Heart Failure PCA and Classification

March 15, 2023

[2]:
```
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.decomposition import PCA
from sklearn.preprocessing import StandardScaler
import numpy as np
import plotly.express as px
import scipy.stats as stats
from scipy.stats import chi2_contingency, randint
```

1 Heart Failure PCA and Classification

[3]:
```
hfd = pd.read_csv(r'C:\Users\samue\Documents\College Notes\PyRe\Data␣
 ↪sets\heart_failure_dataset.csv')
hfd = hfd.dropna()
hfd.head
```

[3]:
```
<bound method NDFrame.head of       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
..    …       …                       …       …                 …
294  62.0        0                        61         1                  38
295  55.0        0                      1820         0                  38
296  45.0        0                      2060         1                  60
297  45.0        0                      2413         0                  38
298  50.0        0                       196         0                  45

     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
..                   …       …                  …           …  …
294                    1  155000.00               1.1           143    1
295                    0  270000.00               1.2           139    0
296                    0  742000.00               0.8           138    0
297                    0  140000.00               1.4           140    1
298                    0  395000.00               1.6           136    1

     smoking  time  DEATH_EVENT
0          0     4            1
1          0     6            1
2          1     7            1
3          0     7            1
4          0     8            1
..       …   …          …
294        1   270            0
295        0   271            0
296        0   278            0
297        1   280            0
298        1   285            0

[299 rows x 13 columns]>
```

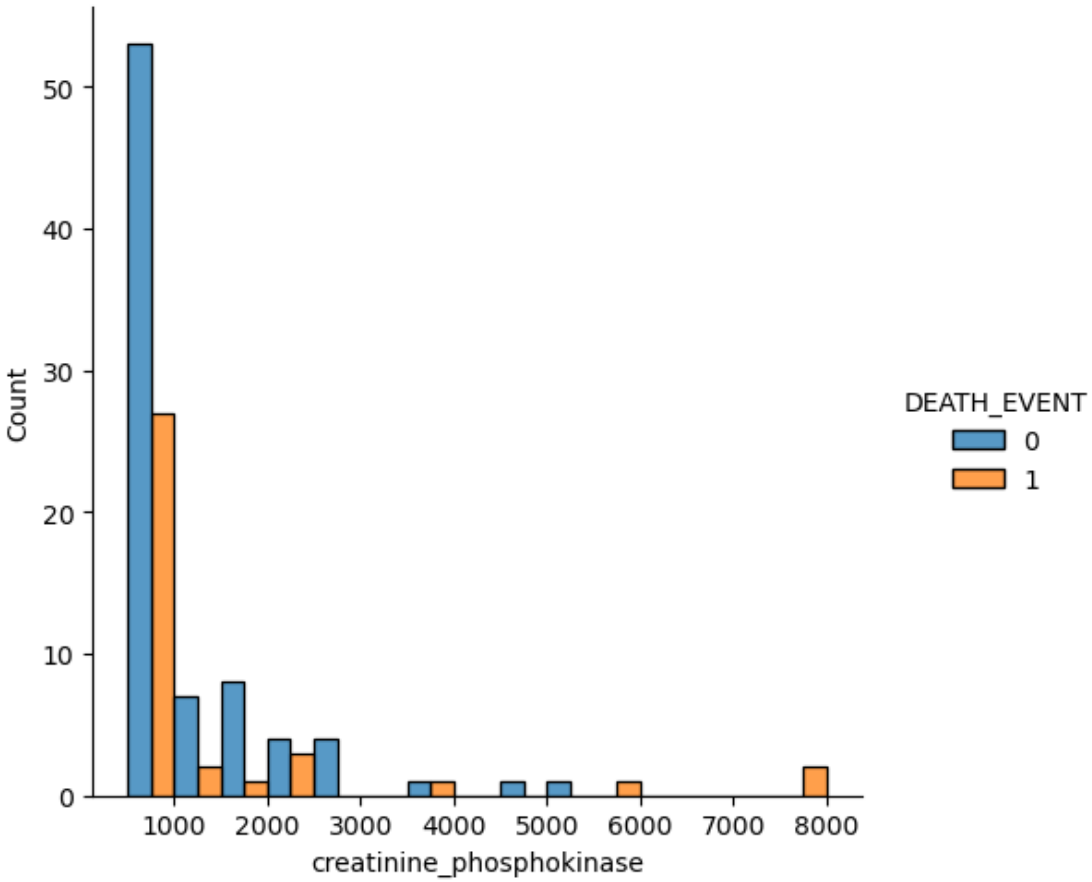
[4]:
```
hfd.describe()
```

[4]:
```
                age     anaemia  creatinine_phosphokinase    diabetes  \
count  299.000000  299.000000                299.000000  299.000000
mean    60.833893    0.431438                581.839465    0.418060
std     11.894809    0.496107                970.287881    0.494067
min     40.000000    0.000000                 23.000000    0.000000
25%     51.000000    0.000000                116.500000    0.000000
50%     60.000000    0.000000                250.000000    0.000000
75%     70.000000    1.000000                582.000000    1.000000
max     95.000000    1.000000               7861.000000    1.000000

       ejection_fraction  high_blood_pressure      platelets  \
count         299.000000           299.000000     299.000000
mean           38.083612             0.351171  263358.029264
std            11.834841             0.478136   97804.236869
min            14.000000             0.000000   25100.000000
25%            30.000000             0.000000  212500.000000
50%            38.000000             0.000000  262000.000000
75%            45.000000             1.000000  303500.000000
max            80.000000             1.000000  850000.000000

       serum_creatinine  serum_sodium         sex    smoking        time  \
count         299.00000    299.000000  299.000000  299.00000  299.000000
```

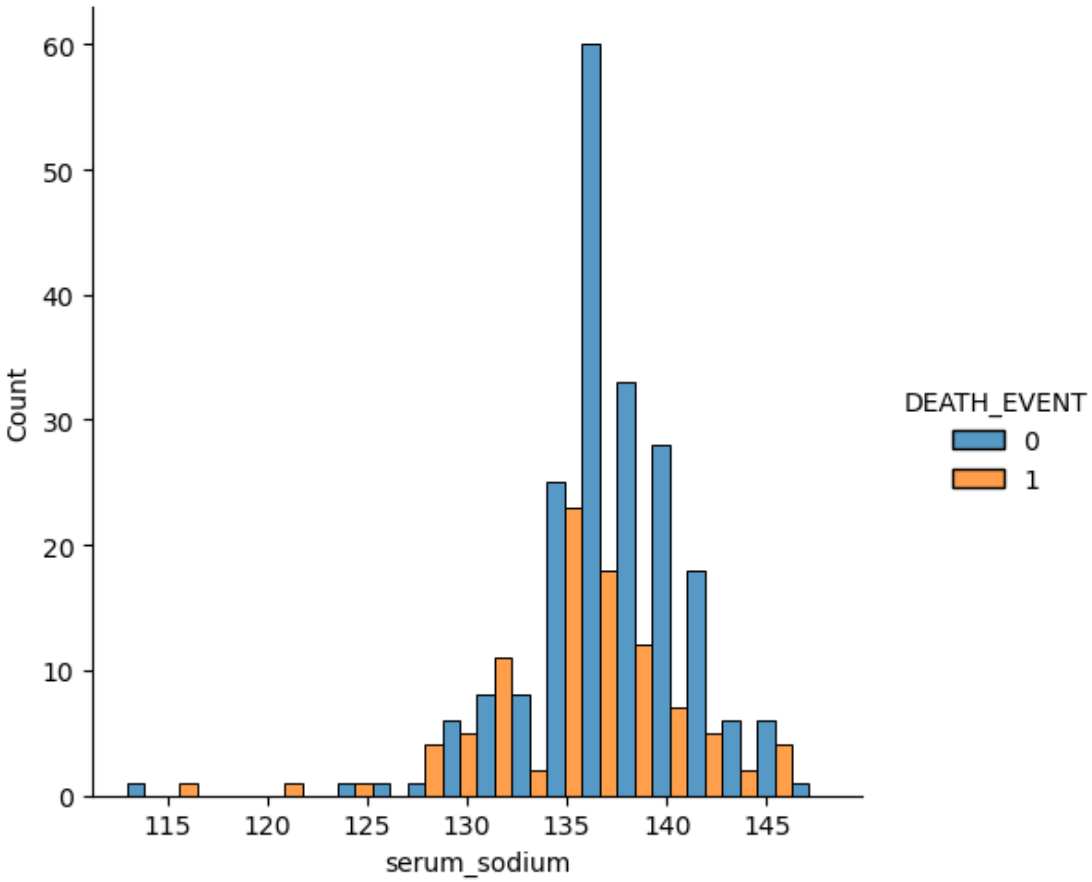
```
mean            1.39388    136.625418    0.648829    0.32107  130.260870
std             1.03451      4.412477    0.478136    0.46767   77.614208
min             0.50000    113.000000    0.000000    0.00000    4.000000
25%             0.90000    134.000000    0.000000    0.00000   73.000000
50%             1.10000    137.000000    1.000000    0.00000  115.000000
75%             1.40000    140.000000    1.000000    1.00000  203.000000
max             9.40000    148.000000    1.000000    1.00000  285.000000
```

```
       DEATH_EVENT
count    299.00000
mean       0.32107
std        0.46767
min        0.00000
25%        0.00000
50%        0.00000
75%        1.00000
max        1.00000
```

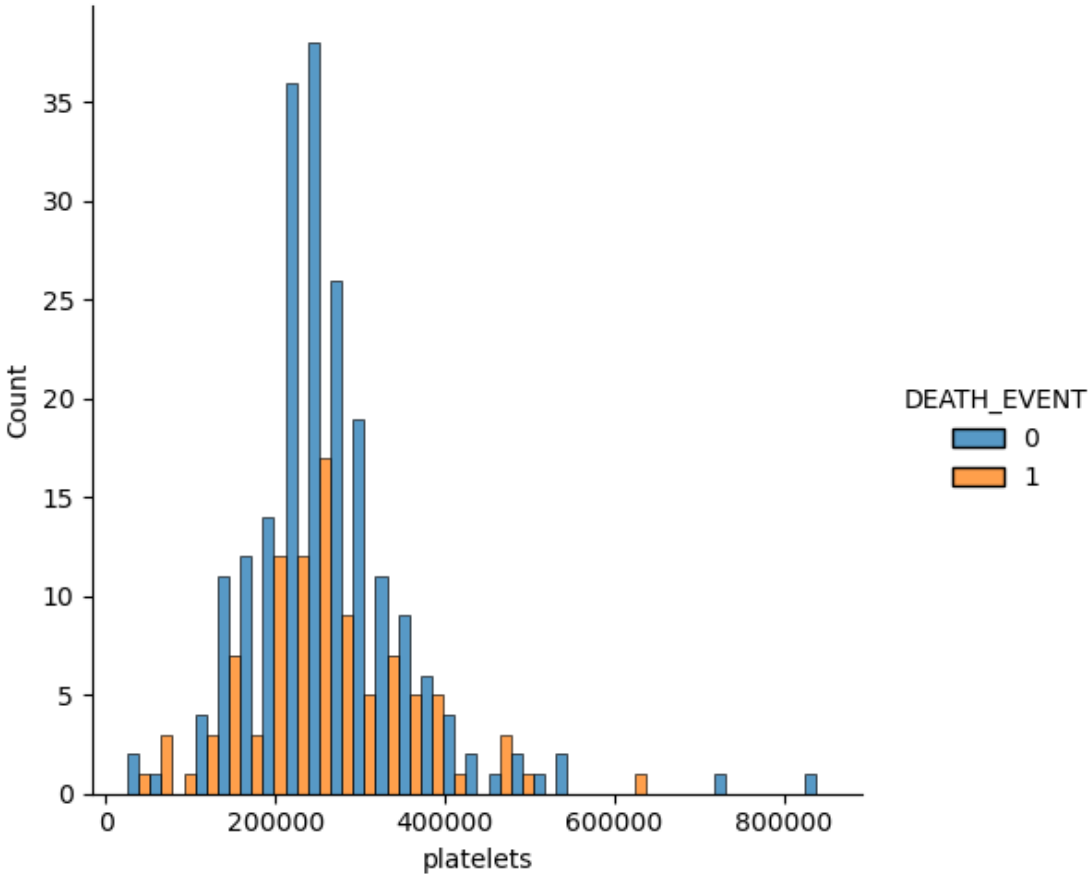
[5]:
```
sns.displot(hfd, x = "creatinine_phosphokinase", hue = "DEATH_EVENT", multiple␣
↪= "dodge",
            bins = [500, 1000, 1500, 2000, 2500, 3000, 3500, 4000, 4500, 5000,␣
↪5500, 6000, 6500, 7000, 7500, 8000])
plt.show()
```



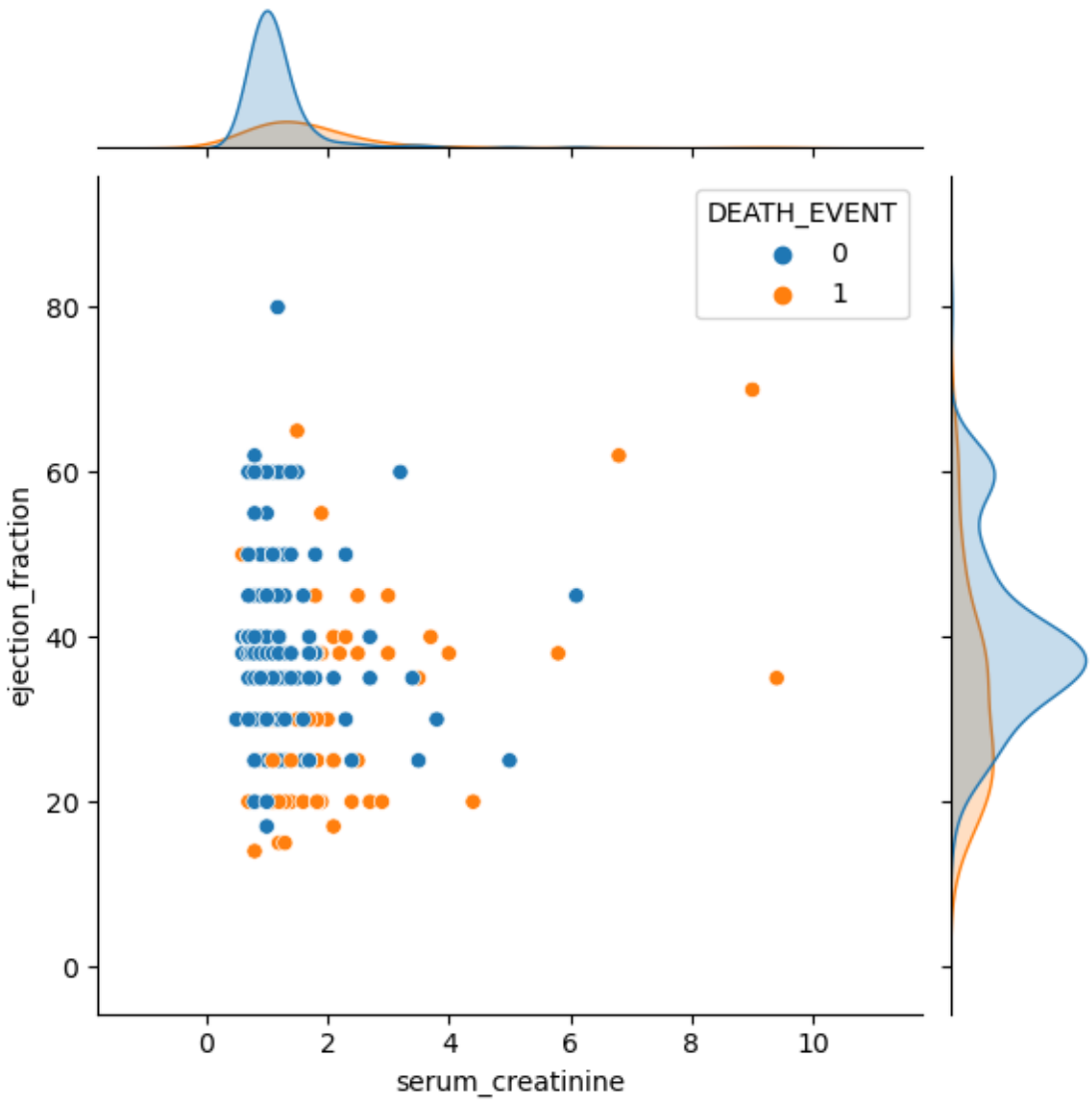
[6]:
```
sns.displot(hfd, x = "serum_sodium", hue = "DEATH_EVENT", multiple = "dodge")
plt.show()
```



[7]:
```
sns.displot(hfd, x = "platelets", hue = "DEATH_EVENT", multiple = "dodge")
plt.show()
```



[8]:
```
sns.jointplot(data = hfd, x = "serum_creatinine", y = "ejection_fraction", hue␣
↪= "DEATH_EVENT")
plt.show()
```



The plots above display the distribution of our continuous variables. As we see the distributions for these variables are relatively normal, save for creatine phosphokinase (CPK) which is skewed right.

[9]:
```
stats.mannwhitneyu(x = hfd['DEATH_EVENT'], y = hfd['creatinine_phosphokinase'],␣
↪alternative = 'two-sided')
```

[9]:
```
MannwhitneyuResult(statistic=0.0, pvalue=7.80940515793462e-104)
```

[10]:
```
stats.mannwhitneyu(x = hfd['DEATH_EVENT'], y = hfd['ejection_fraction'],␣
↪alternative = 'two-sided')
```

[10]:
```
MannwhitneyuResult(statistic=0.0, pvalue=5.748810376178891e-104)
```

[11]:
```
stats.mannwhitneyu(x = hfd['DEATH_EVENT'], y = hfd['platelets'], alternative =␣
↪'two-sided')
```

[11]:
```
MannwhitneyuResult(statistic=0.0, pvalue=8.63331766603266e-104)
```

[12]:
```
stats.mannwhitneyu(x = hfd['DEATH_EVENT'], y = hfd['serum_creatinine'],␣
↪alternative = 'two-sided')
```

[12]:
```
MannwhitneyuResult(statistic=10176.0, pvalue=2.2614587328253158e-63)
```

[13]:
```
stats.mannwhitneyu(x = hfd['DEATH_EVENT'], y = hfd['serum_sodium'], alternative␣
↪= 'two-sided')
```

[13]:
```
MannwhitneyuResult(statistic=0.0, pvalue=6.761757176362062e-104)
```

[14]:
```
stats.mannwhitneyu(x = hfd['DEATH_EVENT'], y = hfd['age'], alternative =␣
↪'two-sided')
```

[14]:
```
MannwhitneyuResult(statistic=0.0, pvalue=7.787877997331131e-104)
```

Assuming an alpha of 0.05, it can be assumed that for our continuous variables (CPK, ejection fraction, platelets, serum creatinine, serum sodium, and age) survival status differed significantly among heart failure patients.

[15]:
```
hfd_target = hfd.loc[:,'DEATH_EVENT']
hfd_target.head

hfd_features = hfd.drop(['anaemia', 'sex','diabetes', 'time', 'smoking',␣
↪'DEATH_EVENT'], axis = 1)
hfd_features.head
```

[15]:
```
<bound method NDFrame.head of       age  creatinine_phosphokinase
ejection_fraction  high_blood_pressure  \
0    75.0                        582                 20                   1
1    55.0                       7861                 38                   0
2    65.0                        146                 20                   0
3    50.0                        111                 20                   0
4    65.0                        160                 20                   0
..    …                          …                   …                    …
294  62.0                         61                 38                   1
295  55.0                       1820                 38                   0
296  45.0                       2060                 60                   0
297  45.0                       2413                 38                   0
298  50.0                        196                 45                   0

     platelets  serum_creatinine  serum_sodium
0    265000.00               1.9           130
```

```
1    263358.03              1.1           136
2    162000.00              1.3           129
3    210000.00              1.9           137
4    327000.00              2.7           116
..         …                …             …
294  155000.00              1.1           143
295  270000.00              1.2           139
296  742000.00              0.8           138
297  140000.00              1.4           140
298  395000.00              1.6           136

[299 rows x 7 columns]>
```

Seperating our target variable from our feature variables. The binary variable 'high blood pressure' is retained.

[16]:
```
x = StandardScaler().fit_transform(hfd_features)

hfd_pcamodel = PCA(n_components = 4)
hfd_pca = hfd_pcamodel.fit_transform(x)
hfd_pca.shape
```

[16]:
```
(299, 4)
```

Creating our PCA model with four principal components to start.

[17]:
```
hfd_pca2 = pd.DataFrame(data = hfd_pca, columns = ['PC1', 'PC2', 'PC3', 'PC4'])
hfd_pca2.head
```

[17]:
```
<bound method NDFrame.head of           PC1       PC2       PC3       PC4
0    2.044649 -0.164567 -1.244152  0.939179
1   -1.784539  3.546248  3.683013  2.623146
2    1.931770  1.397081 -0.695478 -0.648093
3    0.571228  1.433565 -0.519324 -0.430294
4    3.891392  1.654035 -0.789666  1.785356
..        …         …         …         …
294 -0.509334 -1.029473 -0.749240 -1.192754
295 -0.887347  0.977491  0.892423  0.212809
296 -3.324198 -0.178264  1.087546  3.933024
297 -0.954457  1.778759  1.208409 -0.577548
298 -0.650700  0.140269  0.214062  0.828817

[299 rows x 4 columns]>
```

[18]:
```
hfd_final = pd.concat([hfd_pca2, hfd_target], axis = 1, join = 'inner')
hfd_final.head
```

[18]:
```
<bound method NDFrame.head of           PC1       PC2       PC3       PC4
DEATH_EVENT
0    2.044649 -0.164567 -1.244152  0.939179            1
1   -1.784539  3.546248  3.683013  2.623146            1
2    1.931770  1.397081 -0.695478 -0.648093            1
3    0.571228  1.433565 -0.519324 -0.430294            1
4    3.891392  1.654035 -0.789666  1.785356            1
..        …         …         …         …          …
294 -0.509334 -1.029473 -0.749240 -1.192754            0
295 -0.887347  0.977491  0.892423  0.212809            0
296 -3.324198 -0.178264  1.087546  3.933024            0
297 -0.954457  1.778759  1.208409 -0.577548            0
298 -0.650700  0.140269  0.214062  0.828817            0

[299 rows x 5 columns]>
```

[19]:
```
hfd_pcamodel.explained_variance_
```

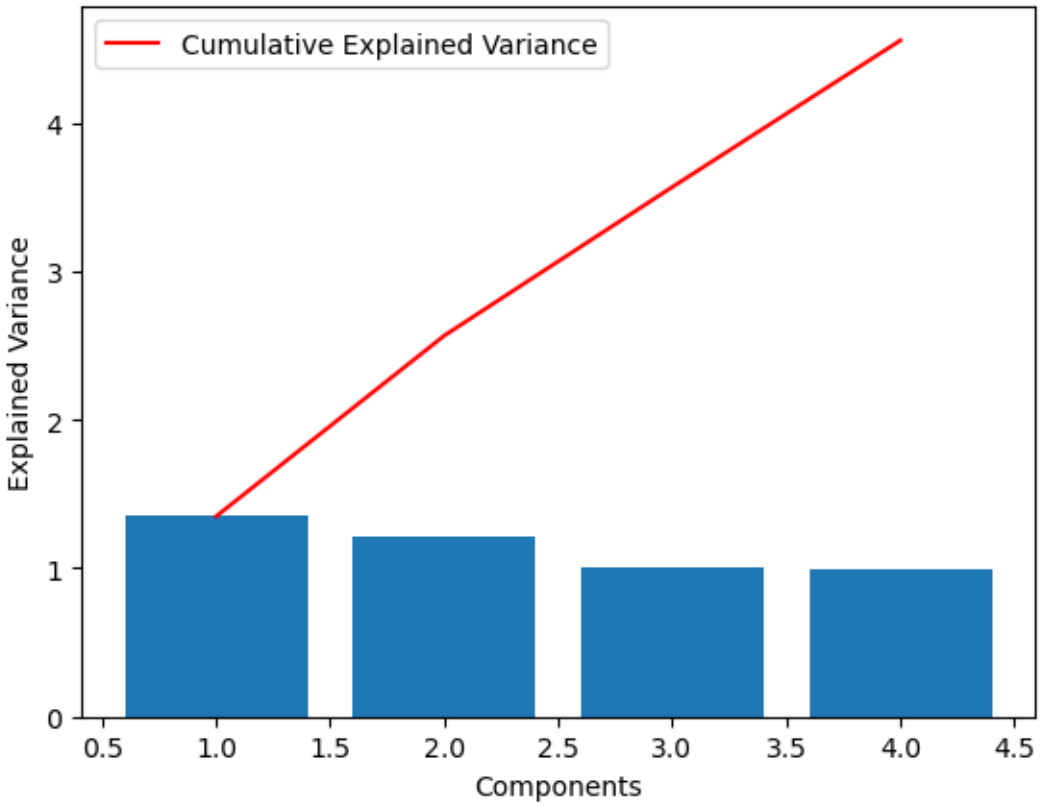
[19]:
```
array([1.34980664, 1.21784302, 1.00188564, 0.98827669])
```

[20]:
```
hfd_pcamodel.explained_variance_ratio_
```

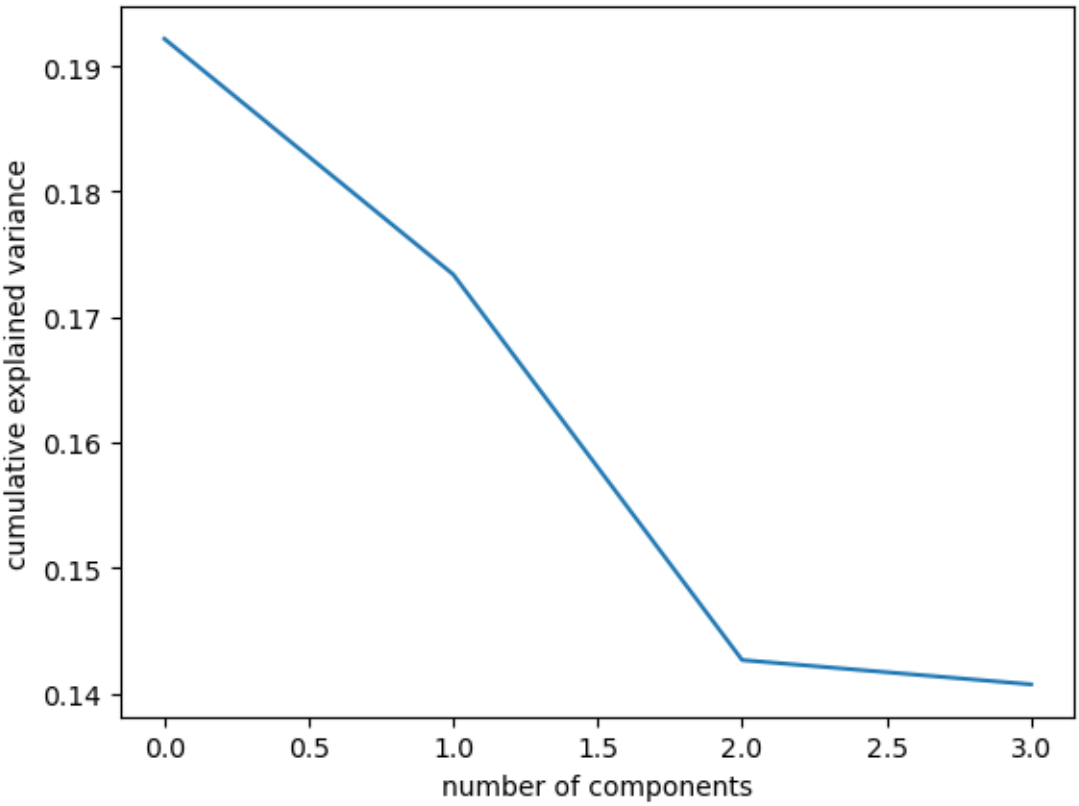
[20]:
```
array([0.1921846 , 0.17339571, 0.14264784, 0.1407102 ])
```

The explained variance (eigenvalues) tells us the first four principal components account for 65% of the variance in the data. Not a great PCA problem likely due to weak relationships between the variables. A correlation matrix should be created to get specific correlation coefficients to determine the true strength of PCA for this data.

[21]:
```
plt.bar(range(1,len(hfd_pcamodel.explained_variance_)+1),hfd_pcamodel.
  ↪explained_variance_)
plt.ylabel('Explained Variance')
plt.xlabel('Components')
plt.plot(range(1,len(hfd_pcamodel.explained_variance_)+1), np.
  ↪cumsum(hfd_pcamodel.explained_variance_), c = 'red',
         label = "Cumulative Explained Variance")
plt.legend(loc = 'upper left')
plt.show()
```

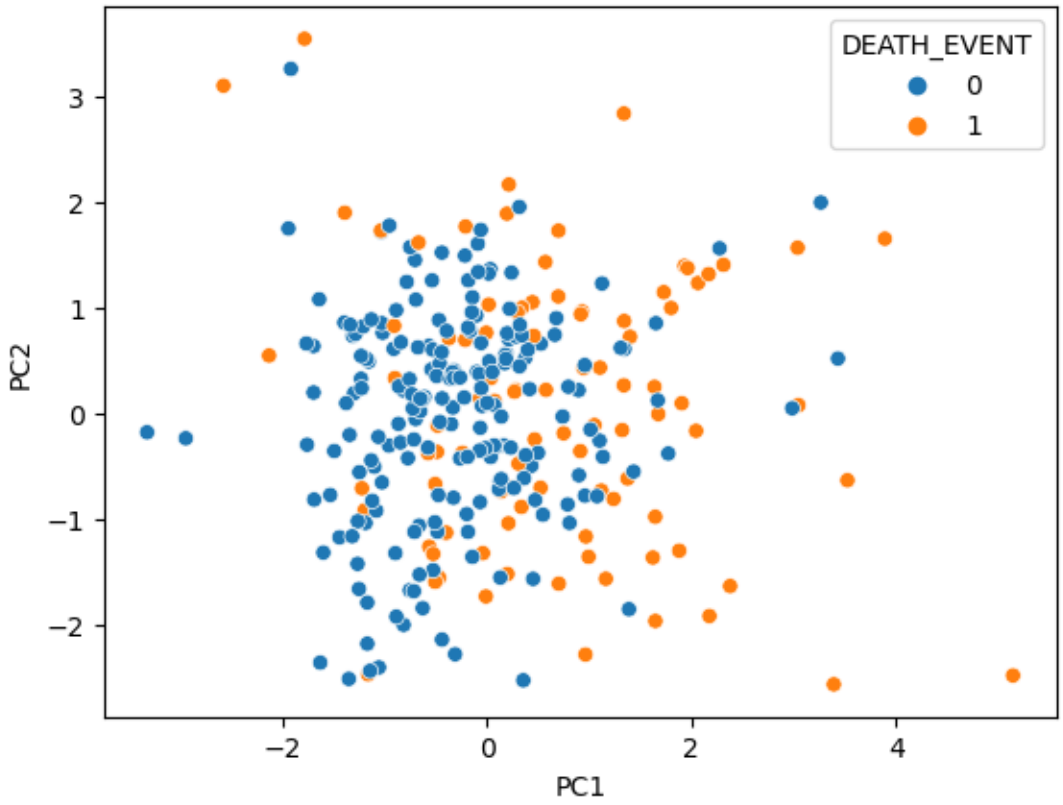


[22]:
```
plt.plot(hfd_pcamodel.explained_variance_ratio_)
plt.xlabel('number of components')
plt.ylabel('cumulative explained variance')
plt.show()
```

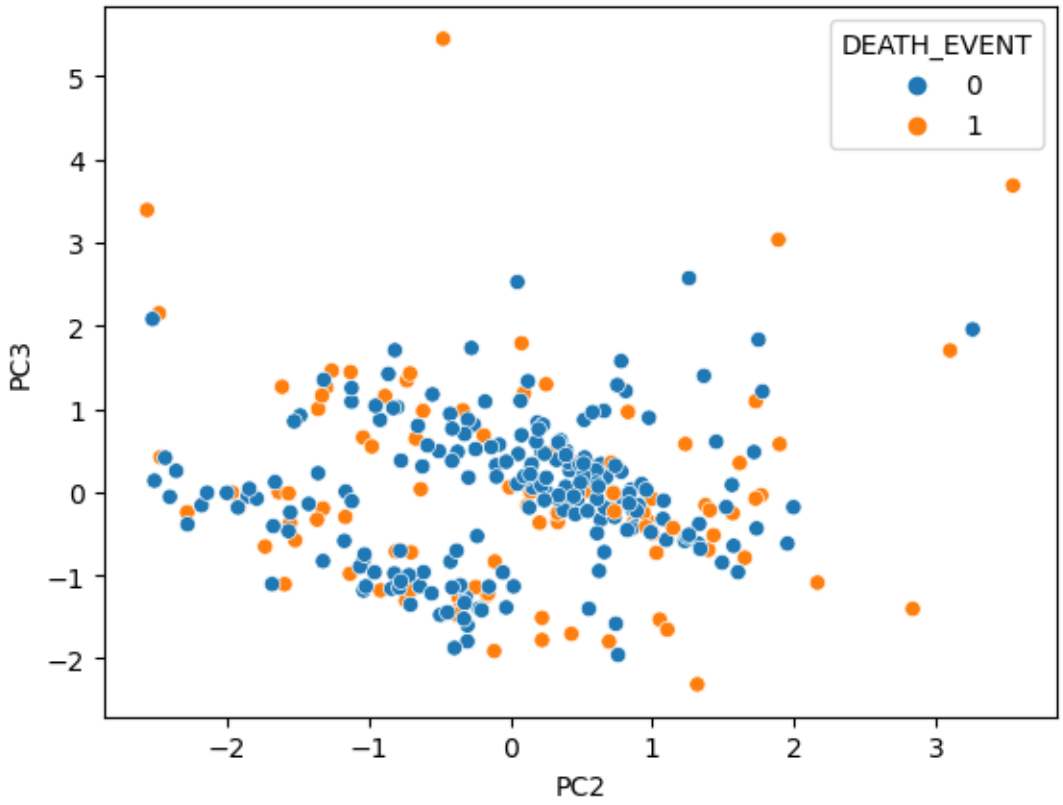


Scree plot shows that only the first two principal components should be retained.

[23]:
```
hfd_pcafig = sns.scatterplot(data = hfd_final, x = 'PC1',y = 'PC2', hue =␣
  ↪"DEATH_EVENT")
plt.show()
```



[24]:
```
hfd_pcafig2 = sns.scatterplot(data = hfd_final, x = 'PC2',y = 'PC3', hue =␣
↪"DEATH_EVENT")
plt.show()
```

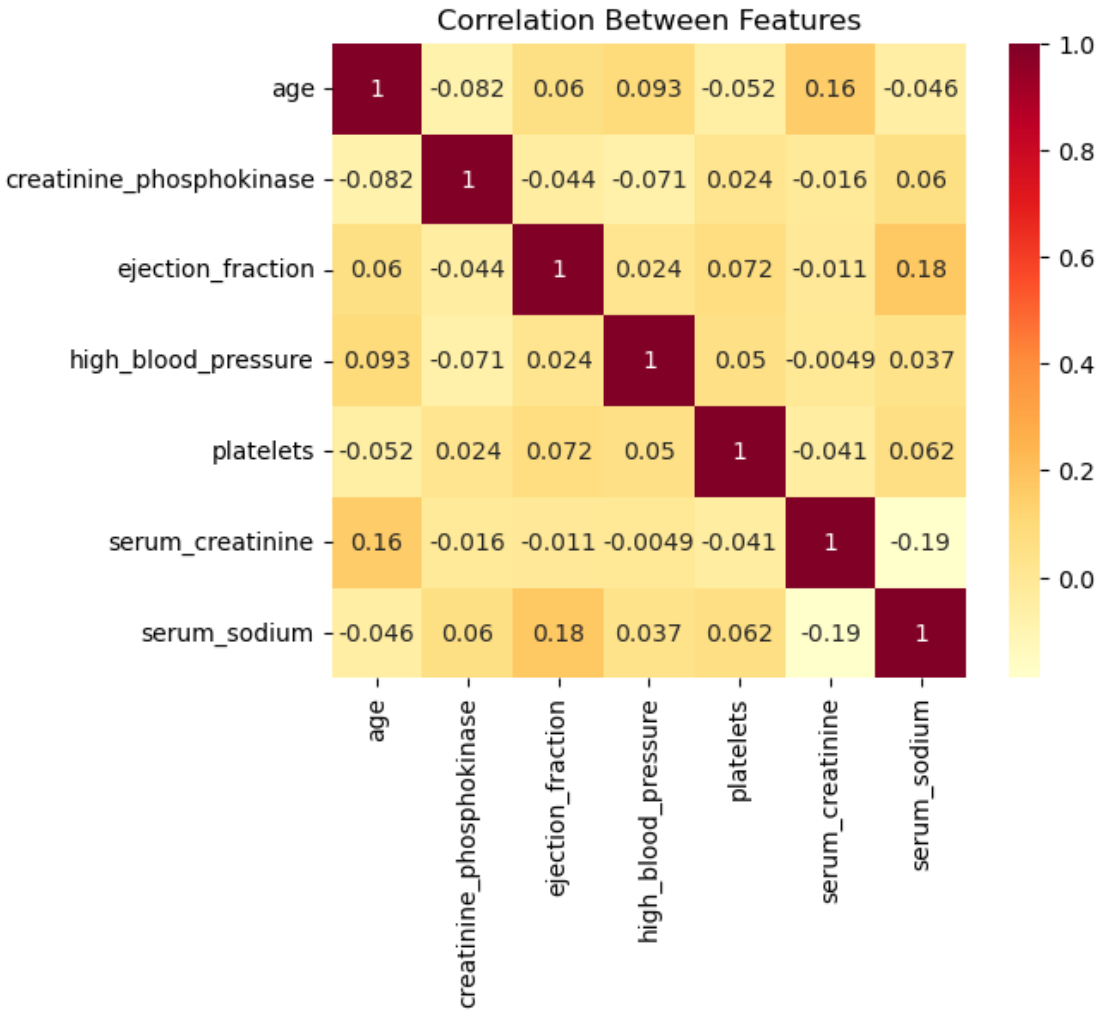


Interesting seperation between the second and third principal components, likely due to the binary variable 'high blood pressure'.

[25]:
```
hfd_pcafig3 = px.scatter_3d(
hfd_final, x = 'PC1', y = 'PC2', z = 'PC3', color = 'DEATH_EVENT',
title = '3 Dimensions',
labels = {'0': 'PC1', '1': 'PC2', '2': 'PC3'})
hfd_pcafig3.show()
```

Created a 3D plot because I wanted to see the seperation between the second and third principal components.

[26]:
```
correlation = hfd_features.corr()
sns.heatmap(correlation, square = True, annot = True, cmap = 'YlOrRd')
plt.title("Correlation Between Features")
plt.show()
```



As we see from the correlation matrix all the variables have weak correlations, less than 0.2, meaning that PCA will not help in reducing the data in a meaningful way.

[27]:
```
from sklearn.model_selection import train_test_split, GridSearchCV
from sklearn.linear_model import LogisticRegression
from sklearn import metrics
from sklearn.metrics import classification_report
from sklearn.metrics import mean_squared_error
from sklearn.model_selection import cross_val_score
from sklearn.ensemble import RandomForestClassifier
from sklearn import tree
from sklearn.metrics import confusion_matrix, accuracy_score, precision_score
```

Logistic Regression

[28]:
```
hfd_features_train, hfd_features_test, hfd_target_train, hfd_target_test =␣
↪train_test_split(hfd_features, hfd_target, test_size = 0.25, random_state =␣
↪10)
```

Partitioning our data between testing and training sets. In this line of code, I'm assigning 75% of the data as our training set and the remaining 25% as our testing set.

[29]:
```
hflogreg = LogisticRegression(random_state = 10)
hflogreg.fit(hfd_features_train, hfd_target_train)
y_pred = hflogreg.predict(hfd_features_test)
```

Creating a logistic regression model.

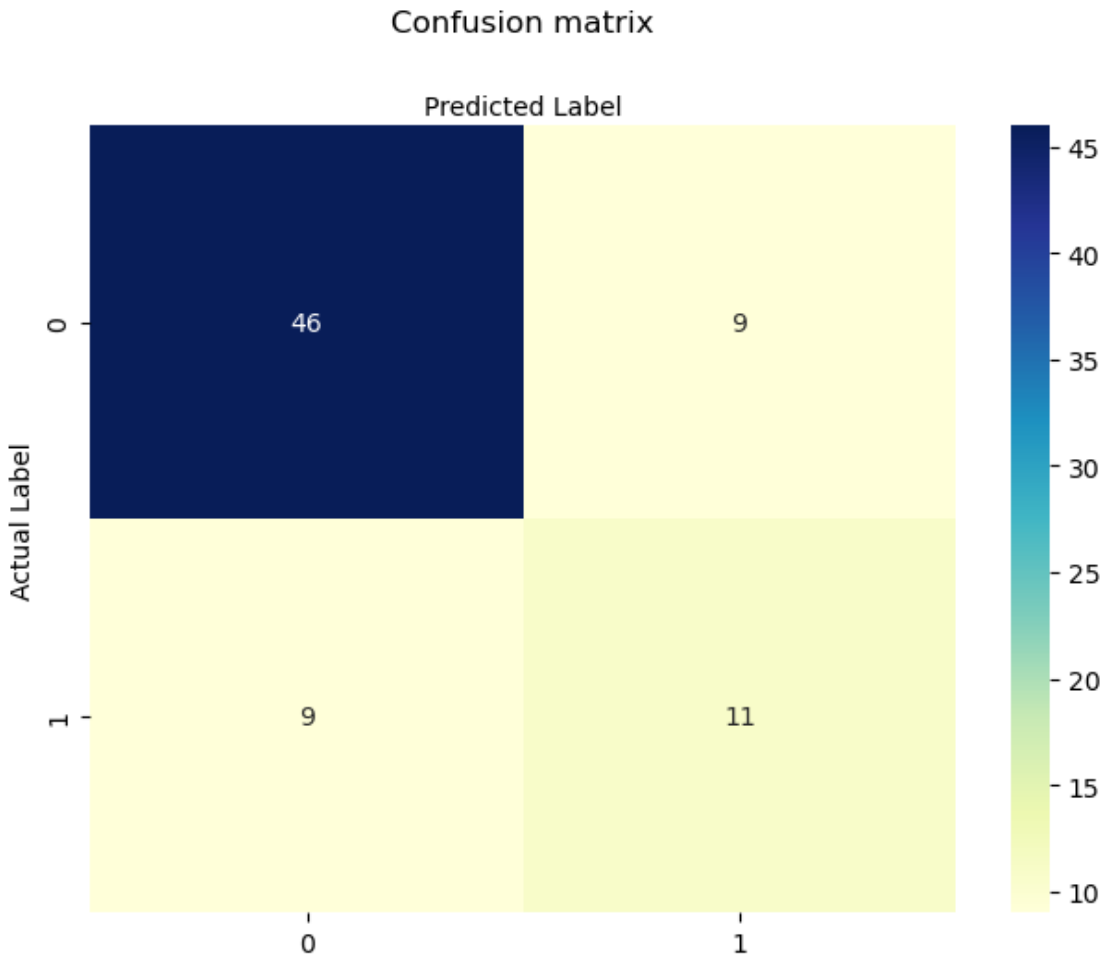
[30]:
```
hf_scores = cross_val_score(hflogreg, hfd_features, hfd_target, scoring =␣
↪"neg_mean_squared_error", cv = 10, n_jobs = 1)

hf_rmse = np.sqrt(-hf_scores)
print("RMSE Values: ", np.round(hf_rmse, 2))
print("RMSE Average: ", np.mean(hf_rmse))
```

```
RMSE Values:  [0.41 0.58 0.45 0.61 0.52 0.58 0.55 0.37 0.45 0.49]
RMSE Average:  0.4983478483772646
```

[31]:
```
con_matrix = metrics.confusion_matrix(hfd_target_test, y_pred)
con_matrix
```

[31]:
```
array([[46,  9],
       [ 9, 11]], dtype=int64)
```

[32]:
```
class_names = [0,1]
fig, ax = plt.subplots()
tick_marks = np.arange(len(class_names))
plt.xticks(tick_marks, class_names)
plt.yticks(tick_marks, class_names)
# Heatmap
sns.heatmap(pd.DataFrame(con_matrix), annot = True, cmap = "YlGnBu", fmt = 'g')
ax.xaxis.set_label_position("top")
plt.tight_layout()
plt.title('Confusion matrix', y = 1.1)
plt.ylabel('Actual Label')
plt.xlabel('Predicted Label')
plt.show()
```



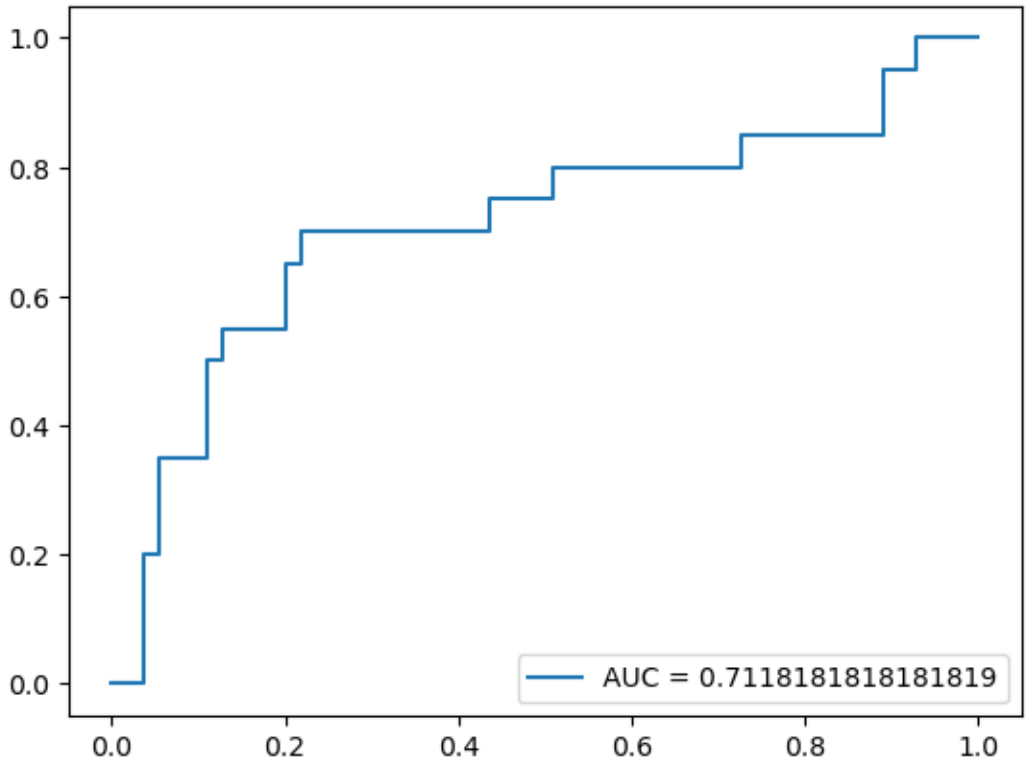
[33]:
```
target_names = ['Alive', 'Death Event']
print(classification_report(hfd_target_test, y_pred, target_names =␣
↪target_names))
```

```
              precision    recall  f1-score   support

       Alive       0.84      0.84      0.84        55
 Death Event       0.55      0.55      0.55        20

    accuracy                           0.76        75
   macro avg       0.69      0.69      0.69        75
weighted avg       0.76      0.76      0.76        75
```

The results from the logistic regression gives us an AUC of 0.71, which means that the model has a 71% chance of predicting survival from a patient afflicted with heart failure. The sensitivity value calculated is 0.55 and the specificity value is 0.84. Given

the model performance (AUC = 0.71) we can say that the model is satisfactory in predicting survival in patients with heart failure, however due to the domain that our question arises (healthcare) a model accuracy of 71% would be unacceptable in a healthcare setting. Because of this, more time should be spent tuning our model further in an attempt to reach a better AUC.

[34]:
```
y_pred_proba = hflogreg.predict_proba(hfd_features_test)[::,1]
fpr, tpr, _ = metrics.roc_curve(hfd_target_test, y_pred_proba)
auc = metrics.roc_auc_score(hfd_target_test, y_pred_proba)
plt.plot(fpr, tpr, label = "AUC = " +str(auc))
plt.legend(loc=4)
plt.show()
```



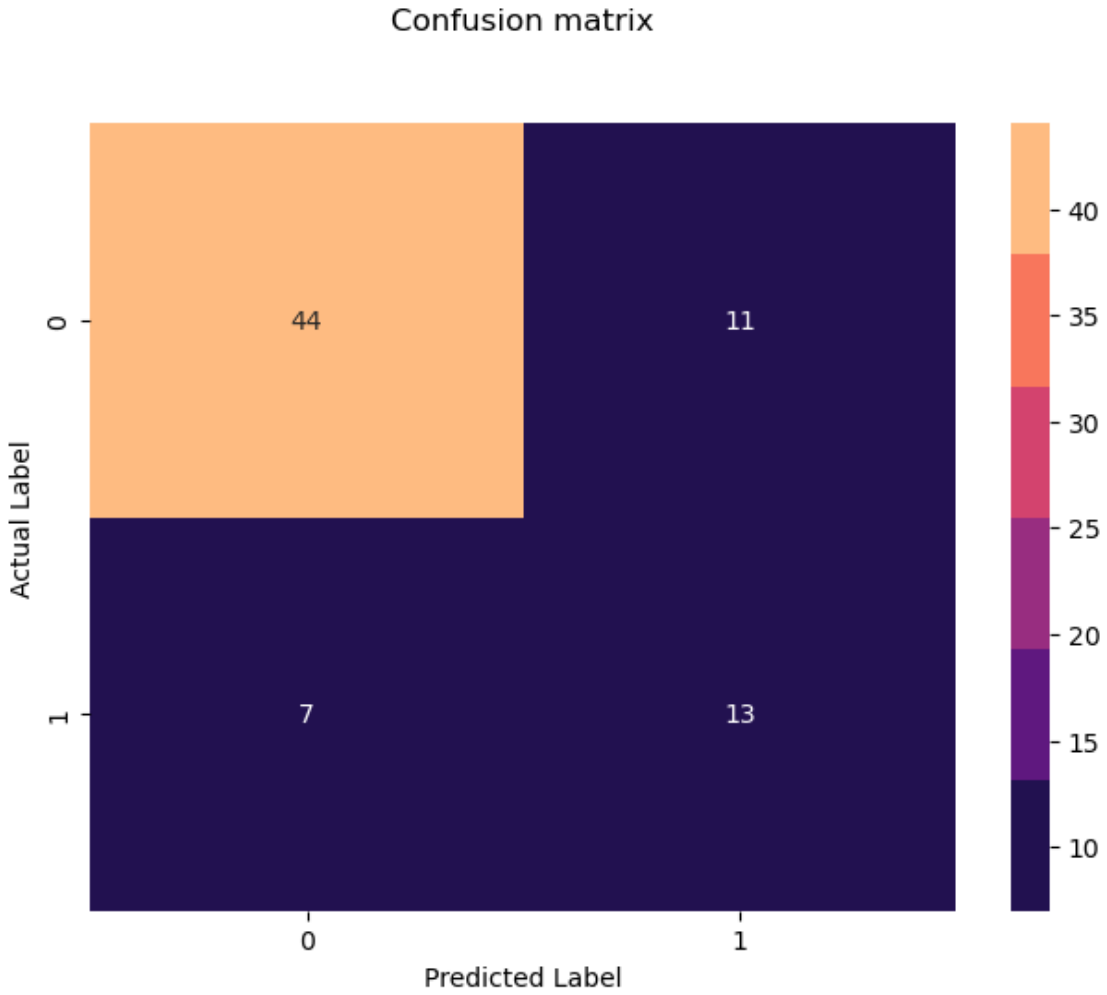
Random Forest

[52]:
```
hfd_features2 = hfd.drop(['anaemia', 'sex','diabetes', 'time', 'smoking',␣
↪'DEATH_EVENT', 'age', 'high_blood_pressure'], axis = 1)
```

[53]:
```
rfc_features_train, rfc_features_test, rfc_target_train, rfc_target_test =␣
↪train_test_split(hfd_features2, hfd_target, test_size = 0.25, random_state =␣
↪10)

hfd_rfc = RandomForestClassifier()
```

```
hfd_rfc.fit(rfc_features_train, rfc_target_train)

y_pred2 = hfd_rfc.predict(rfc_features_test)
```

[47]:
```
con_matrix2 = metrics.confusion_matrix(rfc_target_test, y_pred2)
color = sns.color_palette("magma")

sns.heatmap(pd.DataFrame(con_matrix2), annot = True, cmap = color, fmt = 'g')
ax.xaxis.set_label_position("top")
plt.tight_layout()
plt.title('Confusion matrix', y = 1.1)
plt.ylabel('Actual Label')
plt.xlabel('Predicted Label')
plt.show()
```



[54]:
```
accuracy = accuracy_score(rfc_target_test, y_pred2)
print("Accuracy:", accuracy)
```

```
Accuracy: 0.7733333333333333
```

Computed a random forest, dropping the features high blood pressure and age. A model accuracy of .773 or 77% was found, slightly better than the accuracy found in the logisitic regression. A follow up to this technique would be to use grid search to find the best hyperparameters and tune the model according to the results, then calculate an AUC value.