

<https://github.com/catebros/ML-fundamentals-2025>

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import sklearn
import scipy
import kagglehub
path = 'titanic3.xls'
```

✓ Task 1: Data Loading and Initial Exploration

Lecture material: Lecture 3, slides 4–8, 10, and 11.

- Load the dataset into a Pandas DataFrame.
- Perform basic exploratory data analysis (EDA) to comprehend the structure and characteristics of the data. Note: Your analysis should include appropriate exploratory statistics and visualizations

```
df = pd.read_excel(path)
```

```
df.shape
```

```
(1309, 14)
```

Our dataset contains 1,309 entries, however, historical records indicate that the Titanic had a total of 2,240 passengers, of whom 1,510 lost their lives in 1912.

```
df.head()
```

	pclass	survived	name	sex	age	sibsp	parch	ticket	fare	cabin	embarked	boat	body	home.dest
0	1	1	Allen, Miss. Elisabeth Walton	female	29.0000	0	0	24160	211.3375	B5	S	2	NaN	St Louis, MO
1	1	1	Allison, Master. Hudson Trevor	male	0.9167	1	2	113781	151.5500	C22 C26	S	11	NaN	Montreal, PQ / Chesterville, ON
2	1	0	Allison, Miss. Helen Loraine	female	2.0000	1	2	113781	151.5500	C22 C26	S	NaN	NaN	Montreal, PQ / Chesterville, ON
3	1	0	Allison, Mr. Hudson	male	29.0000	1	2	113781	151.5500	C22	S	NaN	NaN	Montreal, PQ /

```
df.describe()
```

	pclass	survived	age	sibsp	parch	fare	body
count	1309.000000	1309.000000	1046.000000	1309.000000	1309.000000	1308.000000	121.000000
mean	2.294882	0.381971	29.881135	0.498854	0.385027	33.295479	160.809917
std	0.837836	0.486055	14.413500	1.041658	0.865560	51.758668	97.696922
min	1.000000	0.000000	0.166700	0.000000	0.000000	0.000000	1.000000
25%	2.000000	0.000000	21.000000	0.000000	0.000000	7.895800	72.000000
50%	3.000000	0.000000	28.000000	0.000000	0.000000	14.454200	155.000000
75%	3.000000	1.000000	39.000000	1.000000	0.000000	31.275000	256.000000
max	3.000000	1.000000	80.000000	8.000000	9.000000	512.329200	328.000000

```
df.dtypes
```

```
pclass      int64
survived     int64
name         object
sex          object
age          float64
sibsp        int64
parch        int64
ticket       object
fare         float64
cabin        object
embarked     object
boat         object
body         float64
```

```
home.dest    object
dtype: object
```

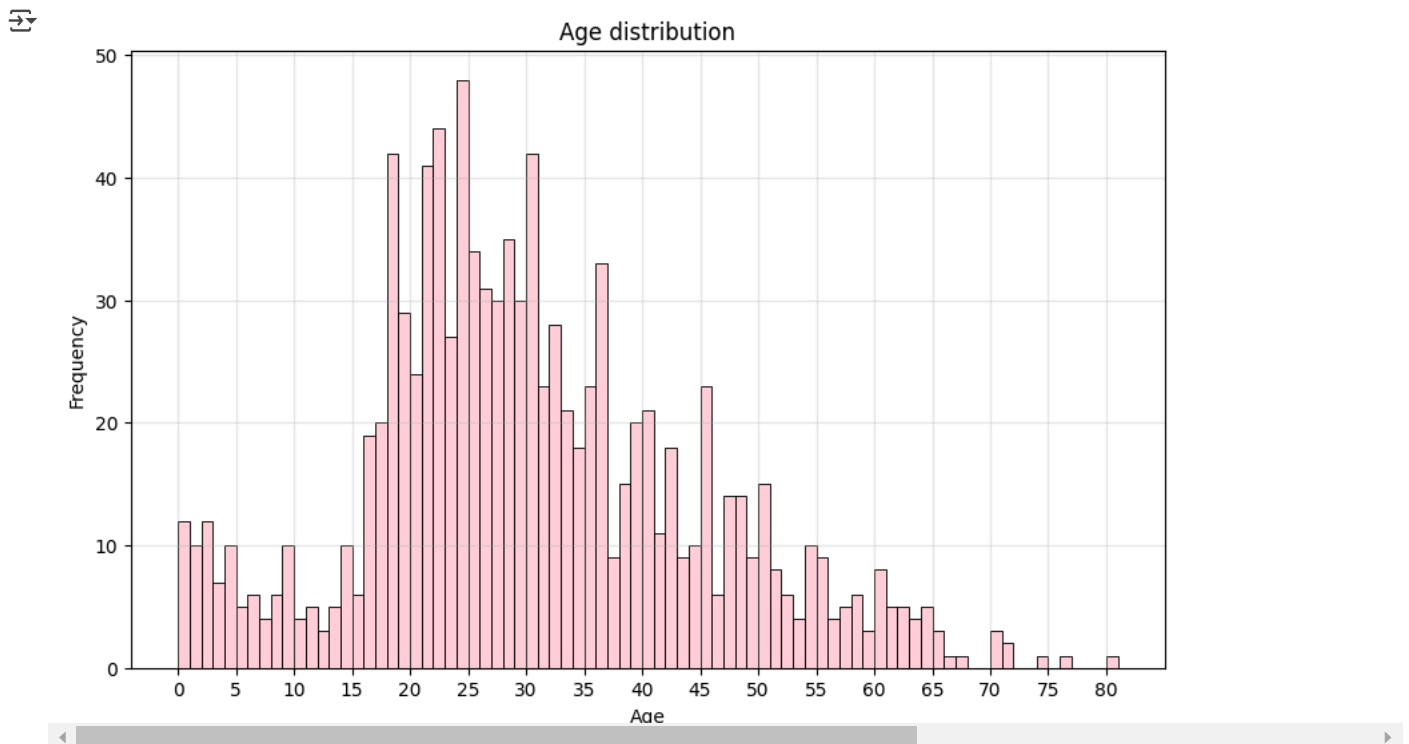
Variables of the Dataset

- pclass: Passenger class, represented as an integer from 1 to 3, indicating socio-economic status (1 = First Class, 2 = Second Class, 3 = Third Class).
- survived: Survival status of the passenger, where 1 = Survived and 0 = Did not survive, this is also out target variable.
- name: Full name of the passenger, including title (e.g., Mr., Mrs., Miss), as a string.
- sex: Gender of the passenger, recorded as a string (female or male).
- age: Age of the passenger as a float.
- sibsp: Number of siblings and spouses the passenger had aboard the Titanic, as an integer
- parch: Number of parents and children the passenger was traveling with, as an integer.
- fare: Amount paid for the ticket, as a float ranging from 0 to 512.329, measured in British Pounds.
- cabin: Cabin number assigned to the passenger, recorded as a string.
- embarked: The port where the passenger boarded the ship. The Titanic's route started at Southampton (S), then stopped at Cherbourg (C), followed by Queenstown (Q), before finally heading to New York.
- boat: Number of the lifeboat the passenger boarded, if they were rescued
- body: If the passenger did not survive, this indicates the body identification number, if recovered, recorded as float.
- home.dest: Final destination of the passenger, indicating where they were traveling to, recorded as a string.
- ticket: passenger/s ticket

✓ Numerical variables

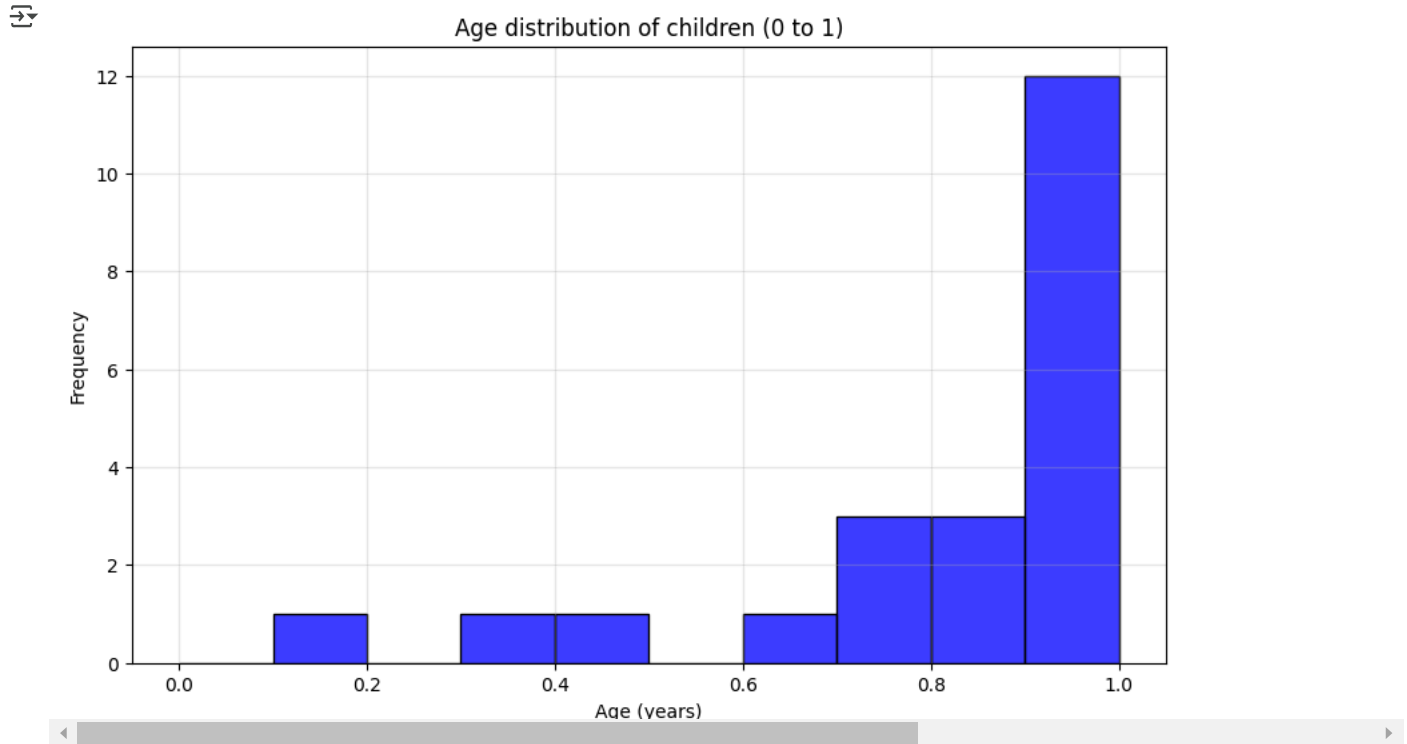
✓ Age

```
# frequency of age
plt.figure(figsize=(10, 6))
# we adapt the bins to the years
bins_survived = np.arange(0, df['age'].max() + 2)
sns.histplot(data=df, x='age', bins=bins_survived, color='pink', binrange=(0, df['age'].max() + 1))
plt.title('Age distribution')
plt.xlabel('Age')
plt.ylabel('Frequency')
plt.xticks(np.arange(0, df['age'].max() + 1, 5))
plt.grid(True, alpha=0.3)
plt.show()
```



The age variable is a float, as we know that there could have been babies aboard the Titanic. The following graph shows the distribution of ages.

```
# frequency of babies
children_0_1 = df[(df['age'] >= 0) & (df['age'] <= 1)]
bins = np.arange(0, 1.1, 0.1)
plt.figure(figsize=(10, 6))
sns.histplot(data=children_0_1, x='age', bins=bins, color='blue')
plt.title('Age distribution of children (0 to 1)')
plt.xlabel('Age (years)')
plt.ylabel('Frequency')
plt.grid(True, alpha=0.3)
plt.show()
```



It is important to check whether individuals older than 1 year have decimal values in their ages.

```
older_than_one_year = df[df['age'] > 1]
ages_with_decimals = older_than_one_year['age'] % 1 != 0

print(f'Total number of people older than 1 year with decimals in their age: {ages_with_decimals.sum()}')

non_integer_ages = older_than_one_year[ages_with_decimals]
print('Rows where age does not end with .0:')
print(non_integer_ages[['age']])
```

```
Total number of people older than 1 year with decimals in their age: 33
Rows where age does not end with .0:
   age
173  32.5
222  28.5
224  45.5
512  32.5
516  36.5
568  18.5
584  32.5
692  18.5
727  70.5
741  22.5
758  36.5
796  40.5
797  40.5
847  23.5
919  18.5
924  34.5
960  34.5
977  20.5
992  30.5
1015 55.5
1066 28.5
1169 38.5
1171 14.5
1192 24.5
1225 60.5
```

```

1251 30.5
1263 11.5
1264 40.5
1285 32.5
1294 28.5
1301 45.5
1304 14.5
1306 26.5

```

As we can see, there are 33 individuals older than 1 year whose age has a decimal, specifically, all of these individuals have their age ending in .5. It is interesting to explore the survival status of these individuals

```

ages_with_decimals = older_than_one_year[older_than_one_year['age'] % 1 != 0]

total_individuals = len(ages_with_decimals)
print(f'Total number of individuals older than 1 year with ages ending in .5: {total_individuals}')

survival_status = ages_with_decimals['survived'].value_counts(normalize=True)

print(f'Proportion of survivors: {survival_status.get(1, 0)}')
print(f'Proportion of non-survivors: {survival_status.get(0, 0)}')

```

```

↗ Total number of individuals older than 1 year with ages ending in .5: 33
Proportion of survivors: 0.060606060606061
Proportion of non-survivors: 0.9393939393939394

```

Even though 94% of individuals whose age ends in .5 did not survive, this data could be more meaningful if the sample of individuals with this specific characteristic were larger. However, it's challenging to generalize this idea to the entire model.

```

age_metrics = {
    'mean': df['age'].mean(),
    'variance': df['age'].var(),
    'standard_deviation': df['age'].std(),
    'median': df['age'].median(),
    'mode': df['age'].mode()[0],
    'min': df['age'].min(),
    'max': df['age'].max(),
    'count': df['age'].count(),
    'missing_values': df['age'].isnull().sum()
}

for metric, value in age_metrics.items():
    print(f'{metric.capitalize()}: {value}')

```

```

↗ Mean: 29.8811345124283
Variance: 207.74897359969773
Standard_deviation: 14.413499699923602
Median: 28.0
Mode: 24.0
Min: 0.1667
Max: 80.0
Count: 1046
Missing_values: 263

```

Based on the previous data, the variance of the age distribution is relatively high, indicating a broad spread of ages within the dataset. Additionally, there are 263 missing values in the age column. However, this will be addressed later.

Important: For all the plots that compare a feature based on survival, it's better to use a proportion plot, as the feature is still imbalanced and this method more accurately reflects the relationship.

```

survived = df[df['survived'] == 1]
not_survived = df[df['survived'] == 0]

plt.figure(figsize=(20, 6))

# we make 1 bin per year, for easier visualization
bins_survived = np.arange(0, survived['age'].max() + 2)
bins_not_survived = np.arange(0, not_survived['age'].max() + 2)

## 1st plot: Age distribution and survived
plt.subplot(1, 3, 1)
sns.histplot(data=survived, x='age', bins=bins_survived,
             stat='probability', color='green',
             binrange=(0, survived['age'].max() + 1), hue='survived')
plt.title('Age distribution (proportional) and survived')

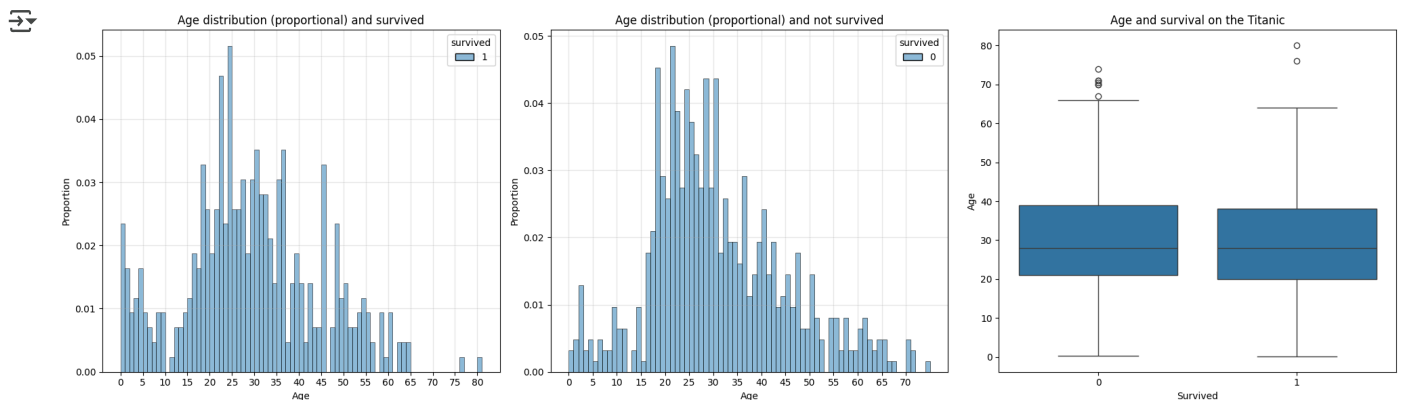
```

```
plt.xlabel('Age')
plt.ylabel('Proportion')
plt.xticks(np.arange(0, survived['age'].max() + 1, 5))
plt.grid(True, alpha=0.3)

# 2nd plot: Age distribution and not survived
plt.subplot(1, 3, 2)
sns.histplot(data=not_survived, x='age', bins=bins_not_survived,
             stat='probability', color='red',
             binrange=(0, not_survived['age'].max() + 1), hue='survived')
plt.title('Age distribution (proportional) and not survived')
plt.xlabel('Age')
plt.ylabel('Proportion')
plt.xticks(np.arange(0, not_survived['age'].max() + 1, 5))
plt.grid(True, alpha=0.3)

# 3rd plot: Boxplot - Age vs Survived
plt.subplot(1, 3, 3)
sns.boxplot(x='survived', y='age', data=df)
plt.xlabel('Survived')
plt.ylabel('Age')
plt.title('Age and survival on the Titanic')

plt.tight_layout()
plt.show()
```



Based on this, we observe a notable difference in the survival rates of individuals, with children between 0 and 10 years old having a higher chance of survival. On the other hand, older individuals, starting from 65 years and above, had a lower chance of survival. However, since the majority of the population falls between the ages of 15 and 40, this does not significantly impact the boxplots, and the mean age remains fairly stable between the survived and not survived groups. It might be interesting to remove the age variable and instead create a new categorical variable with the following age groups: below 15 years, between 15 and 50 years, and above 50 years.

✓ Fare

Fare represents the amount of money paid by a passenger individually

```
fig, axes = plt.subplots(1, 4, figsize=(22, 7))

bin_edges = range(0, int(df['fare'].max()) + 50, 50)

# fare distribution
sns.histplot(df['fare'], color='blue', ax=axes[0], bins=bin_edges)
axes[0].set_title('Overall fare distribution')
axes[0].set_xlabel('Fare')
axes[0].set_ylabel('Frequency')

# fare distribution for class 1 (second plot)
sns.histplot(df[df['pclass'] == 1]['fare'], color='lightblue', ax=axes[1], bins=bin_edges, alpha=0.7)
axes[1].set_title('Fare distribution and first class')
axes[1].set_xlabel('Fare')
```

```

axes[1].set_ylabel('Frequency')

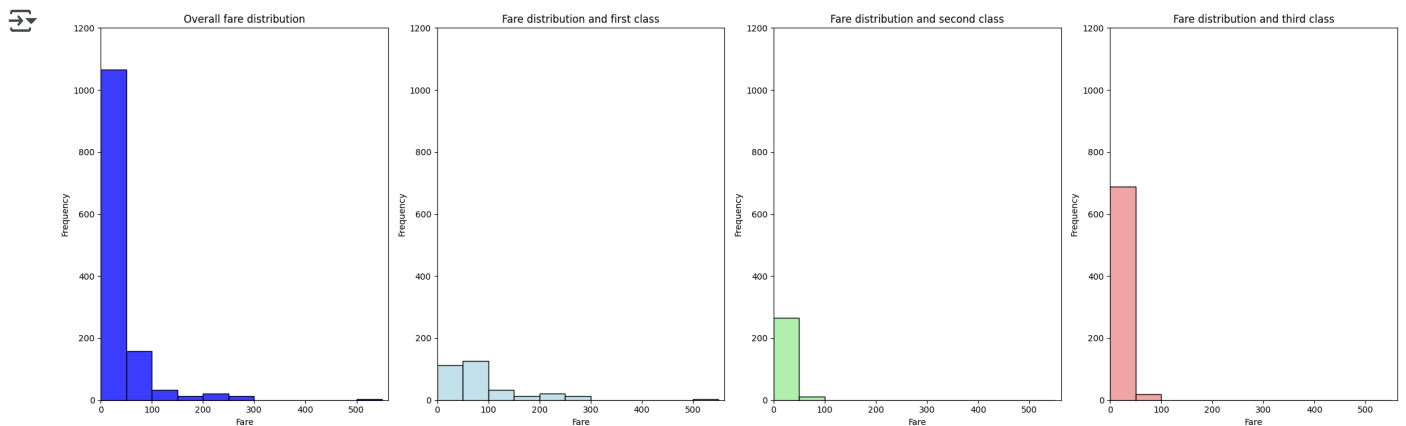
# fare distribution for class 2 (third plot)
sns.histplot(df[df['pclass'] == 2]['fare'], color='lightgreen', ax=axes[2], bins=bin_edges, alpha=0.7)
axes[2].set_title('Fare distribution and second class')
axes[2].set_xlabel('Fare')
axes[2].set_ylabel('Frequency')

# fare distribution for class 3 (fourth plot)
sns.histplot(df[df['pclass'] == 3]['fare'], color='lightcoral', ax=axes[3], bins=bin_edges, alpha=0.7)
axes[3].set_title('Fare distribution and third class')
axes[3].set_xlabel('Fare')
axes[3].set_ylabel('Frequency')

# apply the same x and y limits to all plots for consistency
max_fare = df['fare'].max()
axes[0].set_xlim(0, max_fare + 50)
axes[1].set_xlim(0, max_fare + 50)
axes[2].set_xlim(0, max_fare + 50)
axes[3].set_xlim(0, max_fare + 50)
axes[0].set_ylim(0, 1200)
axes[1].set_ylim(0, 1200)
axes[2].set_ylim(0, 1200)
axes[3].set_ylim(0, 1200)

plt.tight_layout()
plt.show()

```



```

bin_width = 10
max_fare = df['fare'].max()
bins = np.arange(0, max_fare + bin_width, bin_width)

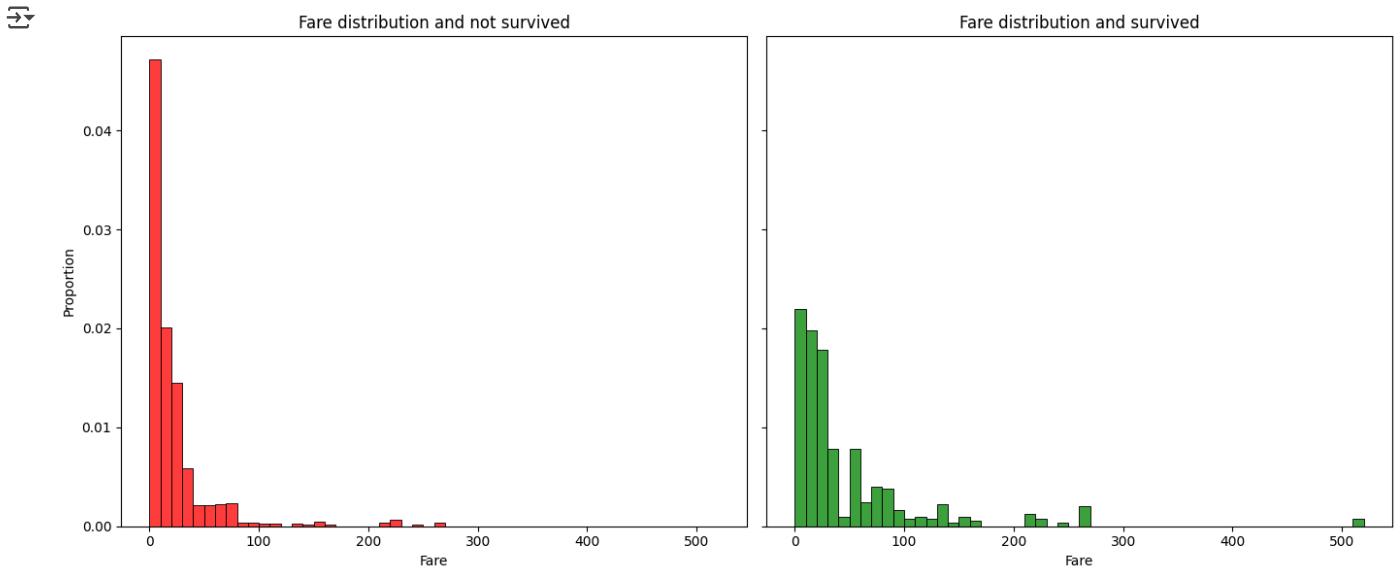
fig, axes = plt.subplots(1, 2, figsize=(14, 6), sharey=True, sharex=True)

# compare the fare of those who survived and not survived
sns.histplot(df[df['survived'] == 0]['fare'],
              bins=bins, color='red', stat='density', ax=axes[0])
axes[0].set_title('Fare distribution and not survived')
axes[0].set_xlabel('Fare')
axes[0].set_ylabel('Proportion')

sns.histplot(df[df['survived'] == 1]['fare'],
              bins=bins, color='green', stat='density', ax=axes[1])
axes[1].set_title('Fare distribution and survived')
axes[1].set_xlabel('Fare')

plt.tight_layout()
plt.show()

```



```
# these values looks like outliers,
max_fare = df['fare'].max()
person_max_fare = df[df['fare'] == max_fare]
print(person_max_fare)
```

```

49      1      1      Cardeza, Mr. Thomas Drake Martinez
50      1      1  Cardeza, Mrs. James Warburton Martinez (Charlo...
183     1      1      Lesurer, Mr. Gustave J
302     1      1      Ward, Miss. Anna

      sex  age  sibsp  parch  ticket      fare      cabin embarked \
49  male  36.0     0     1  PC 17755  512.3292  B51 B53 B55      C
50  female  58.0     0     1  PC 17755  512.3292  B51 B53 B55      C
183  male  35.0     0     0  PC 17755  512.3292      B101      C
302  female  35.0     0     0  PC 17755  512.3292      NaN      C

      boat  body      home.dest
49      3  NaN  Austria-Hungary / Germantown, Philadelphia, PA
50      3  NaN      Germantown, Philadelphia, PA
183     3  NaN      NaN
302     3  NaN      NaN
```

Body

This is a clear case of data leakage because it directly indicates the outcome we are trying to predict, whether someone survived or not.

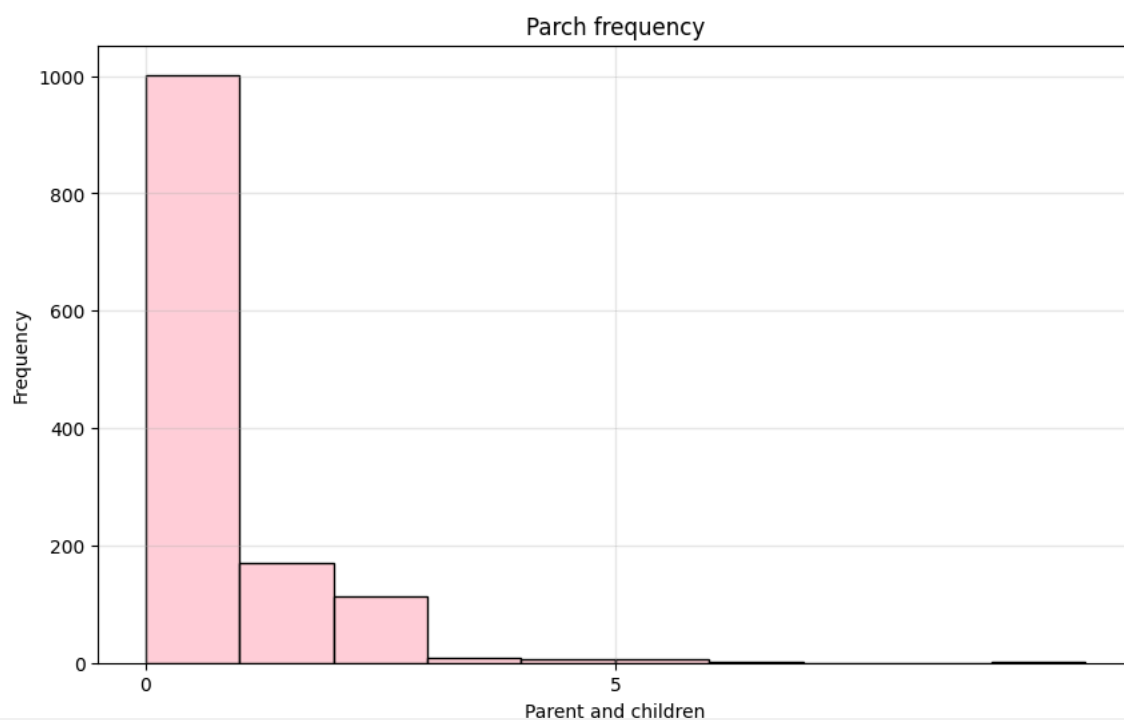
```
nobody_df = df.drop(columns=['body'])
print(nobody_df.columns)
```

```
Index(['pclass', 'survived', 'name', 'sex', 'age', 'sibsp', 'parch', 'ticket',
      'fare', 'cabin', 'embarked', 'boat', 'home.dest'],
      dtype='object')
```

Parch

```
# frequency of parch
plt.figure(figsize=(10, 6))
bins_survived = np.arange(0, nobody_df['parch'].max() + 2)
sns.histplot(data=nobody_df, x='parch', bins=bins_survived, color='pink', binrange=(0, nobody_df['parch'].max() + 1))
plt.title('Parch frequency')
plt.xlabel('Parent and children')
plt.ylabel('Frequency')
plt.xticks(np.arange(0, nobody_df['parch'].max() + 1, 5))
```

```
plt.grid(True, alpha=0.3)
plt.show()
```



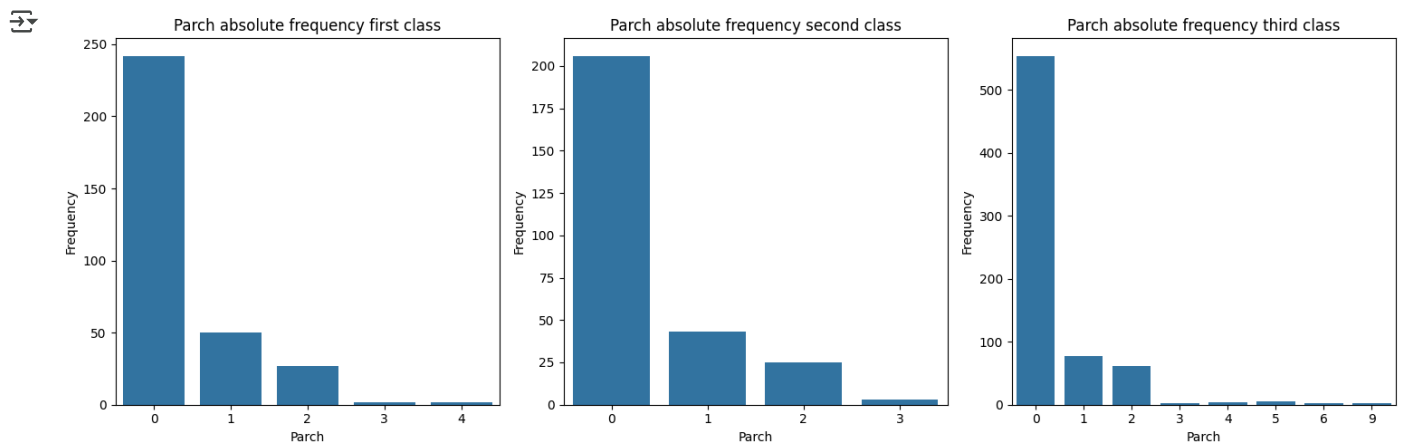
```
plt.figure(figsize=(15, 5))
```

```
plt.subplot(1, 3, 1)
sns.countplot(data=df[nobody_df['pclass'] == 1], x='parch')
plt.title('Parch absolute frequency first class')
plt.xlabel('Parch')
plt.ylabel('Frequency')
```

```
plt.subplot(1, 3, 2)
sns.countplot(data=df[nobody_df['pclass'] == 2], x='parch')
plt.title('Parch absolute frequency second class')
plt.xlabel('Parch')
plt.ylabel('Frequency')
```

```
plt.subplot(1, 3, 3)
sns.countplot(data=df[nobody_df['pclass'] == 3], x='parch')
plt.title('Parch absolute frequency third class')
plt.xlabel('Parch')
plt.ylabel('Frequency')
```

```
plt.tight_layout()
plt.show()
```

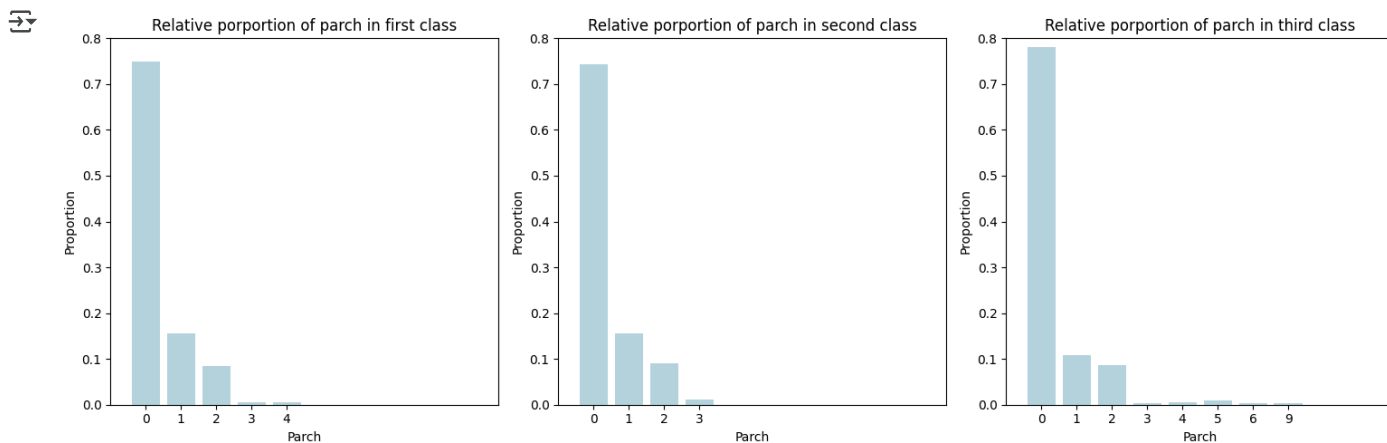
```
plt.figure(figsize=(15, 5))

class_data = df[nobody_df['pclass'] == 1]
parch_counts = class_data['parch'].value_counts(normalize=True).sort_index()
plt.subplot(1, 3, 1)
sns.barplot(x=parch_counts.index, y=parch_counts.values, color='lightblue')
plt.ylim(0, 0.8)
plt.xlim(-1, 10)
plt.title(f'Relative porportion of parch in first class')
plt.xlabel('Parch')
plt.ylabel('Proportion')

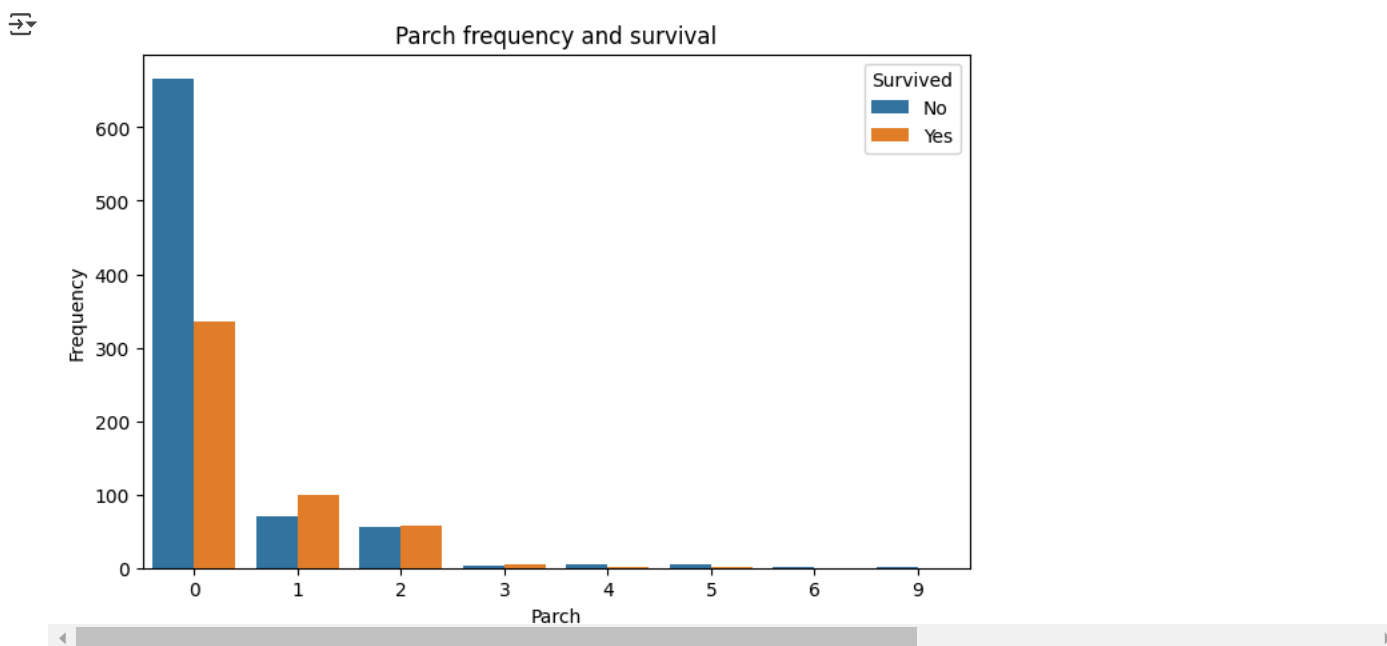
class_data = df[nobody_df['pclass'] == 2]
parch_counts = class_data['parch'].value_counts(normalize=True).sort_index()
plt.subplot(1, 3, 2)
sns.barplot(x=parch_counts.index, y=parch_counts.values, color='lightblue')
plt.ylim(0, 0.8)
plt.xlim(-1, 10)
plt.title(f'Relative porportion of parch in second class')
plt.xlabel('Parch')
plt.ylabel('Proportion')

class_data = df[nobody_df['pclass'] == 3]
parch_counts = class_data['parch'].value_counts(normalize=True).sort_index()
plt.subplot(1, 3, 3)
sns.barplot(x=parch_counts.index, y=parch_counts.values, color='lightblue')
plt.ylim(0, 0.8)
plt.xlim(-1, 10)
plt.title(f'Relative porportion of parch in third class')
plt.xlabel('Parch')
plt.ylabel('Proportion')

plt.tight_layout()
plt.show()
```

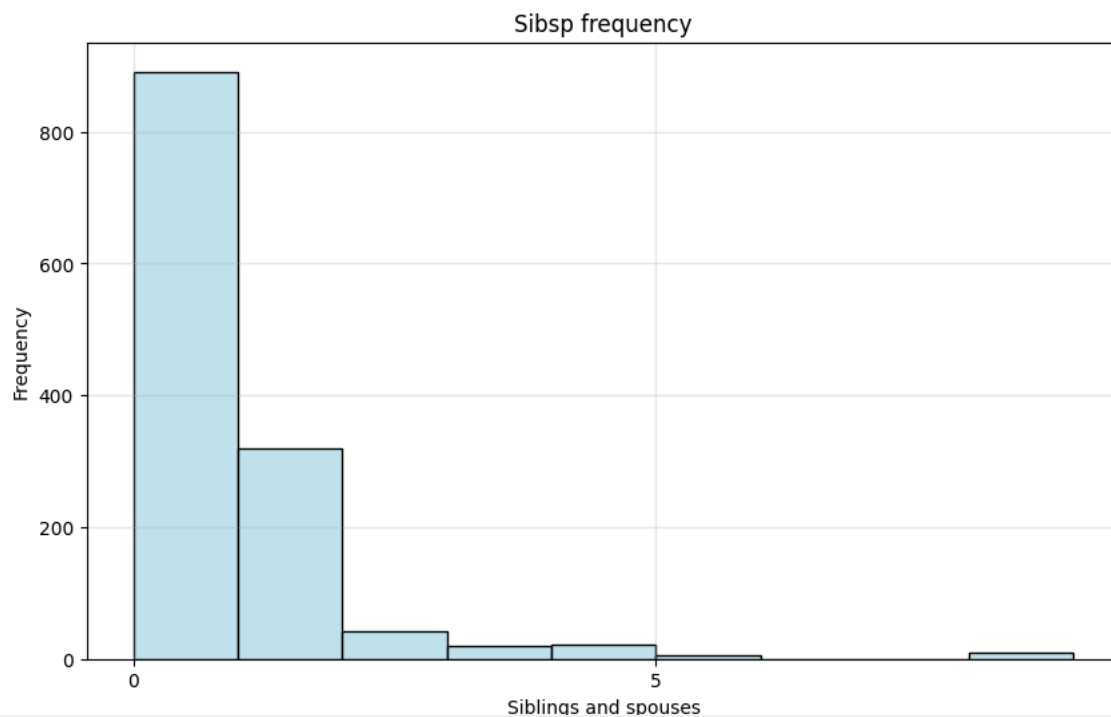


```
plt.figure(figsize=(8, 5))
sns.countplot(data=nobody_df, x='parch', hue='survived')
plt.title('Parch frequency and survival')
plt.xlabel('Parch')
plt.ylabel('Frequency')
plt.legend(title='Survived', labels=['No', 'Yes'])
plt.show()
```



▽ Sibsp

```
# frequency of sibsp
plt.figure(figsize=(10, 6))
bins_survived = np.arange(0, nobody_df['sibsp'].max() + 2)
sns.histplot(data=nobody_df, x='sibsp', bins=bins_survived, color='lightblue', binrange=(0, df['sibsp'].max() + 1))
plt.title('Sibsp frequency')
plt.xlabel('Siblings and spouses')
plt.ylabel('Frequency')
plt.xticks(np.arange(0, nobody_df['sibsp'].max() + 1, 5))
plt.grid(True, alpha=0.3)
plt.show()
```



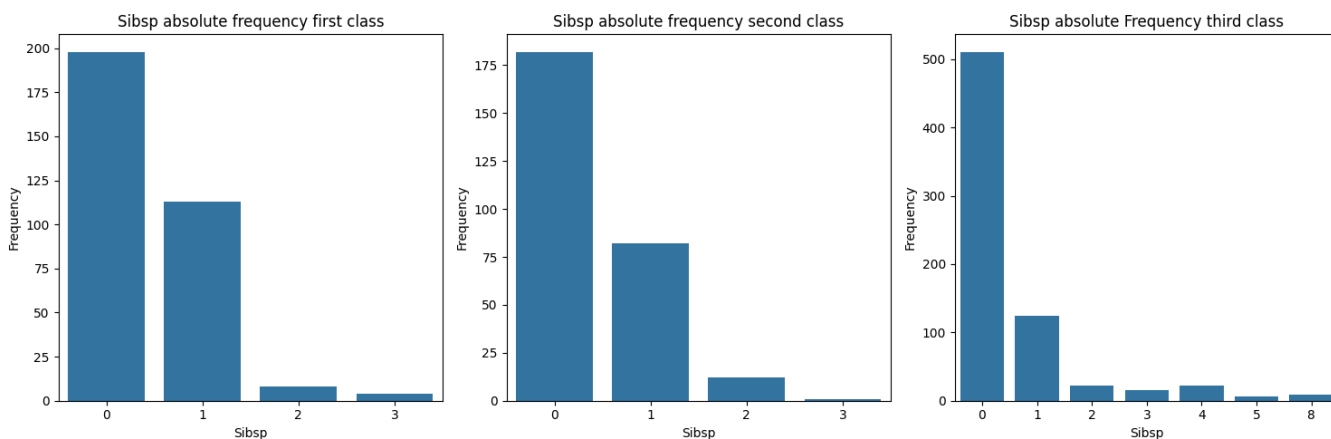
```
plt.figure(figsize=(15, 5))
```

```
plt.subplot(1, 3, 1)
sns.countplot(data=df[nobody_df['pclass'] == 1], x='sibsp')
plt.title('Sibsp absolute frequency first class')
plt.xlabel('Sibsp')
plt.ylabel('Frequency')
```

```
plt.subplot(1, 3, 2)
sns.countplot(data=df[nobody_df['pclass'] == 2], x='sibsp')
plt.title('Sibsp absolute frequency second class')
plt.xlabel('Sibsp')
plt.ylabel('Frequency')
```

```
plt.subplot(1, 3, 3)
sns.countplot(data=df[nobody_df['pclass'] == 3], x='sibsp')
plt.title('Sibsp absolute Frequency third class')
plt.xlabel('Sibsp')
plt.ylabel('Frequency')
```

```
plt.tight_layout()
plt.show()
```



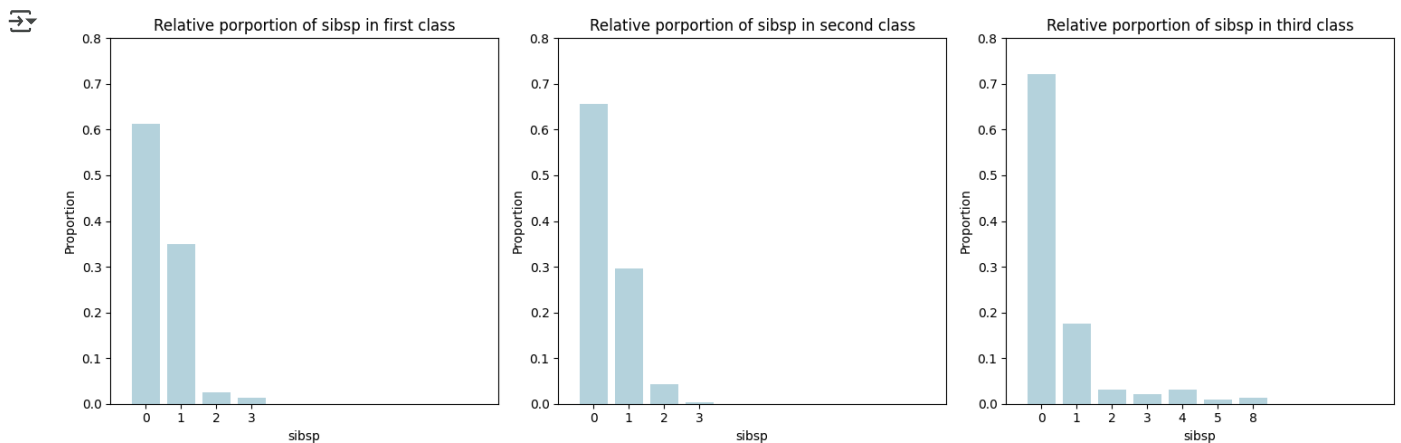
```
plt.figure(figsize=(15, 5))

class_data = df[nobody_df['pclass'] == 1]
parch_counts = class_data['sibsp'].value_counts(normalize=True).sort_index()
plt.subplot(1, 3, 1)
sns.barplot(x=parch_counts.index, y=parch_counts.values, color='lightblue')
plt.ylim(0, 0.8)
plt.xlim(-1, 10)
plt.title(f'Relative porportion of sibsp in first class')
plt.xlabel('sibsp')
plt.ylabel('Proportion')

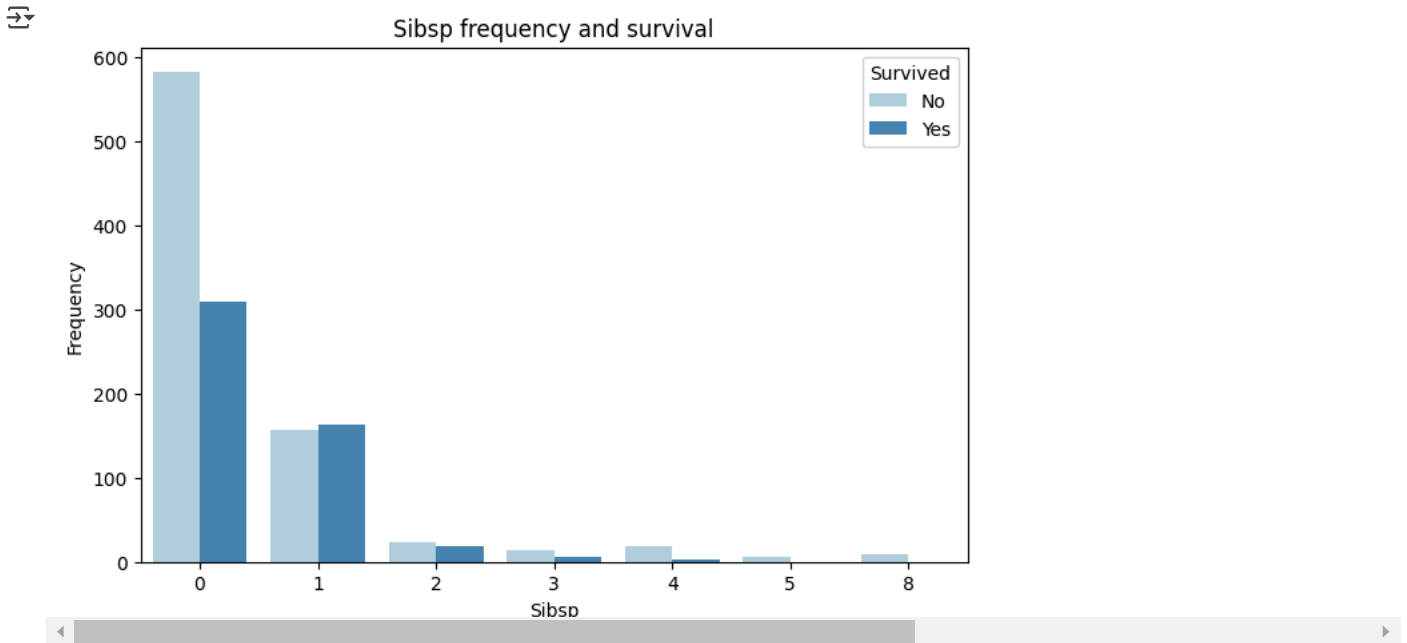
class_data = df[nobody_df['pclass'] == 2]
parch_counts = class_data['sibsp'].value_counts(normalize=True).sort_index()
plt.subplot(1, 3, 2)
sns.barplot(x=parch_counts.index, y=parch_counts.values, color='lightblue')
plt.ylim(0, 0.8)
plt.xlim(-1, 10)
plt.title(f'Relative porportion of sibsp in second class')
plt.xlabel('sibsp')
plt.ylabel('Proportion')

class_data = df[nobody_df['pclass'] == 3]
parch_counts = class_data['sibsp'].value_counts(normalize=True).sort_index()
plt.subplot(1, 3, 3)
sns.barplot(x=parch_counts.index, y=parch_counts.values, color='lightblue')
plt.ylim(0, 0.8)
plt.xlim(-1, 10)
plt.title(f'Relative porportion of sibsp in third class')
plt.xlabel('sibsp')
plt.ylabel('Proportion')

plt.tight_layout()
plt.show()
```



```
plt.figure(figsize=(8, 5))
sns.countplot(data=nobody_df, x='sibsp', hue='survived', palette='Blues')
plt.title('Sibsp frequency and survival')
plt.xlabel('Sibsp')
plt.ylabel('Frequency')
plt.legend(title='Survived', labels=['No', 'Yes'])
plt.show()
```



✓ Sibsp + Parch

It may be beneficial for our model to introduce two new features derived from parch and sibsp: a boolean variable, 'alone', indicating whether a passenger was traveling alone, and another feature, 'relatives', representing the total number of family members on board.

```
# alone: 0/boolean
nobody_df['alone'] = ((nobody_df['sibsp'] == 0) & (nobody_df['parch'] == 0)).astype(int)
```

```
# relatives: numerical
nobody_df['relatives'] = nobody_df['sibsp'] + nobody_df['parch']
```

```
print(nobody_df.head())
```

```

pclass  survived      name  sex \
0      1         1  Allen, Miss. Elisabeth Walton  female
1      1         1  Allison, Master. Hudson Trevor  male
2      1         0  Allison, Miss. Helen Loraine  female
3      1         0  Allison, Mr. Hudson Joshua Creighton  male
4      1         0  Allison, Mrs. Hudson J C (Bessie Waldo Daniels)  female

age  sibsp  parch  ticket  fare  cabin embarked boat \
0  29.0000  0     0   24160  211.3375  B5      S      2
1   0.9167  1     2  113781  151.5500  C22 C26  S     11
2   2.0000  1     2  113781  151.5500  C22 C26  S    NaN
3  30.0000  1     2  113781  151.5500  C22 C26  S    NaN
4  25.0000  1     2  113781  151.5500  C22 C26  S    NaN

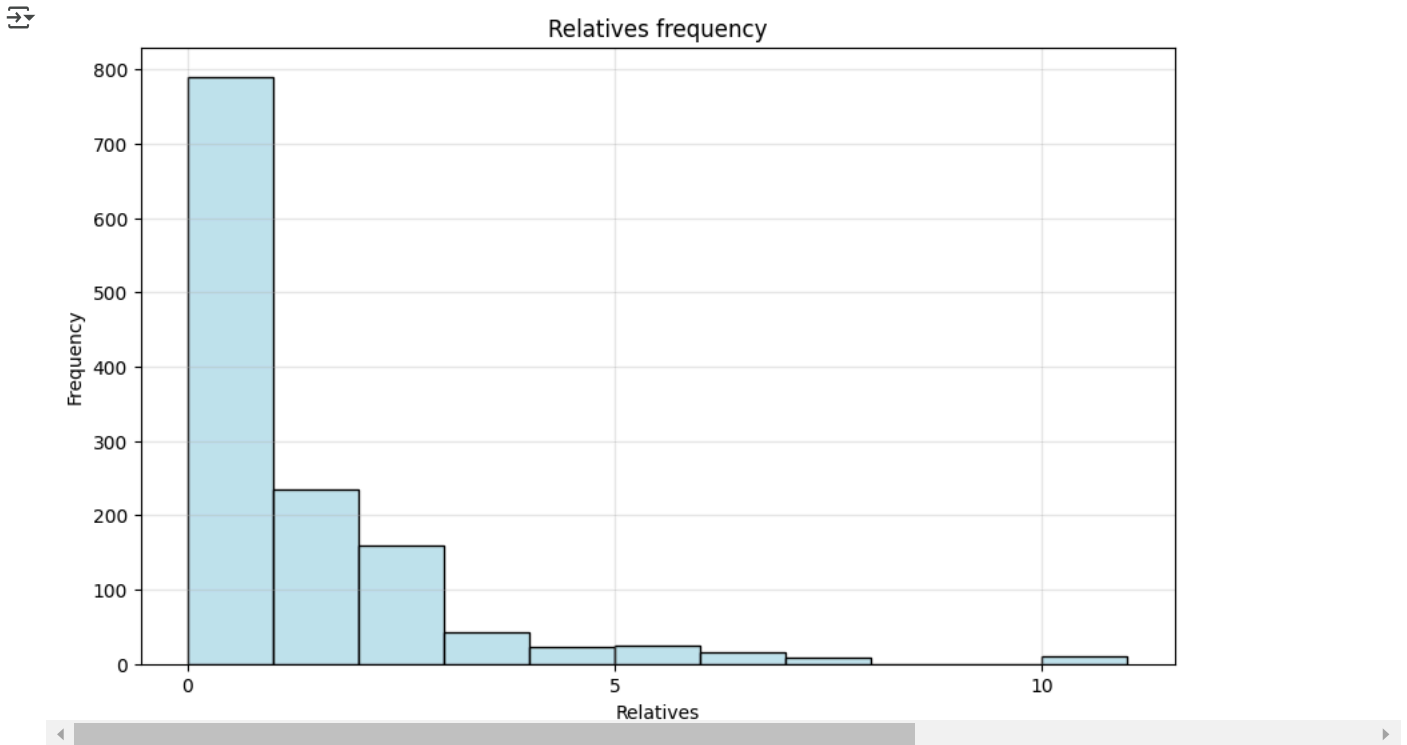
home.dest  alone  relatives
0      St Louis, MO      1         0
1  Montreal, PQ / Chesterville, ON      0         3
2  Montreal, PQ / Chesterville, ON      0         3
3  Montreal, PQ / Chesterville, ON      0         3
4  Montreal, PQ / Chesterville, ON      0         3

```

```

# Plot frequency of sibsp
plt.figure(figsize=(10, 6))
bins_survived = np.arange(0, nobody_df['relatives'].max() + 2)
sns.histplot(data=nobody_df, x='relatives', bins=bins_survived, color='lightblue', binrange=(0, nobody_df['sibsp'].max() + 1))
plt.title('Relatives frequency')
plt.xlabel('Relatives')
plt.ylabel('Frequency')
plt.xticks(np.arange(0, nobody_df['relatives'].max() + 1, 5))
plt.grid(True, alpha=0.3)
plt.show()

```



```
relatives_percentage = pd.crosstab(nobody_df['relatives'], nobody_df['survived'], normalize='index') * 100
relatives_percentage.columns = ['Did not survive (%)', 'Survived (%)']
```

```
# For 'alone' (0/1) by survival status with percentages
```

```
alone_percentage = pd.crosstab(nobody_df['alone'], nobody_df['survived'], normalize='index') * 100
alone_percentage.columns = ['Did not survive (%)', 'Survived (%)']
```

```
# Display the tables with percentages by level
```

```
print("Percentage distribution for 'relatives' by survival:")
print(relatives_percentage)
```

```
print("\nPercentage distribution for 'alone' by survival:")
print(alone_percentage)
```

```
Percentage distribution for 'relatives' by survival:
```

	Did not survive (%)	Survived (%)
relatives		
0	69.746835	30.253165
1	46.382979	53.617021
2	43.396226	56.603774
3	30.232558	69.767442
4	72.727273	27.272727
5	80.000000	20.000000
6	75.000000	25.000000
7	100.000000	0.000000
10	100.000000	0.000000

```
Percentage distribution for 'alone' by survival:
```

	Did not survive (%)	Survived (%)
alone		
0	49.710983	50.289017
1	69.746835	30.253165

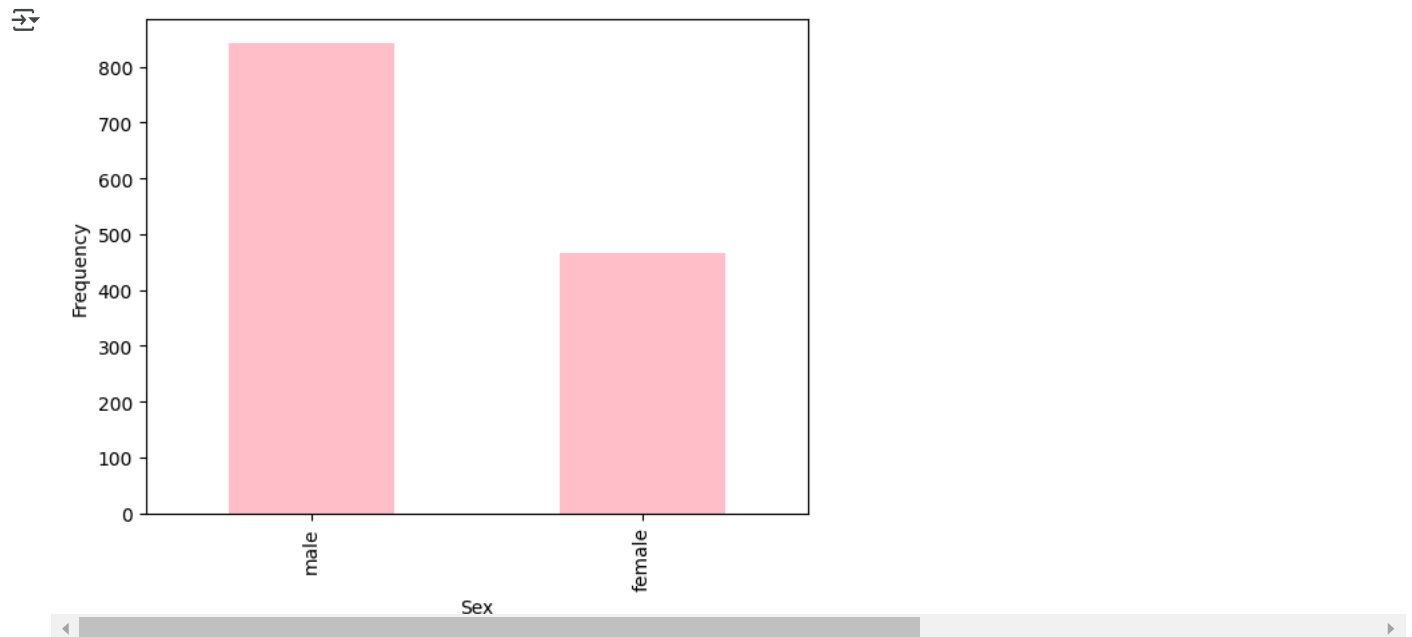
Passengers traveling alone had a significantly lower survival rate (30.25%) compared to those with at least one relative (50.29%), suggesting that family presence played a crucial role in survival. The highest survival rate (69.77%) was observed among those with three relatives, indicating that moderate family support may have facilitated evacuation. However, survival rates dropped for those with four or more relatives, with families of seven or ten experiencing 100% mortality. However, since there were fewer passengers in these larger family groups, it's harder to draw strong conclusions from their survival patterns.

✓ Categorical Variables

- Pclass
- Embarked
- Boat
- Sex
- Survived

▾ Sex

```
nobody_df['sex'].value_counts().plot(kind='bar', edgecolor = 'none', color = 'pink')
plt.title('')
plt.xlabel('Sex')
plt.ylabel('Frequency')
plt.show()
```



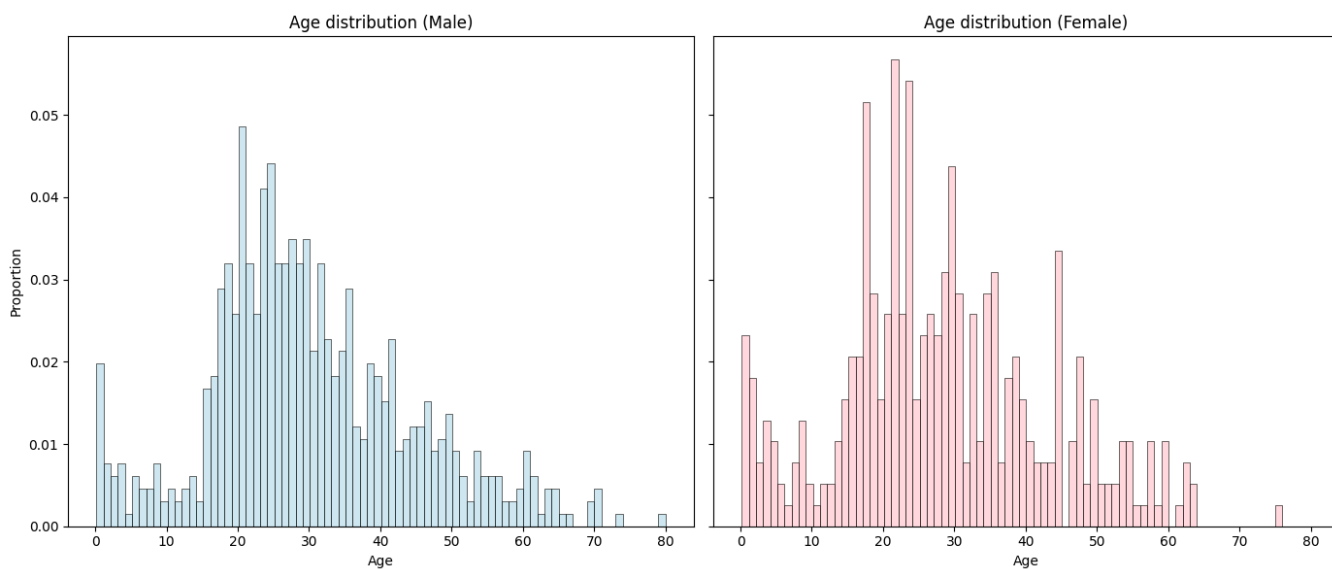
```
bins = np.linspace(nobody_df['age'].min(), nobody_df['age'].max(), 81)
male_ages = df[nobody_df['sex'] == 'male']['age'].dropna()
female_ages = df[nobody_df['sex'] == 'female']['age'].dropna()

fig, axes = plt.subplots(1, 2, figsize=(14, 6), sharey=True)

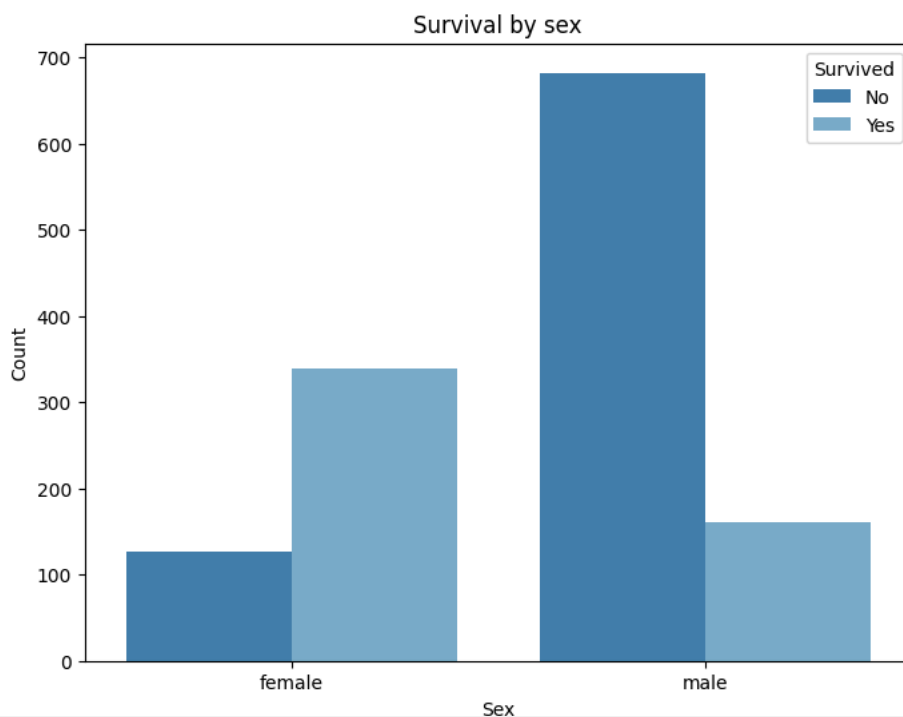
sns.histplot(male_ages, bins=bins, color='lightblue', alpha=0.6, stat='probability', ax=axes[0])
axes[0].set_title('Age distribution (Male)')
axes[0].set_xlabel('Age')
axes[0].set_ylabel('Proportion')

sns.histplot(female_ages, bins=bins, color='pink', alpha=0.6, stat='probability', ax=axes[1])
axes[1].set_title('Age distribution (Female)')
axes[1].set_xlabel('Age')
axes[1].set_ylabel('Proportion')

plt.tight_layout()
plt.show()
```



```
plt.figure(figsize=(8, 6))
sns.countplot(data=nobody_df, x='sex', hue='survived', palette='tab20c')
plt.title('Survival by sex')
plt.xlabel('Sex')
plt.ylabel('Count')
plt.legend(title='Survived', labels=['No', 'Yes'])
plt.show()
```

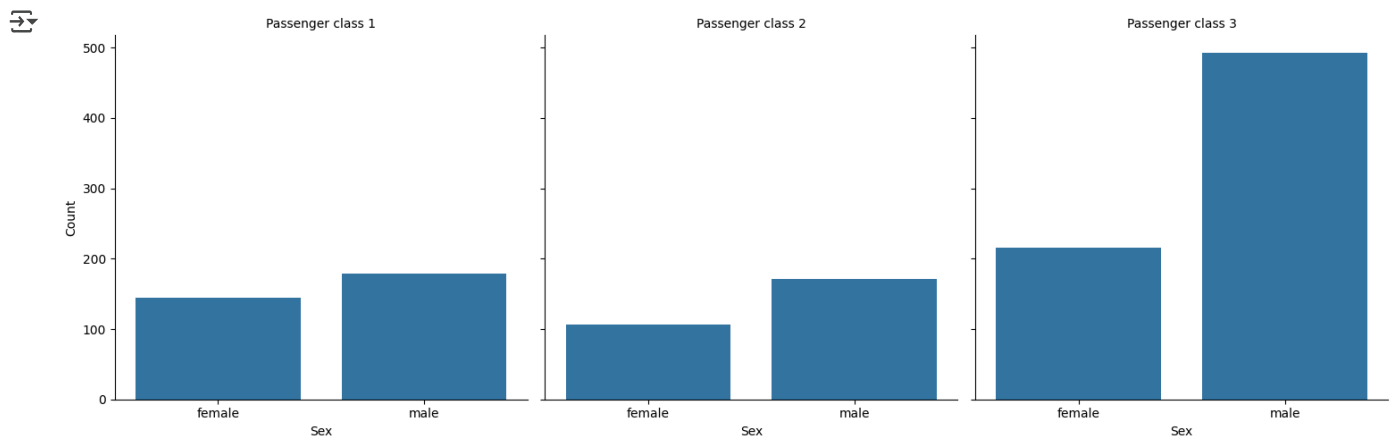


```
graph = sns.catplot(data=df, x='sex', col='pclass', kind='count')

graph.set_titles('Passenger class {col_name}')
graph.set_axis_labels('Sex', 'Count')

for ax in graph.axes.flat:
    ax.text(0.5, 1.05, '', transform=ax.transAxes, ha='center', va='bottom', fontsize=10, color='black')

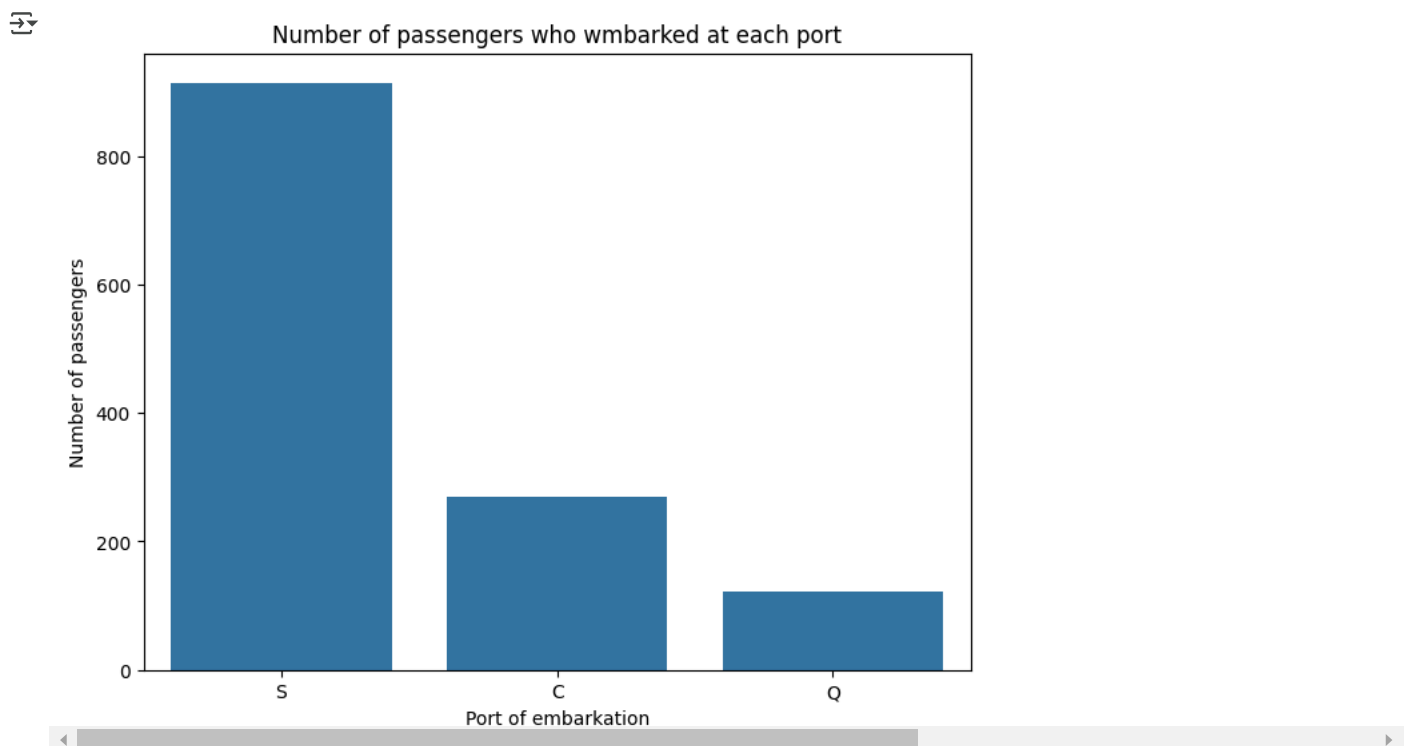
plt.tight_layout()
plt.show()
```

The "sex" variable is likely to be meaningful in predicting survival, as a significant number of women survived the Titanic disaster.

✕ Embarked

```
plt.figure(figsize=(8, 6))
sns.countplot(x='embarked', data=nobody_df)
plt.title('Number of passengers who wmbarked at each port')
plt.xlabel('Port of embarkation')
plt.ylabel('Number of passengers')
plt.show()
```

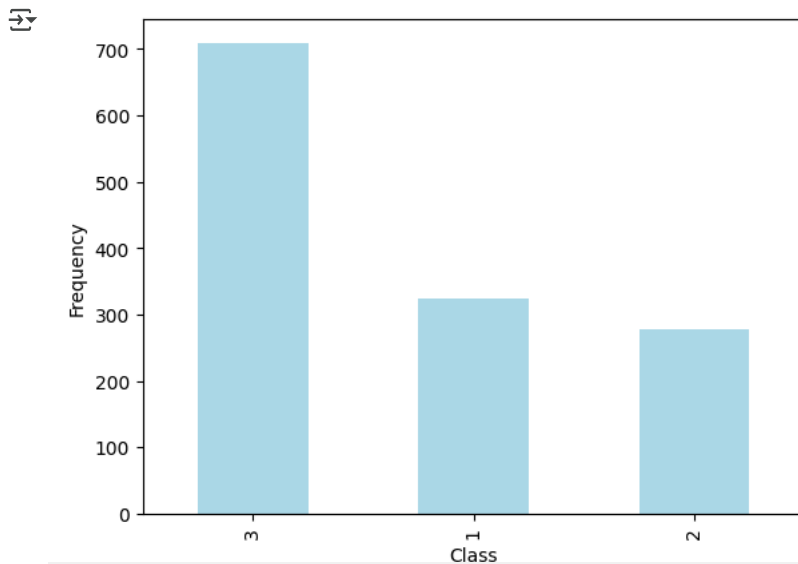


Most of the passengers boarded at port S, but we will explore further in the class section, as this is closely related to the class they boarded in. The class of passengers varied significantly by port, so there might be a high correlation between the two variables.

✕ Pclass

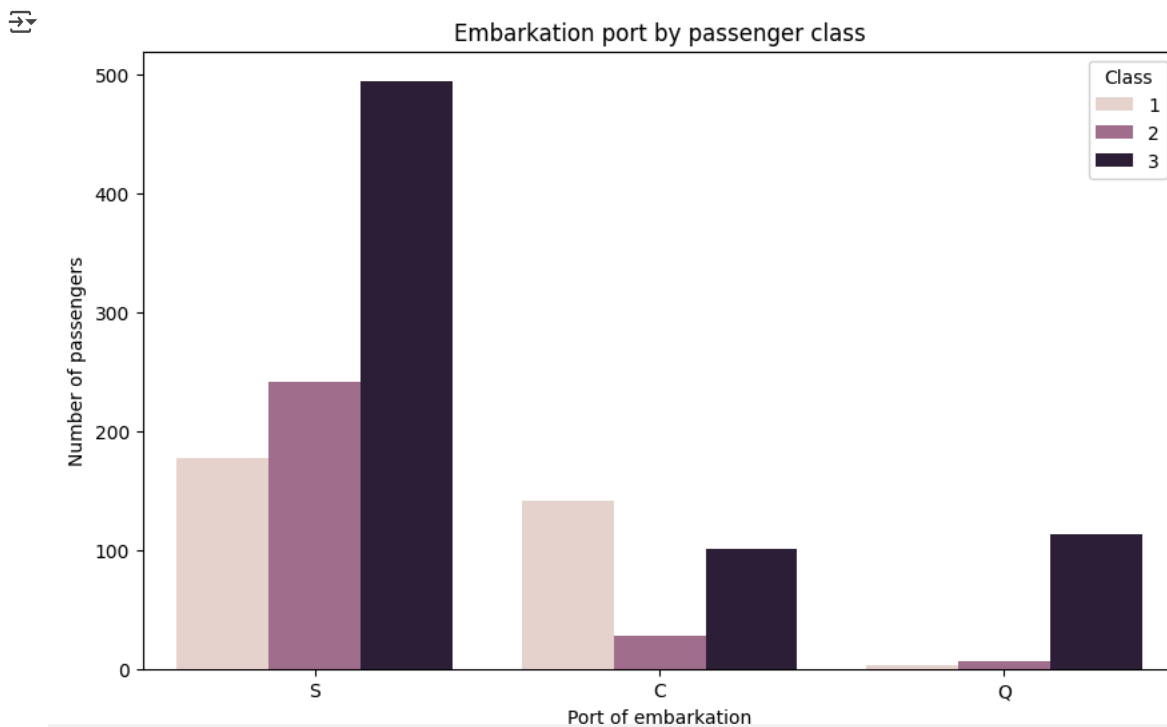
```
nobody_df['pclass'].value_counts().plot(kind='bar', edgecolor = 'none', color='lightblue')
plt.title('')
plt.xlabel('Class')
```

```
plt.ylabel('Frequency')
plt.show()
```



```
plt.figure(figsize=(10, 6))
sns.countplot(x='embarked', hue='pclass', data=nobody_df)
```

```
plt.title('Embarkation port by passenger class')
plt.xlabel('Port of embarkation')
plt.ylabel('Number of passengers')
plt.legend(title='Class')
plt.show()
```



```
embarked_class_counts = nobody_df.groupby('embarked')['pclass'].value_counts(normalize=True).unstack() * 100
embarked_class_counts.columns = ['Class 1 (%)', 'Class 2 (%)', 'Class 3 (%)']
print(embarked_class_counts.round(2))
```

```
embarked
```

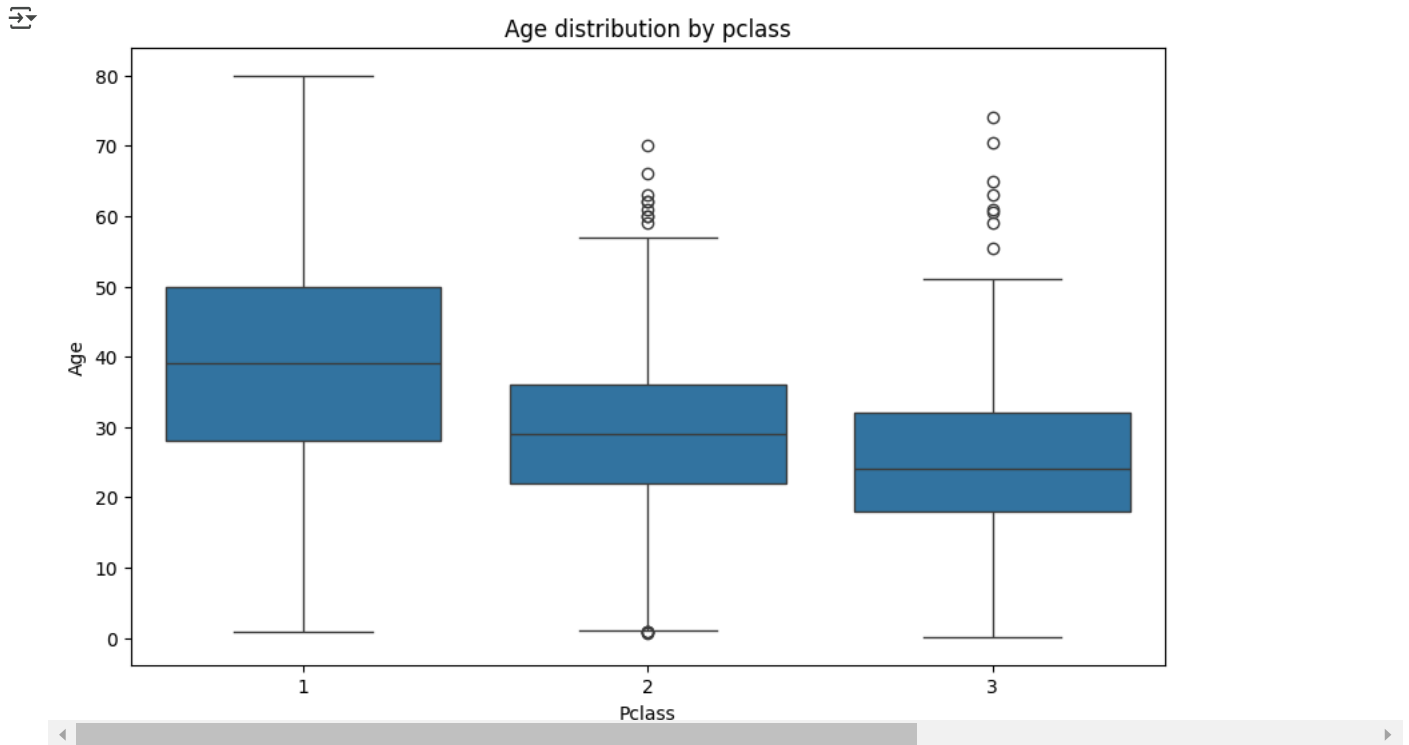
	Class 1 (%)	Class 2 (%)	Class 3 (%)
C	52.22	10.37	37.41
Q	2.44	5.69	91.87
S	19.37	26.48	54.16

As we mentioned, passengers from different classes did not board in equal proportions, and this distribution varies significantly depending on the port of embarkation

```
plt.figure(figsize=(10, 6))

sns.boxplot(x='pclass', y='age', data=nobody_df)

plt.title('Age distribution by pclass')
plt.xlabel('Pclass')
plt.ylabel('Age')
plt.show()
```



Age is also related to class, older passengers tended to belong to higher classes. This suggests that as age increased, passengers were more likely to have been in the wealthier and more privileged groups.

✓ Boat

The boat variable in the Titanic dataset is considered data leakage because it directly correlates with the target variable survived, allowing the model to "cheat" by using future information that wouldn't be available at the time of prediction.

However, just to mention, there are in total nine individual who have a boat assigned but did not survive.

```
in_boat = df[nobody_df['boat'].notnull()]
did_not_survive = in_boat[in_boat['survived'] == 0]

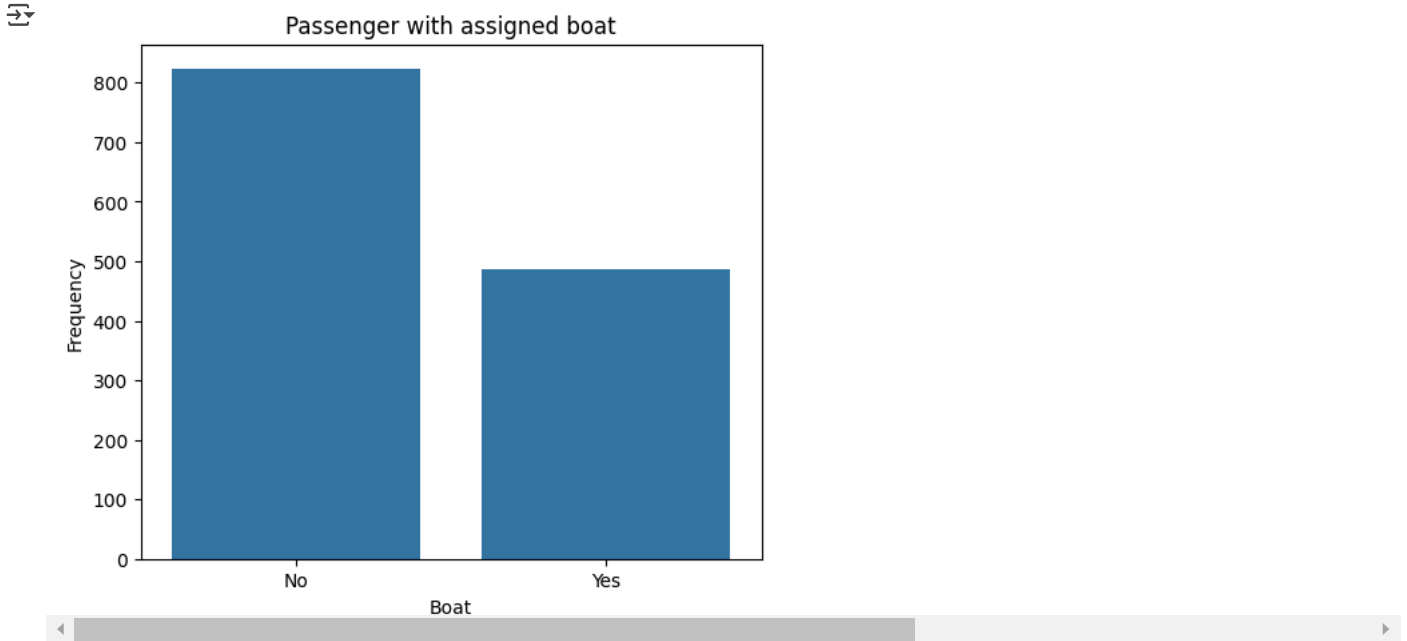
print(did_not_survive[['name', 'pclass', 'sex', 'age', 'boat', 'survived']])
```

	name	pclass	sex	age
19	Beattie, Mr. Thomson	1	male	36.0
166	Hoyt, Mr. William Fisher	1	male	NaN
544	Renouf, Mr. Peter Henry	2	male	34.0
655	Backstrom, Mr. Karl Alfred	3	male	32.0
853	Harmer, Mr. Abraham (David Lishin)	3	male	25.0
921	Keefe, Mr. Arthur	3	male	NaN
968	Lindell, Mr. Edvard Bengtsson	3	male	36.0
969	Lindell, Mrs. Edvard Bengtsson (Elin Gerda Per...	3	female	30.0
1299	Yasbeck, Mr. Antoni	3	male	27.0

	boat	survived
19	A	0
166	14	0
544	12	0
655	D	0
853	B	0
921	A	0
968	A	0
969	A	0
1299	C	0

```
plt.figure(figsize=(6, 5))
nobody_df['has_boat'] = nobody_df['boat'].notna()
sns.countplot(data=nobody_df, x='has_boat')
```

```
plt.title('Passenger with assigned boat')
plt.xlabel('Boat')
plt.ylabel('Frequency')
plt.xticks(ticks=[0, 1], labels=['No', 'Yes'])
plt.show()
```



```
noboat_df = nobody_df.drop(columns=['boat', 'has_boat'])
print(noboat_df.columns)
```

```
Index(['pclass', 'survived', 'name', 'sex', 'age', 'sibsp', 'parch', 'ticket',
      'fare', 'cabin', 'embarked', 'home.dest', 'alone', 'relatives'],
      dtype='object')
```

✓ Nominal Variables

- name
- ticket
- home.dest
- cabin

✓ Cabin

```
noboat_df.columns
```

```
Index(['pclass', 'survived', 'name', 'sex', 'age', 'sibsp', 'parch', 'ticket',
      'fare', 'cabin', 'embarked', 'home.dest', 'alone', 'relatives'],
      dtype='object')
```

```
unique_cabins = noboat_df['cabin'].unique()
print("Unique values in 'cabin':")
print(unique_cabins)
```

```
Unique values in 'cabin':
['B5' 'C22 C26' 'E12' 'D7' 'A36' 'C101' nan 'C62 C64' 'B35' 'A23'
 'B58 B60' 'D15' 'C6' 'D35' 'C148' 'C97' 'B49' 'C99' 'C52' 'T' 'A31' 'C7'
 'C103' 'D22' 'E33' 'A21' 'B10' 'B4' 'E40' 'B38' 'E24' 'B51 B53 B55'
 'B96 B98' 'C46' 'E31' 'E8' 'B61' 'B77' 'A9' 'C89' 'A14' 'E58' 'E49' 'E52'
 'E45' 'B22' 'B26' 'C85' 'E17' 'B71' 'B20' 'A34' 'C86' 'A16' 'A20' 'A18'
 'C54' 'C45' 'D20' 'A29' 'C95' 'E25' 'C111' 'C23 C25 C27' 'E36' 'D34'
 'D40' 'B39' 'B41' 'B102' 'C123' 'E63' 'C130' 'B86' 'C92' 'A5' 'C51' 'B42'
 'C91' 'C125' 'D10 D12' 'B82 B84' 'E50' 'D33' 'C83' 'B94' 'D49' 'D45'
 'B69' 'B11' 'E46' 'C39' 'B18' 'D11' 'C93' 'B28' 'C49' 'B52 B54 B56' 'E60'
 'C132' 'B37' 'D21' 'D19' 'C124' 'D17' 'B101' 'D28' 'D6' 'D9' 'B80' 'C106'
 'B79' 'C47' 'D30' 'C90' 'E38' 'C78' 'C30' 'C118' 'D36' 'D48' 'D47' 'C105'
 'B36' 'B30' 'D43' 'B24' 'C2' 'C65' 'B73' 'C104' 'C110' 'C50' 'B3' 'A24'
 'A32' 'A11' 'A10' 'B57 B59 B63 B66' 'C28' 'E44' 'A26' 'A6' 'A7' 'C31'
 'A19' 'B45' 'E34' 'B78' 'B50' 'C87' 'C116' 'C55 C57' 'D50' 'E68' 'E67'
 'C126' 'C68' 'C70' 'C53' 'B19' 'D46' 'D37' 'D26' 'C32' 'C80' 'C82' 'C128'
 'E39 E41' 'D' 'F4' 'D56' 'F33' 'E101' 'E77' 'F2' 'D38' 'F' 'F G63'
 'F E57' 'F E46' 'F G73' 'E121' 'F E69' 'E10' 'G6' 'F38']
```

The first letter of the cabin indicates its height on the boat, with 'A' being the highest. This can provide insights into whether survival rates were linked to the cabins location.

```
def assign_value(cabin):
    letters_to_values = {
        'A': 1, 'B': 2, 'C': 3, 'D': 4, 'E': 5, 'F': 6, 'G': 7, 'T': 8
    }

    if pd.isnull(cabin):
        return -9999999
    else:
        first_letter = cabin[0]
        # here we assign the height or -9999999 to missing values
        return letters_to_values.get(first_letter, -9999999)

noboat_df['height'] = noboat_df['cabin'].apply(assign_value)
```

The cabin column is dropped due to its lack of predictive power and tendency to lead to overfitting, especially considering the many missing values. Instead, we retain only the height feature for analysis.

```
nocabin_df = noboat_df.drop(columns=['cabin'])
print(nocabin_df.columns)

Index(['pclass', 'survived', 'name', 'sex', 'age', 'sibsp', 'parch', 'ticket',
       'fare', 'embarked', 'home.dest', 'alone', 'relatives', 'height'],
      dtype='object')

plt.figure(figsize=(10, 6))

height_survival_counts = nocabin_df.groupby(['height', 'survived']).size().unstack(fill_value=0)

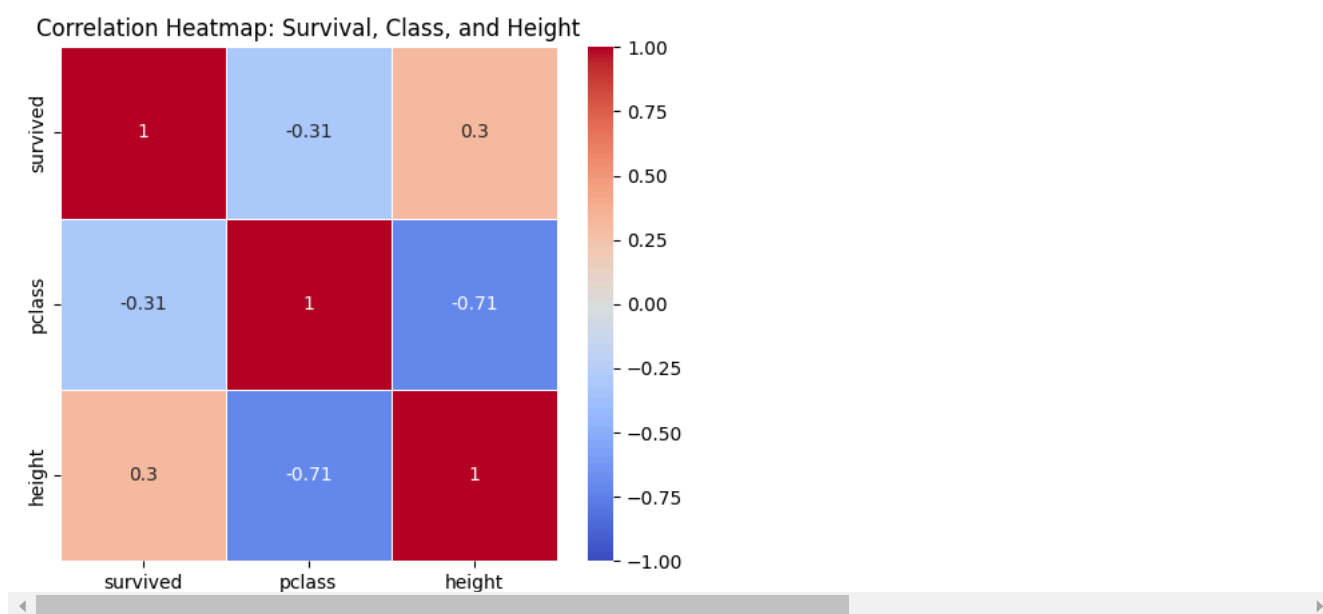
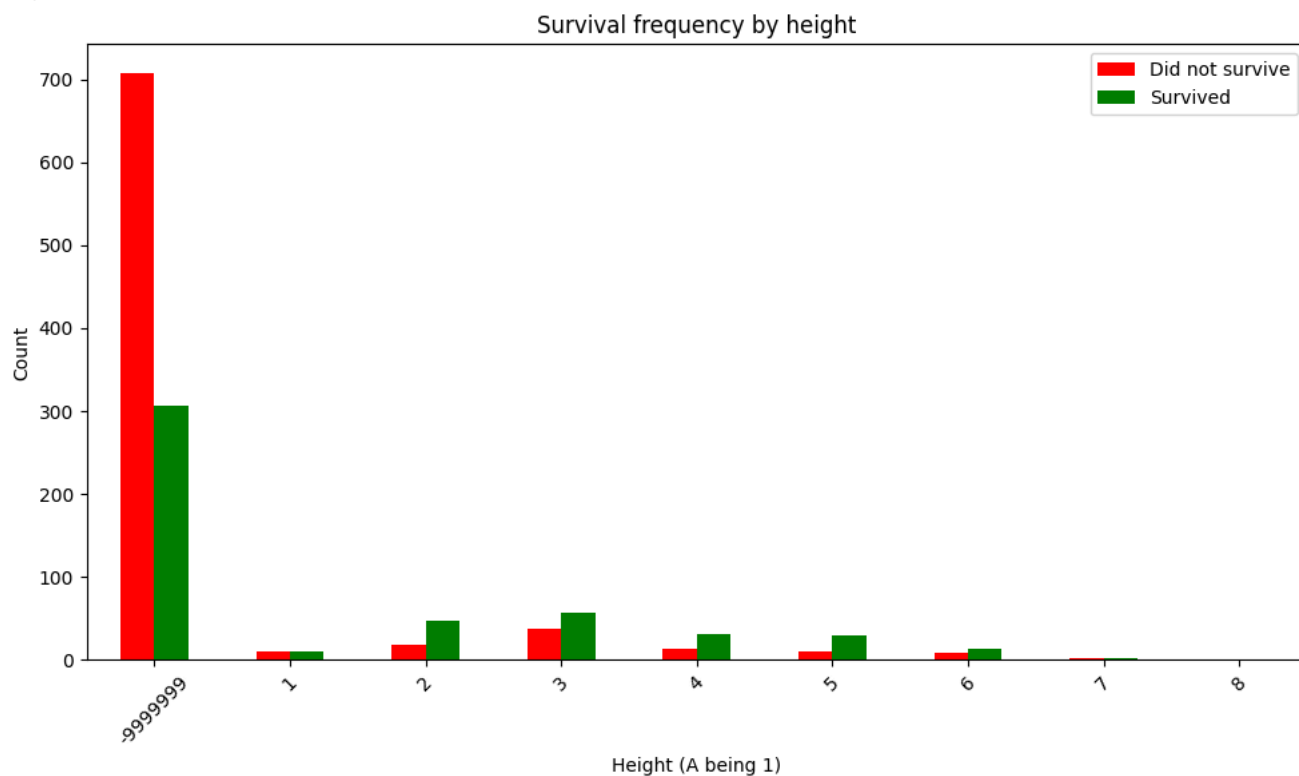
height_survival_counts.plot(kind='bar', stacked=False, color=['red', 'green'], figsize=(10, 6))

plt.title('Survival frequency by height')
plt.xlabel('Height (A being 1)')
plt.ylabel('Count')
plt.xticks(rotation=45)
plt.legend(['Did not survive', 'Survived'])
plt.tight_layout()
plt.show()

correlation_data = nocabin_df[['survived', 'pclass', 'height']].corr()

plt.figure(figsize=(6, 5))
sns.heatmap(correlation_data, annot=True, cmap='coolwarm', vmin=-1, vmax=1, linewidths=0.5)
plt.title('Correlation Heatmap: Survival, Class, and Height')
plt.show()
```

<Figure size 1000x600 with 0 Axes>



As we can see, pclass and height have a high correlation. However, our current threshold for considering correlation is 0.75. This threshold may change as we analyze the correlation with other features. Both pclass and height seem to have a similar correlation with survival.

```
# relatives percentages of survival by height
height_survival_counts = nocabin_df.groupby(['height', 'survived']).size().unstack(fill_value=0)

height_survival_percentages = height_survival_counts.divide(height_survival_counts.sum(axis=1), axis=0) * 100

print(height_survival_percentages)
```

```
survived      0      1
height
-9999999  69.723866  30.276134
1         50.000000  50.000000
2         27.692308  72.307692
3         39.361702  60.638298
4         30.434783  69.565217
5         26.829268  73.170732
6         38.095238  61.904762
7         40.000000  60.000000
8        100.000000   0.000000
```

▼ Name

The name variable includes passenger information, but the actual textual content (e.g., full names) is not useful for predicting survival. However, certain parts of the name, like titles (Mr., Mrs., etc.), may carry some predictive value, which is why we extracted the title from the name. Since the full name is not directly useful for prediction and contains a lot of redundant information, I removed it, leaving the title as a more informative and simplified feature.

```
import re
```

```
def extract_title(name):
    if pd.isnull(name):
        return 'Unknown'
    else:
        match = re.search(r'([A-Za-z]+\.)\.', name)
        if match:
            return match.group(1)
        else:
            return 'Unknown'
```

```
nocabin_df['title'] = nocabin_df['name'].apply(extract_title)
```

```
print(nocabin_df[['name', 'title']].head())
```

```
↗
```

	name	title
0	Allen, Miss. Elisabeth Walton	Miss
1	Allison, Master. Hudson Trevor	Master
2	Allison, Miss. Helen Loraine	Miss
3	Allison, Mr. Hudson Joshua Creighton	Mr
4	Allison, Mrs. Hudson J C (Bessie Waldo Daniels)	Mrs

```
unique_titles = nocabin_df['title'].unique()
print("Unique values in 'cabin':")
print(unique_titles)
```

```
↗ Unique values in 'cabin':
['Miss' 'Master' 'Mr' 'Mrs' 'Col' 'Mme' 'Dr' 'Major' 'Capt' 'Lady' 'Sir'
 'Mlle' 'Dona' 'Jonkheer' 'Countess' 'Don' 'Rev' 'Ms']
```

```
# important title 0 or 1
important = ['Sir', 'Lady', 'Dr', 'Major', 'Capt', 'Rev', 'Countess', 'Dona']
not_important = ['Miss', 'Master', 'Mr', 'Mrs', 'Col', 'Mme', 'Mlle', 'Jonkheer', 'Don', 'Ms']
```

```
def assign_title_importance(title):
    if title in important:
        return 1
    elif title in not_important:
        return 0
    else:
        return 'Unknown'
```

```
nocabin_df['important_title'] = nocabin_df['title'].apply(assign_title_importance)
```

```
print(nocabin_df[['name', 'title', 'important_title']].head())
```

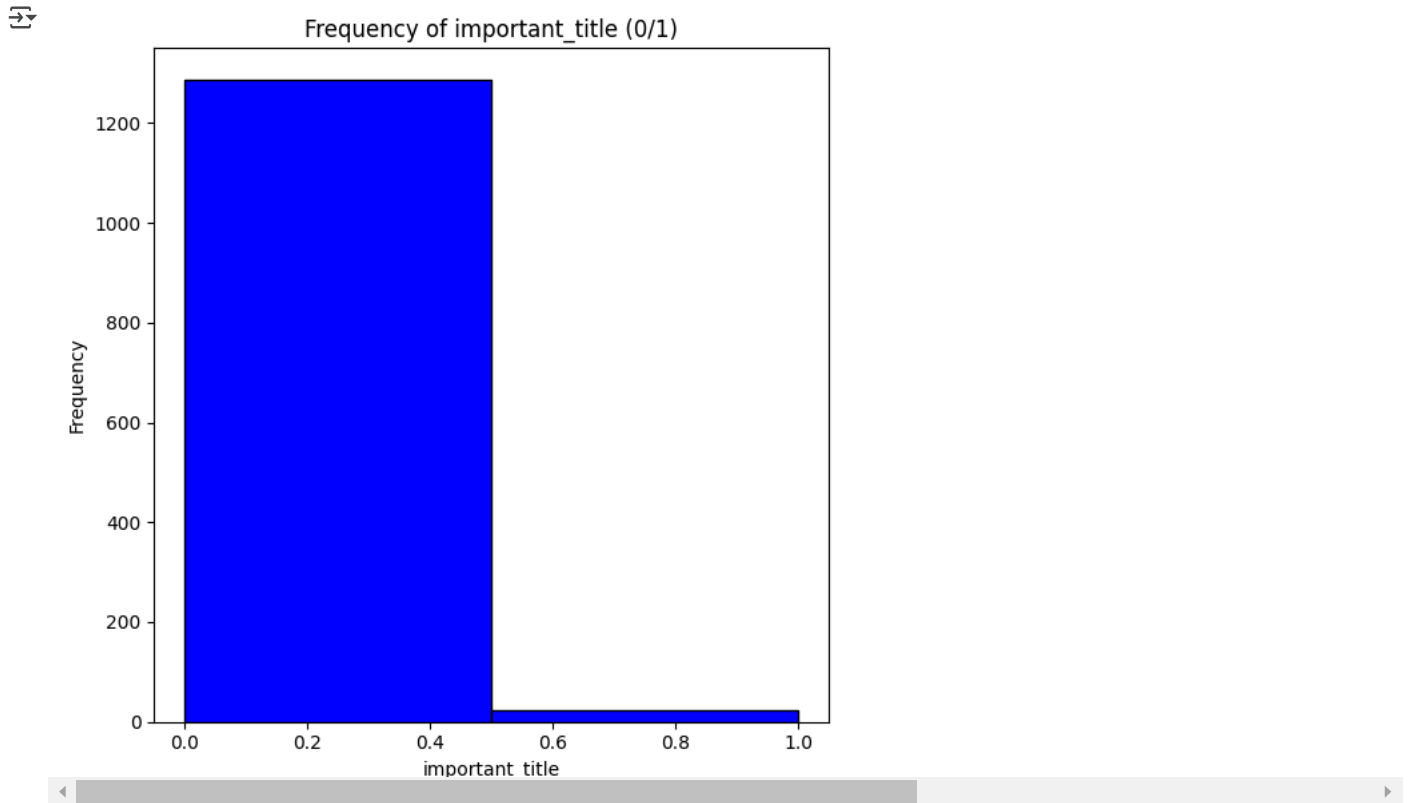
```
↗
```

	name	title	important_title
0	Allen, Miss. Elisabeth Walton	Miss	0
1	Allison, Master. Hudson Trevor	Master	0
2	Allison, Miss. Helen Loraine	Miss	0
3	Allison, Mr. Hudson Joshua Creighton	Mr	0
4	Allison, Mrs. Hudson J C (Bessie Waldo Daniels)	Mrs	0

```
noname_df = nocabin_df.drop(columns=['title', 'name'])
print(noname_df.columns)
```

```
↗ Index(['pclass', 'survived', 'sex', 'age', 'sibsp', 'parch', 'ticket', 'fare',
        'embarked', 'home.dest', 'alone', 'relatives', 'height',
        'important_title'],
        dtype='object')
```

```
plt.figure(figsize=(6, 6))
plt.hist(noname_df['important_title'], bins=2, edgecolor='black', color='blue')
plt.title('Frequency of important_title (0/1)')
plt.xlabel('important_title')
plt.ylabel('Frequency')
plt.tight_layout()
plt.show()
```



```
important_title_sex_table_percentage = pd.crosstab(
    [noname_df['important_title'], noname_df['sex']],
    noname_df['survived'],
    normalize='index'
) * 100

important_title_sex_table_percentage.columns = ['Did not survive (%)', 'Survived (%)']

print("\nPercentage distribution for 'important_title' by survival and sex:")
print(important_title_sex_table_percentage)
```



```
Percentage distribution for 'important_title' by survival and sex:
              Did not survive (%)  Survived (%)
important_title sex
0          female          27.489177      72.510823
              male          81.067961      18.932039
1          female           0.000000     100.000000
              male          73.684211      26.315789
```

The "important_title" variable can be very meaningful, especially when considering the "sex" feature. However, it can have a lot of correlation with pclass.

✕ Ticket and Home.dest

The ticket variable represents a shared ticket for all individuals traveling together, typically indicating families or groups of people. This makes the ticket variable highly similar to the relatives variable. Since relatives already captures the familial aspect of the passengers, ticket becomes redundant and doesn't provide additional predictive power and only introduces noise. The home.dest variable represents the combined information of the passenger's home and their final destination. However, it contains many unique values and, in many cases, seems to provide limited information for predicting survival. Given its high cardinality, inconsistency, and low predictive power, I decided to remove home.dest from the dataset to avoid introducing unnecessary noise into the model.

```
plt.figure(figsize=(12, 6))

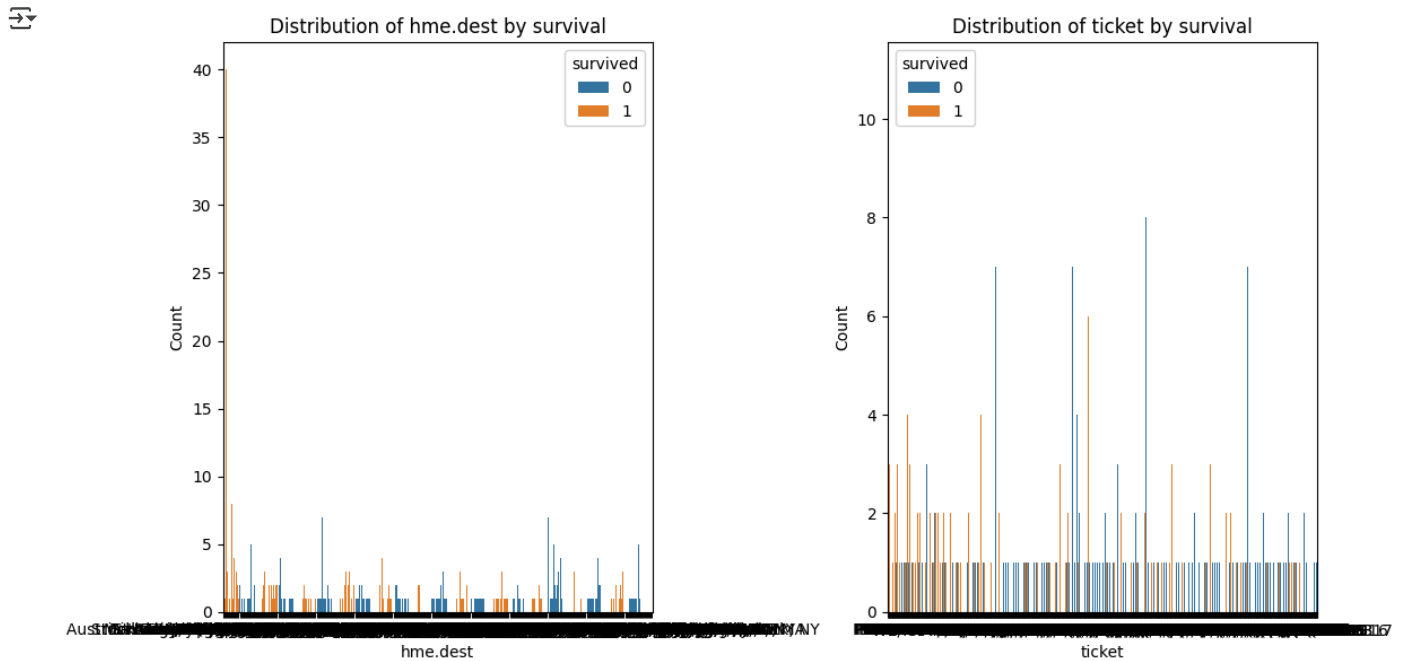
plt.subplot(1, 2, 1)
sns.countplot(x='home.dest', hue='survived', data=noname_df)
plt.title('Distribution of hme.dest by survival')
plt.xlabel('hme.dest')
plt.ylabel('Count')

plt.subplot(1, 2, 2)
sns.countplot(x='ticket', hue='survived', data=noname_df)
plt.title('Distribution of ticket by survival')
```



```
plt.xlabel('ticket')
plt.ylabel('Count')

plt.tight_layout()
plt.show()
```



```
noname_df.columns
```

```
Index(['pclass', 'survived', 'sex', 'age', 'sibsp', 'parch', 'ticket', 'fare',
      'embarked', 'home.dest', 'alone', 'relatives', 'height',
      'important_title'],
      dtype='object')
```

```
clean_df = noname_df.drop(columns=['ticket', 'home.dest'])
print(clean_df.columns)
```

```
Index(['pclass', 'survived', 'sex', 'age', 'sibsp', 'parch', 'fare',
      'embarked', 'alone', 'relatives', 'height', 'important_title'],
      dtype='object')
```

✓ Other Analysis

```
duplicates = df[clean_df.duplicated()]
duplicates = df[df.duplicated(subset=['name', 'pclass', 'sex', 'age'], keep=False)]
print(duplicates)
```

```
Empty DataFrame
Columns: [pclass, survived, name, sex, age, sibsp, parch, ticket, fare, cabin, embarked, boat, body, home.dest]
Index: []
```

No duplicates

- Is the data enough?
Yes, it provides sufficient features to analyze survival prediction.
- Is the data usable?
Yes, after some cleaning and preprocessing.
- Are the data tidy? (Lecture 1, Slide 14)
Not entirely. Some features require feature engineering
- Are data tidy but incomplete? If yes, we need data imputation methods.

There are missing values (e.g., in age, embarked). Imputation is required.

- Are data tidy but with duplicates?
No duplicates detected.
- Are data tidy but expired or significantly out of date?
Not expired, data is from a historical event (Titanic).
- Are data tidy but incomplete or unrepresentative of the phenomenon?
Data is mostly representative but not fully clean.
- Do We Know the Source of Our Data?
Kaggle, unknown provenance, but trusted by lots of users.
- Were gender data manually inputted, or were they the result of a low-quality classifier?
No information.
- Is There Data Leakage? Is the prediction target (implicitly) contained in the training dataset?
There was (boat, body), already removed.
- Are the Data Reliable? Can We Trust the Labels?
Labels are reliable, as they are based on real historical outcomes.
- Are labels delayed? We observe labels now but use them to predict far future events.
No delayed or indirect labels: survival is the direct outcome.
- Do we have feedback loops?
No feedback loops: The model doesn't train on its own predictions.

✓ Task 2: Managing Missing Values (1/2)

Lecture Material: Lecture 3, slides 22–24.

- Identify the columns containing missing values.
- Develop a strategy to address them.

```
missing_values = clean_df.isnull().sum()
print(missing_values)
```

```

pclass      0
survived     0
sex          0
age        263
sibsp       0
parch       0
fare        1
embarked     2
alone       0
relatives   0
height      0
important_title  0
dtype: int64
```

✓ Dealing with embarked missing values

```
missing_embarked = df[clean_df['embarked'].isnull()]
print(missing_embarked)
```

```

pclass  survived      name  sex \
168      1         1  Icard, Miss. Amelie  female
284      1         1  Stone, Mrs. George Nelson (Martha Evelyn)  female

   age  sibsp  parch  ticket  fare  cabin  embarked  boat  body \
168  38.0    0     0  113572   80.0    B28      NaN    6   NaN
284  62.0    0     0  113572   80.0    B28      NaN    6   NaN

   home.dest
168      NaN
284  Cincinatti, OH
```

Same ticket number, but not family. If we search in internet Icard, Miss. Amelie boarded at Southampton (<https://www.encyclopedia-titanica.org/titanic-survivor/amelia-icard.html>) same for Stone, Mrs. George Nelson (Martha Evelyn) (<https://www.encyclopedia-titanica.org/titanic-survivor/martha-evelyn-stone.html>).

```
clean_df['embarked'] = clean_df['embarked'].fillna('S')
print(clean_df['embarked'].isnull().sum())
```

↗ 0

✓ Task 5: Data Splitting

Lecture material: Lecture 2, slides 4–7.

- Split the dataset into training, validation, and test sets.
- Ensure that the split reflects the original distribution of the target variable using stratification. Note: a good strategy is to first split the dataset into 'training' and 'others', and then split 'others' into equally sized 'validation' and 'test' sets. When splitting sets, consider the argument stratify of the train test split method.

For a dataset of 1300 examples, an 80-10-10 split is ideal because it provides enough training data while keeping the validation and test sets statistically meaningful. A 90% training split is better for very small datasets (Under 1000 examples), where cross-validation can replace a separate validation set. On the other hand, a 70% training split is more common when working with large datasets, where validation and test sets need more examples for reliable evaluation. Since 1300 is a small/mid-sized dataset, 80% training ensures the model learns well, while 10% validation and 10% test provide decent performance metrics.

```
# Strategy 80-20 and then 50-50 on the 20 making: 80-10-10
train_df, others_df = sklearn.model_selection.train_test_split(clean_df, test_size=0.2, stratify=df['survived'], random_state=2025)
valid_df, test_df = sklearn.model_selection.train_test_split(others_df, test_size=0.5, stratify=others_df['survived'], random_state=2025)
```

```
# check proportion of survival, should be equal
print('Train set distribution:')
print(train_df['survived'].value_counts(normalize=True))
```

```
print('\nValidation set distribution:')
print(valid_df['survived'].value_counts(normalize=True))
```

```
print('\nTest set distribution:')
print(test_df['survived'].value_counts(normalize=True))
```

↗ Train set distribution:

```
survived
0    0.617956
1    0.382044
Name: proportion, dtype: float64
```

```
Validation set distribution:
survived
0    0.618321
1    0.381679
Name: proportion, dtype: float64
```

```
Test set distribution:
survived
0    0.618321
1    0.381679
Name: proportion, dtype: float64
```

✓ Task 2: Managing Missing Values (2/2)

Lecture Material: Lecture 3, slides 22–24.

- Identify the columns containing missing values.
- Develop a strategy to address them.

```
# train
t_missing_values = train_df.isnull().sum()
print(t_missing_values)
print('-----')
```

```
# validate
v_missing_values = valid_df.isnull().sum()
print(v_missing_values)
print('-----')
```

```
#test
```

```
ts_missing_values = test_df.isnull().sum()
print(ts_missing_values)
```

```
↩ pclass      0
  survived    0
  sex         0
  age        203
  sibsp       0
  parch       0
  fare        1
  embarked    0
  alone       0
  relatives   0
  height      0
  important_title  0
  dtype: int64
-----
pclass      0
  survived    0
  sex         0
  age        29
  sibsp       0
  parch       0
  fare        0
  embarked    0
  alone       0
  relatives   0
  height      0
  important_title  0
  dtype: int64
-----
pclass      0
  survived    0
  sex         0
  age        31
  sibsp       0
  parch       0
  fare        0
  embarked    0
  alone       0
  relatives   0
  height      0
  important_title  0
  dtype: int64
```

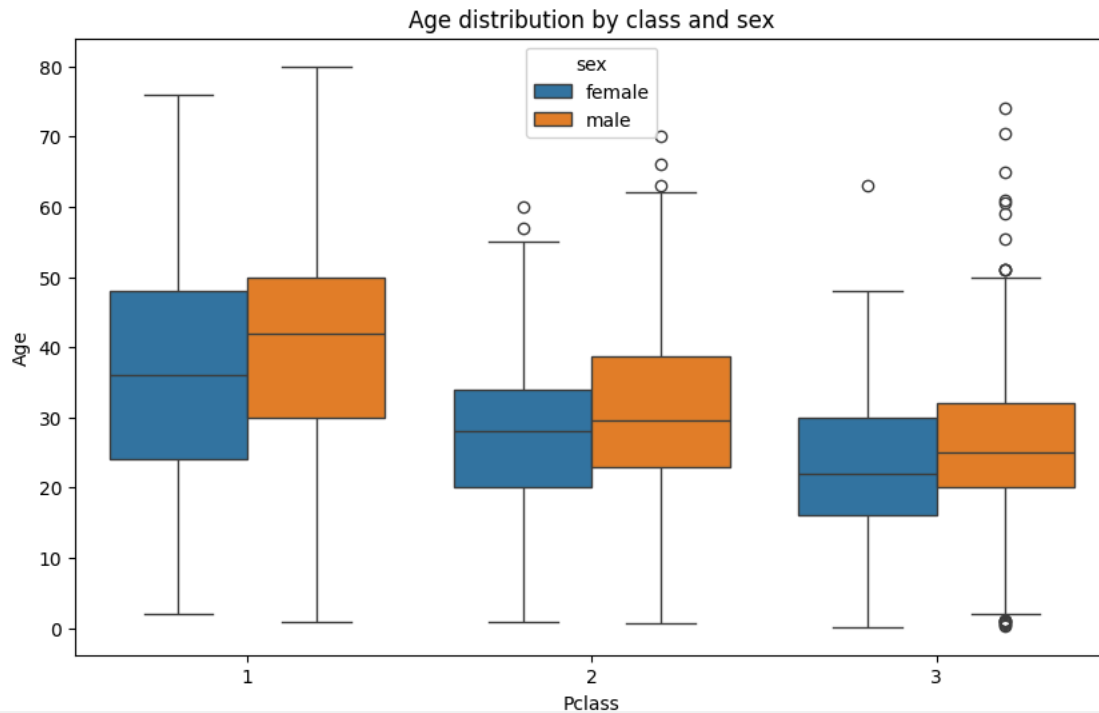
✓ Dealing with age missing values

The most interesting approach is to group the data by class and sex, and then calculate the mean of the features. We use these average values from the training set to fill in the missing values in both the validation and test sets. KNN could also have been used.

```
plt.figure(figsize=(10, 6))

sns.boxplot(x='pclass', y='age', hue='sex', data=clean_df)
plt.title('Age distribution by class and sex')
plt.xlabel('Pclass')
plt.ylabel('Age')

plt.show()
```



```
def fill_missing_age(df, age_grouped):
    def fill_age(row):
        if pd.isna(row['age']):
            # get the mean age for the corresponding pclass and sex from the grouped data
            mean_age = age_grouped[
                (age_grouped['pclass'] == row['pclass']) &
                (age_grouped['sex'] == row['sex'])
            ]['age']

            if not mean_age.empty:
                return mean_age.values[0]
            else:
                return 'Unknown'
        else:
            return row['age']

    # apply the fill_age function to the entire dataset
    df['age'] = df.apply(fill_age, axis=1)

    return df

age_grouped_train = train_df.groupby(['pclass', 'sex'])['age'].mean().reset_index()
print('Mean ages by pclass and sex in train_df:')
print(age_grouped_train)

for dataset_name, dataset in [('train', train_df), ('valid', valid_df), ('test', test_df)]:
    print(f"\nFilling missing values in 'age' for {dataset_name} set:")
    # check how many missing values
    print(f"Missing values in 'age' for {dataset.shape[0]} entries: {dataset['age'].isnull().sum()}")

    # only fill values in valid and test sets using values from train_df
    dataset = fill_missing_age(dataset, age_grouped_train)

    # check again how many missing values
    print(f"Missing values in 'age' after fill: {dataset['age'].isnull().sum()}")
    print(dataset.head())
```



Mean ages by pclass and sex in train_df:

	pclass	sex	age
0	1	female	36.711712
1	1	male	40.889108
2	2	female	26.968107
3	2	male	31.017811
4	3	female	22.442623
5	3	male	26.022365

```
Filling missing values in 'age' for train set:
Missing values in 'age' for 1047 entries: 203
Missing values in 'age' after fill: 0
pclass survived sex age sibsp parch fare embarked \
```

829	3	0	female	16.000000	5	2	46.900	S
889	3	1	male	26.000000	0	0	7.775	S
330	2	0	male	57.000000	0	0	13.000	S
91	1	1	male	31.000000	1	0	57.000	S
808	3	0	male	26.022365	0	0	8.050	S

	alone	relatives	height	important_title
829	0	7	-9999999	0
889	1	0	-9999999	0
330	1	0	-9999999	0
91	0	1	2	0
808	1	0	-9999999	0

Filling missing values in 'age' for valid set:

Missing values in 'age' for 131 entries: 29

Missing values in 'age' after fill: 0

	pclass	survived	sex	age	sibsp	parch	fare	embarked	alone	\
687	3	0	female	20.0	0	0	7.8542	S	1	
664	3	1	male	20.0	0	0	7.2292	C	1	
935	3	1	male	29.0	3	1	22.0250	S	0	
133	1	1	male	49.0	1	0	89.1042	C	0	
339	2	1	male	1.0	2	1	39.0000	S	0	

	relatives	height	important_title
687	0	-9999999	0
664	0	-9999999	0
935	4	-9999999	0
133	1	3	0
339	3	6	0

Filling missing values in 'age' for test set:

Missing values in 'age' for 131 entries: 31

Missing values in 'age' after fill: 0

	pclass	survived	sex	age	sibsp	parch	fare	embarked	\
144	1	1	female	25.000000	1	0	55.4417	C	
1177	3	0	male	26.022365	8	2	69.5500	S	
116	1	1	female	60.000000	1	4	263.0000	S	
620	3	0	male	32.000000	0	0	22.5250	S	
583	2	1	female	40.000000	0	0	15.7500	S	

	alone	relatives	height	important_title
144	0	1	5	0
1177	0	10	-9999999	0
116	0	5	3	0
620	1	0	-9999999	0

✓ Dealing with fare missing values

To estimate the missing fare values, I first looked for passengers with similar characteristics: same class and embarked from the same port. After identifying similar passengers, I analyzed their fare distribution and found that most paid between 7 and 10, with one clear outlier. Based on that, I decided the median fare was the best estimate. Finally, I searched online and found that Storey, Mr. Thomas paid exactly 7 pounds for his ticket (<https://www.encyclopedia-titanica.org/titanic-victim/thomas-storey.html>).

```
def get_similar_fares(train_df, passenger_index):
    passenger = train_df.loc[passenger_index]

    similar_passengers = train_df[
        (train_df['pclass'] == passenger['pclass']) &
        (train_df['embarked'] == passenger['embarked']) &
        (train_df['sibsp'] == passenger['sibsp']) &
        (train_df['parch'] == passenger['parch'])
    ]
    similar_passengers = similar_passengers[similar_passengers['fare'].notnull()]

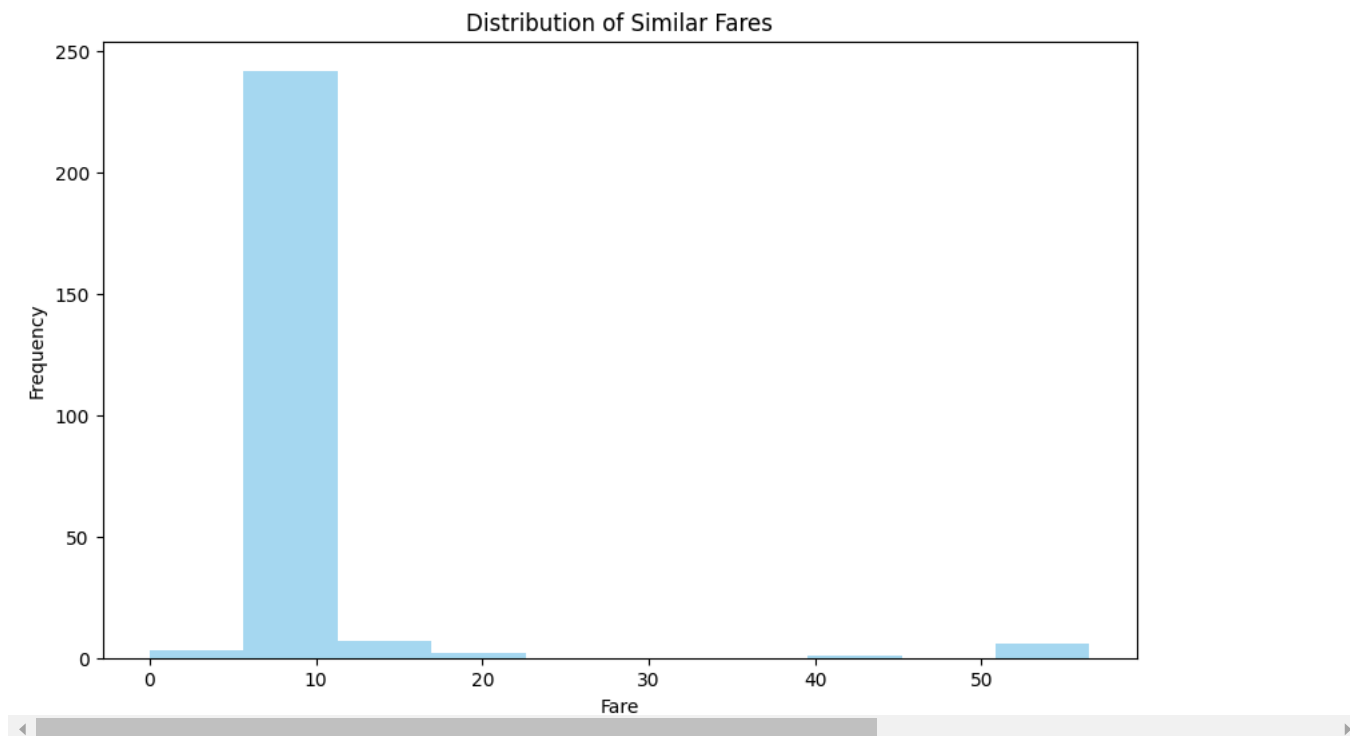
    return similar_passengers['fare'].tolist()

for index in train_df[train_df['fare'].isnull()].index:
    similar_fares = get_similar_fares(train_df, index)

print(train_df['fare'].isnull().sum()) # Should be 0

plt.figure(figsize=(10, 6))
sns.histplot(similar_fares, bins=10, color='skyblue', edgecolor='none')
plt.title('Distribution of Similar Fares')
plt.xlabel('Fare')
plt.ylabel('Frequency')
plt.show()
```

↗ 1



```
missing_fare_rows = df[df['fare'].isna()]
print('Passengers without an assigned fare:')
print(missing_fare_rows)
```

↗ Passengers without an assigned fare:

	pclass	survived	name	sex	age	sibsp	parch	ticket	\
1225	3	0	Storey, Mr. Thomas	male	60.5	0	0	3701	

	fare	cabin	embarked	boat	body	home.dest
1225	NaN	NaN	S	NaN	261.0	NaN

```
train_df['fare'] = train_df['fare'].fillna(7)
```

```
# train
t_missing_values = train_df.isnull().sum()
print(t_missing_values)
print('-----')
```

```
# validate
v_missing_values = valid_df.isnull().sum()
print(v_missing_values)
print('-----')
```

```
#test
ts_missing_values = test_df.isnull().sum()
print(ts_missing_values)
```

```
↗ pclass      0
   survived   0
   sex        0
   age        0
   sibsp      0
   parch      0
   fare       0
   embarked   0
   alone      0
   relatives   0
   height     0
   important_title 0
   dtype: int64
-----
pclass      0
survived     0
sex          0
age          0
sibsp        0
parch        0
fare         0
embarked     0
alone        0
relatives     0
height       0
```

```

important_title    0
dtype: int64
-----
pclass            0
survived          0
sex              0
age              0
sibsp            0
parch            0
fare             0
embarked         0
alone            0
relatives        0
height           0
important_title   0
dtype: int64

```

No more missing values!

✓ Task 3: Encoding Categorical Variables

Lecture material: Lecture 4, slides 10–15, 21.

- Identify the categorical variables in the dataset.
- Utilize OneHotEncoder to encode them.
- Observe the transformation and discuss its impact on machine learning models

I applied one-hot encoding to the sex and embarked columns because they are categorical variables without an hierarchical order, allowing ML models to treat them as distinct categories rather than numerical values. On the other hand, variables like pclass represent a hierarchical order, so encoding them as separate categories would break their structure, not allowing the model to learn correctly.

Encoding categorical variables is crucial for machine learning models, as most algorithms require numerical input. By transforming categorical features into numerical values, models can identify patterns and relationships. One-hot encoding, creates binary columns for each category, which helps the model recognize each category as a separate entity. However, it's important to note that this can increase dimensionality, and if the dataset contains many categories, it could make the model prone to overfitting.

```

categorical_cols = ['sex', 'embarked']

encoder = sklearn.preprocessing.OneHotEncoder(drop='first', sparse_output=False)

# Encoding..
train_encoded = encoder.fit_transform(train_df[categorical_cols])
test_encoded = encoder.transform(test_df[categorical_cols])
valid_encoded = encoder.transform(valid_df[categorical_cols])

# Remake the df
encoded_cols = encoder.get_feature_names_out(categorical_cols)
train_encoded_df = pd.DataFrame(train_encoded, columns=encoded_cols, index=train_df.index)
test_encoded_df = pd.DataFrame(test_encoded, columns=encoded_cols, index=test_df.index)
valid_encoded_df = pd.DataFrame(valid_encoded, columns=encoded_cols, index=valid_df.index)

# Merge the df
train_df = pd.concat([train_df.drop(columns=categorical_cols), train_encoded_df], axis=1)
test_df = pd.concat([test_df.drop(columns=categorical_cols), test_encoded_df], axis=1)
valid_df = pd.concat([valid_df.drop(columns=categorical_cols), valid_encoded_df], axis=1)

# just check
print(train_df.head())
print(valid_df.head())
print(test_df.head())

```

```

➡
pclass  survived    age  sibsp  parch    fare  alone  relatives  \
829      3          0  16.000000    5     2   46.900      0          7
889      3          1  26.000000    0     0    7.775      1          0
330      2          0  57.000000    0     0   13.000      1          0
91       1          1  31.000000    1     0   57.000      0          1
808      3          0  26.022365    0     0    8.050      1          0

height  important_title  sex_male  embarked_Q  embarked_S
829 -9999999          0         0.0         0.0         1.0
889 -9999999          0         1.0         0.0         1.0
330 -9999999          0         1.0         0.0         1.0
91  -9999999          0         1.0         0.0         1.0
808 -9999999          0         1.0         0.0         1.0

pclass  survived    age  sibsp  parch    fare  alone  relatives  height  \
687      3          0   20.0     0     0   7.8542      1          0 -9999999
664      3          1   20.0     0     0   7.2292      1          0 -9999999

```


935	3	1	29.0	3	1	22.0250	0	4	-9999999
133	1	1	49.0	1	0	89.1042	0	1	3
339	2	1	1.0	2	1	39.0000	0	3	6

	important_title	sex_male	embarked_Q	embarked_S
687	0	0.0	0.0	1.0
664	0	1.0	0.0	0.0
935	0	1.0	0.0	1.0
133	0	1.0	0.0	0.0
339	0	1.0	0.0	1.0

	pclass	survived	age	sibsp	parch	fare	alone	relatives	\
144	1	1	25.000000	1	0	55.4417	0		1
1177	3	0	26.022365	8	2	69.5500	0		10
116	1	1	60.000000	1	4	263.0000	0		5
620	3	0	32.000000	0	0	22.5250	1		0
583	2	1	40.000000	0	0	15.7500	1		0

	height	important_title	sex_male	embarked_Q	embarked_S
144	5	0	0.0	0.0	0.0
1177	-9999999	0	1.0	0.0	1.0
116	3	0	0.0	0.0	1.0
620	-9999999	0	1.0	0.0	1.0
583	-9999999	0	0.0	0.0	1.0

✓ Task 4: Feature Scaling

Lecture material: Lecture 5, slides 14–20.

- Standardize the numerical variables using StandardScaler.
- Normalize the numerical variables using MinMaxScaler.
- Discuss the differences between standardization and normalization, along with their importance

Feature scaling, in general, is important because it ensures that no individual feature dominates the model due to its scale, and it allows the model to learn from all features equally and prevents features with larger scales (like fare) from dominating the learning process. For this model, standarization is a better choice than normalization. This is becouse logistic regression is sensitive to the variance of the features and standarization escales the data to have a mean of 0 and a standard deviation of 1. Standardization works particularly well when your data is approximately normally distributed, which is often the case for numerical features like age, fare, or sibsp in real-world datasets.

On the other hand, normalization, rescales the data to a fixed range, typically [0, 1]. This method is useful when the absolute magnitude of the features matters. However, normalization can be affected by outliers, which can make smaller the range of normal values and impact the model performance.

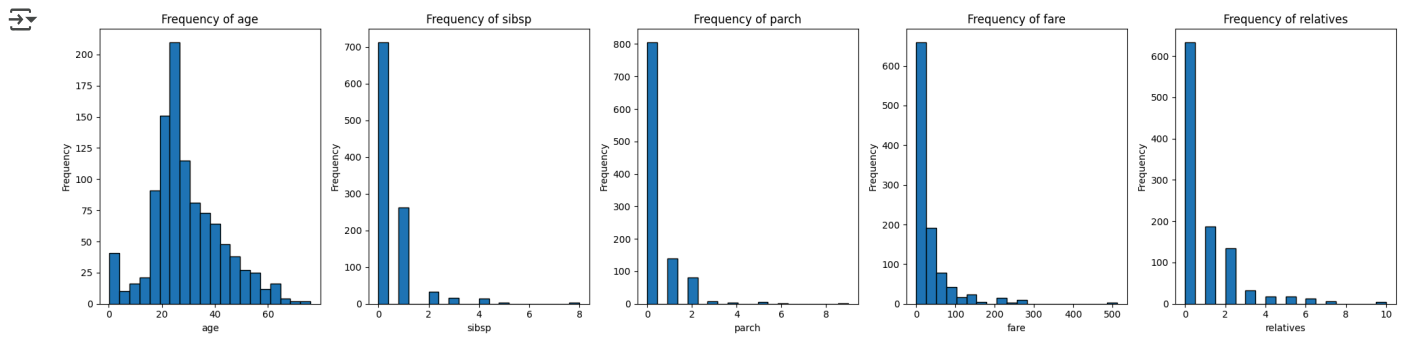
```
print(train_df.dtypes)
numerical_columns = ['age', 'sibsp', 'parch', 'fare', 'relatives']
```

```
↗ pclass          int64
   survived       int64
   age           float64
   sibsp         int64
   parch         int64
   fare          float64
   alone         int64
   relatives     int64
   height        int64
   important_title int64
   sex_male      float64
   embarked_Q    float64
   embarked_S    float64
dtype: object
```

```
# plot each numerical distribution
fig, axes = plt.subplots(1, 5, figsize=(20, 5))

for i, col in enumerate(numerical_columns):
    axes[i].hist(train_df[col], bins=20, edgecolor='black')
    axes[i].set_title(f'Frequency of {col}')
    axes[i].set_xlabel(col)
    axes[i].set_ylabel('Frequency')

plt.tight_layout()
plt.show()
```



```
# scale
scaler = sklearn.preprocessing.StandardScaler()
scaler.fit(train_df[numerical_columns])

train_df[numerical_columns] = scaler.transform(train_df[numerical_columns])
valid_df[numerical_columns] = scaler.transform(valid_df[numerical_columns])
test_df[numerical_columns] = scaler.transform(test_df[numerical_columns])

# verify
print('Train set after scaling:')
print(train_df[numerical_columns].head())

print('\nValidation set after scaling:')
print(valid_df[numerical_columns].head())

print('\nTest set after scaling:')
print(test_df[numerical_columns].head())
```

```
Train set after scaling:
   age  sibsp  parch  fare  relatives
829 -1.038419  5.039298  1.830957  0.247731  4.212663
889 -0.268845 -0.509866 -0.428338 -0.500739 -0.573356
330  2.116833 -0.509866 -0.428338 -0.400783 -0.573356
91   0.115942  0.599967 -0.428338  0.440946  0.110361
808 -0.267124 -0.509866 -0.428338 -0.495478 -0.573356
```

```
Validation set after scaling:
   age  sibsp  parch  fare  relatives
687 -0.730589 -0.509866 -0.428338 -0.499224 -0.573356
664 -0.730589 -0.509866 -0.428338 -0.511180 -0.573356
935 -0.037973  2.819632  0.701309 -0.228133  2.161512
133  1.501174  0.599967 -0.428338  1.055107  0.110361
339 -2.192779  1.709800  0.701309  0.096602  1.477795
```

```
Test set after scaling:
   age  sibsp  parch  fare  relatives
144 -0.345802  0.599967 -0.428338  0.411136  0.110361
1177 -0.267124  8.368796  1.830957  0.681030  6.263814
116  2.347705  0.599967  4.090253  4.381771  2.845229
620  0.192899 -0.509866 -0.428338 -0.218568 -0.573356
583  0.808558 -0.509866 -0.428338 -0.348175 -0.573356
```

✓ Task 6: Addressing Class Imbalance

Lecture material: Lecture 3, slides 25–27; Lecture 4, slides 4–5.

- Apply a method to address class imbalance (e.g., Oversampling Technique (SMOTE), Adaptive Synthetic Sampling Method (ADASYN)).
Note: You can load a SMOTE and/or ADASYN implementation from the Python module imblearn.

Balancing the classes is important because if one class is significantly more common than the other, the model might learn to favor the majority class and ignore the minority class. This can lead to poor performance, especially when predicting the less frequent outcomes. I chose SMOTE because it generates samples for the minority class by "blending" existing data points, helping to create a more balanced and representative dataset.

```
from imblearn.over_sampling import SMOTE
```

```
X_train = train_df.drop('survived', axis=1)
y_train = train_df['survived']

smote = SMOTE(sampling_strategy='auto', random_state=2025)
X_train_res, y_train_res = smote.fit_resample(X_train, y_train)

print(f'Original class distribution in training set: {y_train.value_counts()}')
print(f'Resampled class distribution in training set: {y_train_res.value_counts()}')
```

```
↗ Original class distribution in training set: survived
0    647
1   400
Name: count, dtype: int64
Resampled class distribution in training set: survived
0    647
1    647
Name: count, dtype: int64
```

✓ Task 7: Feature Selection

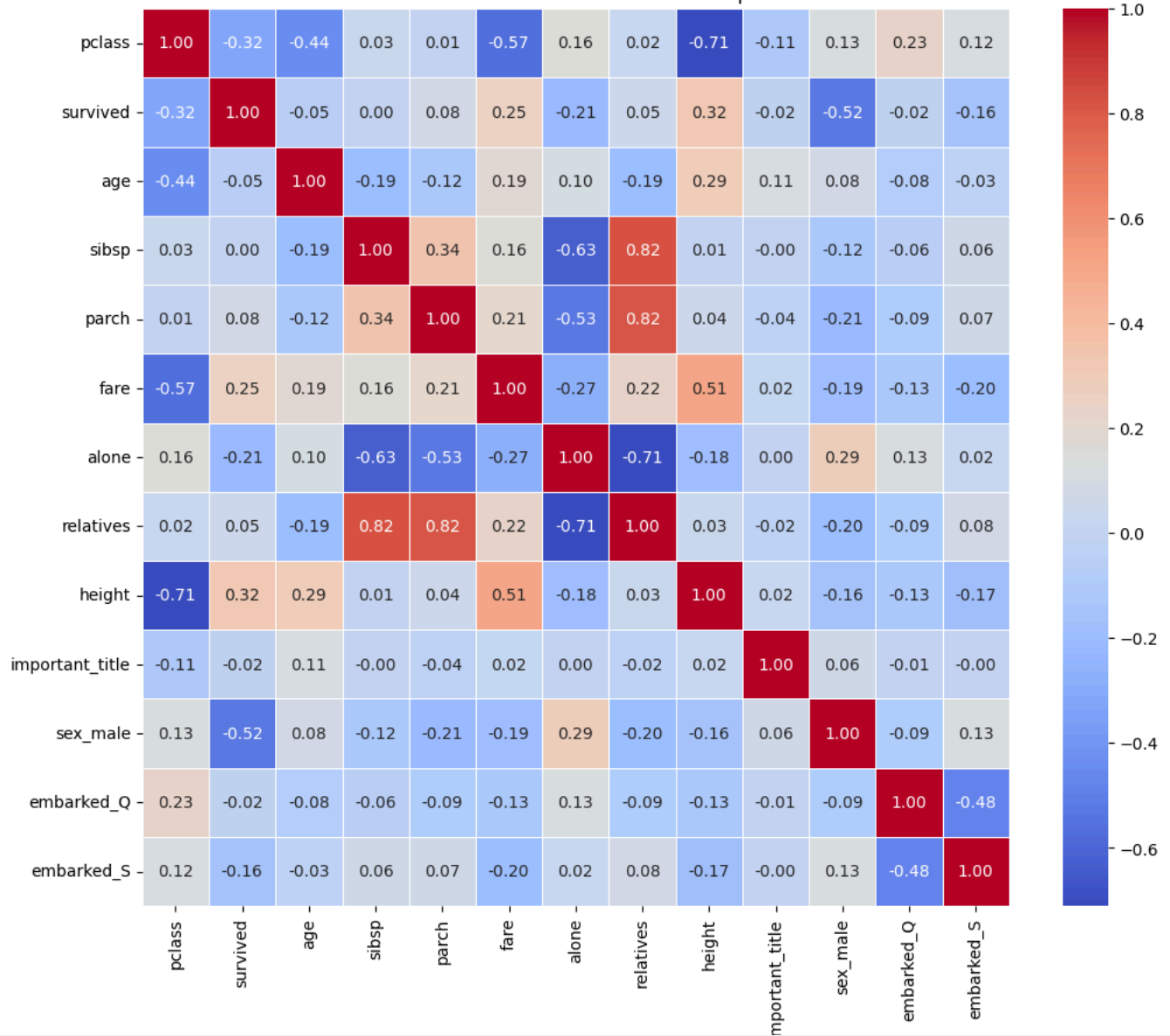
Lecture material: Lecture 5, slides 10–14, 19.

- Eliminate low variance and highly correlated features.
- Why do we carry out tasks 6 and 7 after splitting the dataset into training, validation, and test sets? Could we have conducted them on the entire dataset instead? Please elaborate on your answer.

```
# correlation matrix
corr_matrix = train_df.corr()
plt.figure(figsize=(12, 10))
sns.heatmap(corr_matrix, annot=True, cmap='coolwarm', fmt='.2f', linewidths=0.5, cbar=True)
plt.title('Matriz de Correlación del Dataset Completo')
plt.show()
```



Matriz de Correlación del Dataset Completo



```
# low variance
def remove_low_variance_features(df, threshold=0.1):
    variances = df.var()
    low_variance_features = variances[variances < threshold].index.tolist()
    df_cleaned = df.drop(columns=low_variance_features)
    print(f'Low variance features removed: {low_variance_features}')
    return df_cleaned

# highly correlated features
def remove_highly_correlated_features(df, correlation_threshold=0.5):
    corr_matrix = df.corr().abs()
    upper_triangle = corr_matrix.where(np.triu(np.ones(corr_matrix.shape), k=1).astype(bool))
    to_drop = [column for column in upper_triangle.columns if any(upper_triangle[column] > correlation_threshold)]
    df_cleaned = df.drop(columns=to_drop)
    print(f'Highly correlated features removed: {to_drop}')
    return df_cleaned

X_train = remove_low_variance_features(X_train)
X_train = remove_highly_correlated_features(X_train)

print(X_train.head())
```



```
Low variance features removed: ['important_title', 'embarked_Q']
Highly correlated features removed: ['fare', 'alone', 'relatives', 'height']
```

	pclass	age	sibsp	parch	sex_male	embarked_S
829	3	-1.038419	5.039298	1.830957	0.0	1.0
889	3	-0.268845	-0.509866	-0.428338	1.0	1.0
330	2	2.116833	-0.509866	-0.428338	1.0	1.0
91	1	0.115942	0.599967	-0.428338	1.0	1.0
808	3	-0.267124	-0.509866	-0.428338	1.0	1.0

Features with low variance, such as `important_title` and `embarked_Q`, don't provide meaningful information because they remain mostly constant across the dataset. If a feature doesn't vary much, it won't help the model differentiate between classes, so I set a variance threshold of 0.1 to automatically drop such features.

Additionally, I removed highly correlated features like `fare`, `alone`, `relatives`, and `height` to prevent multicollinearity. When two features have a correlation above 0.5, they likely contain redundant information, meaning keeping both could make the model more complex without adding real value. Interestingly, most of these were features I created, which suggests that they captured relationships already present in other variables.

We balance the classes and select features after splitting the data to avoid data leakage. If we balanced the classes before splitting, we might end up with synthetic or resampled data in both training and test sets, making the model look better than it actually is. Keeping balancing only in the training set ensures that our validation and test sets remain truly unseen.

Feature selection works the same way. If we analyze the whole dataset before splitting, we might pick features that seem important only because they correlate with patterns in the test data. This could lead to overfitting, where the model does well in training but struggles with new data. By selecting features only from the training set, we make sure the model learns from real patterns without accidentally using future information.

✓ Task 8: Training a Logistic Regression Model

Lecture material: Lecture 6, slides 5–9.

- Train a Logistic Regression Model to predict whether a passenger survives. Note: Use the method `predict` from the class `LogisticRegression` with the validation set. Have fun finding a visually appealing way to display the results of the predictions on the validation set. An analysis of model performance is not required and will not affect your final grade for the assignment. However, I won't