eda-assignment-1

March 24, 2024

[28]:

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
```

[2]:

```
df = pd.read_csv('heart_failure_clinical_records_dataset.csv')
```

[3]:

```
df_cp = df
```

[4]:

```
df.head()
```

[4]:

```
    age  anaemia  creatinine_phosphokinase  diabetes  ejection_fraction  \
0  75.0        0                       582         0                 20
1  55.0        0                      7861         0                 38
2  65.0        0                       146         0                 20
3  50.0        1                       111         0                 20
4  65.0        1                       160         1                 20

   high_blood_pressure  platelets  serum_creatinine  serum_sodium  sex  \
0                    1  265000.00               1.9           130    1
1                    0  263358.03               1.1           136    1
2                    0  162000.00               1.3           129    1
3                    0  210000.00               1.9           137    1
4                    0  327000.00               2.7           116    0

   smoking  time  DEATH_EVENT
0        0     4            1
1        0     6            1
2        1     7            1
3        0     7            1
4        0     8            1
```

[5]:

```
df.shape
```

[5]:

```
(299, 13)
```

[6]:

```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 299 entries, 0 to 298
Data columns (total 13 columns):
 #   Column                    Non-Null Count  Dtype
---  ------                    --------------  -----
 0   age                       299 non-null    float64
 1   anaemia                   299 non-null    int64
 2   creatinine_phosphokinase  299 non-null    int64
 3   diabetes                  299 non-null    int64
 4   ejection_fraction         299 non-null    int64
 5   high_blood_pressure       299 non-null    int64
 6   platelets                 299 non-null    float64
 7   serum_creatinine          299 non-null    float64
 8   serum_sodium              299 non-null    int64
 9   sex                       299 non-null    int64
 10  smoking                   299 non-null    int64
 11  time                      299 non-null    int64
 12  DEATH_EVENT               299 non-null    int64
dtypes: float64(3), int64(10)
memory usage: 30.5 KB
```

[7]:
```
df[df.isnull()].sum()
```

[7]:
```
age                         0.0
anaemia                     0.0
creatinine_phosphokinase    0.0
diabetes                    0.0
ejection_fraction           0.0
high_blood_pressure         0.0
platelets                   0.0
serum_creatinine            0.0
serum_sodium                0.0
sex                         0.0
smoking                     0.0
time                        0.0
DEATH_EVENT                 0.0
dtype: float64
```

[8]:
```
df.DEATH_EVENT
```

[8]:
```
0      1
1      1
2      1
3      1
4      1
      ..
294    0
```

```
295    0
296    0
297    0
298    0
Name: DEATH_EVENT, Length: 299, dtype: int64
```

[9]:

```
df['age']
```

[9]:

```
0      75.0
1      55.0
2      65.0
3      50.0
4      65.0
       …
294    62.0
295    55.0
296    45.0
297    45.0
298    50.0
Name: age, Length: 299, dtype: float64
```

[10]:

```
age_data = df['age']
```

[11]:

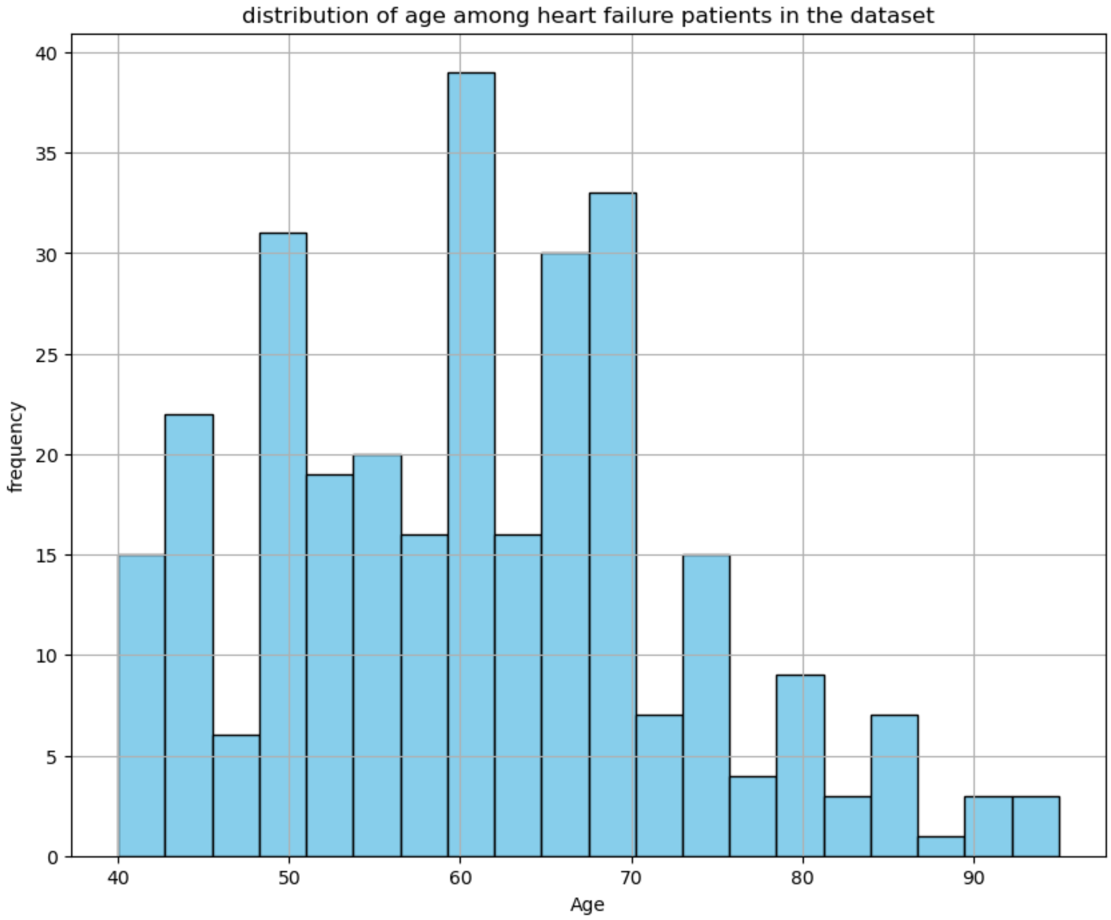
```
# What is the distribution of age among heart failure patients in the dataset
mean_age = age_data.mean()
mode_age = age_data.mode()
median_age = age_data.median()
```

[12]:

```
##visualization
print("Mean_age :",mean_age)
print("Mode_age :",mode_age)
print("median_age :",median_age)
plt.figure(figsize=(10,8))
plt.hist(age_data,bins = 20,color = 'skyblue',edgecolor = 'black')
plt.title('distribution of age among heart failure patients in the dataset')
plt.xlabel("Age")
plt.ylabel("frequency")
plt.grid(True)
plt.show()

##Insights are :
# 1) More number of people die in the age of 60
# 2) So More precosions take at this age of 60
# 3)Age of between 80 and 90 death rate is very less
```

```
Mean_age : 60.83389297658862
Mode_age : 0    60.0
```

```
Name: age, dtype: float64
median_age : 60.0
```

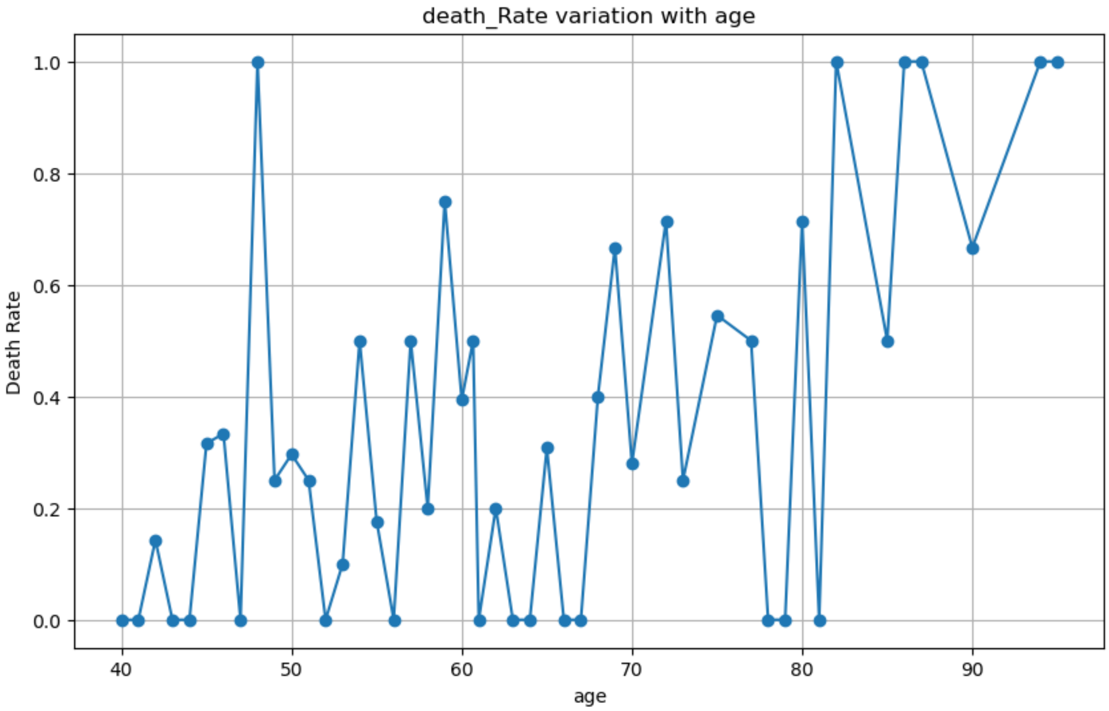


[13]:

```
## ´ How does the death rate vary with age

##Group this data by age and calculate death rate
age_death_rate = df.groupby('age')['DEATH_EVENT'].mean()
```

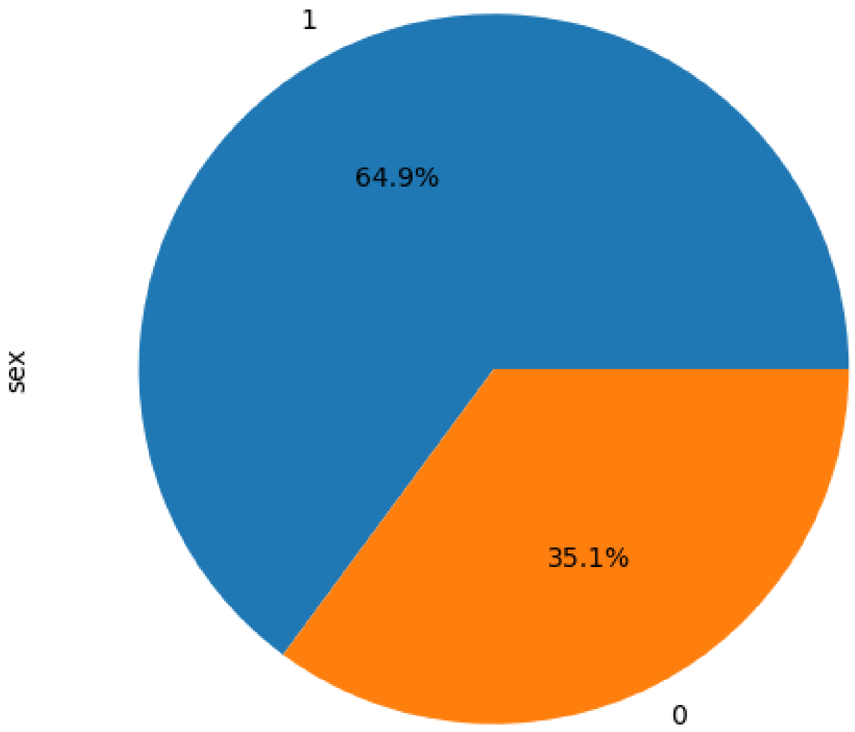
[14]:

```
# Visualize this Group
plt.figure(figsize=(10,6))
plt.plot(age_death_rate.index,age_death_rate.values,marker = 'o',linestyle='-')
plt.title("death_Rate variation with age")
plt.xlabel("age")
plt.ylabel("Death Rate")
plt.grid(True)
plt.show()
```



```
[15]: #What is the percentage of male and female patients in the dataset?
      df["sex"].value_counts()
      df["sex"].value_counts().plot.pie(y = df['sex'],autopct = '%1.1f%%',figsize =␣
       ↪(6,6))
      ##Insights :
      # 1) More heart atacks occure in males
```

```
[15]: <AxesSubplot: ylabel='sex'>
```



[16]:

```
platelet_counts = df.groupby('age')['platelets'].mean()
```

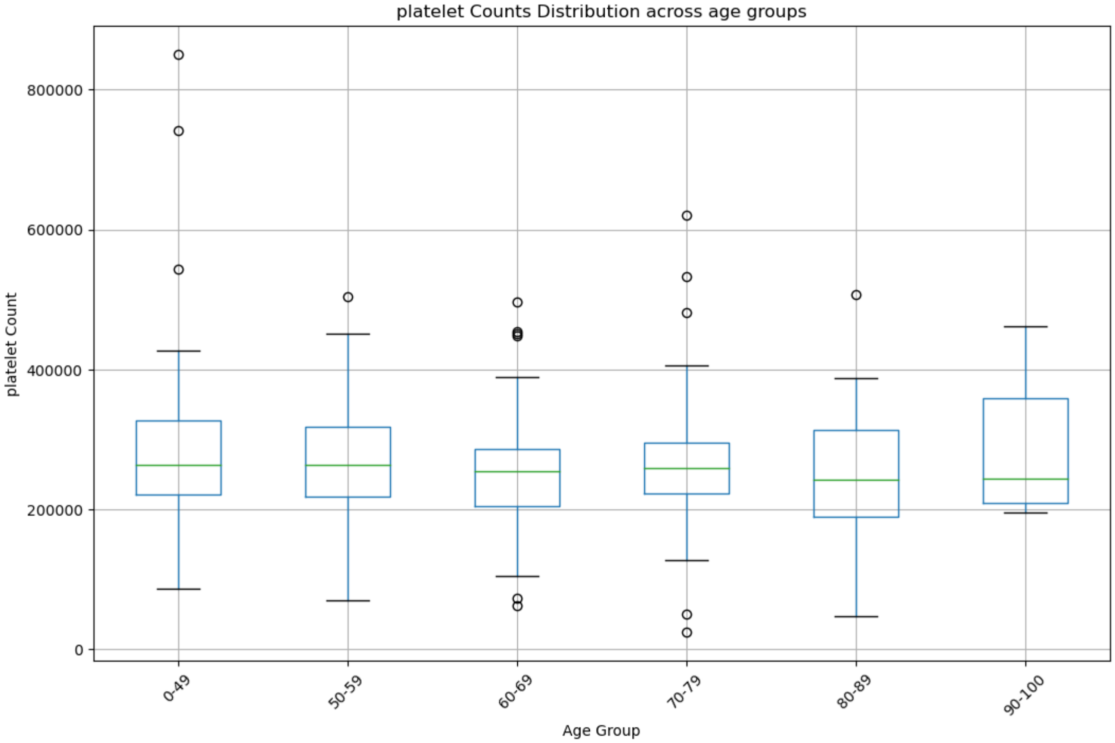
[17]:

```
# How does the platelet count vary among different age groups
bins = [0,50,60,70,80,90,100]
labels = ['0-49','50-59','60-69','70-79','80-89','90-100']

df['age_group'] = pd.cut(df['age'],bins = bins,labels = labels,right = False)
platlet_summary = df.groupby('age_group')['platelets'].describe()

print(platlet_summary)

plt.figure(figsize=(10,6))
df.boxplot(column='platelets',by = 'age_group',figsize=(12,8))
plt.title("platelet Counts Distribution across age groups")
plt.xlabel("Age Group")
plt.ylabel("platelet Count")
plt.suptitle("")
plt.xticks(rotation = 45)
```

```python
plt.show()

##Insights we can see that there are some outliers in all age groups
```

```
           count           mean            std       min       25%  \
age_group
0-49        47.0  285931.705319  141518.402154   87000.0  222000.0
50-59       82.0  265001.807073   83484.172827   70000.0  218250.0
60-69       93.0  248990.840645   76019.870854   62000.0  204000.0
70-79       52.0  267036.349038  101173.880709   25100.0  222250.0
80-89       19.0  252248.213684  105430.556160   47000.0  189000.0
90-100       6.0  290059.671667  109798.700540  196000.0  209500.0

                  50%          75%       max
age_group
0-49       263358.030  326500.0000  850000.0
50-59      263358.030  317750.0000  504000.0
60-69      254000.000  286000.0000  497000.0
70-79      259179.015  296000.0000  621000.0
80-89      243000.000  313500.0000  507000.0
90-100     244679.015  358339.5075  461000.0
```

```
<Figure size 1000x600 with 0 Axes>
```



[18]:
```
# is there a correlation between creatinine and sodium levels in the blood


creatinine_levels = df['creatinine_phosphokinase']
sodium_levels = df['serum_sodium']

correlation_coefficient = creatinine_levels.corr(sodium_levels)
```

[19]:
```
print('Correlation coefficient between creatinine and sodium levels :
  ↪',correlation_coefficient)
##Insights : correlation Score is 59 it means there is some relations exist
```

```
Correlation coefficient between creatinine and sodium levels :
0.05955015583372577
```

[20]:
```
# How does the prevalence of high blood presure differ between male and female␣
  ↪patients

male_patients = df[df['sex'] == 1] ##Assume males are coded as 1
female_patients = df[df['sex'] == 0] ##Assume females are coded as 0

male_bp_prevalence = (male_patients['high_blood_pressure']).mean()*100
female_bp_prevalence = (female_patients['high_blood_pressure']).mean()*100
```

[21]:
```
print(f"Prevalence of High Blood Pressure among Male Patients:
  ↪{male_bp_prevalence:.5f}")
print(f"Prevalence of High Blood Pressure among FeMale Patients:
  ↪{female_bp_prevalence:.5f}")
```

```
Prevalence of High Blood Pressure among Male Patients:31.44330
Prevalence of High Blood Pressure among FeMale Patients:41.90476
```

[22]:
```
df.high_blood_pressure
```

[22]:
```
0      1
1      0
2      0
3      0
4      0
      ..
294    1
295    0
296    0
297    0
298    0
Name: high_blood_pressure, Length: 299, dtype: int64
```

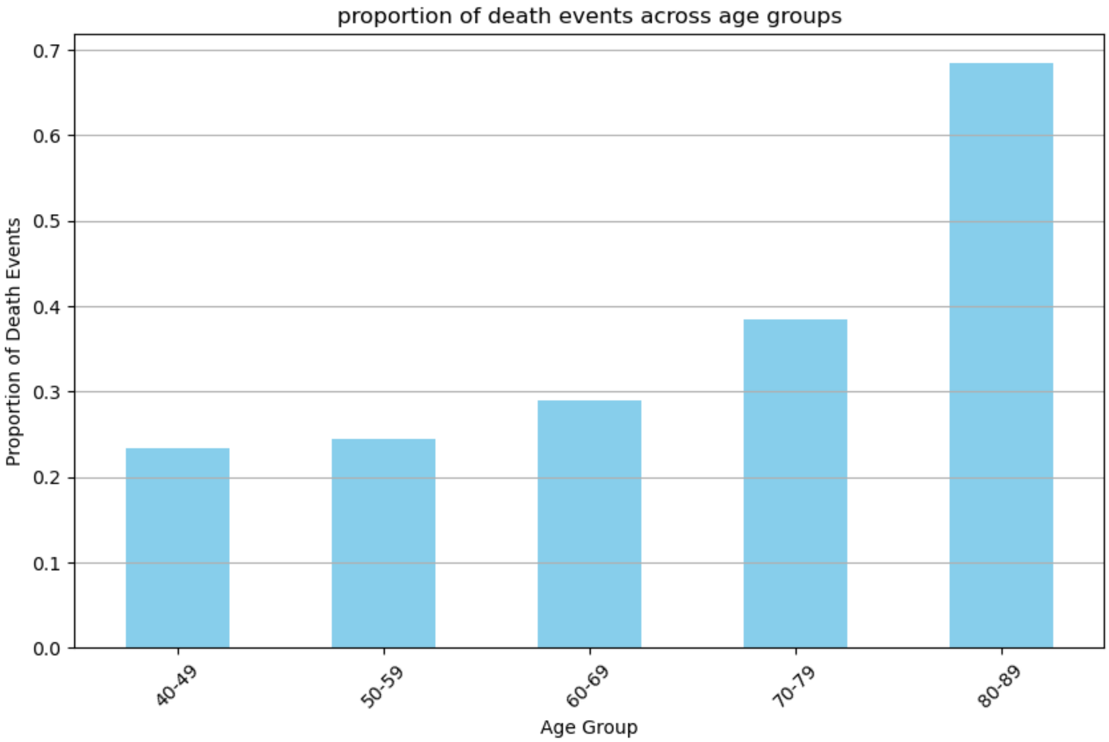
[23]:

```
##What is the relationship between smoking habits and the occurence of heart␣
  ↪failure
smoking_habbits = df.groupby('smoking')['DEATH_EVENT'].mean()

print(smoking_habbits[0])
print(smoking_habbits[1])
```

```
0.3251231527093596
0.3125
```

[24]:

```
# Are there any noticeable patterns in the distribution of death events across␣
  ↪different age groups ?
bins = [40, 50, 60, 70, 80, 90]  # Define age bins according to your dataset
labels = ['40-49', '50-59', '60-69', '70-79', '80-89']  # Labels for the age␣
  ↪groups
df['age_group'] = pd.cut(df['age'],bins = bins ,labels= labels,right=False)
death_proposition_by_age = df.groupby('age_group')['DEATH_EVENT'].mean()

plt.figure(figsize=(10,6))
death_proposition_by_age.plot(kind = 'bar',color = 'skyblue')
plt.title('proportion of death events across age groups')
plt.xlabel('Age Group')
plt.ylabel('Proportion of Death Events')
plt.xticks(rotation=45)
plt.grid(axis='y')
plt.show()
##Insights::more portion of deaths at age of 80-89
```



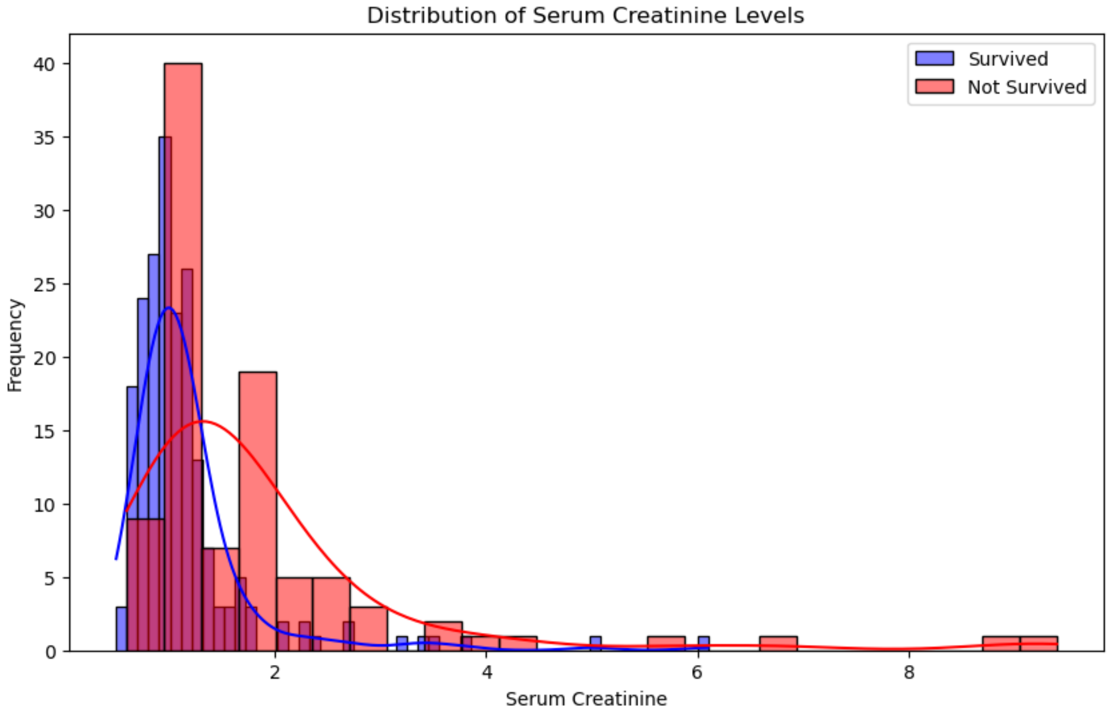
[25]:
```
##Is there any significant different in ejection faraction between patients␣
↪with and without diabetes ?
from scipy.stats import chi2_contingency

contingency_table = pd.crosstab(df['diabetes'],df['DEATH_EVENT'])
# Perform Chi-square test of independence
chi2,p_value,_,_= chi2_contingency(contingency_table)

# Check if the p-value is significant
alpha = 0.05  # Significance level
if p_value < alpha:
    print("There is a significant difference in the occurrence of death events␣
↪between patients with and without diabetes.")
else:
    print("There is no significant difference in the occurrence of death events␣
↪between patients with and without diabetes.")
```

```
There is no significant difference in the occurrence of death events between
patients with and without diabetes.
```

[29]:
```
##How does the serum creatinine level vary between patients who survived and␣
↪those who did not ?
serum_creatinine_survived = df[df['DEATH_EVENT']==0]['serum_creatinine']
```

```
serum_creatinine_not_survived = df[df['DEATH_EVENT']==1]['serum_creatinine']


from scipy.stats import ttest_ind
t_statistic,p_value =␣
 ↪ttest_ind(serum_creatinine_survived,serum_creatinine_not_survived)
print("Mean serum creatinine (Survived):",serum_creatinine_survived.mean())
print("Mean Serum Creatinine (Not Survived):", serum_creatinine_not_survived.
 ↪mean())
print("T-statistic:", t_statistic)
print("P-value:", p_value)

plt.figure(figsize=(10, 6))
sns.histplot(serum_creatinine_survived, color='blue', kde=True,␣
 ↪label='Survived', alpha=0.5)
sns.histplot(serum_creatinine_not_survived, color='red', kde=True, label='Not␣
 ↪Survived', alpha=0.5)
plt.title('Distribution of Serum Creatinine Levels')
plt.xlabel('Serum Creatinine')
plt.ylabel('Frequency')
plt.legend()
plt.show()
```

```
Mean serum creatinine (Survived): 1.1848768472906404
Mean Serum Creatinine (Not Survived): 1.8358333333333334
T-statistic: -5.306457599754319
P-value: 2.1901978548979685e-07
```


Distribution of Serum Creatinine Levels
Survived
Not Survived
Frequency
0
5
10
15
20
25
30
35
40
2
4
6
8
Serum Creatinine

[ ]:

[ ]:

[ ]:

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[ ]: