Final Project - Predicting survival of people with Heart Failure

Libraries

In [1]:
```
import pandas as pd
import numpy as np
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler
from sklearn import linear_model
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn import metrics

from sklearn.tree import DecisionTreeClassifier
from sklearn.neighbors import KNeighborsClassifier
from sklearn.naive_bayes import GaussianNB
from sklearn.svm import SVC

from scipy.cluster.hierarchy import linkage, fcluster
from sklearn.cluster import KMeans, DBSCAN
```

Data Import

In [2]:
```
data = pd.read_csv('heart_failure_clinical_records_dataset.csv')
data.head()
```

Out[2]:

	age	anaemia	creatinine_phosphokinase	diabetes	ejection_fraction	high_blood_pressure	platelets	serum_creatinine	serum_sodium	sex
0	75.0	0	582	0	20	1	265000.00	1.9	130	1
1	55.0	0	7861	0	38	0	263358.03	1.1	136	1
2	65.0	0	146	0	20	0	162000.00	1.3	129	1
3	50.0	1	111	0	20	0	210000.00	1.9	137	1
4	65.0	1	160	1	20	0	327000.00	2.7	116	0

In [3]:
```
data.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
```

Number of variables: 13

Types of variables: int64, float64

Redundant Variables: None

```
In [4]: data.dropna(0)
```

Out[4]:

	age	anaemia	creatinine_phosphokinase	diabetes	ejection_fraction	high_blood_pressure	platelets	serum_creatinine	serum_sodium	se
0	75.0	0	582	0	20	1	265000.00	1.9	130	1
1	55.0	0	7861	0	38	0	263358.03	1.1	136	1
2	65.0	0	146	0	20	0	162000.00	1.3	129	1
3	50.0	1	111	0	20	0	210000.00	1.9	137	1
4	65.0	1	160	1	20	0	327000.00	2.7	116	0
...	...	...	...	...	...	...	...	...	...	..
294	62.0	0	61	1	38	1	155000.00	1.1	143	1
295	55.0	0	1820	0	38	0	270000.00	1.2	139	0
296	45.0	0	2060	1	60	0	742000.00	0.8	138	0
297	45.0	0	2413	0	38	0	140000.00	1.4	140	1
298	50.0	0	196	0	45	0	395000.00	1.6	136	1

299 rows × 13 columns

```
In [5]: data.shape
Out[5]: (299, 13)
```

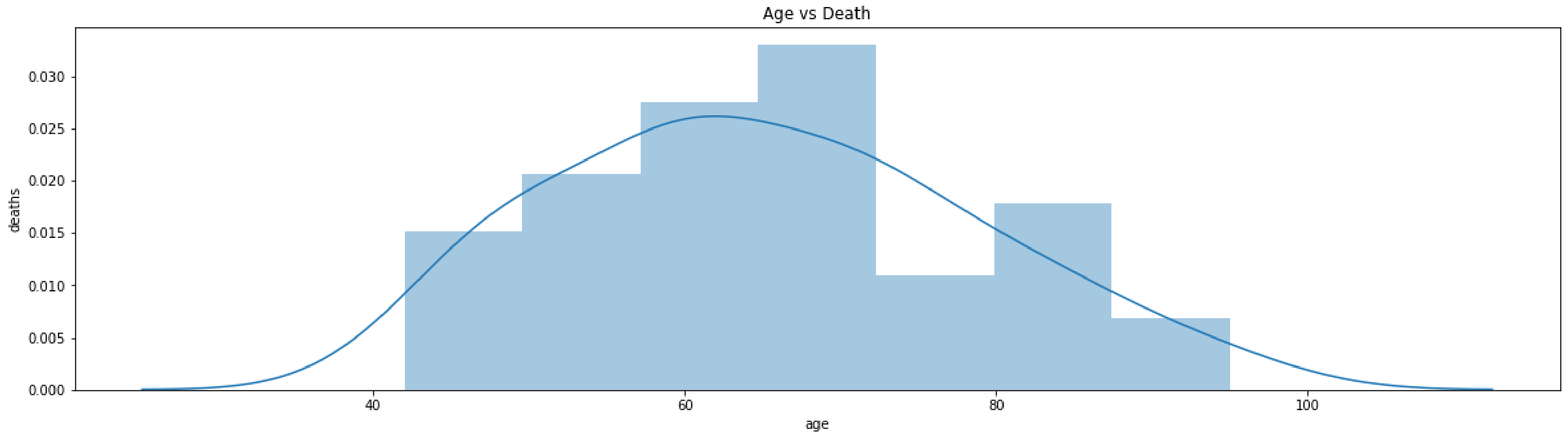
There are no missing data, noise, outliers

In [6]:
```python
# statistic description for heart failure data
data.describe().transpose().round(2)
```

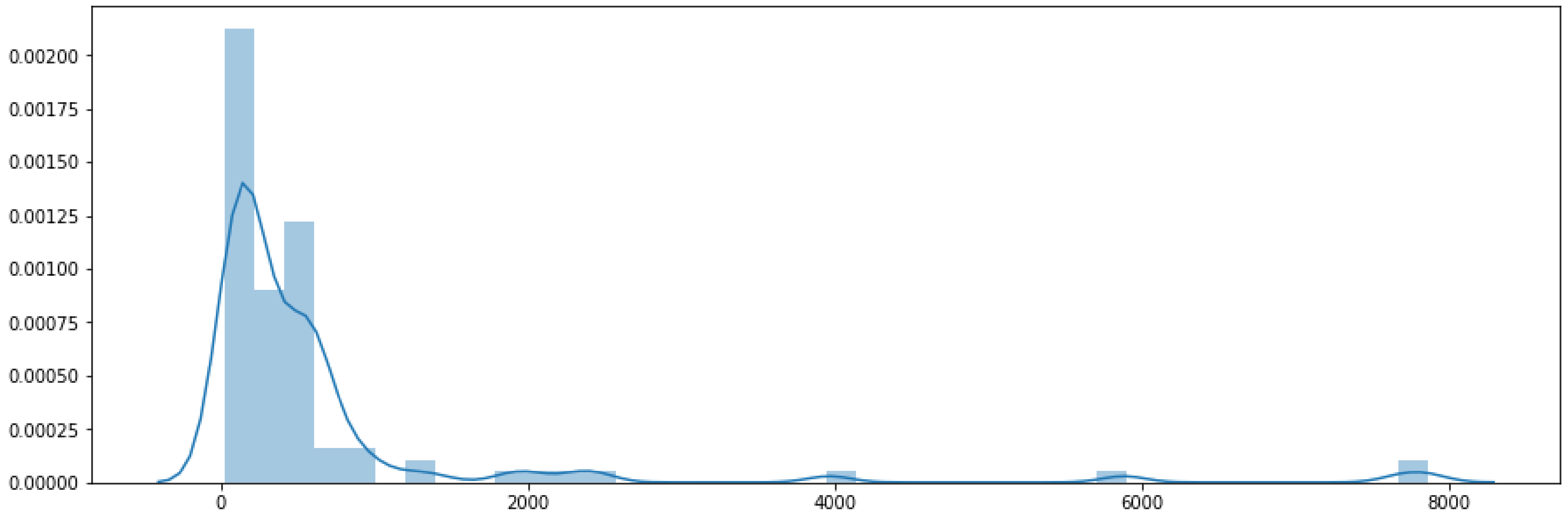
Out[6]:

	count	mean	std	min	25%	50%	75%	max
age	299.0	60.83	11.89	40.0	51.0	60.0	70.0	95.0
anaemia	299.0	0.43	0.50	0.0	0.0	0.0	1.0	1.0
creatinine_phosphokinase	299.0	581.84	970.29	23.0	116.5	250.0	582.0	7861.0
diabetes	299.0	0.42	0.49	0.0	0.0	0.0	1.0	1.0
ejection_fraction	299.0	38.08	11.83	14.0	30.0	38.0	45.0	80.0
high_blood_pressure	299.0	0.35	0.48	0.0	0.0	0.0	1.0	1.0
platelets	299.0	263358.03	97804.24	25100.0	212500.0	262000.0	303500.0	850000.0
serum_creatinine	299.0	1.39	1.03	0.5	0.9	1.1	1.4	9.4
serum_sodium	299.0	136.63	4.41	113.0	134.0	137.0	140.0	148.0
sex	299.0	0.65	0.48	0.0	0.0	1.0	1.0	1.0
smoking	299.0	0.32	0.47	0.0	0.0	0.0	1.0	1.0
time	299.0	130.26	77.61	4.0	73.0	115.0	203.0	285.0
DEATH_EVENT	299.0	0.32	0.47	0.0	0.0	0.0	1.0	1.0

```
In [7]: ax = sns.distplot(data[data['DEATH_EVENT'] == 1][['age']])
        ax.figure.set_size_inches(20, 5)
        ax.set(title = 'Age vs Death', xlabel = 'age', ylabel = 'deaths')

Out[7]: [Text(0, 0.5, 'deaths'), Text(0.5, 0, 'age'), Text(0.5, 1.0, 'Age vs Death')]
```

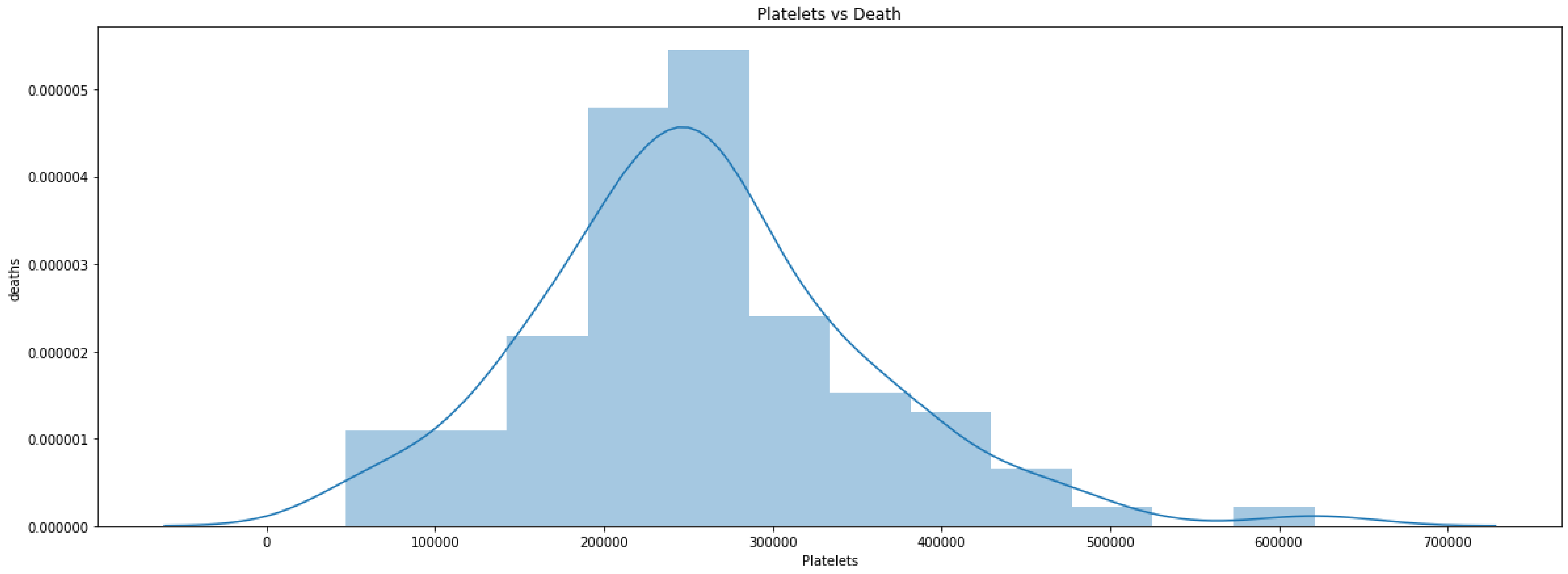


In [8]:
```
fig, axs = plt.subplots(1)
fig.set_size_inches(15, 5)
axs = sns.distplot(data[data['DEATH_EVENT'] == 1][['creatinine_phosphokinase']])
```



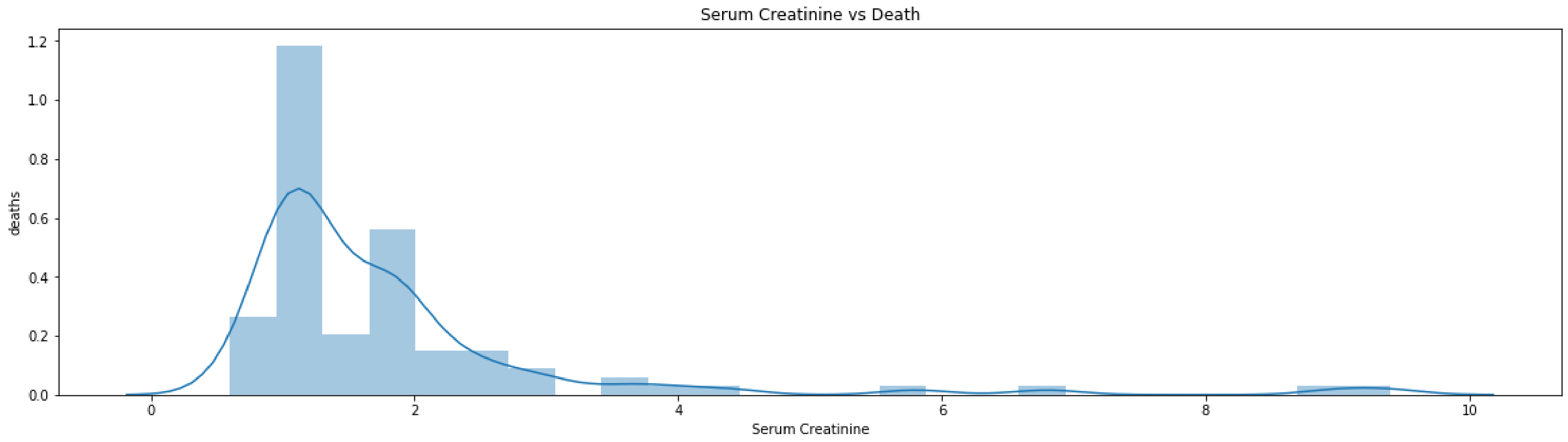
```
In [9]: ax = sns.distplot(data[data['DEATH_EVENT'] == 1][['platelets']])
        ax.figure.set_size_inches(20, 7)
        ax.set(title = 'Platelets vs Death', xlabel = 'Platelets', ylabel = 'deaths')
```

```
Out[9]: [Text(0, 0.5, 'deaths'),
         Text(0.5, 0, 'Platelets'),
         Text(0.5, 1.0, 'Platelets vs Death')]
```

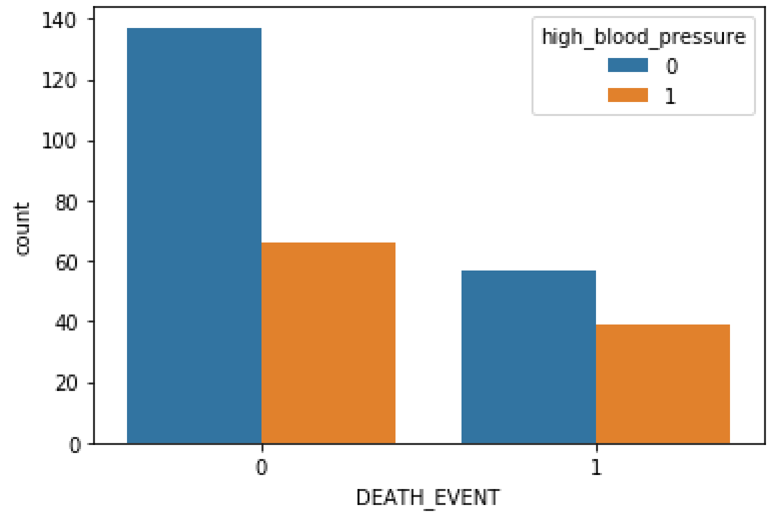


```
In [10]: ax = sns.distplot(data[data['DEATH_EVENT'] == 1][['serum_creatinine']])
         ax.figure.set_size_inches(20, 5)
         ax.set(title = 'Serum Creatinine vs Death', xlabel = 'Serum Creatinine', ylabel = 'deaths')
```

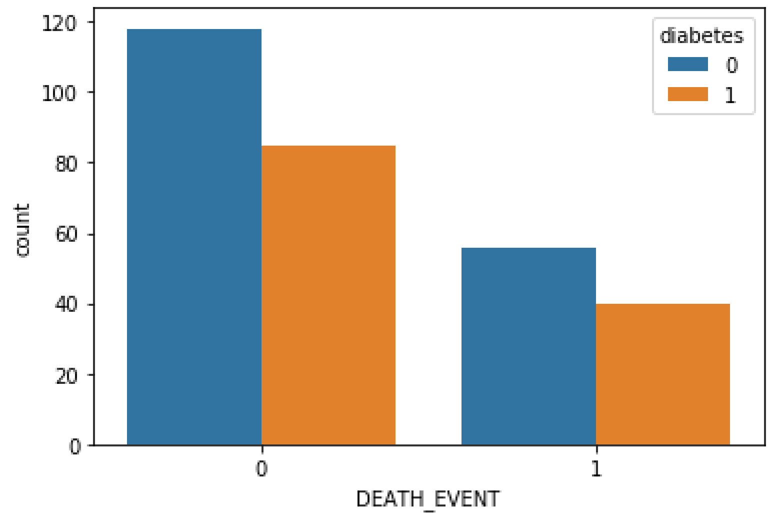
```
Out[10]: [Text(0, 0.5, 'deaths'),
          Text(0.5, 0, 'Serum Creatinine'),
          Text(0.5, 1.0, 'Serum Creatinine vs Death')]
```



```
In [11]: sns.countplot(x = 'DEATH_EVENT', hue = 'high_blood_pressure', data = data)
Out[11]: <matplotlib.axes._subplots.AxesSubplot at 0x7faa66ed0890>
```

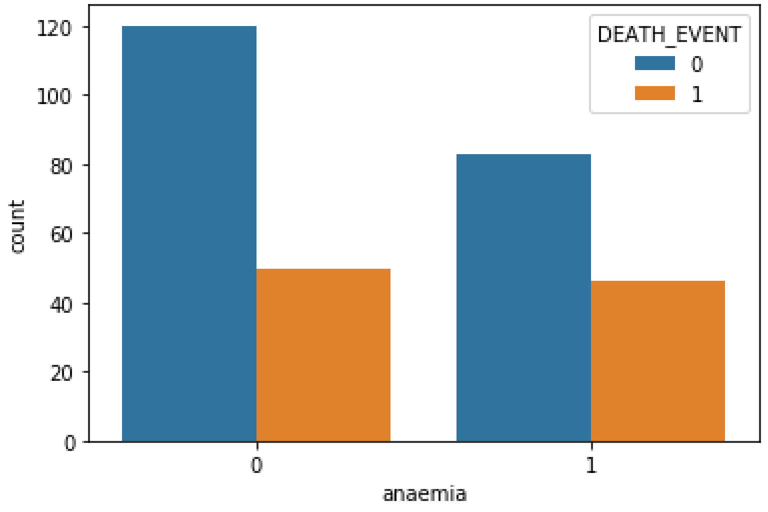


```
In [12]: sns.countplot(x = 'DEATH_EVENT', hue = 'diabetes', data = data)
Out[12]: <matplotlib.axes._subplots.AxesSubplot at 0x7faa66e3d450>
```



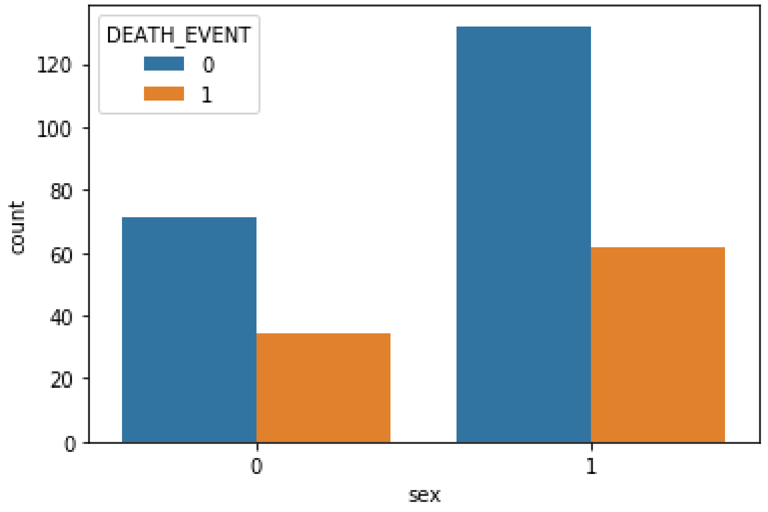
```
In [13]: sns.countplot(x = 'anaemia', hue = 'DEATH_EVENT', data = data)
```

```
Out[13]: <matplotlib.axes._subplots.AxesSubplot at 0x7faa66dbd050>
```



```
In [14]: sns.countplot(x = 'sex', hue = 'DEATH_EVENT', data = data)
```

```
Out[14]: <matplotlib.axes._subplots.AxesSubplot at 0x7faa66d25150>
```



Data Preparation

```
In [15]: X_train, X_val, y_train, y_val = train_test_split(data.iloc[:,:-1], data.iloc[:, [-1]], test_size = 0.25,
         random_state = 0)
         # X_train, X_val, y_train, y_val = train_test_split(data.iloc[:,:12], data.iloc[:, 12:], test_size = 0.2
         5, random_state = 0)
```

```
In [16]: scaler = StandardScaler()
         scaler.fit(X_train)
         x_train_scaled = scaler.transform(X_train)
         x_val_scaled = scaler.transform(X_val)
         # x_val = X_val.select_dtypes(include=[np.int64,np.float64])
         x_train_scaled_df = pd.DataFrame(x_train_scaled,index = X_train.index,columns=X_train.columns)
         x_val_scaled_df = pd.DataFrame(x_val_scaled,index = X_val.index,columns=X_val.columns)
```

Classification

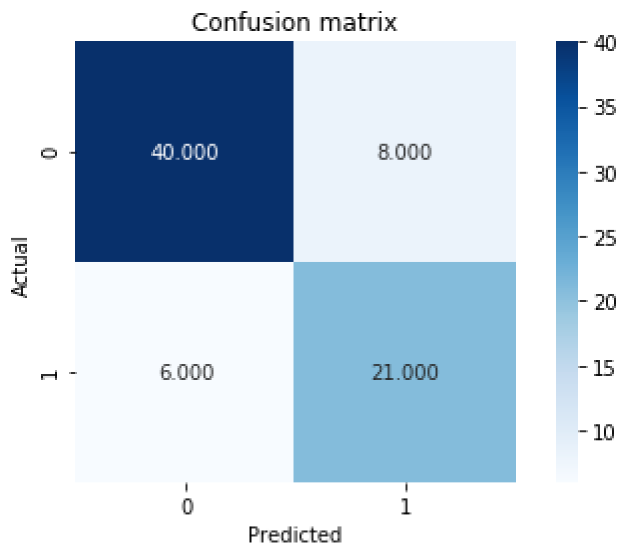
1: Decision Tree

1.1: Using all predictor variables

```
In [17]: classifier = DecisionTreeClassifier(criterion='entropy', random_state=0)
         classifier.fit(x_train_scaled, y_train)
```

```
Out[17]: DecisionTreeClassifier(ccp_alpha=0.0, class_weight=None, criterion='entropy',
                                max_depth=None, max_features=None, max_leaf_nodes=None,
                                min_impurity_decrease=0.0, min_impurity_split=None,
                                min_samples_leaf=1, min_samples_split=2,
                                min_weight_fraction_leaf=0.0, presort='deprecated',
                                random_state=0, splitter='best')
```

```
In [18]: y_pred = classifier.predict(x_val_scaled)
In [19]: conf_matrix = metrics.confusion_matrix(y_val, y_pred)
         sns.heatmap(conf_matrix, annot = True, fmt = ".3f", square = True, cmap = plt.cm.Blues)
         plt.ylabel('Actual')
         plt.xlabel('Predicted')
         plt.title('Confusion matrix')
         plt.tight_layout()
```



```
In [20]: accuracy = metrics.accuracy_score(y_val, y_pred)
         print("Accuracy: ", accuracy)
         error = 1 - accuracy
         print("Error: ", error)
         precision = metrics.precision_score(y_val, y_pred)
         print("Precision: ", precision)
         recall = metrics.recall_score(y_val, y_pred)
         print("Recall: ", recall)
         F1_score = metrics.f1_score(y_val, y_pred)
         print("F1 score: ", F1_score)
```

```
Accuracy:  0.8133333333333334
Error:  0.18666666666666665
Precision:  0.7241379310344828
Recall:  0.7777777777777778
F1 score:  0.75
```

1.2: Using Age and Gender as predictor variables

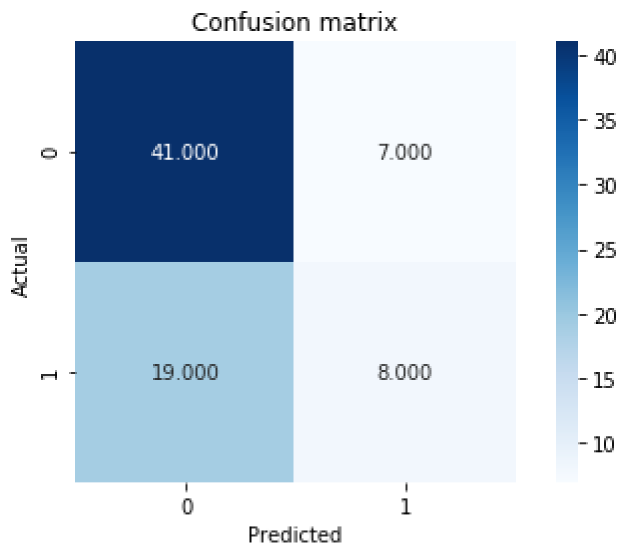
In [21]:
```
selected_predictor_variables = ['age',
                                'sex']
```

In [22]:
```
classifier = DecisionTreeClassifier(criterion='entropy', random_state=0)
classifier.fit(x_train_scaled_df[selected_predictor_variables], y_train)
```

Out[22]:
```
DecisionTreeClassifier(ccp_alpha=0.0, class_weight=None, criterion='entropy',
                       max_depth=None, max_features=None, max_leaf_nodes=None,
                       min_impurity_decrease=0.0, min_impurity_split=None,
                       min_samples_leaf=1, min_samples_split=2,
                       min_weight_fraction_leaf=0.0, presort='deprecated',
                       random_state=0, splitter='best')
```

In [23]:
```
y_pred = classifier.predict(x_val_scaled_df[selected_predictor_variables])
```

```
In [24]: conf_matrix = metrics.confusion_matrix(y_val, y_pred)
         sns.heatmap(conf_matrix, annot = True, fmt = ".3f", square = True, cmap = plt.cm.Blues)
         plt.ylabel('Actual')
         plt.xlabel('Predicted')
         plt.title('Confusion matrix')
         plt.tight_layout()
```



```
In [25]: accuracy = metrics.accuracy_score(y_val, y_pred)
         print("Accuracy: ", accuracy)
         error = 1 - accuracy
         print("Error: ", error)
         precision = metrics.precision_score(y_val, y_pred)
         print("Precision: ", precision)
         recall = metrics.recall_score(y_val, y_pred)
         print("Recall: ", recall)
         F1_score = metrics.f1_score(y_val, y_pred)
         print("F1 score: ", F1_score)
```

```
Accuracy:  0.6533333333333333
Error:  0.3466666666666667
Precision:  0.5333333333333333
Recall:  0.2962962962962963
F1 score:  0.38095238095238093
```

1.3: Using Diabetes, High Blood Pressure and anaemia, platelets, smoking as predictor variables

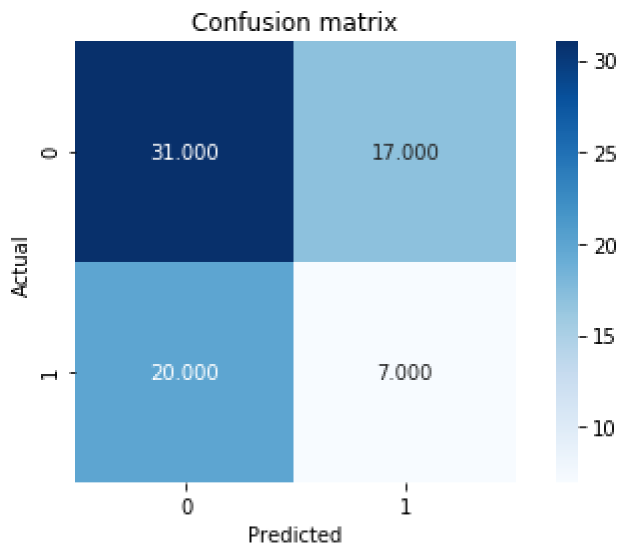
```
In [26]: # print(data.head())
         selected_predictor_variables = ['anaemia',
                                          'diabetes',
                                         'platelets', 'high_blood_pressure', 'smoking']
```

```
In [27]: classifier = DecisionTreeClassifier(criterion='entropy', random_state=0)
         classifier.fit(x_train_scaled_df[selected_predictor_variables], y_train)
```

```
Out[27]: DecisionTreeClassifier(ccp_alpha=0.0, class_weight=None, criterion='entropy',
                                max_depth=None, max_features=None, max_leaf_nodes=None,
                                min_impurity_decrease=0.0, min_impurity_split=None,
                                min_samples_leaf=1, min_samples_split=2,
                                min_weight_fraction_leaf=0.0, presort='deprecated',
                                random_state=0, splitter='best')
```

```
In [28]: y_pred = classifier.predict(x_val_scaled_df[selected_predictor_variables])
```

In [29]:
```
conf_matrix = metrics.confusion_matrix(y_val, y_pred)
sns.heatmap(conf_matrix, annot = True, fmt = ".3f", square = True, cmap = plt.cm.Blues)
plt.ylabel('Actual')
plt.xlabel('Predicted')
plt.title('Confusion matrix')
plt.tight_layout()
```



In [30]:
```
accuracy = metrics.accuracy_score(y_val, y_pred)
print("Accuracy: ", accuracy)
error = 1 - accuracy
print("Error: ", error)
precision = metrics.precision_score(y_val, y_pred)
print("Precision: ", precision)
recall = metrics.recall_score(y_val, y_pred)
print("Recall: ", recall)
F1_score = metrics.f1_score(y_val, y_pred)
print("F1 score: ", F1_score)
```

```
Accuracy:  0.5066666666666667
Error:  0.49333333333333333
Precision:  0.2916666666666667
Recall:  0.25925925925925924
F1 score:  0.27450980392156865
```

1.4: Using creatinine_phosphokinase, serum_creatinine, serum_sodium and ejection_fraction as predictor variables

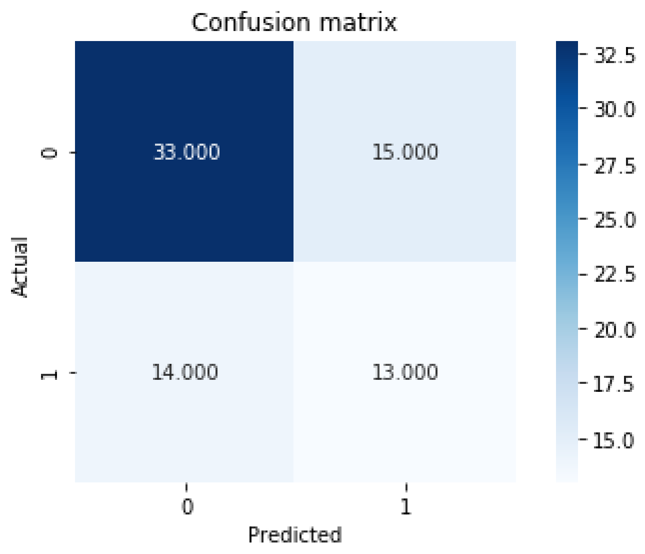
```
In [31]: selected_predictor_variables = ['creatinine_phosphokinase',
                                          'serum_creatinine',
                                         'serum_sodium',
                                         'ejection_fraction']
```

```
In [32]: classifier = DecisionTreeClassifier(criterion='entropy', random_state=0)
         classifier.fit(x_train_scaled_df[selected_predictor_variables], y_train)
```

```
Out[32]: DecisionTreeClassifier(ccp_alpha=0.0, class_weight=None, criterion='entropy',
                                max_depth=None, max_features=None, max_leaf_nodes=None,
                                min_impurity_decrease=0.0, min_impurity_split=None,
                                min_samples_leaf=1, min_samples_split=2,
                                min_weight_fraction_leaf=0.0, presort='deprecated',
                                random_state=0, splitter='best')
```

```
In [33]: y_pred = classifier.predict(x_val_scaled_df[selected_predictor_variables])
```

In [34]:
```
conf_matrix = metrics.confusion_matrix(y_val, y_pred)
sns.heatmap(conf_matrix, annot = True, fmt = ".3f", square = True, cmap = plt.cm.Blues)
plt.ylabel('Actual')
plt.xlabel('Predicted')
plt.title('Confusion matrix')
plt.tight_layout()
```



In [35]:
```
accuracy = metrics.accuracy_score(y_val, y_pred)
print("Accuracy: ", accuracy)
error = 1 - accuracy
print("Error: ", error)
precision = metrics.precision_score(y_val, y_pred)
print("Precision: ", precision)
recall = metrics.recall_score(y_val, y_pred)
print("Recall: ", recall)
F1_score = metrics.f1_score(y_val, y_pred)
print("F1 score: ", F1_score)
```

```
Accuracy:  0.6133333333333333
Error:  0.3866666666666667
Precision:  0.4642857142857143
Recall:  0.48148148148148145
F1 score:  0.4727272727272727
```

1.5: Using serum_creatinine and ejection_fraction as predictor variables

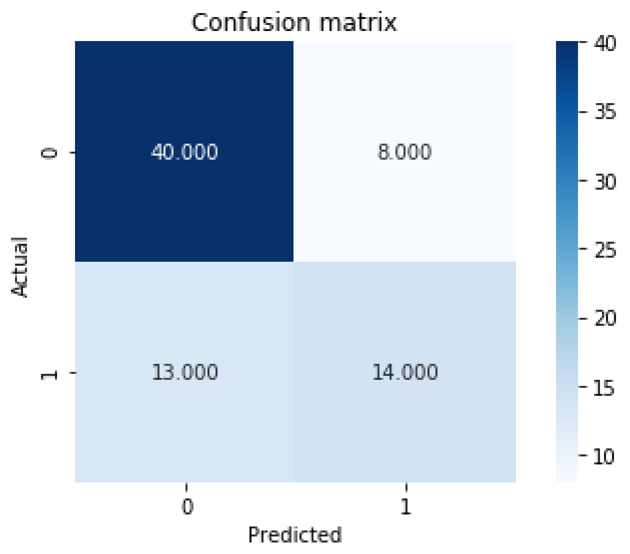
In [36]:
```
selected_predictor_variables = ['serum_creatinine',
                                'ejection_fraction']
```

In [37]:
```
classifier = DecisionTreeClassifier(criterion='entropy', random_state=0)
classifier.fit(x_train_scaled_df[selected_predictor_variables], y_train)
```

Out[37]:
```
DecisionTreeClassifier(ccp_alpha=0.0, class_weight=None, criterion='entropy',
                       max_depth=None, max_features=None, max_leaf_nodes=None,
                       min_impurity_decrease=0.0, min_impurity_split=None,
                       min_samples_leaf=1, min_samples_split=2,
                       min_weight_fraction_leaf=0.0, presort='deprecated',
                       random_state=0, splitter='best')
```

In [38]:
```
y_pred = classifier.predict(x_val_scaled_df[selected_predictor_variables])
```

In [39]:
```
conf_matrix = metrics.confusion_matrix(y_val, y_pred)
sns.heatmap(conf_matrix, annot = True, fmt = ".3f", square = True, cmap = plt.cm.Blues)
plt.ylabel('Actual')
plt.xlabel('Predicted')
plt.title('Confusion matrix')
plt.tight_layout()
```



In [40]:
```
accuracy = metrics.accuracy_score(y_val, y_pred)
print("Accuracy: ", accuracy)
error = 1 - accuracy
print("Error: ", error)
precision = metrics.precision_score(y_val, y_pred)
print("Precision: ", precision)
recall = metrics.recall_score(y_val, y_pred)
print("Recall: ", recall)
F1_score = metrics.f1_score(y_val, y_pred)
print("F1 score: ", F1_score)
```

```
Accuracy:  0.72
Error:  0.28
Precision:  0.6363636363636364
Recall:  0.5185185185185185
F1 score:  0.5714285714285714
```

2) K Nearest Neighbors

2.1: Using all predictor variables

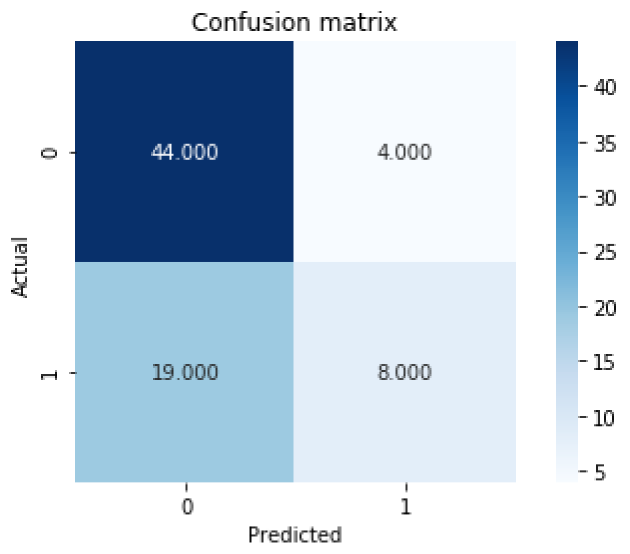
```
In [41]: classifier = KNeighborsClassifier(n_neighbors=3)
         classifier.fit(x_train_scaled, y_train)
```

```
/home/ashwin/anaconda3/lib/python3.7/site-packages/ipykernel_launcher.py:2: DataConversionWarning: A colum
n-vector y was passed when a 1d array was expected. Please change the shape of y to (n_samples, ), for exa
mple using ravel().
```

```
Out[41]: KNeighborsClassifier(algorithm='auto', leaf_size=30, metric='minkowski',
                              metric_params=None, n_jobs=None, n_neighbors=3, p=2,
                              weights='uniform')
```

```
In [42]: y_pred = classifier.predict(x_val_scaled)
```

In [43]:
```
conf_matrix = metrics.confusion_matrix(y_val, y_pred)
sns.heatmap(conf_matrix, annot = True, fmt = ".3f", square = True, cmap = plt.cm.Blues)
plt.ylabel('Actual')
plt.xlabel('Predicted')
plt.title('Confusion matrix')
plt.tight_layout()
```



In [44]:
```
accuracy = metrics.accuracy_score(y_val, y_pred)
print("Accuracy: ", accuracy)
error = 1 - accuracy
print("Error: ", error)
precision = metrics.precision_score(y_val, y_pred)
print("Precision: ", precision)
recall = metrics.recall_score(y_val, y_pred)
print("Recall: ", recall)
F1_score = metrics.f1_score(y_val, y_pred)
print("F1 score: ", F1_score)
```

```
Accuracy:  0.6933333333333334
Error:  0.30666666666666664
Precision:  0.6666666666666666
Recall:  0.2962962962962963
F1 score:  0.41025641025641024
```

2.2: Using Age and Gender Variables

In [45]:
```
selected_predictor_variables = ['age',
                                'sex']
```

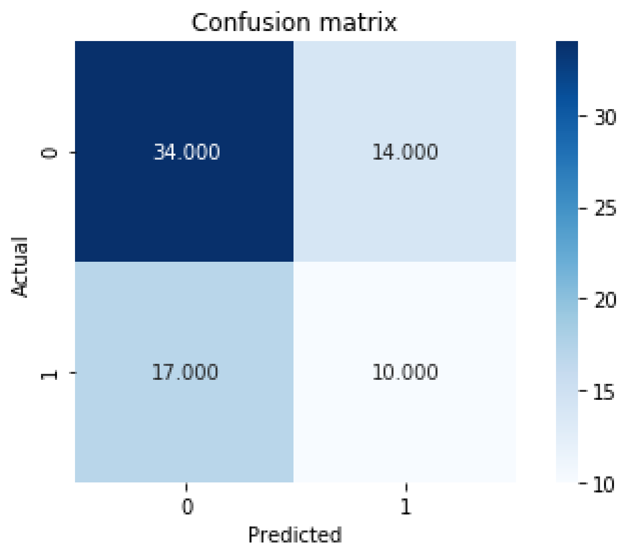
In [46]:
```
classifier = KNeighborsClassifier(n_neighbors=3)
classifier.fit(x_train_scaled_df[selected_predictor_variables], y_train)
```

```
/home/ashwin/anaconda3/lib/python3.7/site-packages/ipykernel_launcher.py:2: DataConversionWarning: A colum
n-vector y was passed when a 1d array was expected. Please change the shape of y to (n_samples, ), for exa
mple using ravel().
```

Out[46]:
```
KNeighborsClassifier(algorithm='auto', leaf_size=30, metric='minkowski',
                     metric_params=None, n_jobs=None, n_neighbors=3, p=2,
                     weights='uniform')
```

In [47]:
```
y_pred = classifier.predict(x_val_scaled_df[selected_predictor_variables])
```

In [48]:
```
conf_matrix = metrics.confusion_matrix(y_val, y_pred)
sns.heatmap(conf_matrix, annot = True, fmt = ".3f", square = True, cmap = plt.cm.Blues)
plt.ylabel('Actual')
plt.xlabel('Predicted')
plt.title('Confusion matrix')
plt.tight_layout()
```



In [49]:
```
accuracy = metrics.accuracy_score(y_val, y_pred)
print("Accuracy: ", accuracy)
error = 1 - accuracy
print("Error: ", error)
precision = metrics.precision_score(y_val, y_pred)
print("Precision: ", precision)
recall = metrics.recall_score(y_val, y_pred)
print("Recall: ", recall)
F1_score = metrics.f1_score(y_val, y_pred)
print("F1 score: ", F1_score)
```

```
Accuracy:  0.5866666666666667
Error:  0.41333333333333333
Precision:  0.4166666666666667
Recall:  0.37037037037037035
F1 score:  0.39215686274509803
```

2.3: Using Diabetes, High Blood Pressure and anaemia, platelets, smoking as predictor variables

In [50]:
```
selected_predictor_variables = ['anaemia',
                                 'diabetes',
                                'platelets', 'high_blood_pressure', 'smoking']
```

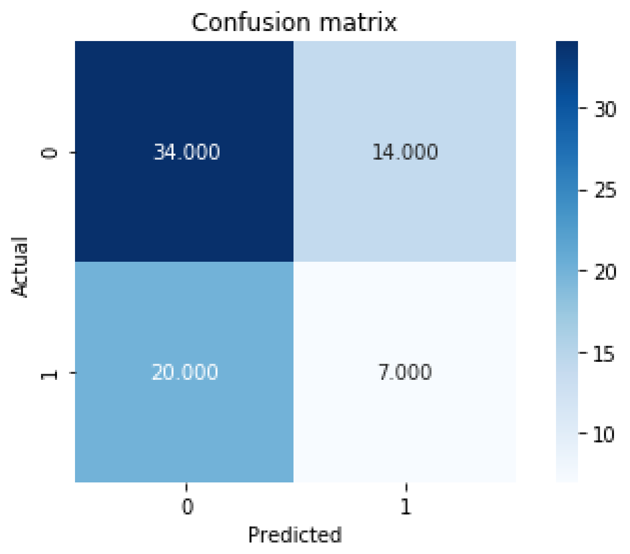
In [51]:
```
classifier = KNeighborsClassifier(n_neighbors=3)
classifier.fit(x_train_scaled_df[selected_predictor_variables], y_train)
```

```
/home/ashwin/anaconda3/lib/python3.7/site-packages/ipykernel_launcher.py:2: DataConversionWarning: A colum
n-vector y was passed when a 1d array was expected. Please change the shape of y to (n_samples, ), for exa
mple using ravel().
```

Out[51]:
```
KNeighborsClassifier(algorithm='auto', leaf_size=30, metric='minkowski',
                     metric_params=None, n_jobs=None, n_neighbors=3, p=2,
                     weights='uniform')
```

In [52]:
```
y_pred = classifier.predict(x_val_scaled_df[selected_predictor_variables])
```

In [53]:
```
conf_matrix = metrics.confusion_matrix(y_val, y_pred)
sns.heatmap(conf_matrix, annot = True, fmt = ".3f", square = True, cmap = plt.cm.Blues)
plt.ylabel('Actual')
plt.xlabel('Predicted')
plt.title('Confusion matrix')
plt.tight_layout()
```



In [54]:
```
accuracy = metrics.accuracy_score(y_val, y_pred)
print("Accuracy: ", accuracy)
error = 1 - accuracy
print("Error: ", error)
precision = metrics.precision_score(y_val, y_pred)
print("Precision: ", precision)
recall = metrics.recall_score(y_val, y_pred)
print("Recall: ", recall)
F1_score = metrics.f1_score(y_val, y_pred)
print("F1 score: ", F1_score)
```

```
Accuracy:  0.5466666666666666
Error:  0.45333333333333337
Precision:  0.3333333333333333
Recall:  0.25925925925925924
F1 score:  0.2916666666666667
```

2.4: Using creatinine_phosphokinase, serum_creatinine, serum_sodium and ejection_fraction as predictor variables

In [55]:
```
selected_predictor_variables = ['creatinine_phosphokinase',
                                 'serum_creatinine',
                                'serum_sodium',
                                'ejection_fraction']
```

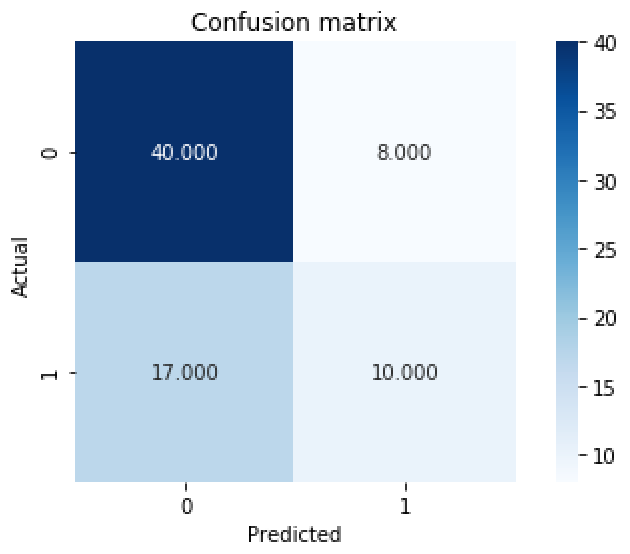
In [56]:
```
classifier = KNeighborsClassifier(n_neighbors=3)
classifier.fit(x_train_scaled_df[selected_predictor_variables], y_train)
```

```
/home/ashwin/anaconda3/lib/python3.7/site-packages/ipykernel_launcher.py:2: DataConversionWarning: A colum
n-vector y was passed when a 1d array was expected. Please change the shape of y to (n_samples, ), for exa
mple using ravel().
```

Out[56]:
```
KNeighborsClassifier(algorithm='auto', leaf_size=30, metric='minkowski',
                     metric_params=None, n_jobs=None, n_neighbors=3, p=2,
                     weights='uniform')
```

In [57]:
```
y_pred = classifier.predict(x_val_scaled_df[selected_predictor_variables])
```

In [58]:
```
conf_matrix = metrics.confusion_matrix(y_val, y_pred)
sns.heatmap(conf_matrix, annot = True, fmt = ".3f", square = True, cmap = plt.cm.Blues)
plt.ylabel('Actual')
plt.xlabel('Predicted')
plt.title('Confusion matrix')
plt.tight_layout()
```



In [59]:
```
accuracy = metrics.accuracy_score(y_val, y_pred)
print("Accuracy: ", accuracy)
error = 1 - accuracy
print("Error: ", error)
precision = metrics.precision_score(y_val, y_pred)
print("Precision: ", precision)
recall = metrics.recall_score(y_val, y_pred)
print("Recall: ", recall)
F1_score = metrics.f1_score(y_val, y_pred)
print("F1 score: ", F1_score)
```

```
Accuracy:  0.6666666666666666
Error:  0.33333333333333337
Precision:  0.5555555555555556
Recall:  0.37037037037037035
F1 score:  0.4444444444444445
```

2.5: Using serum_creatinine and ejection_fraction as predictor variables

In [60]:
```
selected_predictor_variables = ['serum_creatinine',
                                'ejection_fraction']
```

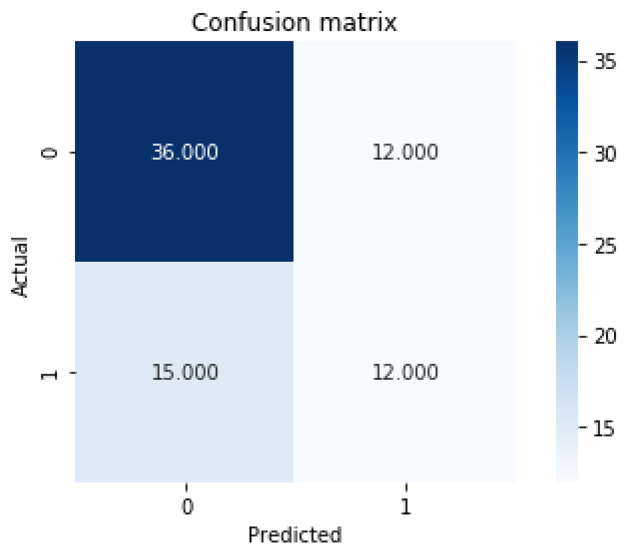
In [61]:
```
classifier_k_nearest = KNeighborsClassifier(n_neighbors=3)
classifier_k_nearest.fit(x_train_scaled_df[selected_predictor_variables], y_train)
```

```
/home/ashwin/anaconda3/lib/python3.7/site-packages/ipykernel_launcher.py:2: DataConversionWarning: A colum
n-vector y was passed when a 1d array was expected. Please change the shape of y to (n_samples, ), for exa
mple using ravel().
```

Out[61]:
```
KNeighborsClassifier(algorithm='auto', leaf_size=30, metric='minkowski',
                     metric_params=None, n_jobs=None, n_neighbors=3, p=2,
                     weights='uniform')
```

In [62]:
```
y_pred = classifier_k_nearest.predict(x_val_scaled_df[selected_predictor_variables])
```

In [63]:
```python
conf_matrix = metrics.confusion_matrix(y_val, y_pred)
sns.heatmap(conf_matrix, annot = True, fmt = ".3f", square = True, cmap = plt.cm.Blues)
plt.ylabel('Actual')
plt.xlabel('Predicted')
plt.title('Confusion matrix')
plt.tight_layout()
```



In [64]:
```python
accuracy = metrics.accuracy_score(y_val, y_pred)
print("Accuracy: ", accuracy)
error = 1 - accuracy
print("Error: ", error)
precision = metrics.precision_score(y_val, y_pred)
print("Precision: ", precision)
recall = metrics.recall_score(y_val, y_pred)
print("Recall: ", recall)
F1_score = metrics.f1_score(y_val, y_pred)
print("F1 score: ", F1_score)
```

```
Accuracy:  0.64
Error:  0.36
Precision:  0.5
Recall:  0.4444444444444444
F1 score:  0.47058823529411764
```

3) Naive Bayes

3.1: Using all predictor variables

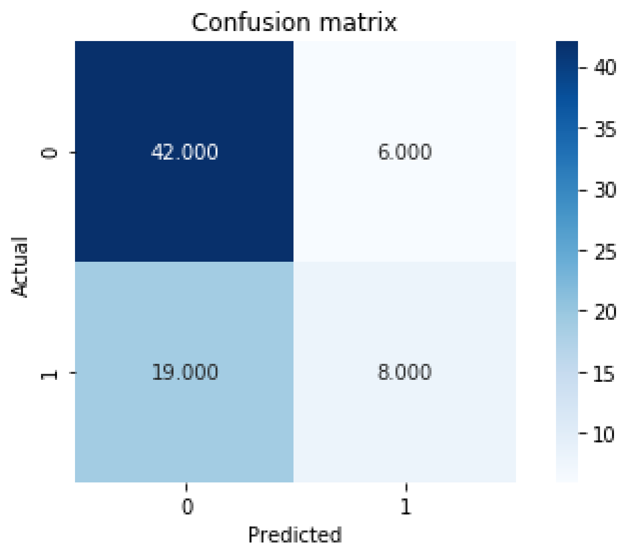
In [65]:
```
classifier = GaussianNB()
classifier.fit(x_train_scaled, y_train)
```

```
/home/ashwin/anaconda3/lib/python3.7/site-packages/sklearn/naive_bayes.py:206: DataConversionWarning: A co
lumn-vector y was passed when a 1d array was expected. Please change the shape of y to (n_samples, ), for
example using ravel().
  y = column_or_1d(y, warn=True)
```

Out[65]:
```
GaussianNB(priors=None, var_smoothing=1e-09)
```

In [66]:
```
y_pred = classifier.predict(x_val_scaled)
```

```
In [67]: conf_matrix = metrics.confusion_matrix(y_val, y_pred)
         sns.heatmap(conf_matrix, annot = True, fmt = ".3f", square = True, cmap = plt.cm.Blues)
         plt.ylabel('Actual')
         plt.xlabel('Predicted')
         plt.title('Confusion matrix')
         plt.tight_layout()
```



```
In [68]: accuracy = metrics.accuracy_score(y_val, y_pred)
         print("Accuracy: ", accuracy)
         error = 1 - accuracy
         print("Error: ", error)
         precision = metrics.precision_score(y_val, y_pred)
         print("Precision: ", precision)
         recall = metrics.recall_score(y_val, y_pred)
         print("Recall: ", recall)
         F1_score = metrics.f1_score(y_val, y_pred)
         print("F1 score: ", F1_score)
```

```
Accuracy:  0.6666666666666666
Error:  0.33333333333333337
Precision:  0.5714285714285714
Recall:  0.2962962962962963
F1 score:  0.3902439024390244
```

3.2: Using Age and Gender Variables

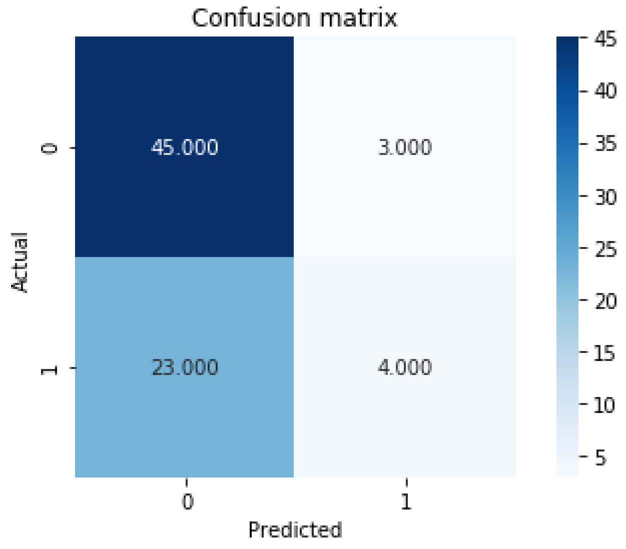
```
In [69]: selected_predictor_variables = ['age',
                                         'sex']
```

```
In [70]: classifier = GaussianNB()
         classifier.fit(x_train_scaled_df[selected_predictor_variables], y_train)
```

```
/home/ashwin/anaconda3/lib/python3.7/site-packages/sklearn/naive_bayes.py:206: DataConversionWarning: A co
lumn-vector y was passed when a 1d array was expected. Please change the shape of y to (n_samples, ), for
example using ravel().
  y = column_or_1d(y, warn=True)
```

```
Out[70]: GaussianNB(priors=None, var_smoothing=1e-09)
```

```
In [71]: y_pred = classifier.predict(x_val_scaled_df[selected_predictor_variables])
In [72]: conf_matrix = metrics.confusion_matrix(y_val, y_pred)
         sns.heatmap(conf_matrix, annot = True, fmt = ".3f", square = True, cmap = plt.cm.Blues)
         plt.ylabel('Actual')
         plt.xlabel('Predicted')
         plt.title('Confusion matrix')
         plt.tight_layout()
```



```
In [73]: accuracy = metrics.accuracy_score(y_val, y_pred)
         print("Accuracy: ", accuracy)
         error = 1 - accuracy
         print("Error: ", error)
         precision = metrics.precision_score(y_val, y_pred)
         print("Precision: ", precision)
         recall = metrics.recall_score(y_val, y_pred)
         print("Recall: ", recall)
         F1_score = metrics.f1_score(y_val, y_pred)
         print("F1 score: ", F1_score)
```

```
Accuracy:  0.6533333333333333
Error:  0.3466666666666667
Precision:  0.5714285714285714
Recall:  0.14814814814814814
F1 score:  0.23529411764705882
```

3.3: Using Diabetes, High Blood Pressure and anaemia, platelets, smoking as predictor variables

```
In [74]: selected_predictor_variables = ['anaemia',
                                          'diabetes',
                                         'platelets', 'high_blood_pressure', 'smoking']
```

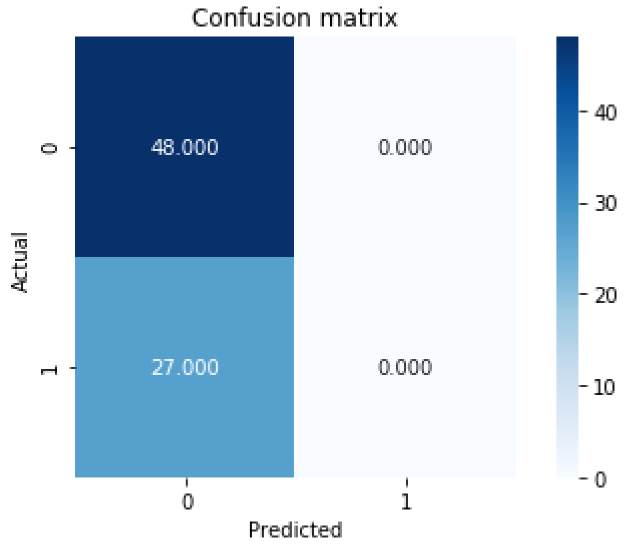
```
In [75]: classifier = GaussianNB()
         classifier.fit(x_train_scaled_df[selected_predictor_variables], y_train)
```

```
/home/ashwin/anaconda3/lib/python3.7/site-packages/sklearn/naive_bayes.py:206: DataConversionWarning: A co
lumn-vector y was passed when a 1d array was expected. Please change the shape of y to (n_samples, ), for
example using ravel().
  y = column_or_1d(y, warn=True)
```

```
Out[75]: GaussianNB(priors=None, var_smoothing=1e-09)
```

```
In [76]: y_pred = classifier.predict(x_val_scaled_df[selected_predictor_variables])
```

In [77]:
```python
conf_matrix = metrics.confusion_matrix(y_val, y_pred)
sns.heatmap(conf_matrix, annot = True, fmt = ".3f", square = True, cmap = plt.cm.Blues)
plt.ylabel('Actual')
plt.xlabel('Predicted')
plt.title('Confusion matrix')
plt.tight_layout()
```



```
In [78]: accuracy = metrics.accuracy_score(y_val, y_pred)
         print("Accuracy: ", accuracy)
         error = 1 - accuracy
         print("Error: ", error)
         precision = metrics.precision_score(y_val, y_pred)
         print("Precision: ", precision)
         recall = metrics.recall_score(y_val, y_pred)
         print("Recall: ", recall)
         F1_score = metrics.f1_score(y_val, y_pred)
         print("F1 score: ", F1_score)
```

```
Accuracy:  0.64
Error:  0.36
Precision:  0.0
Recall:  0.0
F1 score:  0.0

/home/ashwin/anaconda3/lib/python3.7/site-packages/sklearn/metrics/_classification.py:1272: UndefinedMetri
cWarning: Precision is ill-defined and being set to 0.0 due to no predicted samples. Use `zero_division` p
arameter to control this behavior.
  _warn_prf(average, modifier, msg_start, len(result))
```

3.4: Using creatinine_phosphokinase, serum_creatinine, serum_sodium and ejection_fraction as predictor variables

```
In [79]: selected_predictor_variables = ['creatinine_phosphokinase',
                                          'serum_creatinine',
                                         'serum_sodium',
                                         'ejection_fraction']
```

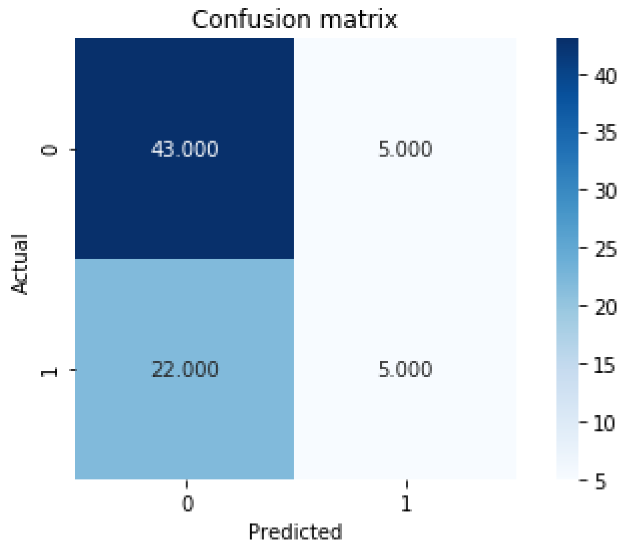
```
In [80]: classifier = GaussianNB()
         classifier.fit(x_train_scaled_df[selected_predictor_variables], y_train)
```

```
/home/ashwin/anaconda3/lib/python3.7/site-packages/sklearn/naive_bayes.py:206: DataConversionWarning: A co
lumn-vector y was passed when a 1d array was expected. Please change the shape of y to (n_samples, ), for
example using ravel().
  y = column_or_1d(y, warn=True)
```

```
Out[80]: GaussianNB(priors=None, var_smoothing=1e-09)
```

In [81]:
```
y_pred = classifier.predict(x_val_scaled_df[selected_predictor_variables])
```

In [82]:
```
conf_matrix = metrics.confusion_matrix(y_val, y_pred)
sns.heatmap(conf_matrix, annot = True, fmt = ".3f", square = True, cmap = plt.cm.Blues)
plt.ylabel('Actual')
plt.xlabel('Predicted')
plt.title('Confusion matrix')
plt.tight_layout()
```



In [83]:
```
accuracy = metrics.accuracy_score(y_val, y_pred)
print("Accuracy: ", accuracy)
error = 1 - accuracy
print("Error: ", error)
precision = metrics.precision_score(y_val, y_pred)
print("Precision: ", precision)
recall = metrics.recall_score(y_val, y_pred)
print("Recall: ", recall)
F1_score = metrics.f1_score(y_val, y_pred)
print("F1 score: ", F1_score)
```

```
Accuracy:  0.64
Error:  0.36
Precision:  0.5
Recall:  0.18518518518518517
F1 score:  0.2702702702702703
```

3.5: Using serum_creatinine and ejection_fraction as predictor variables

In [84]:
```
selected_predictor_variables = ['serum_creatinine',
                                'ejection_fraction']
```

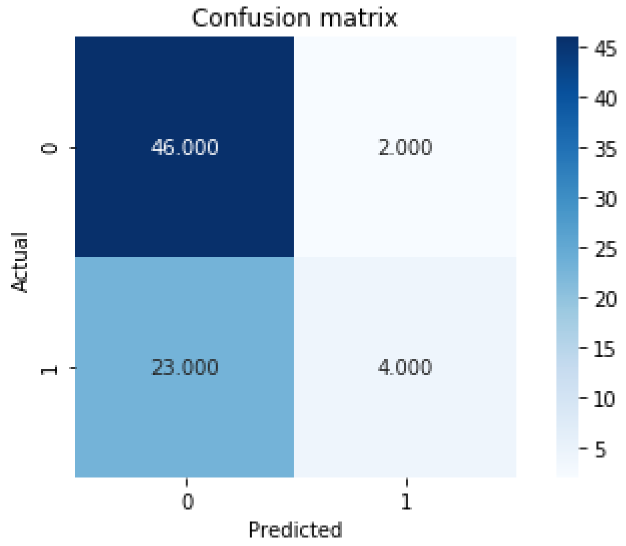
In [85]:
```
classifier = GaussianNB()
classifier.fit(x_train_scaled_df[selected_predictor_variables], y_train)
```

```
/home/ashwin/anaconda3/lib/python3.7/site-packages/sklearn/naive_bayes.py:206: DataConversionWarning: A co
lumn-vector y was passed when a 1d array was expected. Please change the shape of y to (n_samples, ), for
example using ravel().
  y = column_or_1d(y, warn=True)
```

Out[85]:
```
GaussianNB(priors=None, var_smoothing=1e-09)
```

In [86]:
```
y_pred = classifier.predict(x_val_scaled_df[selected_predictor_variables])
```

In [87]:
```
conf_matrix = metrics.confusion_matrix(y_val, y_pred)
sns.heatmap(conf_matrix, annot = True, fmt = ".3f", square = True, cmap = plt.cm.Blues)
plt.ylabel('Actual')
plt.xlabel('Predicted')
plt.title('Confusion matrix')
plt.tight_layout()
```



In [88]:
```
accuracy = metrics.accuracy_score(y_val, y_pred)
print("Accuracy: ", accuracy)
error = 1 - accuracy
print("Error: ", error)
precision = metrics.precision_score(y_val, y_pred)
print("Precision: ", precision)
recall = metrics.recall_score(y_val, y_pred)
print("Recall: ", recall)
F1_score = metrics.f1_score(y_val, y_pred)
print("F1 score: ", F1_score)
```

```
Accuracy:  0.6666666666666666
Error:  0.33333333333333337
Precision:  0.6666666666666666
Recall:  0.14814814814814814
F1 score:  0.24242424242424243
```

4) Support Vector Machine

4.1: Using all predictor variables

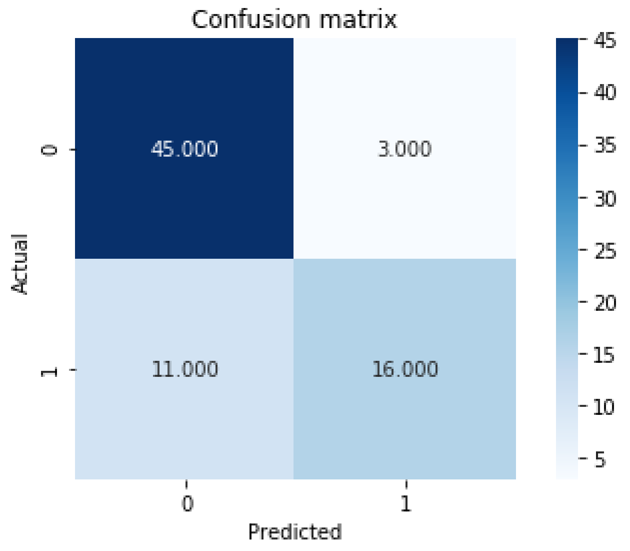
In [89]:
```
classifier = SVC(kernel='rbf')
classifier.fit(x_train_scaled, y_train)
```

```
/home/ashwin/anaconda3/lib/python3.7/site-packages/sklearn/utils/validation.py:760: DataConversionWarning:
A column-vector y was passed when a 1d array was expected. Please change the shape of y to (n_samples, ),
for example using ravel().
  y = column_or_1d(y, warn=True)
```

Out[89]:
```
SVC(C=1.0, break_ties=False, cache_size=200, class_weight=None, coef0=0.0,
    decision_function_shape='ovr', degree=3, gamma='scale', kernel='rbf',
    max_iter=-1, probability=False, random_state=None, shrinking=True,
    tol=0.001, verbose=False)
```

In [90]:
```
y_pred = classifier.predict(x_val_scaled)
```

```
In [91]: conf_matrix = metrics.confusion_matrix(y_val, y_pred)
         sns.heatmap(conf_matrix, annot = True, fmt = ".3f", square = True, cmap = plt.cm.Blues)
         plt.ylabel('Actual')
         plt.xlabel('Predicted')
         plt.title('Confusion matrix')
         plt.tight_layout()
```



```
In [92]: accuracy = metrics.accuracy_score(y_val, y_pred)
         print("Accuracy: ", accuracy)
         error = 1 - accuracy
         print("Error: ", error)
         precision = metrics.precision_score(y_val, y_pred)
         print("Precision: ", precision)
         recall = metrics.recall_score(y_val, y_pred)
         print("Recall: ", recall)
         F1_score = metrics.f1_score(y_val, y_pred)
         print("F1 score: ", F1_score)
```

```
Accuracy:  0.8133333333333334
Error:  0.18666666666666665
Precision:  0.8421052631578947
Recall:  0.5925925925925926
F1 score:  0.6956521739130435
```

4.2: Using Age and Gender Variables

```
In [93]: selected_predictor_variables = ['age',
                                         'sex']
```

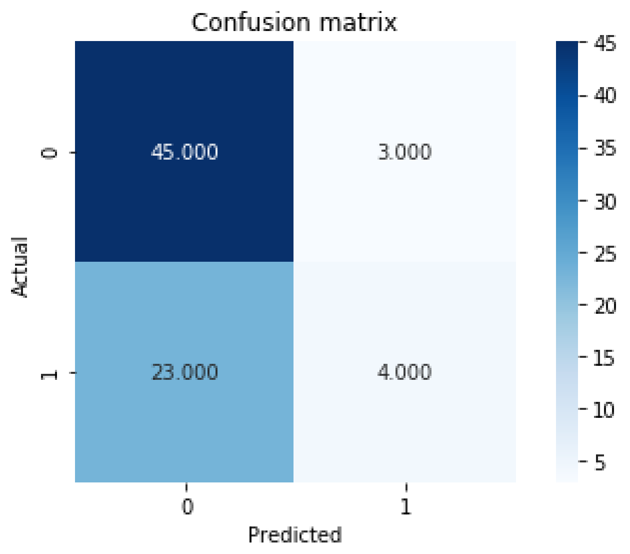
```
In [94]: classifier = SVC(kernel='rbf')
         classifier.fit(x_train_scaled_df[selected_predictor_variables], y_train)
```

```
/home/ashwin/anaconda3/lib/python3.7/site-packages/sklearn/utils/validation.py:760: DataConversionWarning:
A column-vector y was passed when a 1d array was expected. Please change the shape of y to (n_samples, ),
for example using ravel().
  y = column_or_1d(y, warn=True)
```

```
Out[94]: SVC(C=1.0, break_ties=False, cache_size=200, class_weight=None, coef0=0.0,
             decision_function_shape='ovr', degree=3, gamma='scale', kernel='rbf',
             max_iter=-1, probability=False, random_state=None, shrinking=True,
             tol=0.001, verbose=False)
```

```
In [95]: y_pred = classifier.predict(x_val_scaled_df[selected_predictor_variables])
```

In [96]:
```
conf_matrix = metrics.confusion_matrix(y_val, y_pred)
sns.heatmap(conf_matrix, annot = True, fmt = ".3f", square = True, cmap = plt.cm.Blues)
plt.ylabel('Actual')
plt.xlabel('Predicted')
plt.title('Confusion matrix')
plt.tight_layout()
```



In [97]:
```
accuracy = metrics.accuracy_score(y_val, y_pred)
print("Accuracy: ", accuracy)
error = 1 - accuracy
print("Error: ", error)
precision = metrics.precision_score(y_val, y_pred)
print("Precision: ", precision)
recall = metrics.recall_score(y_val, y_pred)
print("Recall: ", recall)
F1_score = metrics.f1_score(y_val, y_pred)
print("F1 score: ", F1_score)
```

```
Accuracy:  0.6533333333333333
Error:  0.3466666666666667
Precision:  0.5714285714285714
Recall:  0.14814814814814814
F1 score:  0.23529411764705882
```

4.3: Using Diabetes, High Blood Pressure and anaemia, platelets, smoking as predictor variables

In [98]:
```
selected_predictor_variables = ['anaemia',
                                 'diabetes',
                                'platelets', 'high_blood_pressure', 'smoking']
```

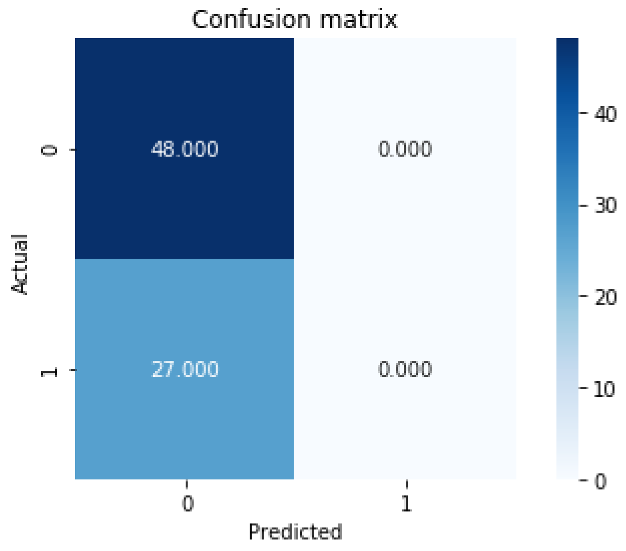
In [99]:
```
classifier = SVC(kernel='rbf')
classifier.fit(x_train_scaled_df[selected_predictor_variables], y_train)
```

```
/home/ashwin/anaconda3/lib/python3.7/site-packages/sklearn/utils/validation.py:760: DataConversionWarning:
A column-vector y was passed when a 1d array was expected. Please change the shape of y to (n_samples, ),
for example using ravel().
  y = column_or_1d(y, warn=True)
```

Out[99]:
```
SVC(C=1.0, break_ties=False, cache_size=200, class_weight=None, coef0=0.0,
    decision_function_shape='ovr', degree=3, gamma='scale', kernel='rbf',
    max_iter=-1, probability=False, random_state=None, shrinking=True,
    tol=0.001, verbose=False)
```

In [100]:
```
y_pred = classifier.predict(x_val_scaled_df[selected_predictor_variables])
```

```
In [101]: conf_matrix = metrics.confusion_matrix(y_val, y_pred)
          sns.heatmap(conf_matrix, annot = True, fmt = ".3f", square = True, cmap = plt.cm.Blues)
          plt.ylabel('Actual')
          plt.xlabel('Predicted')
          plt.title('Confusion matrix')
          plt.tight_layout()
```



```
In [102]: accuracy = metrics.accuracy_score(y_val, y_pred)
          print("Accuracy: ", accuracy)
          error = 1 - accuracy
          print("Error: ", error)
          precision = metrics.precision_score(y_val, y_pred)
          print("Precision: ", precision)
          recall = metrics.recall_score(y_val, y_pred)
          print("Recall: ", recall)
          F1_score = metrics.f1_score(y_val, y_pred)
          print("F1 score: ", F1_score)
```

```
Accuracy:  0.64
Error:  0.36
Precision:  0.0
Recall:  0.0
F1 score:  0.0

/home/ashwin/anaconda3/lib/python3.7/site-packages/sklearn/metrics/_classification.py:1272: UndefinedMetri
cWarning: Precision is ill-defined and being set to 0.0 due to no predicted samples. Use `zero_division` p
arameter to control this behavior.
  _warn_prf(average, modifier, msg_start, len(result))
```

4.4: Using creatinine_phosphokinase, serum_creatinine, serum_sodium and ejection_fraction as predictor variables

```
In [103]: selected_predictor_variables = ['creatinine_phosphokinase',
                                          'serum_creatinine',
                                         'serum_sodium',
                                         'ejection_fraction']
```

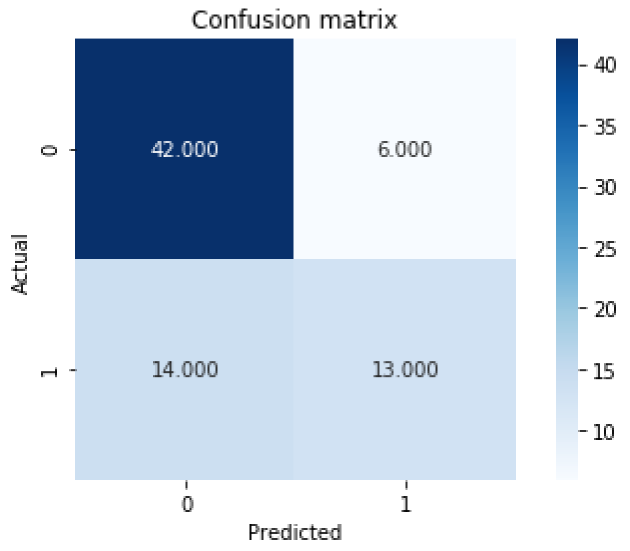
In [104]:
```
classifier = SVC(kernel='rbf')
classifier.fit(x_train_scaled_df[selected_predictor_variables], y_train)
```

```
/home/ashwin/anaconda3/lib/python3.7/site-packages/sklearn/utils/validation.py:760: DataConversionWarning:
A column-vector y was passed when a 1d array was expected. Please change the shape of y to (n_samples, ),
for example using ravel().
  y = column_or_1d(y, warn=True)
```

Out[104]:
```
SVC(C=1.0, break_ties=False, cache_size=200, class_weight=None, coef0=0.0,
    decision_function_shape='ovr', degree=3, gamma='scale', kernel='rbf',
    max_iter=-1, probability=False, random_state=None, shrinking=True,
    tol=0.001, verbose=False)
```

In [105]:
```
y_pred = classifier.predict(x_val_scaled_df[selected_predictor_variables])
```

In [106]:
```
conf_matrix = metrics.confusion_matrix(y_val, y_pred)
sns.heatmap(conf_matrix, annot = True, fmt = ".3f", square = True, cmap = plt.cm.Blues)
plt.ylabel('Actual')
plt.xlabel('Predicted')
plt.title('Confusion matrix')
plt.tight_layout()
```



In [107]:
```
accuracy = metrics.accuracy_score(y_val, y_pred)
print("Accuracy: ", accuracy)
error = 1 - accuracy
print("Error: ", error)
precision = metrics.precision_score(y_val, y_pred)
print("Precision: ", precision)
recall = metrics.recall_score(y_val, y_pred)
print("Recall: ", recall)
F1_score = metrics.f1_score(y_val, y_pred)
print("F1 score: ", F1_score)
```

```
Accuracy:  0.7333333333333333
Error:  0.2666666666666667
Precision:  0.6842105263157895
Recall:  0.48148148148148145
F1 score:  0.5652173913043478
```

4.5: Using serum_creatinine and ejection_fraction as predictor variables

In [108]:
```
selected_predictor_variables = ['serum_creatinine',
                                'ejection_fraction']
```

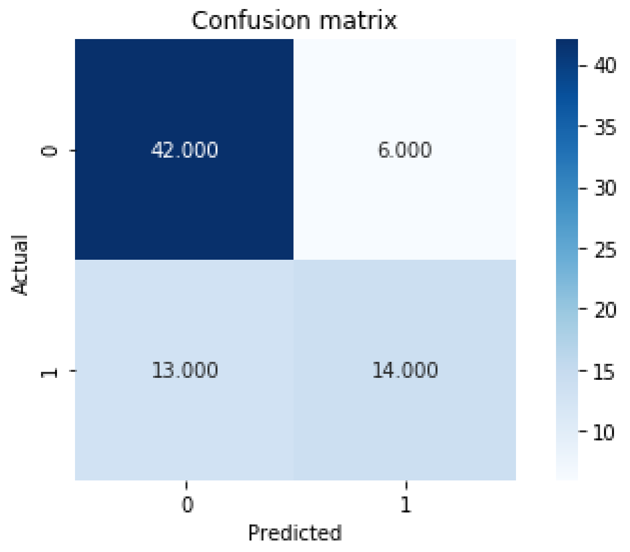
In [109]:
```
classifier = SVC(kernel='rbf')
classifier.fit(x_train_scaled_df[selected_predictor_variables], y_train)
```

```
/home/ashwin/anaconda3/lib/python3.7/site-packages/sklearn/utils/validation.py:760: DataConversionWarning:
A column-vector y was passed when a 1d array was expected. Please change the shape of y to (n_samples, ),
for example using ravel().
  y = column_or_1d(y, warn=True)
```

Out[109]:
```
SVC(C=1.0, break_ties=False, cache_size=200, class_weight=None, coef0=0.0,
    decision_function_shape='ovr', degree=3, gamma='scale', kernel='rbf',
    max_iter=-1, probability=False, random_state=None, shrinking=True,
    tol=0.001, verbose=False)
```

In [110]:
```
y_pred = classifier.predict(x_val_scaled_df[selected_predictor_variables])
```

In [111]:
```
conf_matrix = metrics.confusion_matrix(y_val, y_pred)
sns.heatmap(conf_matrix, annot = True, fmt = ".3f", square = True, cmap = plt.cm.Blues)
plt.ylabel('Actual')
plt.xlabel('Predicted')
plt.title('Confusion matrix')
plt.tight_layout()
```



In [112]:
```
accuracy = metrics.accuracy_score(y_val, y_pred)
print("Accuracy: ", accuracy)
error = 1 - accuracy
print("Error: ", error)
precision = metrics.precision_score(y_val, y_pred)
print("Precision: ", precision)
recall = metrics.recall_score(y_val, y_pred)
print("Recall: ", recall)
F1_score = metrics.f1_score(y_val, y_pred)
print("F1 score: ", F1_score)
```

```
Accuracy:  0.7466666666666667
Error:  0.2533333333333333
Precision:  0.7
Recall:  0.5185185185185185
F1 score:  0.5957446808510639
```

Classification: Model Performances

- **Decision Tree**

Variables	Accuracy	Precision	Recall	F1 Score
All	0.81	0.72	0.78	0.75
Age & Gender	0.65	0.53	0.30	0.38
Diabetes, High BP, Platelets, Anaemia & Smoking	0.51	0.29	0.26	0.27
creatinine_phosphokinase, serum_creatinine,serum_sodium and ejection_fraction	0.61	0.46	0.48	0.47
serum_sodium and ejection_fraction	0.72	0.64	0.52	0.57

- **K Nearest Neighbors**

Variables	Accuracy	Precision	Recall	F1 Score
All	0.69	0.67	0.30	0.41
Age & Gender	0.59	0.42	0.37	0.39
Diabetes, High BP, Platelets, Anaemia & Smoking	0.55	0.33	0.26	0.29
creatinine_phosphokinase, serum_creatinine,serum_sodium and ejection_fraction	0.67	0.56	0.37	0.44
serum_sodium and ejection_fraction	0.64	0.50	0.44	0.47

- **Naive Bayes**

Variables	Accuracy	Precision	Recall	F1 Score
All	0.67	0.57	0.30	0.39
Age & Gender	0.65	0.57	0.15	0.24
Diabetes, High BP, Platelets, Anaemia & Smoking	0.64	0.00	0.00	0.00
creatinine_phosphokinase, serum_creatinine,serum_sodium and ejection_fraction	0.64	0.50	0.19	0.27
serum_sodium and ejection_fraction	0.67	0.67	0.15	0.24

- **Support Vector Machines**

Variables	Accuracy	Precision	Recall	F1 Score
All	0.81	0.84	0.59	0.70
Age & Gender	0.65	0.57	0.15	0.24
Diabetes, High BP, Platelets, Anaemia & Smoking	0.64	0.00	0.00	0.00
creatinine_phosphokinase, serum_creatinine,serum_sodium and ejection_fraction	0.73	0.68	0.48	0.57
serum_sodium and ejection_fraction	0.75	0.70	0.52	0.60

Best performing classification model

Decision Tree using all predictor variables gives the best F1 Score

The performance of the model

- Accuracy: 0.81
- Precision: 0.72
- Recall: 0.78
- F1 Score: 0.75

Selection of the parameters of the model

- Upon trial of many different combinations we understand that few group of variables do not contribute to the best performance of a model. So we chose all predictor variables for the classification as they give the best F1 score and performance.

In [113]:
```
# Best performing classifiers & variables\n",
# (DecisionTreeClassifier(criterion='entropy', random_state=0), ('age', 'anaemia', 'creatinine_phosphokin
ase', 'platelets', 'serum_creatinine', 'serum_sodium', 'smoking', 'time'))\n",
# (DecisionTreeClassifier(criterion='entropy', random_state=0), ('age', 'creatinine_phosphokinase', 'diab
etes', 'platelets', 'serum_creatinine', 'serum_sodium', 'smoking', 'time'))\n",
# (DecisionTreeClassifier(criterion='entropy', random_state=0), ('creatinine_phosphokinase', 'diabetes',
 'ejection_fraction', 'high_blood_pressure', 'platelets', 'serum_creatinine', 'serum_sodium', 'smoking',
 'time'))\n",
# (DecisionTreeClassifier(criterion='entropy', random_state=0), ('ejection_fraction', 'serum_creatinine',
'serum_sodium', 'time'))\n",
# (DecisionTreeClassifier(criterion='entropy', random_state=0), ('ejection_fraction', 'high_blood_pressur
e', 'serum_creatinine', 'serum_sodium', 'time'))"
```

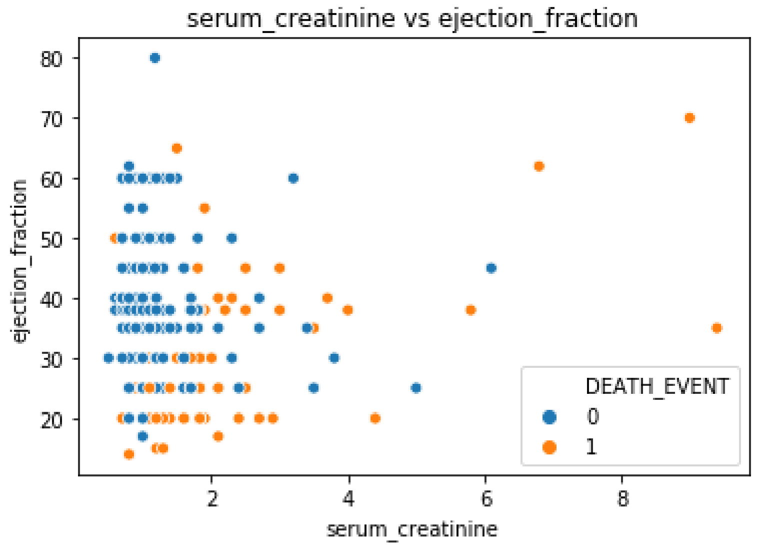
5 Clustering

In [114]:
```
data = pd.read_csv('heart_failure_clinical_records_dataset.csv')
data.head()

x_train = data.iloc[:, :-1]
y_train = data.iloc[:, -1].to_numpy().flatten()

scaler = StandardScaler()
scaler.fit(x_train)
x_train_scaled = scaler.transform(x_train)
x_train_scaled_df = pd.DataFrame(x_train_scaled, index=x_train.index, columns=x_train.columns)
```

Following are the two true clusters based on "Serum Creatinine" and "Ejection Fraction"

```
In [115]: # clustering = linkage(all_x, method = "single", metric = "euclidean")
          # clusters = fcluster(clustering, 2, criterion = 'maxclust')
          col1 = 'serum_creatinine'
          col2 = 'ejection_fraction'
          ax = sns.scatterplot(data=data, x=col1, y=col2, hue='DEATH_EVENT')
          ax.set(title = '{} vs {}'.format(col1, col2), xlabel = col1, ylabel = col2)
```

```
Out[115]: [Text(0, 0.5, 'ejection_fraction'),
           Text(0.5, 0, 'serum_creatinine'),
           Text(0.5, 1.0, 'serum_creatinine vs ejection_fraction')]
```



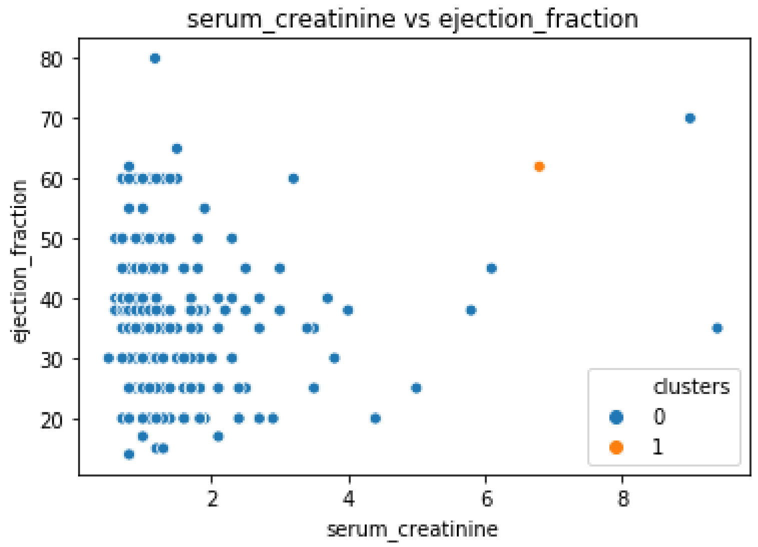
5.1 Hierarchical Clustering - Single Linkage

5.1.1 All variables

```
In [116]: all_x = x_train_scaled_df.to_numpy()
In [117]: clustering = linkage(all_x, method="single", metric = "euclidean")
          clusters = fcluster(clustering, 2, criterion = 'maxclust')
```

```
In [118]: adjusted_rand_index = metrics.adjusted_rand_score(y_train, clusters)
          silhouette_coefficient = metrics.silhouette_score(all_x, clusters, metric = "euclidean")
          print([adjusted_rand_index, silhouette_coefficient])

          [0.007441167976633384, 0.41639364203172197]
```

```
In [119]: data['clusters'] = clusters - 1
          ax = sns.scatterplot(data=data, x=col1, y=col2, hue='clusters')
          ax.set(title = '{} vs {}'.format(col1, col2), xlabel = col1, ylabel = col2)

Out[119]: [Text(0, 0.5, 'ejection_fraction'),
           Text(0.5, 0, 'serum_creatinine'),
           Text(0.5, 1.0, 'serum_creatinine vs ejection_fraction')]
```



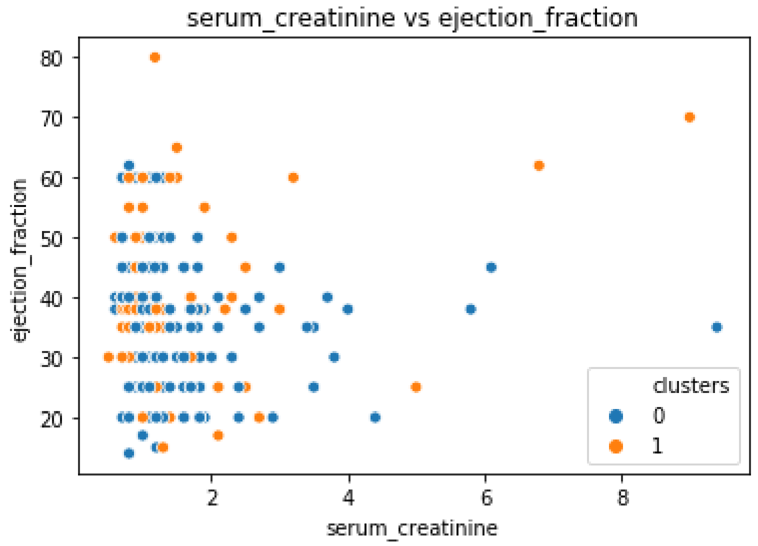
5.1.2: Using Age and Gender Variables

```
In [120]: selected_predictor_variables = ['age',
                                          'sex']
          x = x_train_scaled_df.loc[:, selected_predictor_variables].to_numpy()
```

```
In [121]: clustering = linkage(x, method="single", metric = "euclidean")
          clusters = fcluster(clustering, 2, criterion = 'maxclust')
```

```
In [122]: adjusted_rand_index = metrics.adjusted_rand_score(y_train, clusters)
          silhouette_coefficient = metrics.silhouette_score(x, clusters, metric = "euclidean")
          print([adjusted_rand_index, silhouette_coefficient])

          [-0.0018582102712868956, 0.551937322742283]
```

```
In [123]: data['clusters'] = clusters - 1
          ax = sns.scatterplot(data=data, x=col1, y=col2, hue='clusters')
          ax.set(title = '{} vs {}'.format(col1, col2), xlabel = col1, ylabel = col2)

Out[123]: [Text(0, 0.5, 'ejection_fraction'),
           Text(0.5, 0, 'serum_creatinine'),
           Text(0.5, 1.0, 'serum_creatinine vs ejection_fraction')]
```



5.1.3: Using Health Problem Variables

In [124]:
```
selected_predictor_variables = ['anaemia',
                                 'diabetes',
                                'platelets', 'high_blood_pressure', 'smoking']
x = x_train_scaled_df.loc[:, selected_predictor_variables].to_numpy()
```

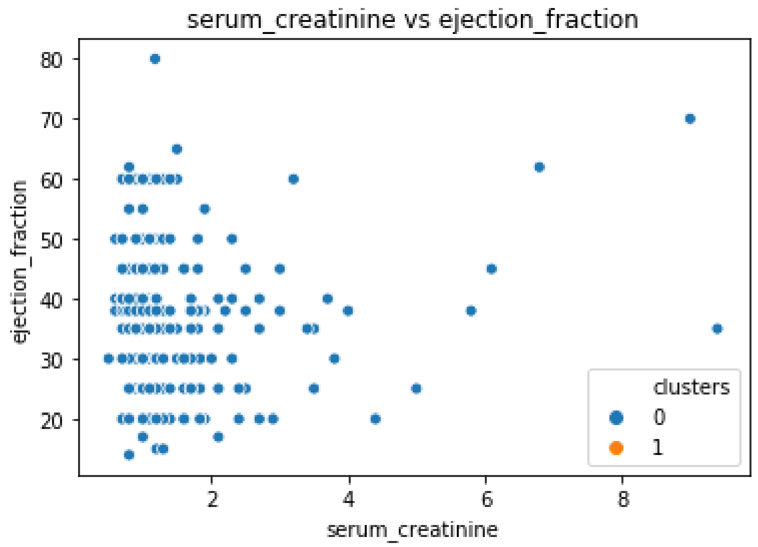
In [125]:
```
clustering = linkage(x, method="single", metric = "euclidean")
clusters = fcluster(clustering, 2, criterion = 'maxclust')
```

In [126]:
```
adjusted_rand_index = metrics.adjusted_rand_score(y_train, clusters)
silhouette_coefficient = metrics.silhouette_score(x, clusters, metric = "euclidean")
print([adjusted_rand_index, silhouette_coefficient])
```

```
[-0.0035189759889497152, 0.5427711036936387]
```

```
In [127]: data['clusters'] = clusters - 1
          ax = sns.scatterplot(data=data, x=col1, y=col2, hue='clusters')
          ax.set(title = '{} vs {}'.format(col1, col2), xlabel = col1, ylabel = col2)
```

```
Out[127]: [Text(0, 0.5, 'ejection_fraction'),
           Text(0.5, 0, 'serum_creatinine'),
           Text(0.5, 1.0, 'serum_creatinine vs ejection_fraction')]
```



5.1.4: Using Body Parameter Variables

```
In [128]: selected_predictor_variables = ['creatinine_phosphokinase',
                                           'serum_creatinine',
                                          'serum_sodium',
                                          'ejection_fraction']
          x = x_train_scaled_df.loc[:, selected_predictor_variables].to_numpy()
```

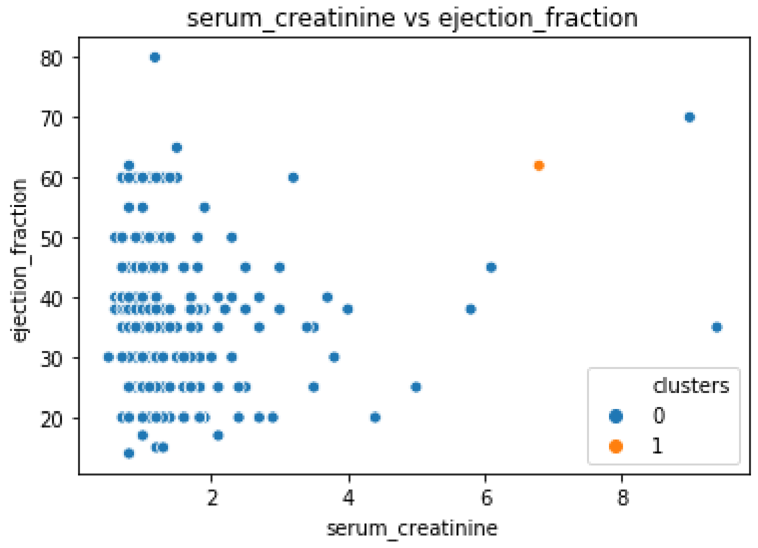
```
In [129]: clustering = linkage(x, method="single", metric = "euclidean")
          clusters = fcluster(clustering, 2, criterion = 'maxclust')
```

```
In [130]: adjusted_rand_index = metrics.adjusted_rand_score(y_train, clusters)
          silhouette_coefficient = metrics.silhouette_score(x, clusters, metric = "euclidean")
          print([adjusted_rand_index, silhouette_coefficient])
```

```
[0.007441167976633384, 0.6662613003976123]
```

```
In [131]: data['clusters'] = clusters - 1
          ax = sns.scatterplot(data=data, x=col1, y=col2, hue='clusters')
          ax.set(title = '{} vs {}'.format(col1, col2), xlabel = col1, ylabel = col2)
```

```
Out[131]: [Text(0, 0.5, 'ejection_fraction'),
           Text(0.5, 0, 'serum_creatinine'),
           Text(0.5, 1.0, 'serum_creatinine vs ejection_fraction')]
```



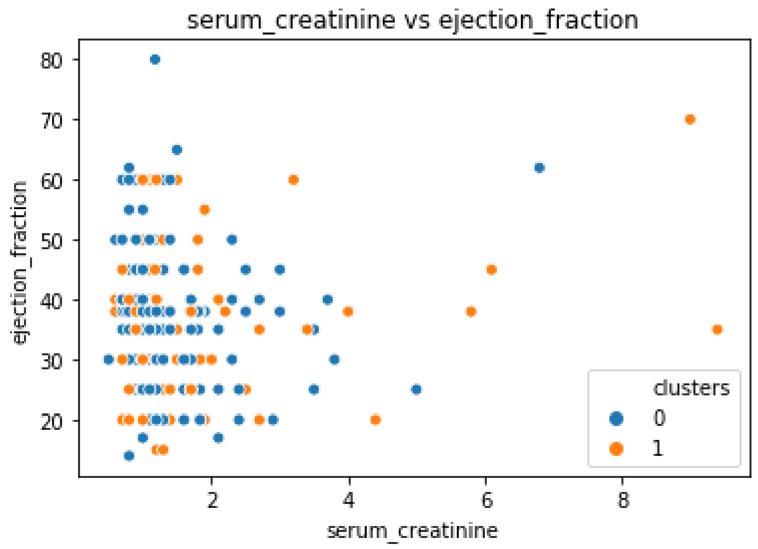
5.1.5: Using Anaemia

```
In [132]: selected_predictor_variables = ['anaemia']
          x = x_train_scaled_df.loc[:, selected_predictor_variables].to_numpy()
```

```
In [133]: clustering = linkage(x, method="single", metric = "euclidean")
          clusters = fcluster(clustering, 2, criterion = 'maxclust')
```

```
In [134]: adjusted_rand_index = metrics.adjusted_rand_score(y_train, clusters)
          silhouette_coefficient = metrics.silhouette_score(x, clusters, metric = "euclidean")
          print([adjusted_rand_index, silhouette_coefficient])

          [0.006938789172657143, 1.0]
```

```
In [135]: data['clusters'] = clusters - 1
          ax = sns.scatterplot(data=data, x=col1, y=col2, hue='clusters')
          ax.set(title = '{} vs {}'.format(col1, col2), xlabel = col1, ylabel = col2)

Out[135]: [Text(0, 0.5, 'ejection_fraction'),
           Text(0.5, 0, 'serum_creatinine'),
           Text(0.5, 1.0, 'serum_creatinine vs ejection_fraction')]
```



2) Hierarchical Clustering - Complete Linkage

5.2.1 All variables

In [136]:
```
all_x = x_train_scaled_df.to_numpy()
```

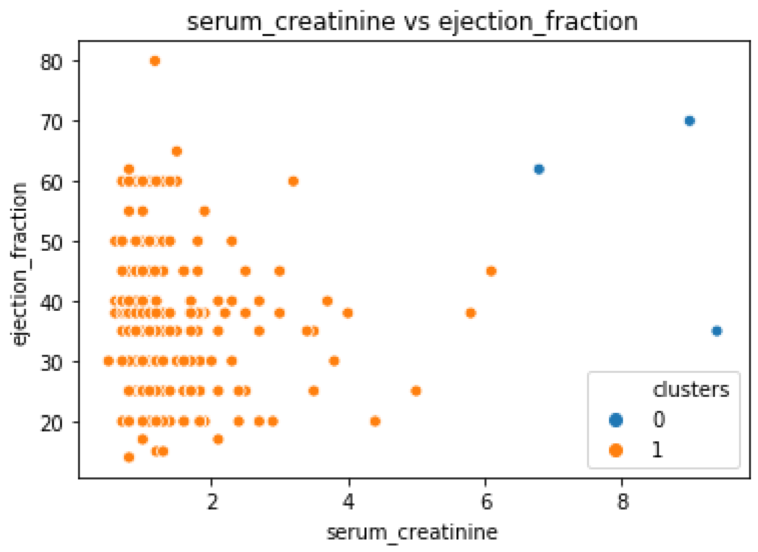
In [137]:
```
clustering = linkage(all_x, method="complete", metric = "euclidean")
clusters = fcluster(clustering, 2, criterion = 'maxclust')
```

In [138]:
```
adjusted_rand_index = metrics.adjusted_rand_score(y_train, clusters)
silhouette_coefficient = metrics.silhouette_score(all_x, clusters, metric = "euclidean")
print([adjusted_rand_index, silhouette_coefficient])
```

```
[0.022507236951381675, 0.46861144710828245]
```

In [139]:
```
data['clusters'] = clusters - 1
ax = sns.scatterplot(data=data, x=col1, y=col2, hue='clusters')
ax.set(title = '{} vs {}'.format(col1, col2), xlabel = col1, ylabel = col2)
```

Out[139]:
```
[Text(0, 0.5, 'ejection_fraction'),
 Text(0.5, 0, 'serum_creatinine'),
 Text(0.5, 1.0, 'serum_creatinine vs ejection_fraction')]
```



5.2.2: Using Age and Gender Variables

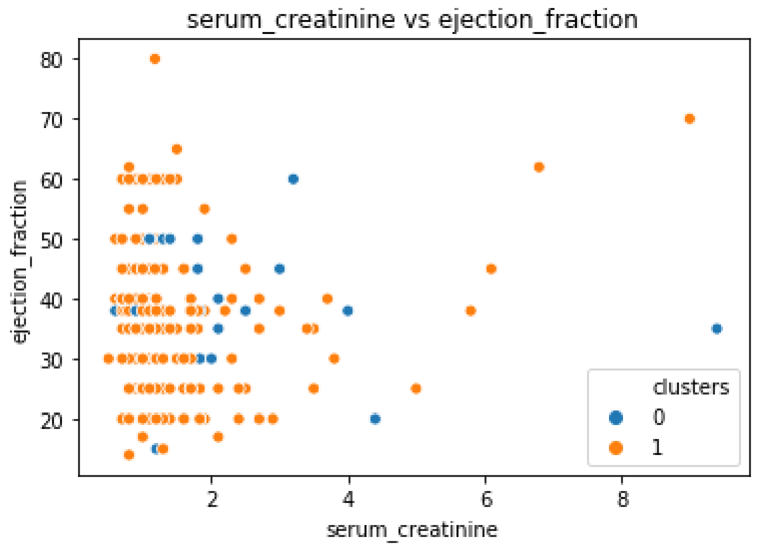
In [140]:
```
selected_predictor_variables = ['age',
                                'sex']
x = x_train_scaled_df.loc[:, selected_predictor_variables].to_numpy()
```

In [141]:
```
clustering = linkage(x, method="complete", metric = "euclidean")
clusters = fcluster(clustering, 2, criterion = 'maxclust')
```

In [142]:
```
adjusted_rand_index = metrics.adjusted_rand_score(y_train, clusters)
silhouette_coefficient = metrics.silhouette_score(x, clusters, metric = "euclidean")
print([adjusted_rand_index, silhouette_coefficient])
```

```
[0.11142775349398941, 0.3419871555832537]
```

```
In [143]: data['clusters'] = clusters - 1
          ax = sns.scatterplot(data=data, x=col1, y=col2, hue='clusters')
          ax.set(title = '{} vs {}'.format(col1, col2), xlabel = col1, ylabel = col2)

Out[143]: [Text(0, 0.5, 'ejection_fraction'),
           Text(0.5, 0, 'serum_creatinine'),
           Text(0.5, 1.0, 'serum_creatinine vs ejection_fraction')]
```



5.2.3: Using Health Problem Variables

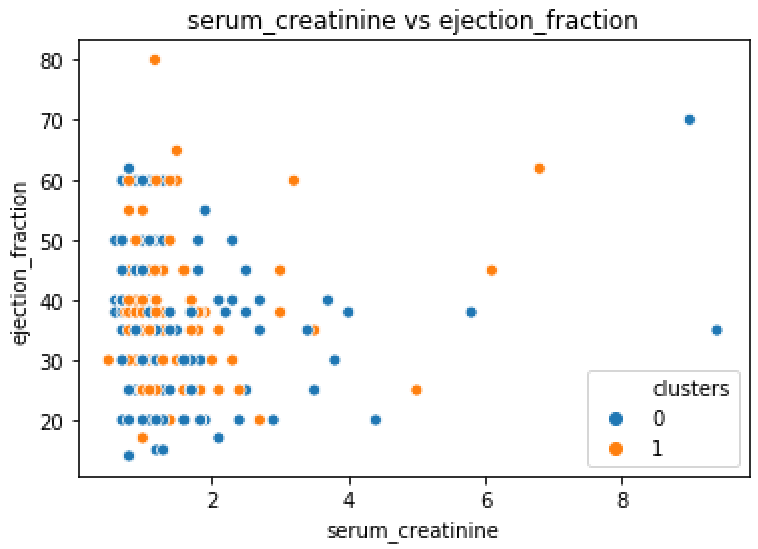
```
In [144]: selected_predictor_variables = ['anaemia',
                                           'diabetes',
                                          'platelets', 'high_blood_pressure', 'smoking']
          x = x_train_scaled_df.loc[:, selected_predictor_variables].to_numpy()

In [145]: clustering = linkage(x, method="complete", metric = "euclidean")
          clusters = fcluster(clustering, 2, criterion = 'maxclust')
```

```
In [146]: adjusted_rand_index = metrics.adjusted_rand_score(y_train, clusters)
          silhouette_coefficient = metrics.silhouette_score(x, clusters, metric = "euclidean")
          print([adjusted_rand_index, silhouette_coefficient])
```

```
[-0.007387031337951726, 0.11014816465932352]
```

```
In [147]: data['clusters'] = clusters - 1
          ax = sns.scatterplot(data=data, x=col1, y=col2, hue='clusters')
          ax.set(title = '{} vs {}'.format(col1, col2), xlabel = col1, ylabel = col2)
```

```
Out[147]: [Text(0, 0.5, 'ejection_fraction'),
           Text(0.5, 0, 'serum_creatinine'),
           Text(0.5, 1.0, 'serum_creatinine vs ejection_fraction')]
```



5.2.4: Using Body Parameter Variables

```
In [148]: selected_predictor_variables = ['creatinine_phosphokinase',
                                           'serum_creatinine',
                                          'serum_sodium',
                                          'ejection_fraction']
          x = x_train_scaled_df.loc[:, selected_predictor_variables].to_numpy()
```

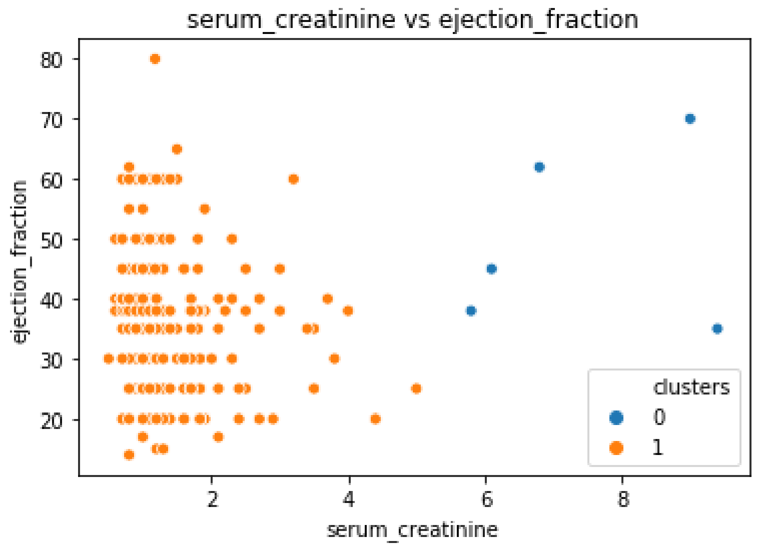
```
In [149]: clustering = linkage(x, method="complete", metric = "euclidean")
          clusters = fcluster(clustering, 2, criterion = 'maxclust')
```

```
In [150]: adjusted_rand_index = metrics.adjusted_rand_score(y_train, clusters)
          silhouette_coefficient = metrics.silhouette_score(x, clusters, metric = "euclidean")
          print([adjusted_rand_index, silhouette_coefficient])
```

```
[0.02612613619798278, 0.6567989004211781]
```

```
In [151]: data['clusters'] = clusters - 1
          ax = sns.scatterplot(data=data, x=col1, y=col2, hue='clusters')
          ax.set(title = '{} vs {}'.format(col1, col2), xlabel = col1, ylabel = col2)
```

```
Out[151]: [Text(0, 0.5, 'ejection_fraction'),
           Text(0.5, 0, 'serum_creatinine'),
           Text(0.5, 1.0, 'serum_creatinine vs ejection_fraction')]
```



5.2.5: Using Anaemia

```
In [152]: selected_predictor_variables = ['anaemia']
          x = x_train_scaled_df.loc[:, selected_predictor_variables].to_numpy()
```

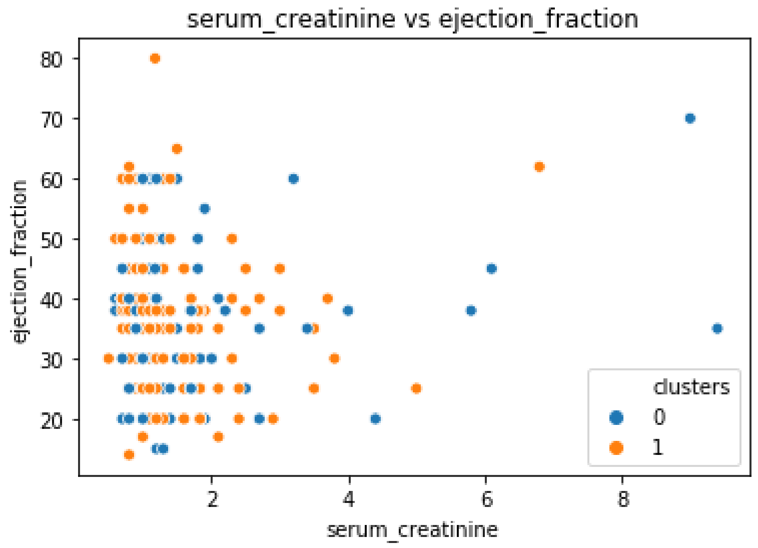
```
In [153]: clustering = linkage(x, method="complete", metric = "euclidean")
          clusters = fcluster(clustering, 2, criterion = 'maxclust')
```

In [154]:
```
adjusted_rand_index = metrics.adjusted_rand_score(y_train, clusters)
silhouette_coefficient = metrics.silhouette_score(x, clusters, metric = "euclidean")
print([adjusted_rand_index, silhouette_coefficient])
```

```
[0.006938789172657143, 1.0]
```

In [155]:
```
data['clusters'] = clusters - 1
ax = sns.scatterplot(data=data, x=col1, y=col2, hue='clusters')
ax.set(title = '{} vs {}'.format(col1, col2), xlabel = col1, ylabel = col2)
```

Out[155]:
```
[Text(0, 0.5, 'ejection_fraction'),
 Text(0.5, 0, 'serum_creatinine'),
 Text(0.5, 1.0, 'serum_creatinine vs ejection_fraction')]
```



3) KMeans Clustering

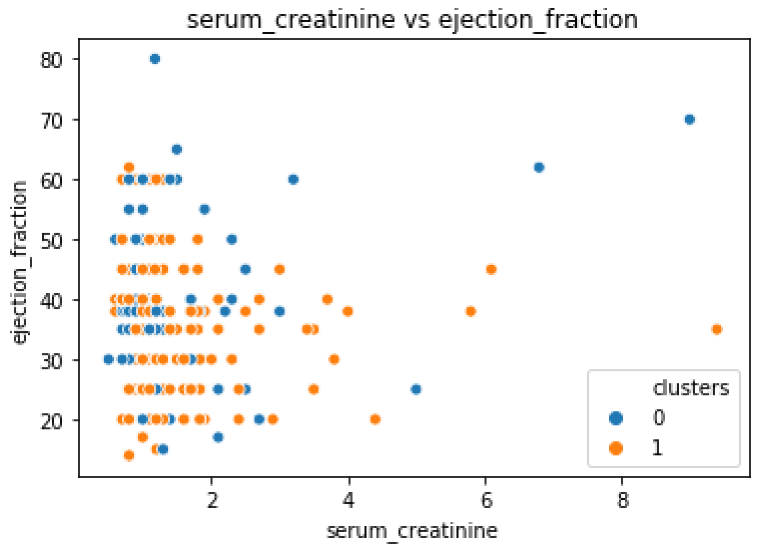
5.3.1: All variables

```
In [156]: all_x = x_train_scaled_df.to_numpy()
```

```
In [157]: clustering = KMeans(n_clusters = 2, init = 'random', n_init = 10, random_state=0).fit(all_x)
          clusters = clustering.labels_
```

```
In [158]: adjusted_rand_index = metrics.adjusted_rand_score(y_train, clusters)
          silhouette_coefficient = metrics.silhouette_score(all_x, clusters, metric = "euclidean")
          print([adjusted_rand_index, silhouette_coefficient])

          [-0.0036799581865726927, 0.1178512561512019]
```

```
In [159]: data['clusters'] = clusters
          ax = sns.scatterplot(data=data, x=col1, y=col2, hue='clusters')
          ax.set(title = '{} vs {}'.format(col1, col2), xlabel = col1, ylabel = col2)

Out[159]: [Text(0, 0.5, 'ejection_fraction'),
           Text(0.5, 0, 'serum_creatinine'),
           Text(0.5, 1.0, 'serum_creatinine vs ejection_fraction')]
```



5.3.2 Using Age and Gender Variables

In [160]:
```
selected_predictor_variables = ['age',
                                'sex']
x = x_train_scaled_df.loc[:, selected_predictor_variables].to_numpy()
```

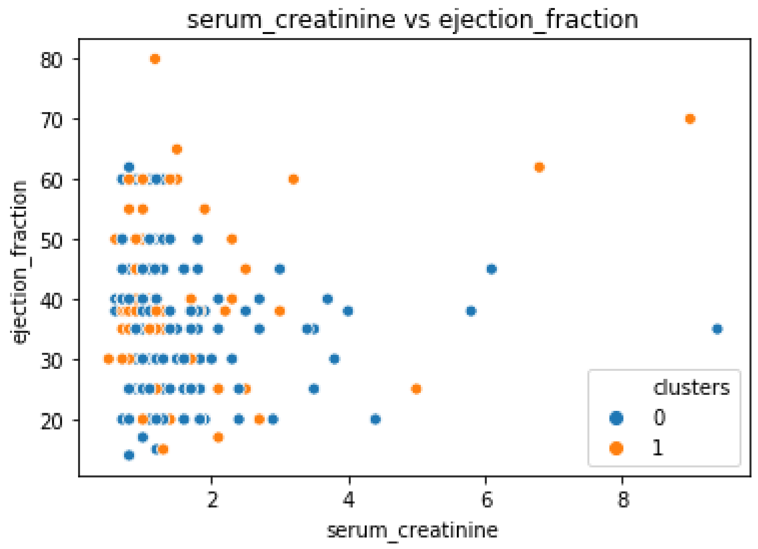
In [161]:
```
clustering = KMeans(n_clusters = 2, init = 'random', n_init = 10, random_state=0).fit(x)
clusters = clustering.labels_
```

In [162]:
```
adjusted_rand_index = metrics.adjusted_rand_score(y_train, clusters)
silhouette_coefficient = metrics.silhouette_score(x, clusters, metric = "euclidean")
print([adjusted_rand_index, silhouette_coefficient])
```

```
[-0.0018582102712868956, 0.551937322742283]
```

In [163]:
```
data['clusters'] = clusters
ax = sns.scatterplot(data=data, x=col1, y=col2, hue='clusters')
ax.set(title = '{} vs {}'.format(col1, col2), xlabel = col1, ylabel = col2)
```

Out[163]:
```
[Text(0, 0.5, 'ejection_fraction'),
 Text(0.5, 0, 'serum_creatinine'),
 Text(0.5, 1.0, 'serum_creatinine vs ejection_fraction')]
```



5.3.3 Using Health Problem Variables

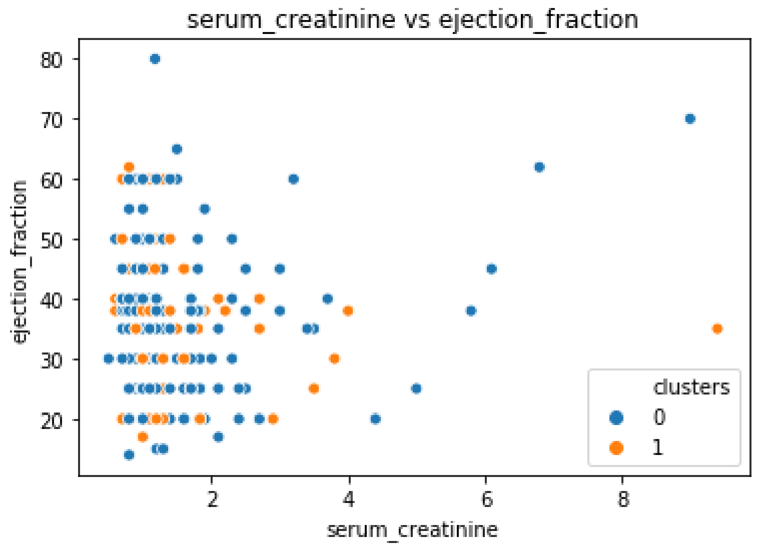
In [164]:
```
selected_predictor_variables = ['anaemia',
                                 'diabetes',
                                'platelets', 'high_blood_pressure', 'smoking']
x = x_train_scaled_df.loc[:, selected_predictor_variables].to_numpy()
```

In [165]:
```
clustering = KMeans(n_clusters = 2, init = 'random', n_init = 10, random_state=0).fit(x)
clusters = clustering.labels_
```

In [166]:
```
adjusted_rand_index = metrics.adjusted_rand_score(y_train, clusters)
silhouette_coefficient = metrics.silhouette_score(x, clusters, metric = "euclidean")
print([adjusted_rand_index, silhouette_coefficient])
```

```
[-0.005350592860670945, 0.245870014784830 37]
```

```
In [167]: data['clusters'] = clusters
          ax = sns.scatterplot(data=data, x=col1, y=col2, hue='clusters')
          ax.set(title = '{} vs {}'.format(col1, col2), xlabel = col1, ylabel = col2)

Out[167]: [Text(0, 0.5, 'ejection_fraction'),
           Text(0.5, 0, 'serum_creatinine'),
           Text(0.5, 1.0, 'serum_creatinine vs ejection_fraction')]
```



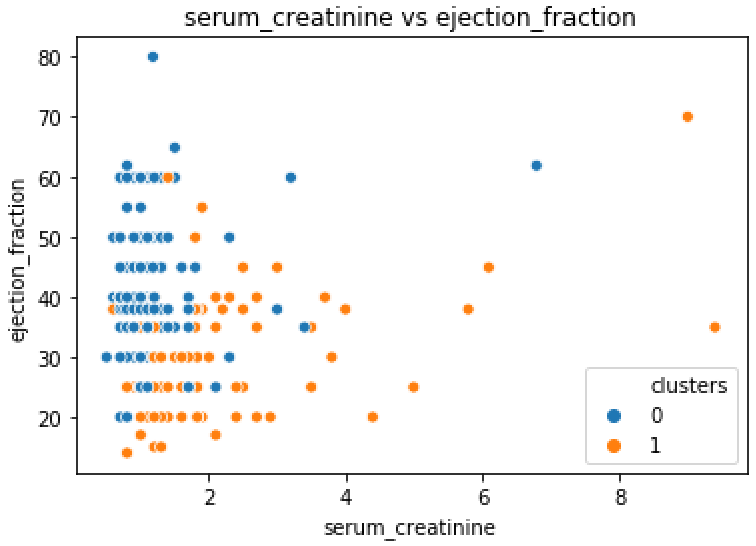
5.3.4 Using Body Parameter Variables

```
In [168]: selected_predictor_variables = ['creatinine_phosphokinase',
                                           'serum_creatinine',
                                          'serum_sodium',
                                          'ejection_fraction']
          x = x_train_scaled_df.loc[:, selected_predictor_variables].to_numpy()
```

```
In [169]: clustering = KMeans(n_clusters = 2, init = 'random', n_init = 10, random_state=0).fit(x)
          clusters = clustering.labels_
```

```
In [170]: adjusted_rand_index = metrics.adjusted_rand_score(y_train, clusters)
          silhouette_coefficient = metrics.silhouette_score(x, clusters, metric = "euclidean")
          print([adjusted_rand_index, silhouette_coefficient])

          [0.15419143591523968, 0.24027667508494274]
```

```
In [171]: data['clusters'] = clusters
          ax = sns.scatterplot(data=data, x=col1, y=col2, hue='clusters')
          ax.set(title = '{} vs {}'.format(col1, col2), xlabel = col1, ylabel = col2)

Out[171]: [Text(0, 0.5, 'ejection_fraction'),
           Text(0.5, 0, 'serum_creatinine'),
           Text(0.5, 1.0, 'serum_creatinine vs ejection_fraction')]
```



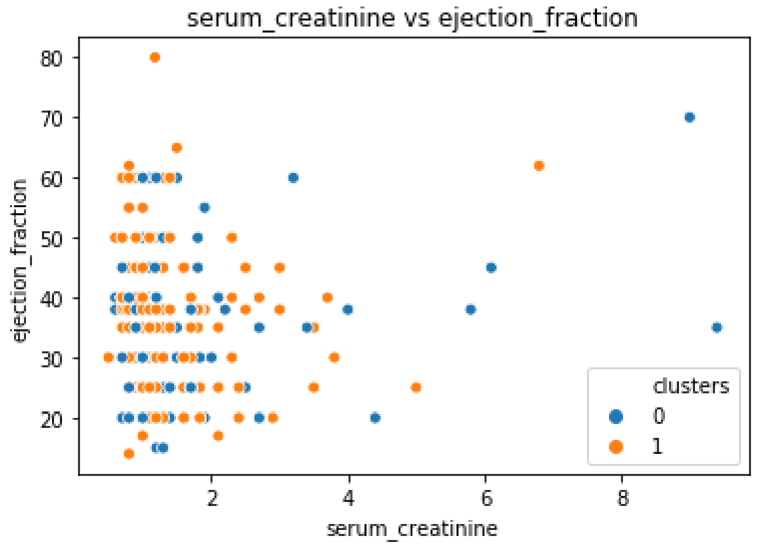
5.3.5 Using Anaemia

```
In [172]: selected_predictor_variables = ['anaemia']
          x = x_train_scaled_df.loc[:, selected_predictor_variables].to_numpy()
```

```
In [173]: clustering = KMeans(n_clusters = 2, init = 'random', n_init = 10, random_state=0).fit(x)
          clusters = clustering.labels_
```

```
In [174]: adjusted_rand_index = metrics.adjusted_rand_score(y_train, clusters)
          silhouette_coefficient = metrics.silhouette_score(x, clusters, metric = "euclidean")
          print([adjusted_rand_index, silhouette_coefficient])

          [0.006938789172657143, 1.0]
```

```
In [175]: data['clusters'] = clusters
          ax = sns.scatterplot(data=data, x=col1, y=col2, hue='clusters')
          ax.set(title = '{} vs {}'.format(col1, col2), xlabel = col1, ylabel = col2)

Out[175]: [Text(0, 0.5, 'ejection_fraction'),
           Text(0.5, 0, 'serum_creatinine'),
           Text(0.5, 1.0, 'serum_creatinine vs ejection_fraction')]
```



Classification: Model Performances

- **Hierarchical Clustering - Single Linkage**

Variables	Rand Index	Silhouette Coefficient
All	0.007	0.416
Age & Gender	-0.001	0.552
Health Problem	-0.003	0.543
Body Parameters	0.007	0.666
Anaemia	0.007	1.0

- **Hierarchical Clustering - Complete Linkage**

Variables	Rand Index	Silhouette Coefficient
All	0.022	0.469
Age & Gender	0.111	0.342
Health Problem	-0.007	0.11
Body Parameters	0.026	0.657
Anaemia	0.007	1.0

- **KMeans Clustering**

Variables	Rand Index	Silhouette Coefficient
All	-0.003	0.117
Age & Gender	-0.001	0.552
Health Problem	-0.005	0.246
Body Parameters	0.154	0.240
Anaemia	0.007	1.0

In [ ]:

```

```