Exercise 2

For this exercise , you will be working with the Titanic Data Set from Kaggle. This is a very famous data set and very often is a student's first step in Data Analytics!

The Dataset has been given to you on D2L. You need to download the .csv file from your assignment folder. The above link is just for a reference story about the data.

1- For this assignment, you need to perform explorotary data analysis and answer at least three hypotheses based on the dataset. You may need to use your knowledge of statiscts to analyze this data.

Here are three possible hypotheses that you can define for this dataset (you can define your own hypotheses as well):

- Determine if the survival rate is associated to the class of passenger
- Determine if the survival rate is associated to the gender
- Determine the survival rate is associated to the age

2- For each hypothesis, you need to make at least one plot.

3- Write a summary of your findings in one page (e.g., summary statistics, plots) and submit the pdf file. Therefore, for part 2 of your assignment, you need to submit one jupyter notebook file and one pdf file.

This will be your first end to end data analysis project. For this assignment, you will be graded on you overall analysis, and your final report.

4- Push your code and project to github and provide the link to your code here.

Ensure that your github project is organized to at least couple of main folders, ensure that you have the README file as well:

- Src
- Data
- Docs
- Results

Read this link for further info:
https://gist.github.com/ericmjl/27e50331f24db3e8f957d1fe7bbbe510

Overview

Variable Notes

pclass: A proxy for socio-economic status (SES)

- **1st** = Upper
- **2nd** = Middle
- **3rd** = Lower

age: Age is fractional if less than 1.

sibsp: The dataset defines family relations in this way:

- **Sibling** = brother, sister, stepbrother, stepsister
- **Spouse** = husband, wife (mistresses and fiancés were ignored)

parch: The dataset defines family relations in this way:

- **Parent** = mother, father
- **Child** = daughter, son, stepdaughter, stepson
  Some children travelled only with a nanny, therefore parch=0 for them.

Read Data

In [1]:
```
import pandas as pd
df=pd.read_csv('..\\Data\\titanic.csv')
```

General review

First, it is important to know the data type of every column and the number of missing values present

---

Missing Data

In [2]:
```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 891 entries, 0 to 890
Data columns (total 12 columns):
 #   Column       Non-Null Count  Dtype  
---  ------       --------------  -----  
 0   PassengerId  891 non-null    int64  
 1   Survived     891 non-null    int64  
 2   Pclass       891 non-null    int64  
 3   Name         891 non-null    object 
 4   Sex          891 non-null    object 
 5   Age          714 non-null    float64
 6   SibSp        891 non-null    int64  
 7   Parch        891 non-null    int64  
 8   Ticket       891 non-null    object 
 9   Fare         891 non-null    float64
 10  Cabin        204 non-null    object 
 11  Embarked     889 non-null    object 
dtypes: float64(2), int64(5), object(5)
memory usage: 83.7+ KB
```

There are two columns with missing values.

- Age
- Cabin

In [3]:
```
for x in ['Age','Cabin']:
    print('{}: {} records are null out of {}. This means {:.2f}% of all records are mi
```

```
Age: 177 records are null out of 891. This means 19.87% of all records are missing
Cabin: 687 records are null out of 891. This means 77.10% of all records are missing
```

For Exploratory Data Analysis the variable **Age** will be taken into account to check some inference with Survival rate.	For Exploratory Data Analysis the variable **Cabin** does not have enough data for find out its stadistics and relationship with other variables. So, this variables will not be included.

Data Type

Considering Data type of all columns are not consistent with their content, Dataframe aatributes should be converted

In [4]:
```
for i in df.columns:
    print(i,len(df[i].unique()))
```

```
PassengerId 891
Survived 2
Pclass 3
Name 891
Sex 2
Age 89
SibSp 7
Parch 7
Ticket 681
Fare 248
Cabin 148
Embarked 4
```

From the previous code the columns that can be considered as categorical are :

Survived	Pclass	Sex	SibSp	Parch	Embarked

From the previous code the columns that can be considered as numerical are :

Fare	Age

The following variables won´t be analyzed due to missing values or quality data.

Ticket	PassengerId	Cabin
Low Quality Data	Key of the rows	Not enough data

In [5]:
```
df1=df.copy()
df1.drop(['Cabin','Ticket'],axis=1)
df1.set_index('PassengerId')
```

Out[5]:

PassengerId	Survived	Pclass	Name	Sex	Age	SibSp	Parch	Ticket	Fare	Cabin	Eml
1	0	3	Braund, Mr. Owen Harris	male	22.0	1	0	A/5 21171	7.2500	NaN	
2	1	1	Cumings, Mrs. John Bradley (Florence Briggs Th...	female	38.0	1	0	PC 17599	71.2833	C85	
3	1	3	Heikkinen, Miss. Laina	female	26.0	0	0	STON/O2. 3101282	7.9250	NaN	
4	1	1	Futrelle, Mrs. Jacques Heath (Lily May Peel)	female	35.0	1	0	113803	53.1000	C123	
5	0	3	Allen, Mr. William Henry	male	35.0	0	0	373450	8.0500	NaN	
...	...	...	...	...	...	...	...	...	...	...	
887	0	2	Montvila, Rev. Juozas	male	27.0	0	0	211536	13.0000	NaN	
888	1	1	Graham, Miss. Margaret Edith	female	19.0	0	0	112053	30.0000	B42	
889	0	3	Johnston, Miss. Catherine Helen "Carrie"	female	NaN	1	2	W./C. 6607	23.4500	NaN	
890	1	1	Behr, Mr. Karl Howell	male	26.0	0	0	111369	30.0000	C148	
891	0	3	Dooley, Mr. Patrick	male	32.0	0	0	370376	7.7500	NaN	

891 rows × 11 columns

In [6]:

```
df1.Survived=df1.Survived.astype('category')
df1.Pclass=df1.Pclass.astype('category')
df1.Sex=df1.Sex.astype('category')
df1.SibSp=df1.SibSp.astype('category')
```

```
df1.Parch=df1.Parch.astype('category')
df1.Embarked=df1.Embarked.astype('category')
```

As Age should be integer and this data type cannot be a empty value, all null values will be replace to -1

In [7]:
```
df1.Age=df1.Age.fillna(-1)
df1.Age=df1.Age.astype('int64')
df1.Fare=df1.Fare.astype('float64')
```

Let ´s see the result

In [ ]:
```
```

In [8]:
```
df1.describe()
```

Out[8]:

	PassengerId	Age	Fare
count	891.000000	891.000000	891.000000
mean	446.000000	23.584736	32.204208
std	257.353842	17.868570	49.693429
min	1.000000	-1.000000	0.000000
25%	223.500000	6.000000	7.910400
50%	446.000000	24.000000	14.454200
75%	668.500000	35.000000	31.000000
max	891.000000	80.000000	512.329200

Determine if the survival rate is associated to the class of passenger

In [9]:
```
survived_results=df.Survived.value_counts(normalize=True)
print('Only {:.2f}% of persons survived'.format(survived_results[1]/sum(survived_resul
```

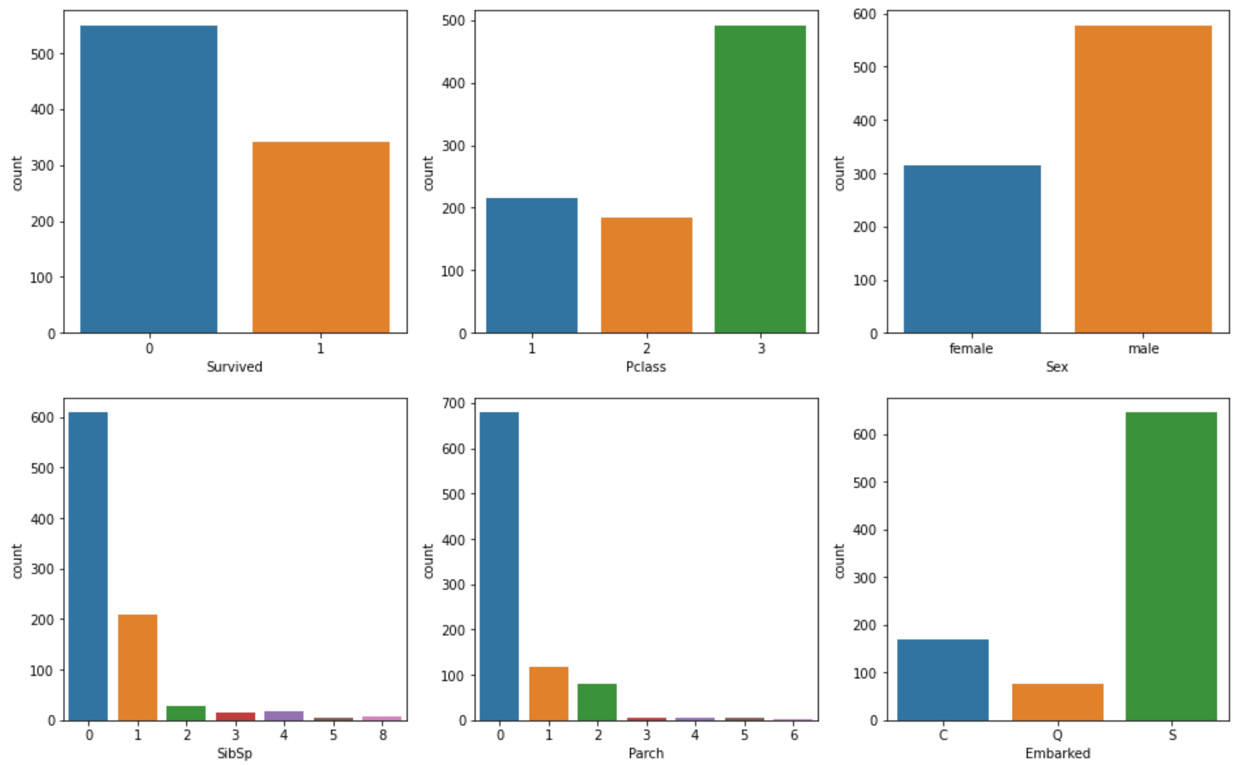
```
Only 38.38% of persons survived
```

Univariable Analysis Categorical Variable

In [10]:
```
import seaborn as sns
import matplotlib.pyplot as plt
plt.figure(figsize=(16,10))
plt.subplot(2,3,1)
fig=sns.countplot(data=df1, x='Survived')
plt.subplot(2,3,2)
sns.countplot(x='Pclass',data=df1)
plt.subplot(2,3,3)
sns.countplot(x='Sex',data=df1)
plt.subplot(2,3,4)
sns.countplot(x='SibSp',data=df1)
```

```
plt.subplot(2,3,5)
sns.countplot(x='Parch',data=df1)
plt.subplot(2,3,6)
sns.countplot(x='Embarked',data=df1)
```

Out[10]: <AxesSubplot:xlabel='Embarked', ylabel='count'>

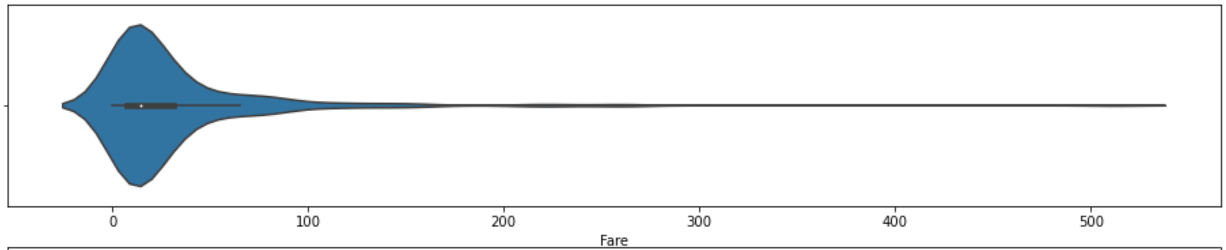


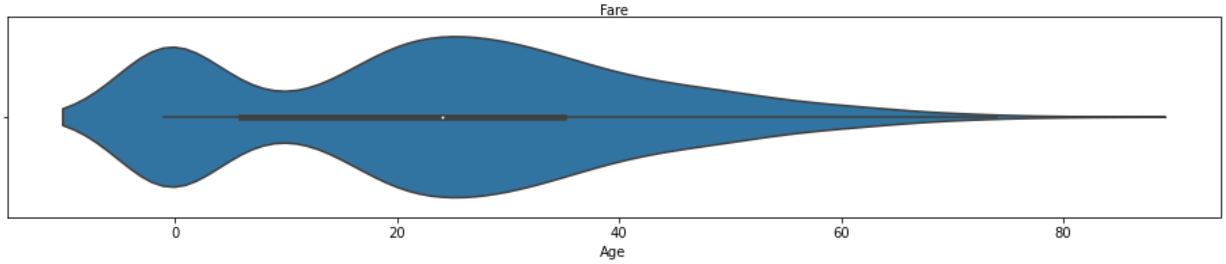
- Mayority of people were death
- Between all classes, class 3 was almost the double amount compared to class 1 y 2.
- Mayority of people were men.
- Majority of people did not have any siblings / spouses aboard the Titanic
- Majority of people did not have any parents / children aboard the Titanic
- Majority of the people embarked by the port S

Univariable Analysis Numerical Variable

In [11]:
```
import seaborn as sns
plt.figure(figsize=(16,6))
plt.subplot(2,1,1)
sns.violinplot(data=df1, x='Fare')
plt.subplot(2,1,2)
sns.violinplot(data=df1, x='Age')
```

Out[11]: <AxesSubplot:xlabel='Age'>





- Fare are too many outliers where some persons paid much more than others.
- The Age has a bimodal distribution, which means two peaks located around 0 and 25 years. The number of young people was significantly higher than the elderly. So the number of babies or newly born was almost the same amount as 25-year-old people.

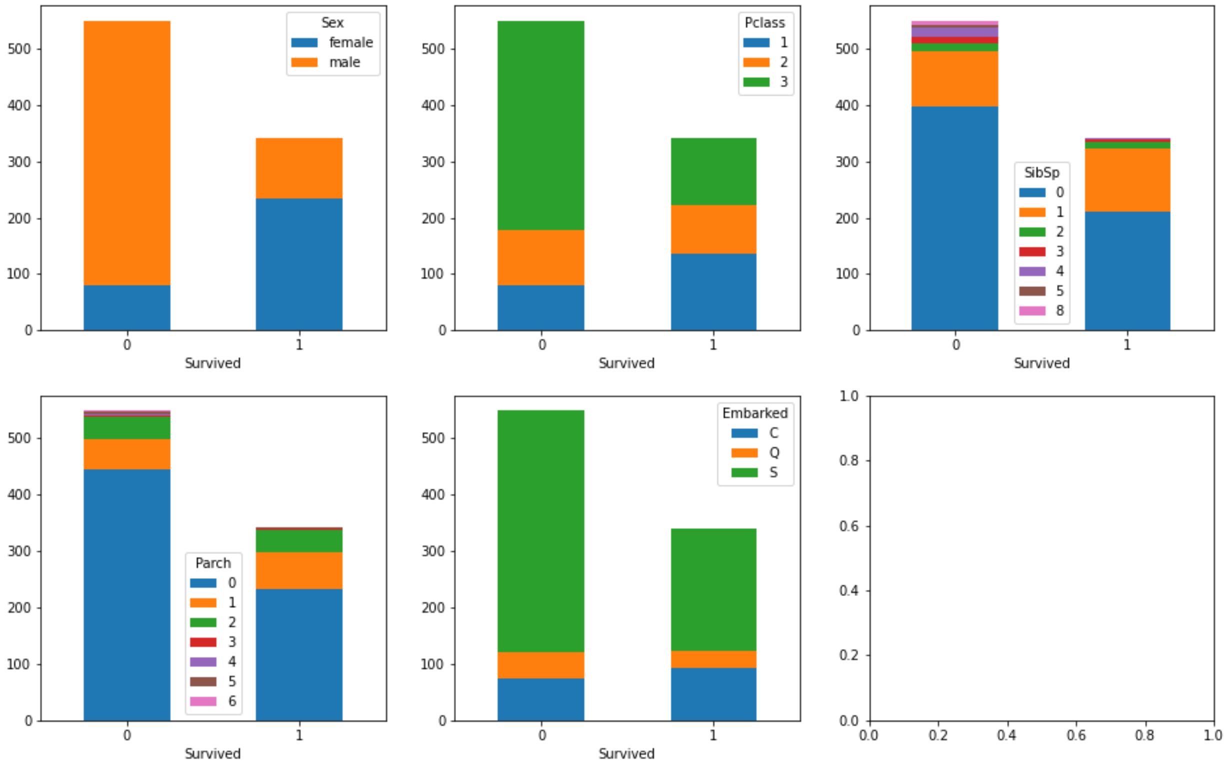
Bivariable Analysis Categorical Variable

Survived

In [12]:
```
my_crosstab_sex = pd.crosstab(index=df1["Survived"],
                            columns=df1["Sex"],)
my_crosstab_class = pd.crosstab(index=df1["Survived"],
                            columns=df1["Pclass"],)

my_crosstab_SibSp = pd.crosstab(index=df1["Survived"],
                            columns=df1["SibSp"],)
my_crosstab_Parch = pd.crosstab(index=df1["Survived"],
                            columns=df1["Parch"],)
my_crosstab_Embarked = pd.crosstab(index=df1["Survived"],
                            columns=df1["Embarked"],)
#plt.figure(figsize=(16,6))
fig, axes=plt.subplots(2,3,figsize=(16,10))
my_crosstab_sex.plot(kind='bar', stacked=True, rot=0,ax=axes[0,0])
my_crosstab_class.plot(kind='bar', stacked=True, rot=0,ax=axes[0,1])
my_crosstab_SibSp.plot(kind='bar', stacked=True, rot=0,ax=axes[0,2])
my_crosstab_Parch.plot(kind='bar', stacked=True, rot=0,ax=axes[1,0])
my_crosstab_Embarked.plot(kind='bar', stacked=True, rot=0,ax=axes[1,1])
```

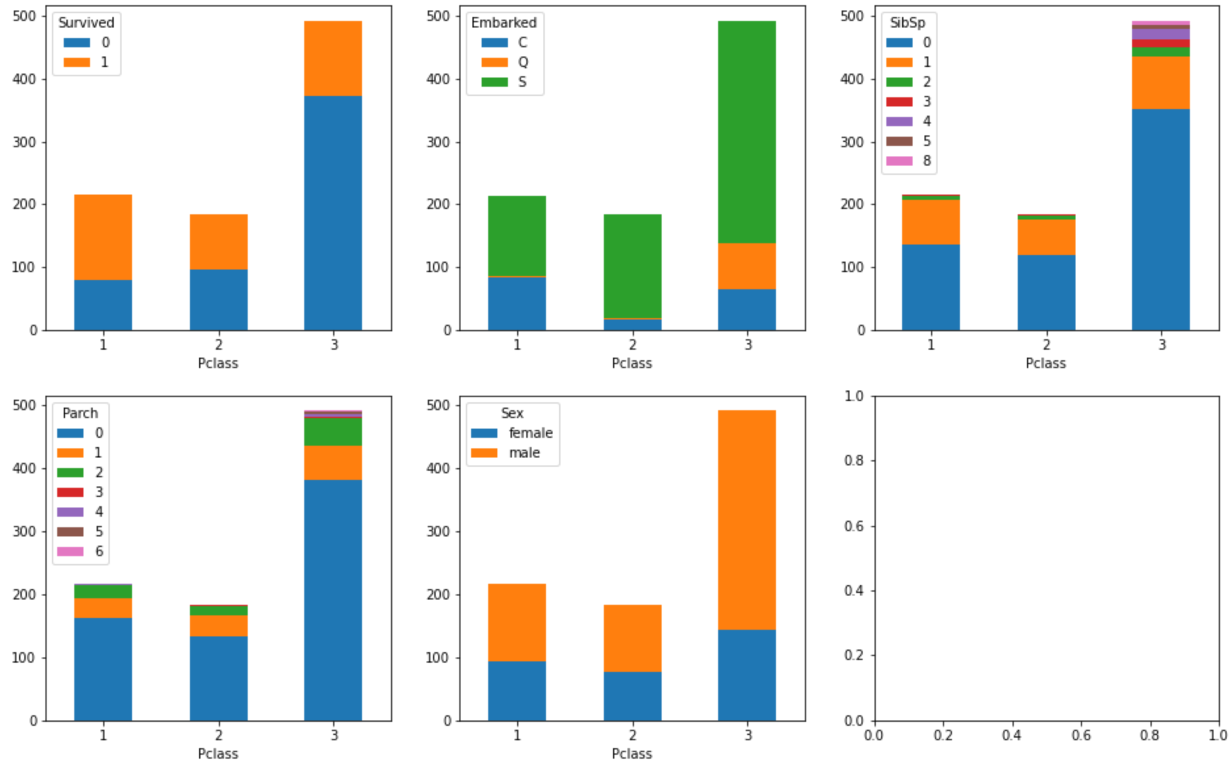
Out[12]:
```
<AxesSubplot:xlabel='Survived'>
```



Class

In [13]:
```
my_crosstab_class = pd.crosstab(index=df1["Pclass"],
                            columns=df1["Survived"],)
my_crosstab_class2 = pd.crosstab(index=df1["Pclass"],
                            columns=df1["Embarked"],)
my_crosstab_class3 = pd.crosstab(index=df1["Pclass"],
                            columns=df1["SibSp"],)
my_crosstab_class4 = pd.crosstab(index=df1["Pclass"],
                            columns=df1["Parch"],)
my_crosstab_class5 = pd.crosstab(index=df1["Pclass"],
                            columns=df1["Sex"],)
fig, axes=plt.subplots(2,3,figsize=(16,10))
my_crosstab_class.plot(kind='bar', stacked=True, rot=0,ax=axes[0,0])
my_crosstab_class2.plot(kind='bar', stacked=True, rot=0,ax=axes[0,1])
my_crosstab_class3.plot(kind='bar', stacked=True, rot=0,ax=axes[0,2])
my_crosstab_class4.plot(kind='bar', stacked=True, rot=0,ax=axes[1,0])
my_crosstab_class5.plot(kind='bar', stacked=True, rot=0,ax=axes[1,1])
```

Out[13]: <AxesSubplot:xlabel='Pclass'>

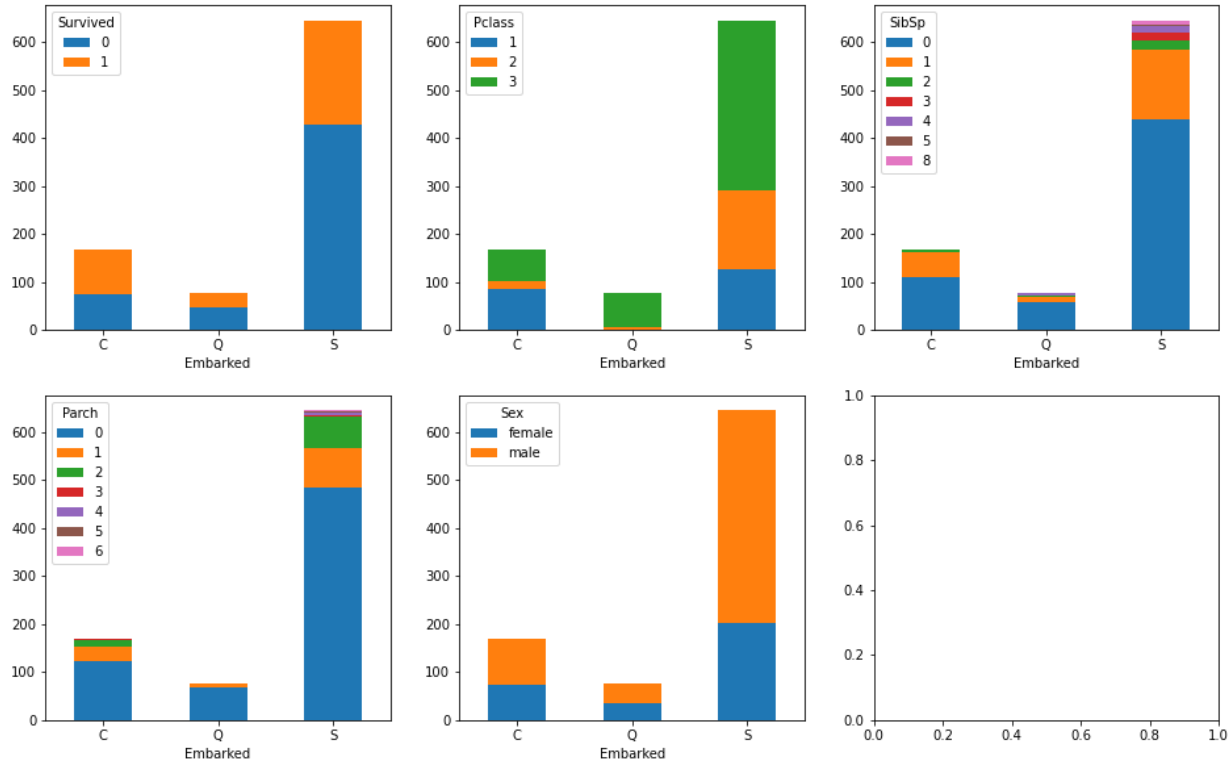


Embarked

In [14]:
```
my_crosstab_e = pd.crosstab(index=df1["Embarked"],
                            columns=df1["Survived"],)
my_crosstab_e2 = pd.crosstab(index=df1["Embarked"],
                             columns=df1["Pclass"],)
my_crosstab_e3 = pd.crosstab(index=df1["Embarked"],
                             columns=df1["SibSp"],)
my_crosstab_e4 = pd.crosstab(index=df1["Embarked"],
                             columns=df1["Parch"],)
my_crosstab_e5 = pd.crosstab(index=df1["Embarked"],
                             columns=df1["Sex"],)

fig, axes=plt.subplots(2,3,figsize=(16,10))
my_crosstab_e.plot(kind='bar', stacked=True, rot=0,ax=axes[0,0])
my_crosstab_e2.plot(kind='bar', stacked=True, rot=0,ax=axes[0,1])
my_crosstab_e3.plot(kind='bar', stacked=True, rot=0,ax=axes[0,2])
my_crosstab_e4.plot(kind='bar', stacked=True, rot=0,ax=axes[1,0])
my_crosstab_e5.plot(kind='bar', stacked=True, rot=0,ax=axes[1,1])
```

Out[14]:
```
<AxesSubplot:xlabel='Embarked'>
```



Insights

- High Proportion of people who survived were Female.
- High proportion of people who no survived were in class 3
- High proportion of people who did not have any siblings / sposes aboard the Titanic did not survived
- High proportion of people who did not have any parents / children aboard the Titanic did not survived
- High porportion of people who embarked by port S were from class 3
- The proportion of numbers of parents / children does not have any relation whether they survived or not.
- The proportion of numbers of siblings / sposes does not have any relation whether they survived or not.
- The proportion of surviver does not correlate with the sex
- The majority of people who embarked in port Q were from class 3
- The proportion of people who did not survived Embarked in the Port S

Analysis for continous variables

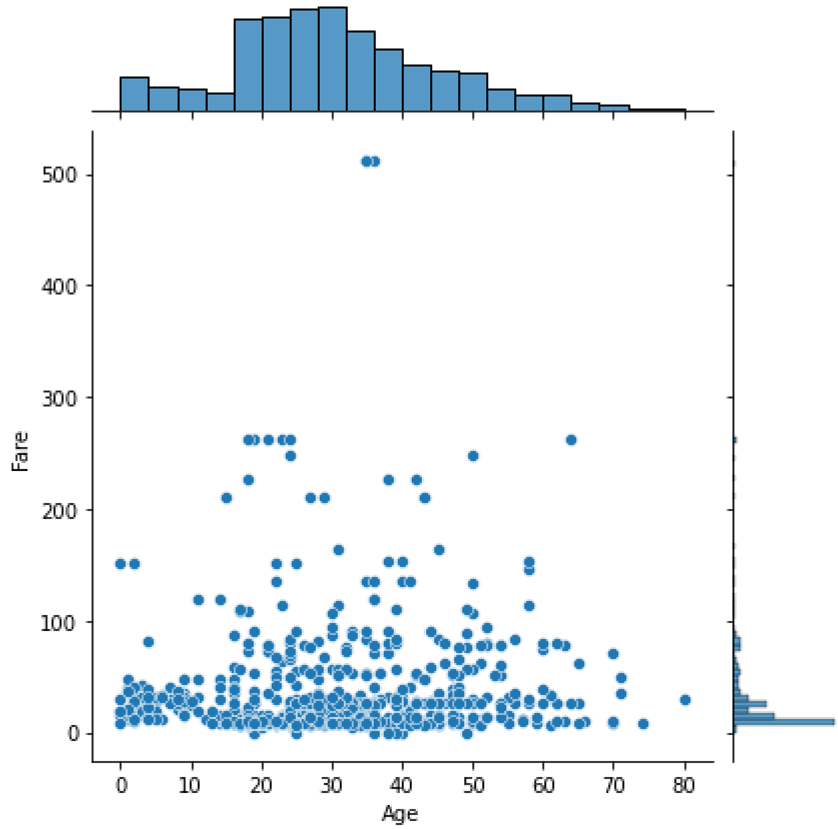
This analysis for continous variables rows with Age in null (-1) will drop.

In [15]:
```
import numpy as np
df1_numerical=df1.loc[df1.Age!=-1]
```

In [16]:
```
plt.figure(figsize=(16,10))
sns.jointplot(x="Age", y="Fare", data=df1_numerical)
```

Out[16]: <seaborn.axisgrid.JointGrid at 0x24922946460>

<Figure size 1152x720 with 0 Axes>



- Two values of Fare can be considered outliers
- Distribution of Age is not uniform due to there being a lack of people lower than 20. The among of young people was comparatively low with adults.
- The Fare distribution is right-skewed, its peak raises around 10 or 20.

Hypotesis

Once we did the **EDA**, we have enough understanding of the data to test the hypothesis

Determine if the survival rate is associated to the class of passenger

The hypothesis will be test looks like:

H_0: *Survival rate* and *class of passenger* are independent to each other among all subjects in the population

H_a: *Survival rate* and *class of passenger* are **NOT** independent to each other among all subjects in the population

In [17]:
```
contingency_class_sr_freq=pd.crosstab(index=df1.Survived,columns=df1.Embarked)
contingency_class_sr_freq
```

Out[17]:

Embarked	C	Q	S
Survived			
0	75	47	427
1	93	30	217

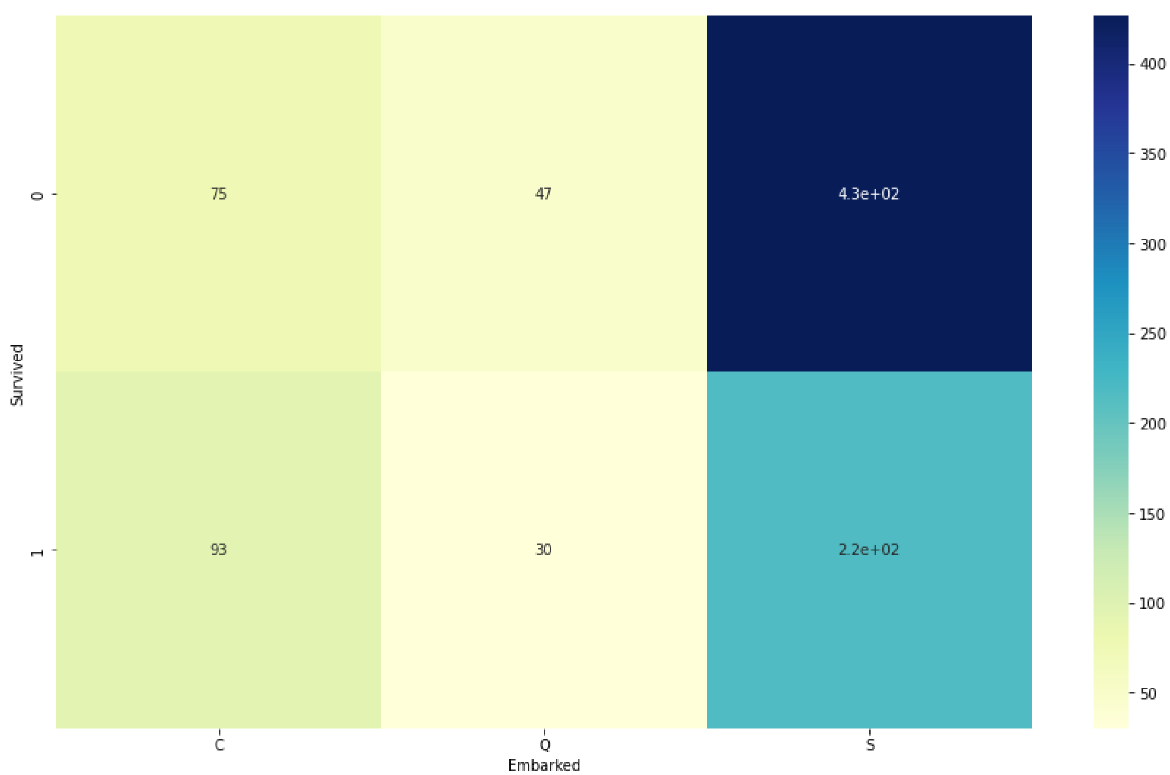
In [18]:
```
contingency_class_sr_percentage=pd.crosstab(index=df1.Survived,columns=df1.Pclass
contingency_class_sr_percentage
```

Out[18]:

Pclass	1	2	3	All
Survived				
0	37.037037	52.717391	75.763747	61.616162
1	62.962963	47.282609	24.236253	38.383838

In [19]:
```
plt.figure(figsize=(15,9))
sns.heatmap(contingency_class_sr_freq, annot=True, cmap="YlGnBu")
```

Out[19]: <AxesSubplot:xlabel='Embarked', ylabel='Survived'>



In [20]:
```
from scipy.stats import chi2_contingency
# Chi-square test of independence.
c, p, dof, expected = chi2_contingency(contingency_class_sr_freq)
# Print the p-value
print(p)
```

```
1.769922284120912e-06
```

The p value was so much less than 0.05, so there is enough statistical evidence to reject the null hypothesis and conclude that the variables are not significatly independent to each other among all the subject in the population .

Determine if the survival rate is associated to the gender

The hypothesis will be test looks like:

H_0: _Survival rate_ and _gender_ are independent to each other among all subjects in the population

H_a: _Survival rate_ and _gender_ are **NOT** independent to each other among all subjects in the population

In [21]:
```
contingency_sex_sr_freq=pd.crosstab(index=df1.Survived,columns=df1.Sex)
contingency_sex_sr_freq
```

Out[21]:

Sex	female	male
Survived		
0	81	468
1	233	109

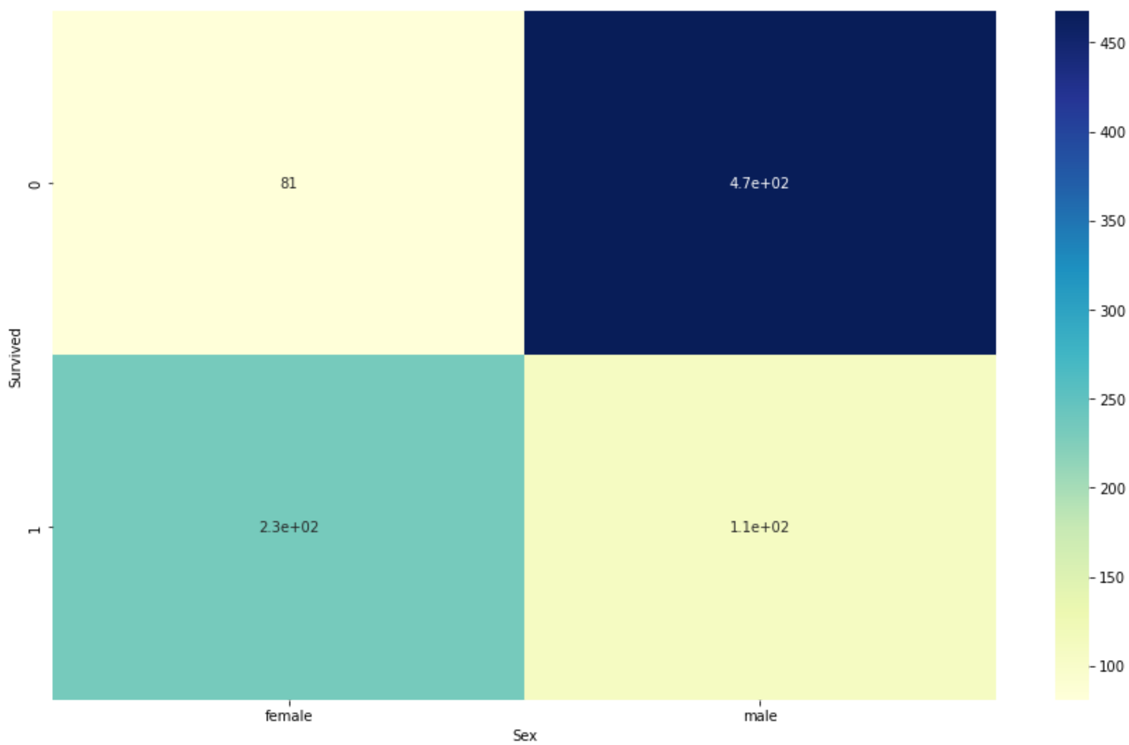
In [22]:
```
contingency_sex_sr_percentage=pd.crosstab(index=df1.Survived,columns=df1.Sex,nc
contingency_sex_sr_percentage
```

Out[22]:

Sex	female	male	All
Survived			
0	25.796178	81.109185	61.616162
1	74.203822	18.890815	38.383838

In [23]:
```
plt.figure(figsize=(15,9))
sns.heatmap(contingency_sex_sr_freq, annot=True, cmap="YlGnBu")
```

Out[23]: <AxesSubplot:xlabel='Sex', ylabel='Survived'>



In [24]:
```
from scipy.stats import chi2_contingency
# Chi-square test of independence.
c, p, dof, expected = chi2_contingency(contingency_sex_sr_freq)
# Print the p-value
print(p)
```

```
1.1973570627755645e-58
```

The p value was so much less than 0.05, so there is enough statistical evidence to reject the null hypothesis and conclude that the variables are not significantly independent to each other among all the subject in the population .

Determine the survival rate is associated to the age

The hypothesis will be test looks like:

H_0**:** *Survival rate* and *age* are independent to each other among all subjects in the population

H_a**:** *Survival rate* and *age* are **NOT** independent to each other among all subjects in the population

Even though the variable **Age** is numerical, doing a data analysis with range of ages

would be more insightful than only the ages as integers.
The ranges to change this variable into categorical with 5 levels will be like this:

- **minors :** 0 to 17
- **young :** 18 to 29
- **adults :** 30 to 44
- **adults-2 :** 45 to 60
- **elderly :** greater than 60
- **No values :** null

In [26]:
```
import numpy as np
df['Age_t']=0
df.loc[(df.Age>=0) & (df.Age<18),'Age_t']='minors'
df.loc[(df.Age>=18) & (df.Age<30),'Age_t']='young'
df.loc[(df.Age>=30) & (df.Age<45),'Age_t']='adults'
df.loc[(df.Age>=45) & (df.Age<60),'Age_t']='adults-2'
df.loc[(df.Age>=60),'Age_t']='elderly'
df.loc[np.isnan(df.Age),'Age_t']='No values'
```

In [27]:
```
df.Age_t.unique()
```

Out[27]:
```
array(['young', 'adults', 'No values', 'adults-2', 'minors', 'elderly'],
      dtype=object)
```

The hypothesis will be test looks like:

H_0: _Survival rate_ and _Age Ranges_ are independent to each other among all subjects in the population

H_a: _Survival rate_ and _Age Ranges_ are **NOT** independent to each other among all subjects in the population

In [28]:
```
contingency_age_sr_freq=pd.crosstab(index=df.Survived,columns=df.Age_t)
contingency_age_sr_freq
```

Out[28]:

Age_t / Survived	No values	adults	adults-2	elderly	minors	young
0	125	124	53	19	52	176
1	52	91	36	7	61	95

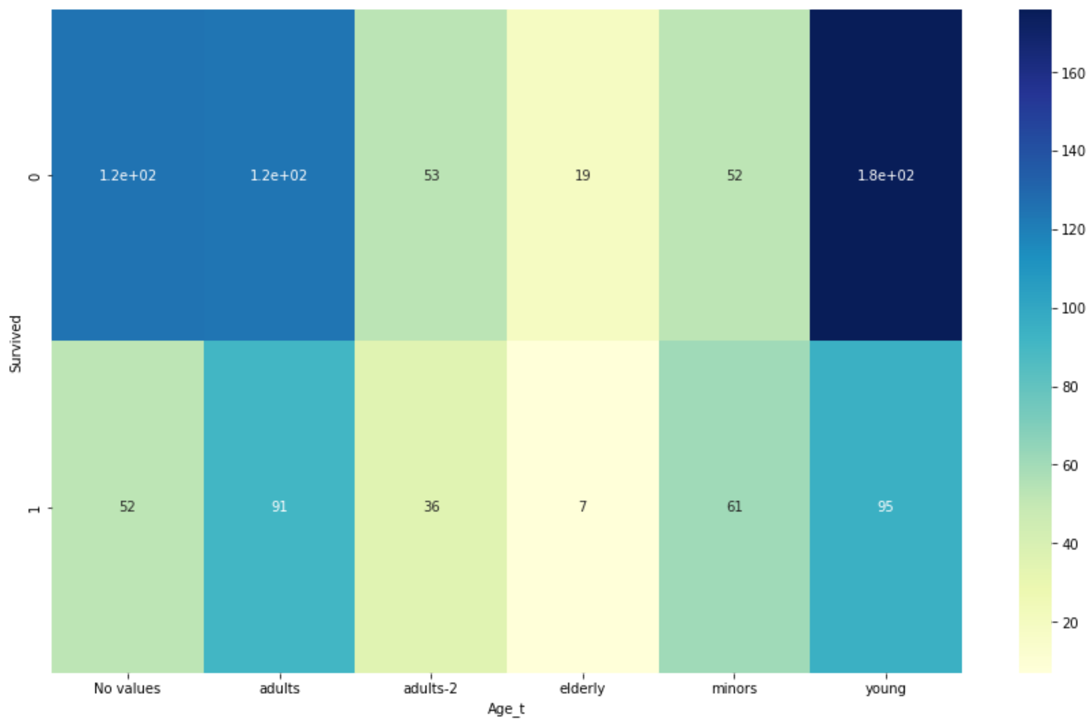
In [29]:
```
contingency_age_sr_percentage=pd.crosstab(index=df.Survived,columns=df.Age_t
contingency_age_sr_percentage
```

Out[29]:

Age_t / Survived	No values	adults	adults-2	elderly	minors	young	All
0	70.621469	57.674419	59.550562	73.076923	46.017699	64.944649	61.616162
1	29.378531	42.325581	40.449438	26.923077	53.982301	35.055351	38.383838

In [30]:
```
plt.figure(figsize=(15,9))
sns.heatmap(contingency_age_sr_freq, annot=True, cmap="YlGnBu")
```

Out[30]: <AxesSubplot:xlabel='Age_t', ylabel='Survived'>



In [31]:
```
from scipy.stats import chi2_contingency
# Chi-square test of independence.
c, p, dof, expected = chi2_contingency(contingency_age_sr_freq)
# Print the p-value
print(p)
```

```
0.0005280305666542873
```

The p value was so much less than 0.05, so there is enough statistical evidence to reject the null hypothesis and conclude that the variables are not significatly independent to each other among all the subject in the population .