare
         0.001432 0.002531 0.566 0.57165
         -0.823545 0.600229 -1.372 0.17005
{\tt EmbarkedQ}
EmbarkedS -0.401213 0.270283 -1.484 0.13770
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Dispersion parameter for binomial family taken to be 1)
   Null deviance: 960.90 on 711 degrees of freedom
Residual deviance: 632.34 on 703 degrees of freedom
 (177 observations deleted due to missingness)
AIC: 650.34
Number of Fisher Scoring iterations: 5
```

4.2 VIF and multicollinearity

### vif(model1)

```
GVIF Df GVIF^(1/(2*Df))
Pclass
        1.887735 1
                           1.373949
Sex
        1.191874 1
                           1.091730
Age
        1.424118 1
                           1.193364
        1.274012 1
SibSp
                           1.128721
Parch
        1.274248 1
                           1.128826
Fare
        1.538521 1
                           1.240371
Embarked 1.139441 2
                           1.033173
```

#### 4.3 Further improving our model

```
- Fare 1 632.68 648.68

- Embarked 2 635.30 649.30

<none> 632.34 650.34

- SibSp 1 640.91 656.91

- Age 1 662.75 678.75

- Pclass 1 686.64 702.64

- Sex 1 808.42 824.42
```

Step: AIC=648.58

Survived ~ Pclass + Sex + Age + SibSp + Fare + Embarked

Df Deviance 1 632.82 646.82 - Fare - Embarked 2 635.54 647.54 <none> 632.58 648.58 + Parch 1 632.34 650.34 1 642.73 656.73 - SibSp - Age 1 662.96 676.96 - Pclass 1 689.97 703.97 1 813.74 827.74 - Sex

Step: AIC=646.82

Survived ~ Pclass + Sex + Age + SibSp + Embarked

Df Deviance AIC - Embarked 2 636.18 646.18 <none> 632.82 646.82 1 632.58 648.58 + Fare + Parch 1 632.68 648.68 1 642.75 654.75 - SibSp - Age 1 663.68 675.68 1 719.21 731.21 - Pclass - Sex 1 816.03 828.03

Step: AIC=646.18

Survived ~ Pclass + Sex + Age + SibSp

Df Deviance AIC 636.18 646.18 <none> + Embarked 2 632.82 646.82 + Fare 1 635.54 647.54 1 636.09 648.09 + Parch 1 646.70 654.70 - SibSp 1 669.11 677.11 - Age - Pclass 1 741.12 749.12 - Sex 1 821.40 829.40

#### summary(model2)

```
Call:
glm(formula = Survived ~ Pclass + Sex + Age + SibSp, family = binomial,
   data = data_clean)
Coefficients:
          Estimate Std. Error z value Pr(>|z|)
(Intercept) 5.59083 0.54342 10.288 < 2e-16 ***
         -1.31392
                    0.14091 -9.324 < 2e-16 ***
Pclass
Sexmale
         Age
SibSp
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Dispersion parameter for binomial family taken to be 1)
   Null deviance: 960.90 on 711 degrees of freedom
Residual deviance: 636.18 on 707 degrees of freedom
  (177 observations deleted due to missingness)
AIC: 646.18
Number of Fisher Scoring iterations: 5
```

#### 5 Model validation

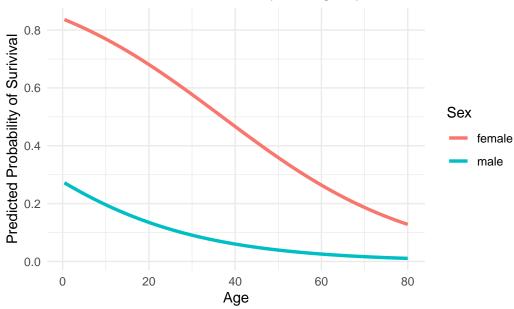
#### 5.1 Prediction plot

```
# Vary sex
data1<-data%>%
  filter(!is.na(Age))
new_data <- expand.grid(
  Age = seq(min(data1$Age), max(data1$Age), length.out = 100),
  Sex = factor(c("male", "female")),
  Pclass=3,
  SibSp=0
)

# Predict
new_data$predicted_prob <- predict(model2, newdata = new_data, type = "response")</pre>
```

```
# Plot by sex
ggplot(new_data, aes(x = Age, y = predicted_prob, color = Sex)) +
  geom_line(linewidth = 1.2) +
  labs(
    title = "Predicted Survived Probability vs. Age by Sex",
    x = "Age",
    y = "Predicted Probability of Surivival"
  ) +
  theme_minimal()
```

#### Predicted Survived Probability vs. Age by Sex



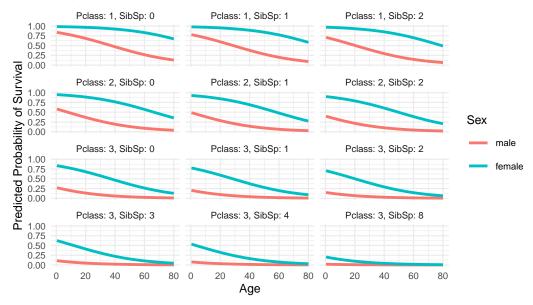
```
library(purrr)
# 1. Find top 12 profiles (excluding sex)
top_profiles <- data %>%
    group_by(Pclass, SibSp) %>%
    summarise(count = n(), .groups = "drop") %>%
    arrange(desc(count)) %>%
    slice_head(n = 12)

# 2. Generate prediction data for each profile + both sexes
age_seq <- seq(min(data1$Age), max(data1$Age), length.out = 100)

# Expand to both Male and Female
new_data <- top_profiles %>%
    mutate(profile_id = row_number()) %>%
    group_split(profile_id) %>%
```

```
map_dfr(function(profile) {
    profile_info <- profile %>% select(-count, -profile_id)
    # Add both sexes
    sexes <- c("male", "female")</pre>
    map_dfr(sexes, function(sex_val) {
      profile_replicated <- profile_info[rep(1, length(age_seq)), ]</pre>
      profile_replicated$Sex <- factor(sex_val, levels = c("male", "female"))</pre>
      profile_replicated$Age <- age_seq</pre>
      profile_replicated
    })
  })
# 3. Predict
new_data$predicted_prob <- predict(model2, newdata = new_data, type = "response")</pre>
# 4. Create facet label
new_data$profile_label <- with(new_data, paste0(</pre>
 "Pclass: ", Pclass, ", SibSp: ", SibSp
))
# 5. Plot with one curve per sex in each profile
ggplot(new_data, aes(x = Age, y = predicted_prob, color = Sex)) +
  geom_line(linewidth = 1) +
  facet_wrap(~ profile_label, ncol = 3) +
   title = "Predicted Survived Probability vs. Age\n(Top 12 Most Common Patient Profiles)
   x = "Age",
   y = "Predicted Probability of Survival",
    color = "Sex"
  ) +
  theme_minimal(base_size = 9) +
  theme(strip.text = element_text(size = 7))
```

## Predicted Survived Probability vs. Age (Top 12 Most Common Patient Profiles)



We plot the most 12 common profile of the passenger and use our model to predict the survival rate. It shows female always have higher survival rate. And the survival rate decrease as the age increases.

#### 5.2 Model accuracy

```
model_data<- model.frame(model2)
actual<-model_data$Survived

Predict_probs<-predict(model2, type="response")
predict_class<-ifelse(Predict_probs>0.5, 1, 0)

Confusion_matrix<-table(Actual=actual, Predict=predict_class)
Confusion_matrix

    Predict
Actual 0 1
    0 366 58
    1 78 210

accuracy=mean(actual==predict_class)</pre>
```

[1] "The model accuracy is 80.9 %."

print(paste("The model accuracy is", round(accuracy\*100, 2), "%."))#%80.9%