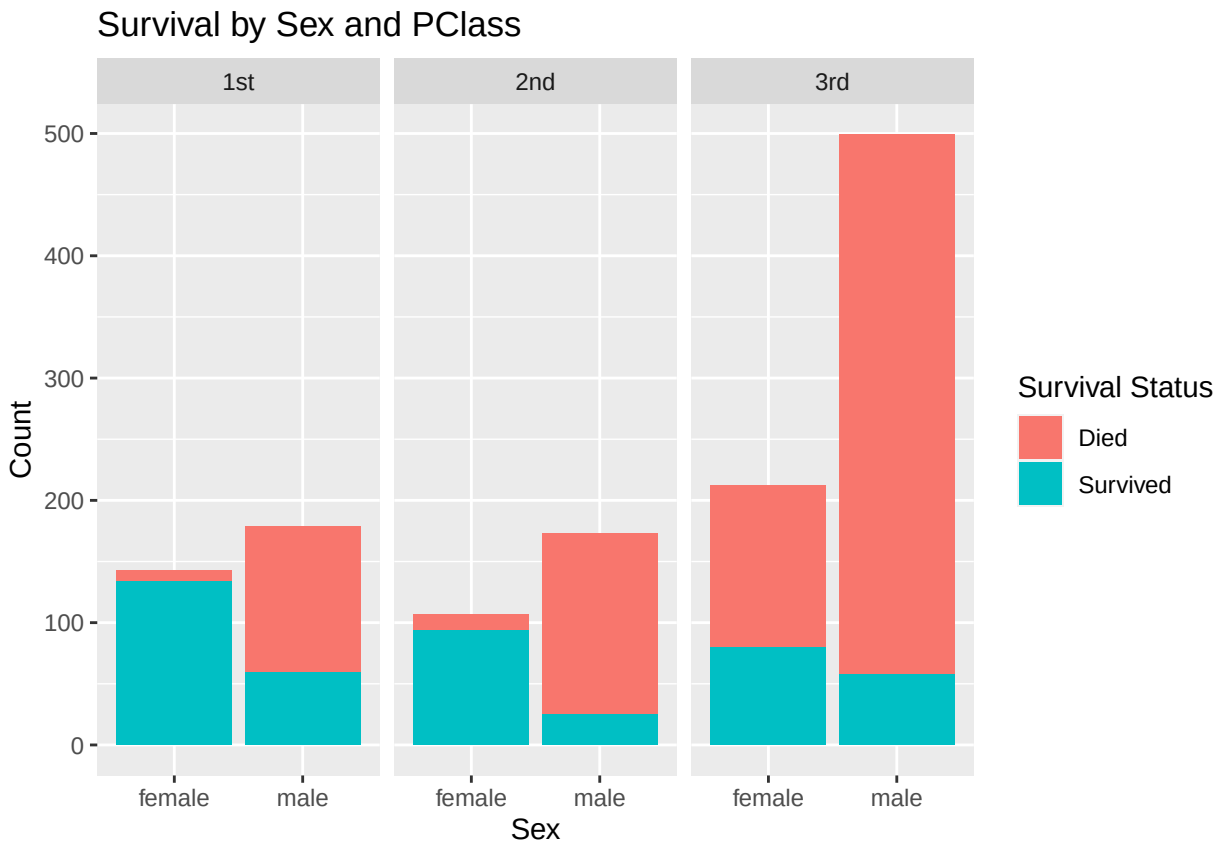
Data Analysis Report

Titanic

a) Overview + liniar model for Survival

Survival based on Sex and PClass

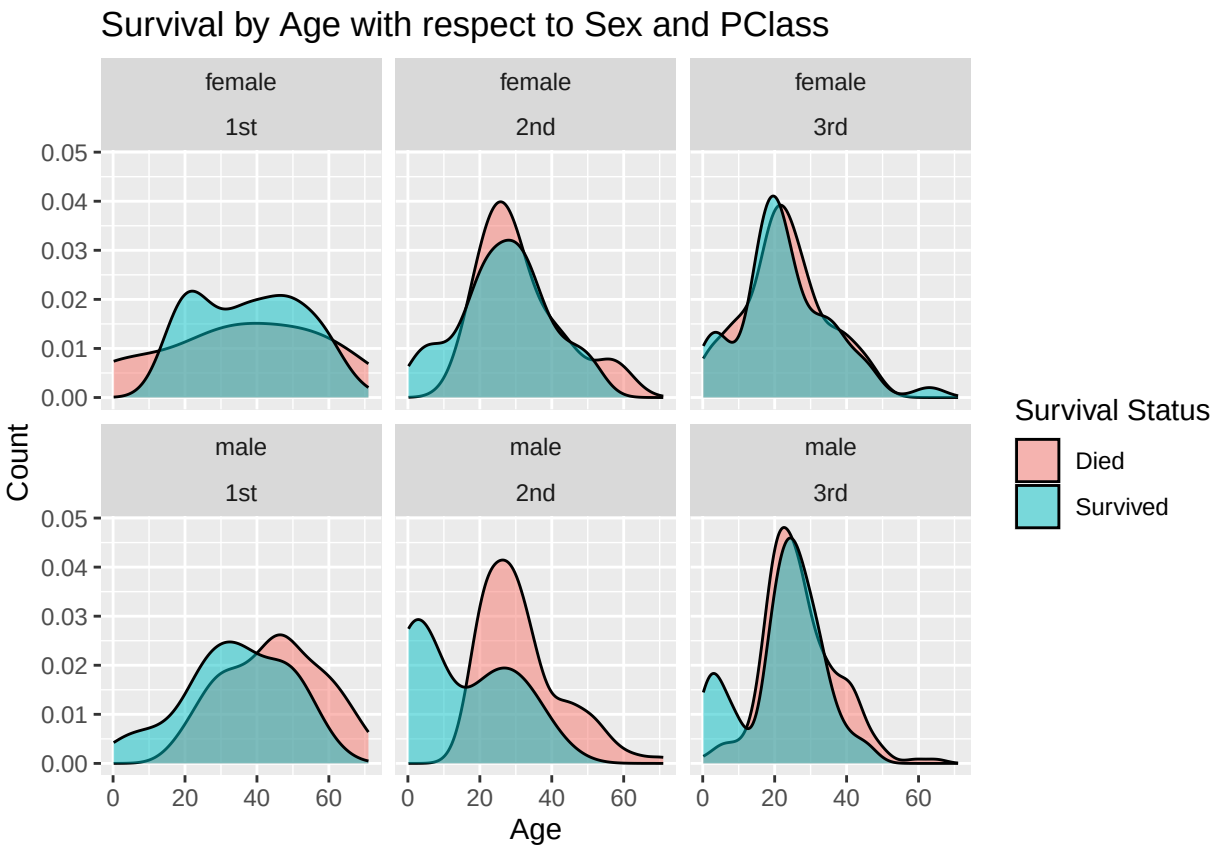
```
titanic %>%
  mutate(Survived = factor(Survived, labels = c("Died", "Survived"))) %>%
  ggplot(aes(x = Sex, fill = Survived)) +
  geom_bar() +
  facet_wrap(~PClass) +
  labs(
    title = "Survival by Sex and PClass",
    x = "Sex",
    y = "Count",
    fill = "Survival Status"
  )
```



Survival based on Age with respect to Sex and PClass

```
titanic %>%
  mutate(Survived = factor(Survived, labels = c("Died", "Survived"))) %>%
  ggplot(aes(x = Age, fill = Survived)) +
  geom_density(alpha = 0.5) +
  facet_wrap(~Sex + PClass) +
  labs(x = "Age",
       y = "Count",
       title = "Survival by Age with respect to Sex and PClass",
       fill = "Survival Status")
```

```
## Warning: Removed 557 rows containing non-finite values (`stat_density()`).
```



We will fit a liniar model, having `Survived` as the effect and, independently, `PClass`, `Age` and `Sex` as possible causes.

```
model <- glm(Survived ~ PClass + Age + Sex, data = titanic, family = binomial)
model_summary <- summary(model)$coefficients
model_summary
```

```
##                Estimate  Std. Error    z value     Pr(>|z|)
## (Intercept)  3.75966210 0.397567324   9.456668 3.179129e-21
## PClass2nd   -1.29196240 0.260075781  -4.967638 6.777324e-07
## PClass3rd   -2.52141915 0.276656805  -9.113888 7.948131e-20
## Age         -0.03917681 0.007616218  -5.143868 2.691392e-07
## Sexmale     -2.63135683 0.201505379 -13.058494 5.684093e-39
```

```
age_effect_estimate <- summary(model)$coefficients["Age", "Estimate"]
age_p_value <- summary(model)$coefficients["Age", "Pr(>|z|)"]

pclass2nd_p_value <- summary(model)$coefficients["PClass2nd", "Pr(>|z|)"]
pclass3nd_p_value <- summary(model)$coefficients["PClass3rd", "Pr(>|z|)"]
sexmale_p_value <- summary(model)$coefficients["Sexmale", "Pr(>|z|)"]
```

We observe a low p_value (2.6913921×10^{-7}) for Age, therefore were reject the initial hypothesis and conclude that age has an effect on the Survival. Apparently, the chances of survival change with (-0.0391768) with each year.

We observe a low p_values for PClass2nd (6.7773237×10^{-7}), PClass3rd ($7.9481311 \times 10^{-20}$), Sexmale ($5.6840932 \times 10^{-39}$), therefore were reject the initial hypothesis and conclude that being 2nd class, 3rd class or being a male has an effect on the Survival.

b) Interactions + Studying a 55 years old person chances to survive

Interactions

```
model_age_pclass <- glm(Survived ~ Age:PClass, data = titanic, family = "binomial")
age_first_class = summary(model_age_pclass)$coefficients["Age:PClass1st", "Pr(>|z|)"]
age_second_class = summary(model_age_pclass)$coefficients["Age:PClass2nd", "Pr(>|z|)"]
age_third_class = summary(model_age_pclass)$coefficients["Age:PClass3rd", "Pr(>|z|)"]
```

Age * PClass interaction Big P values (> 0.05) for Age:PClass1st (0.0724887) and Age:PClass3rd (5.972008×10^{-14}) suggest there is no strong evidence of an interaction between age and those classes passengers.

Low P value ($\ll 0.05$) for Age:PClass2nd (5.8083981×10^{-6}) suggest therestrong evidence of an interaction between age and 2nd class of passengers.

```
model_age_sex <- glm(Survived ~ Age:Sex, data = titanic, family = "binomial")
age_female = summary(model_age_sex)$coefficients["Age:Sexfemale", "Pr(>|z|)"]
age_male = summary(model_age_sex)$coefficients["Age:Sexmale", "Pr(>|z|)"]
```

Age * Sex interaction Low P values ($\ll 0.05$) for Age:Sexfemale (7.2489359×10^{-7}) and Age:Sexmale (age_male) suggest there is strong evidence of an interaction between age and the sex of the passenger

Hypothetical of a 55 years old person

We build a linear model to predict `Survival` with respect to `Age`, `PClass`, `Sex` and their interactions.

```
model <- glm(Survived ~ Age*PClass*Sex, data = titanic, family = "binomial")
male_first <- predict(model, data.frame(Age = 55, PClass = "1st", Sex = "male"), type = "response")
male_second <- predict(model, data.frame(Age = 55, PClass = "2nd", Sex = "male"), type = "response")
male_third <- predict(model, data.frame(Age = 55, PClass = "3rd", Sex = "male"), type = "response")

female_first <- predict(model, data.frame(Age = 55, PClass = "1st", Sex = "female"), type = "response")
female_second <- predict(model, data.frame(Age = 55, PClass = "2nd", Sex = "female"), type = "response")
female_third <- predict(model, data.frame(Age = 55, PClass = "3rd", Sex = "female"), type = "response")
```

- Male
  - 55 years old `male` of `1st` class has a change of 18.5658098% to survive.
  - 55 years old `male` of `2nd` class has a change of 0.2056975% to survive.
  - 55 years old `male` of `3rd` class has a change of 3.5889482% to survive.

- Female
  - 55 years old `female` of `1st` class has a change of 96.0046036% to survive.
  - 55 years old `female` of `2nd` class has a change of 77.6731219% to survive.
  - 55 years old `female` of `3rd` class has a change of 44.5486448% to survive.

Based on previous predictions we argue that a 1st class 55 years old female 96.0046036% was very likely to survive, while a 2nd class 55 years old male (96.0046036%) would have likely died.

c) Survival status predictor + quality measures

I would use a random forest classifier as a predictor.

First I would fill in the missing data with following heuristic:

- Average age for the missing values on `Age` column.
- 50% male/female for missing values on `Sex` column.

We could use cross-validation to split the dataset into train/test datasets.

Python implementation is pretty straightforward with the usage of sklearn.ensemble.RandomForestClassifier class. As quality measures we could use:

- precision [`TP / (TP + FP)`]
- recall [`TP/ (TP + FN)`]
- accuracy [`(TP + TN) / ALL`]

Due to the stochastic nature of the heuristic chosen for filling in `Sex` column and cross-validation dataset splits, I argue the following:

```
* Multiple experiments should be  with respect to cross-validation heuristic.
* The deviation of the `precision`, `recall` and `accuracy` values should be analysed.
```

d) Contingency table test

We will perform two `chi-squared` tests of independence:

Association between `Survival` and `PClass`

```
class_survival_p_value = chisq.test(table(titanic$Survived, titanic$PClass))$p.value
```

We observe a small (« 0.05) P value ($3.8523155 \times 10^{-38}$) for our test, therefore, we reject the null hypothesis and conclude that there is evidence of an association between the `Survival` and `PClass`.

Association between `Survival` and `Sex`

```
sex_survival_p_value = chisq.test(table(titanic$Survived, titanic$Sex))$p.value
```

We observe a small (« 0.05) P value ($1.0404031 \times 10^{-73}$) for our test, therefore, we reject the null hypothesis and conclude that there is evidence of an association between the `Survival` and `Sex`.

e) `random forest classifier` vs `chi-squared` independence test.

`chi-squared` test provides a statistical significance test to check association between `Survival` and (`PClass` | `Sex`). It was useful and fast to get insights over the dataset and to statistically derive the association between (`PClass` | `Sex`) and `Survival`.

Arguably, `random forest classifier` offers a predictive model which can be used for extensive analysis.

Both methods serve their purposes in a complementary way.