Supervised Machine Learning - Classification

Objective

The main objective of my analysis is to focus on **prediction** of heart failure based on the dataset described

```
%config Completer.use_jedi = False
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
from collections import Counter

data =
pd.read_csv('../input/heart-failure-clinical-data/heart_failure_clinic
al_records_dataset.csv')
data.head()
```

```
    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
```

EDA

```
data.isnull().sum()
```

```
age                         0
anaemia                     0
creatinine_phosphokinase    0
diabetes                    0
ejection_fraction           0
high_blood_pressure         0
platelets                   0
serum_creatinine            0
serum_sodium                0
sex                         0
smoking                     0
time                        0
DEATH_EVENT                 0
dtype: int64
```

```
for feature in data.columns:
    print(feature, ':', len(data[feature].unique()))
```

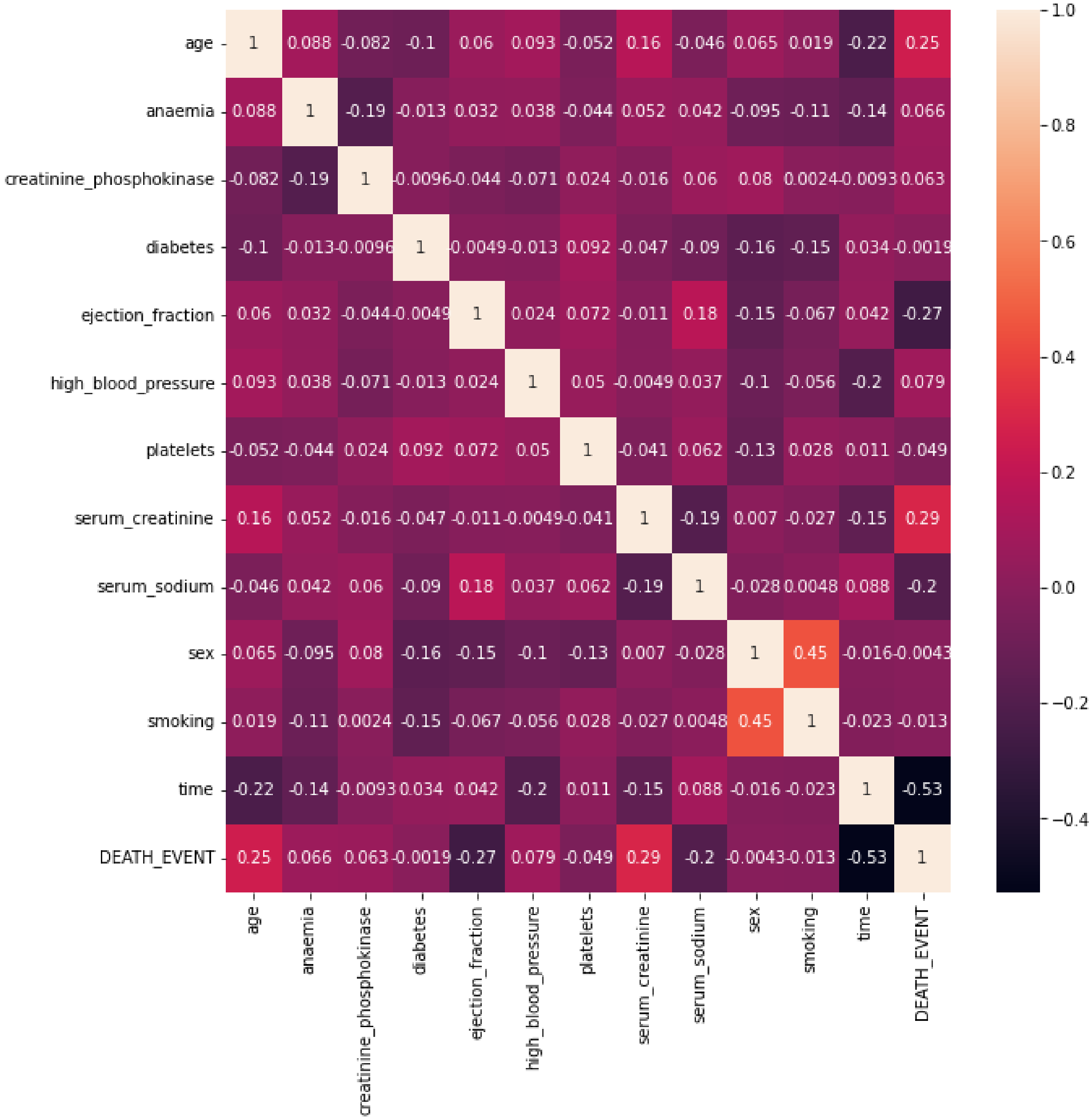
```
age : 47
anaemia : 2
creatinine_phosphokinase : 208
diabetes : 2
ejection_fraction : 17
high_blood_pressure : 2
platelets : 176
serum_creatinine : 40
serum_sodium : 27
sex : 2
smoking : 2
time : 148
DEATH_EVENT : 2
```

```
discrete_features, continuous_features = [], []
for feature in data.columns:
    if feature == 'DEATH_EVENT':
        label = ['DEATH_EVENT']
    elif len(data[feature].unique()) >= 10:
        continuous_features.append(feature)
```

```
    else:
        discrete_features.append(feature)

print('Discrete: ', discrete_features, '\n', 'Continuous',
continuous_features)
```

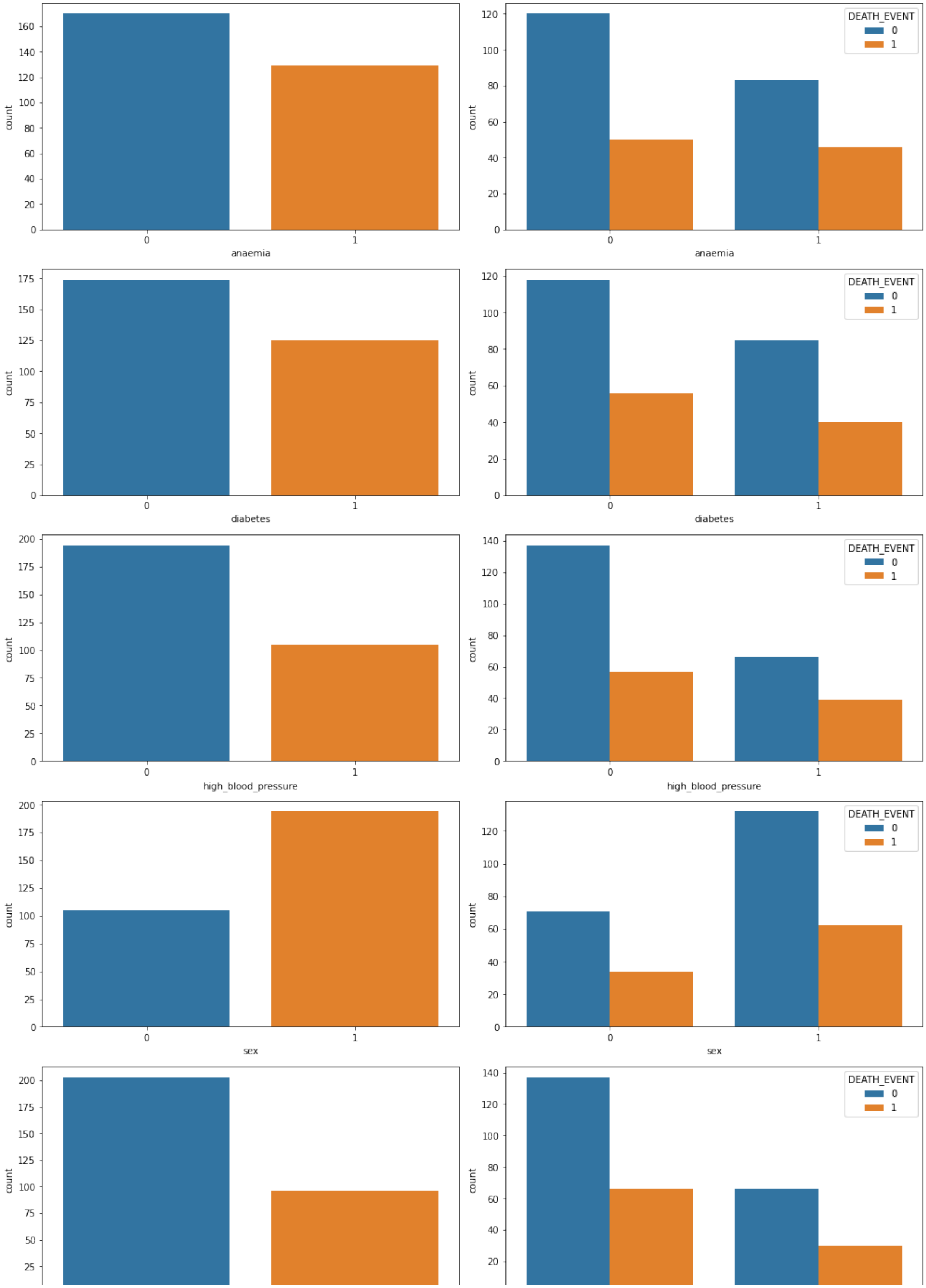
```
Discrete:  ['anaemia', 'diabetes', 'high_blood_pressure', 'sex',
'smoking']
 Continuous ['age', 'creatinine_phosphokinase', 'ejection_fraction',
'platelets', 'serum_creatinine', 'serum_sodium', 'time']
```

```
correlation = data.corr()
plt.figure(figsize=(10, 10))
sns.heatmap(correlation, annot=True)
plt.show()
```



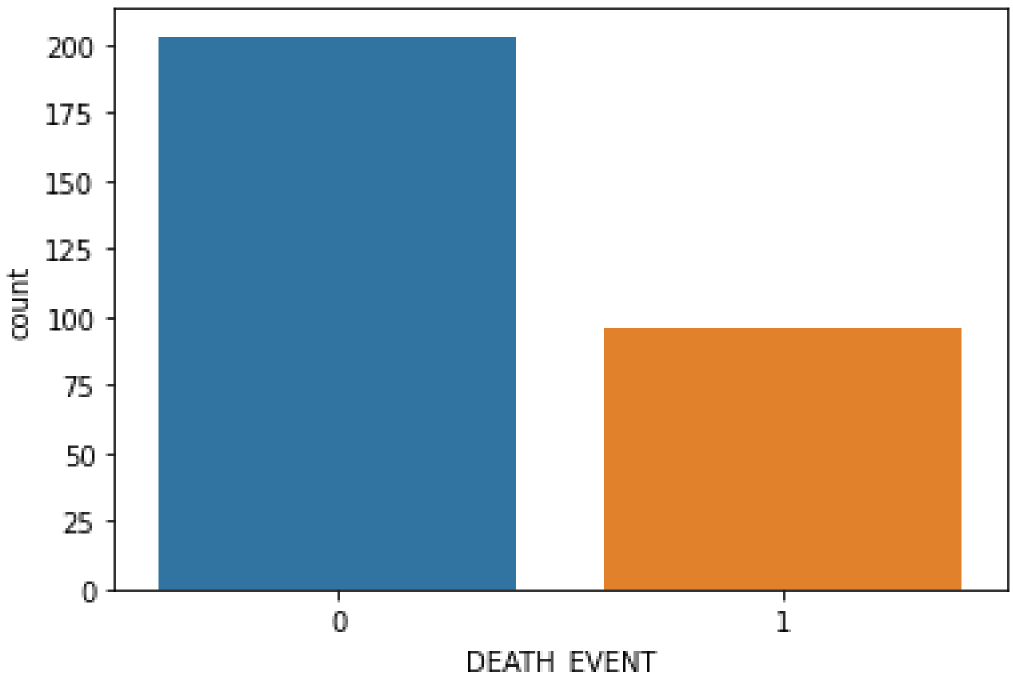
- There is nothing to conclude from discrete features correlation matrix.
- From the correlation matrix for continuous features, time is inversely correlated to death. Thus patients with less follow up time are prone to heart failure.

```
fig, ax = plt.subplots(len(discrete_features), 2, figsize=(14,20))

for i in range(len(discrete_features)):
    sns.countplot(ax=ax[i, 0], x=discrete_features[i], data=data)
    sns.countplot(ax=ax[i, 1], x=discrete_features[i],
hue='DEATH_EVENT', data=data)
fig.tight_layout(pad=1)
plt.show()
```


count
anaemia
DEATH_EVENT
0
1
diabetes
high_blood_pressure
sex

```
sns.countplot(x='DEATH_EVENT', data=data)
```

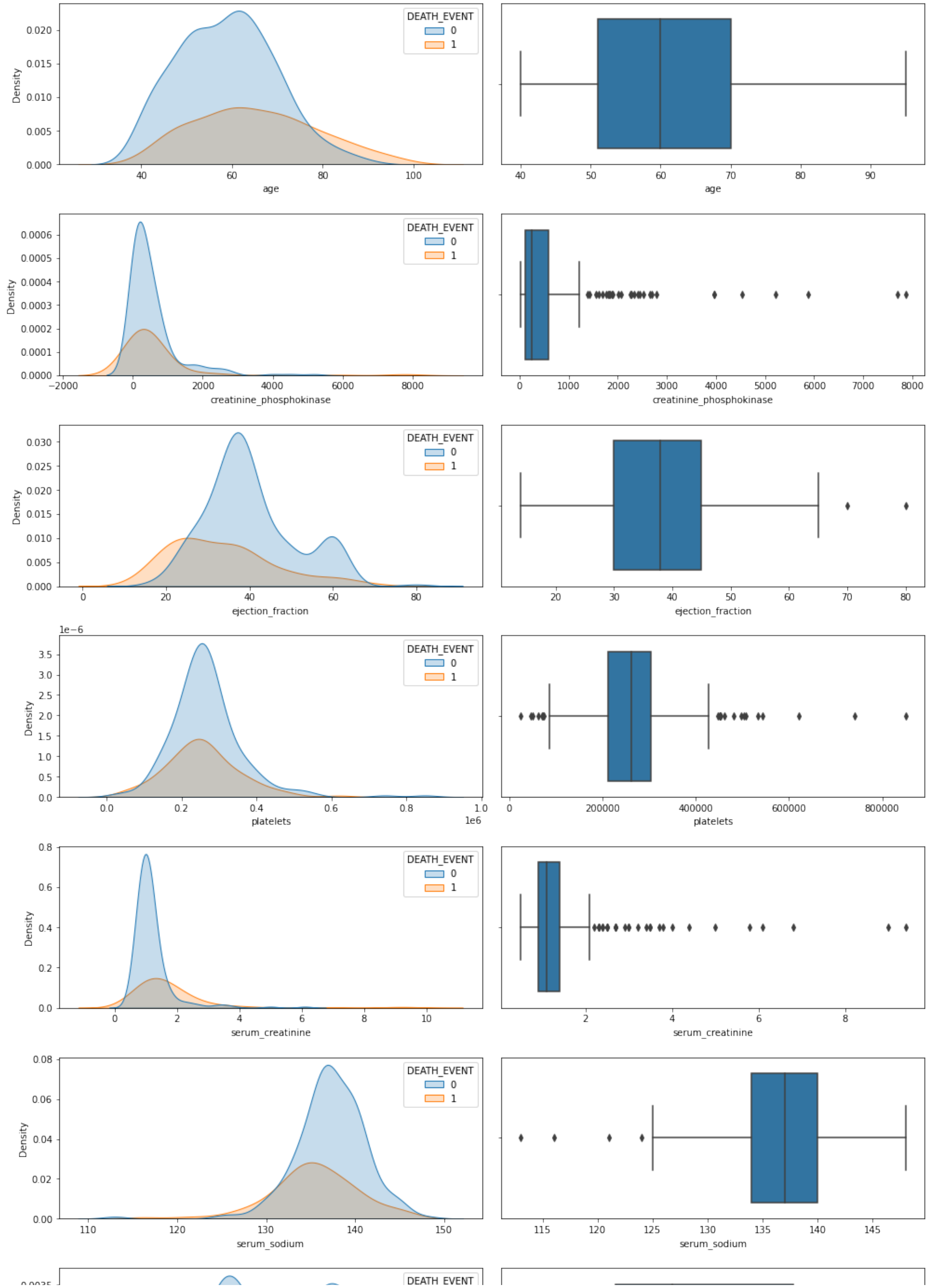
```
<AxesSubplot:xlabel='DEATH_EVENT', ylabel='count'>
```



Observations

- There is an imbalance with the target variable, so we can apply cross validation technique with over sampling method compared to under sampling as the data size is small.

```
fig, ax = plt.subplots(len(continuous_features), 2, figsize=(14,22))

for i in range(len(continuous_features)):
    sns.kdeplot(ax=ax[i, 0], x=continuous_features[i],
hue='DEATH_EVENT', data=data, fill = True)
    sns.boxplot(ax=ax[i, 1], x=continuous_features[i], data=data)
fig.tight_layout(pad=1)
plt.show()
```


DEATH_EVENT
0
1
Density
age
creatinine_phosphokinase
ejection_fraction
1e−6
platelets
1e6
serum_creatinine
serum_sodium

Feature Selection

```
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LogisticRegression, Lasso
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import RandomForestClassifier,
GradientBoostingClassifier
from sklearn.metrics import accuracy_score, classification_report,
confusion_matrix, plot_confusion_matrix
from sklearn.preprocessing import StandardScaler
from sklearn.neighbors import LocalOutlierFactor
from sklearn.feature_selection import chi2, SelectFromModel,
SelectKBest
from sklearn.model_selection import GridSearchCV, RandomizedSearchCV,
cross_val_score, RepeatedStratifiedKFold
from sklearn.svm import SVC
from imblearn.over_sampling import RandomOverSampler, SMOTE
import xgboost

best_features = SelectKBest(chi2, k=10)
features_ranking = best_features.fit(data.drop(['DEATH_EVENT'],
axis=1), data['DEATH_EVENT'])
ranking_dictionary = {}
for i in range(len(features_ranking.scores_)):
    ranking_dictionary[data.columns[i]] =
round(features_ranking.scores_[i], 3)

asc_sort = sorted(ranking_dictionary.items(), key = lambda kv:(kv[1],
kv[0]))

for i, j in asc_sort:
    print(i, ':', j)
```

```
diabetes : 0.001
sex : 0.002
smoking : 0.032
anaemia : 0.747
high_blood_pressure : 1.222
serum_sodium : 1.618
serum_creatinine : 19.814
age : 44.619
ejection_fraction : 79.073
creatinine_phosphokinase : 1897.315
time : 3826.893
platelets : 26135.772
```

```
feature_model = SelectFromModel(Lasso(alpha=0.05, random_state=0))
feature_model.fit(data.drop(['DEATH_EVENT'], axis=1),
data['DEATH_EVENT'])
```

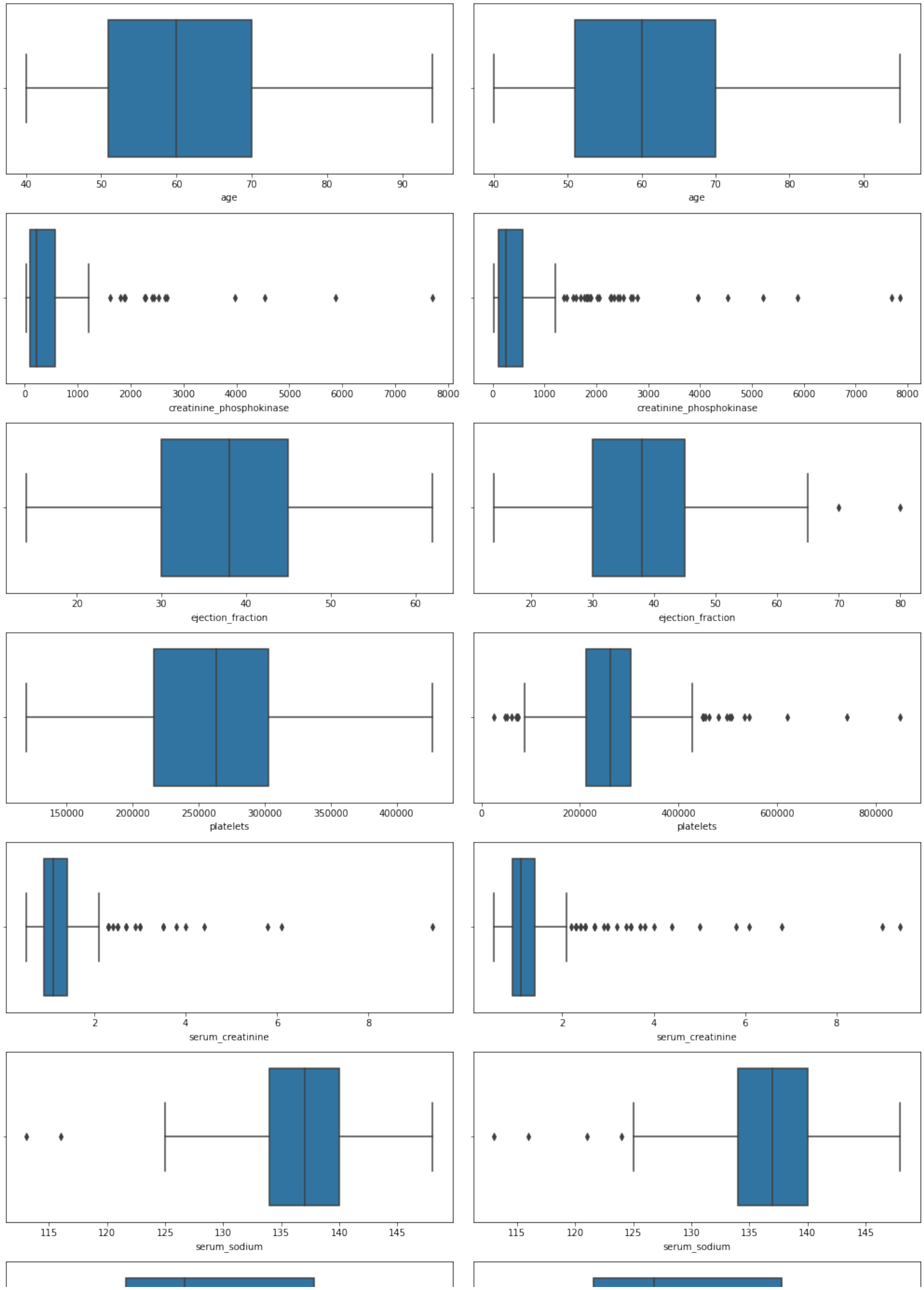
```
SelectFromModel(estimator=Lasso(alpha=0.05, random_state=0))

mask = feature_model.get_support()
for i in range(len(mask)):
    if not mask[i]:
        print(data.drop(['DEATH_EVENT'], axis=1).columns[i])

anaemia
diabetes
high_blood_pressure
platelets
sex
smoking
```

Observations

- Based on EDA and Feature Selection, features such as **anaemia, diabetes, age, sex, smoking** are less contributing.
- Features to be considered are, **platelets, time, creatinine_phosphokinase, ejection_fraction.**

Romove Outliers

```
X = data.drop(['DEATH_EVENT'], axis=1)
y = data['DEATH_EVENT']

X_train, X_test, y_train, y_test = train_test_split(X, y,
test_size=0.2, random_state=0)
print(X_train.shape, X_test.shape)

(239, 12) (60, 12)

features_with_outliers = ['creatinine_phosphokinase', 'platelets',
'serum_creatinine', 'serum_sodium']

lof = LocalOutlierFactor()
outlier_rows = lof.fit_predict(X_train)

mask = outlier_rows != -1
X_train, y_train = X_train[mask], y_train[mask]

fig, ax = plt.subplots(len(continuous_features), 2, figsize=(14,22))

for i in range(len(continuous_features)):
    sns.boxplot(ax=ax[i, 0], x=continuous_features[i], data=X_train)
    sns.boxplot(ax=ax[i, 1], x=continuous_features[i], data=data)
fig.tight_layout(pad=1)
plt.show()
```

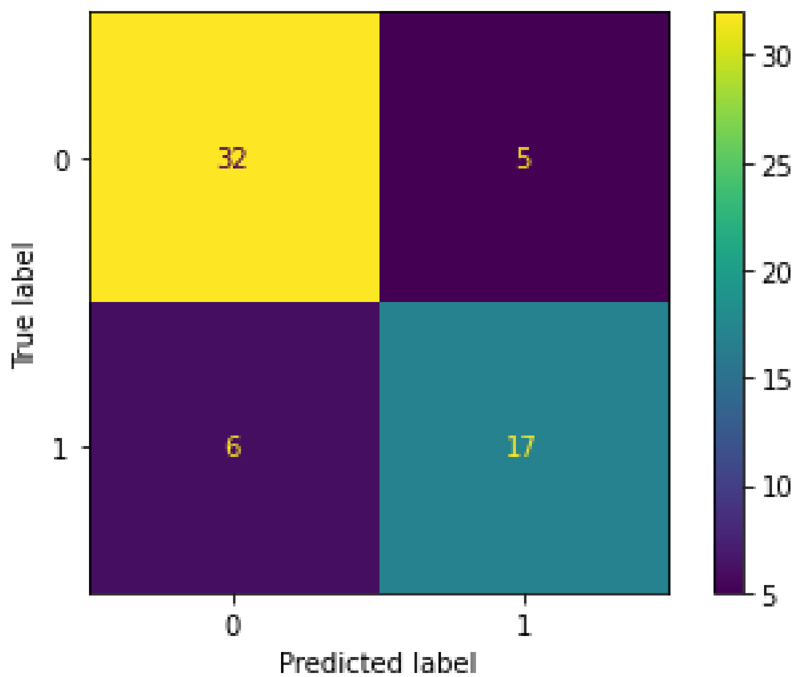


40 50 60 70 80 90
age
40 50 60 70 80 90
age
0 1000 2000 3000 4000 5000 6000 7000 8000
creatinine_phosphokinase
0 1000 2000 3000 4000 5000 6000 7000 8000
creatinine_phosphokinase
20 30 40 50 60
ejection_fraction
20 30 40 50 60 70 80
ejection_fraction
150000 200000 250000 300000 350000 400000
platelets
0 200000 400000 600000 800000
platelets
2 4 6 8
serum_creatinine
2 4 6 8
serum_creatinine
115 120 125 130 135 140 145
serum_sodium
115 120 125 130 135 140 145
serum_sodium

Model Building with SMOTE

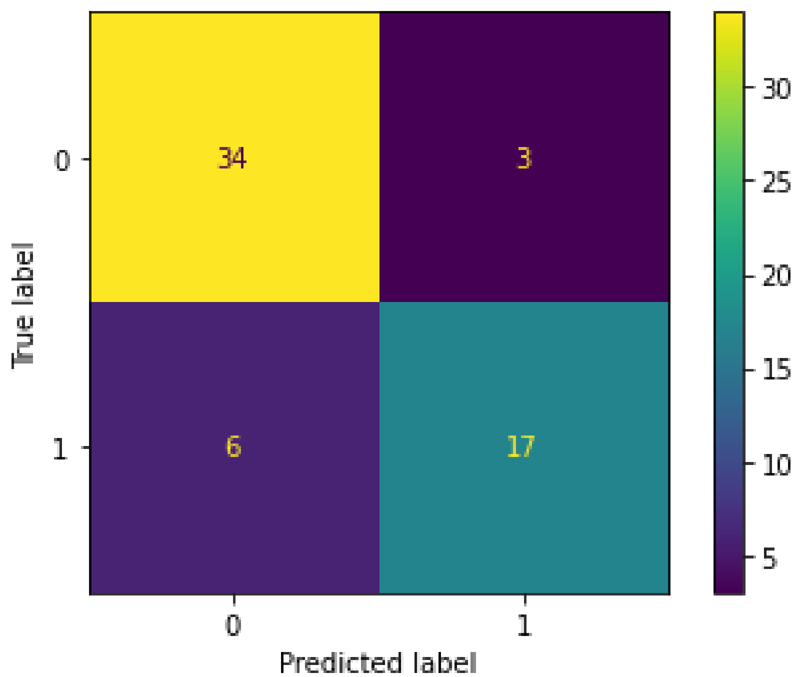
```
X = data[['ejection_fraction', 'serum_creatinine', 'time']]
y = data['DEATH_EVENT']

X_train, X_test, y_train, y_test = train_test_split(X, y,
test_size=0.2, random_state=0)

lof = LocalOutlierFactor()
outlier_rows = lof.fit_predict(X_train)

mask = outlier_rows != -1
X_train, y_train = X_train[mask], y_train[mask]

oversample = SMOTE(sampling_strategy='minority')
X_train, y_train = oversample.fit_resample(X_train, y_train)

scaler = StandardScaler()
X_train = scaler.fit_transform(X_train)
X_test = scaler.transform(X_test)

model = LogisticRegression()
model.fit(X_train, y_train)
y_pred = model.predict(X_test)
conf = plot_confusion_matrix(model, X_test, y_test)
print ("The accuracy of Logistic Regression is : ",
accuracy_score(y_test, y_pred)*100, "%")
print(classification_report(y_test, y_pred))
```

```
The accuracy of Logistic Regression is :  81.66666666666667 %
              precision    recall  f1-score   support

           0       0.84      0.86      0.85        37
           1       0.77      0.74      0.76        23

    accuracy                           0.82        60
   macro avg       0.81      0.80      0.80        60
weighted avg       0.82      0.82      0.82        60
```

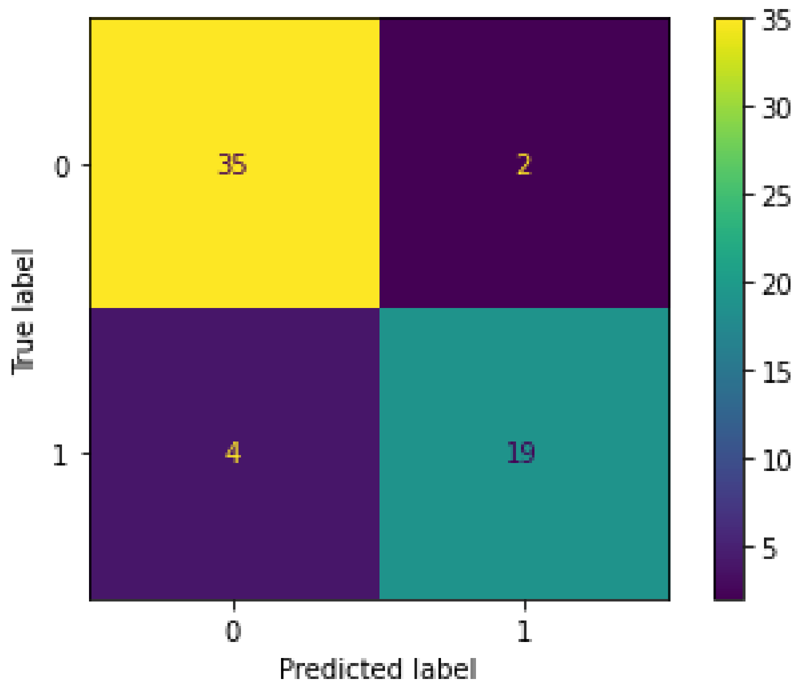



```
model = RandomForestClassifier()
model.fit(X_train, y_train)
y_pred = model.predict(X_test)
conf = plot_confusion_matrix(model, X_test, y_test)
print ("The accuracy of Random Forest is : ", accuracy_score(y_test,
y_pred)*100, "%")
print(classification_report(y_test, y_pred))
```

```
The accuracy of Random Forest is :  85.0 %
              precision    recall  f1-score   support

           0       0.85      0.92      0.88        37
           1       0.85      0.74      0.79        23

    accuracy                           0.85        60
   macro avg       0.85      0.83      0.84        60
weighted avg       0.85      0.85      0.85        60
```




```
model = GradientBoostingClassifier()
model.fit(X_train, y_train)
y_pred = model.predict(X_test)
conf = plot_confusion_matrix(model, X_test, y_test)
print ("The accuracy of Gradient Boost is : ", accuracy_score(y_test,
y_pred)*100, "%")
print(classification_report(y_test, y_pred))

The accuracy of Gradient Boost is :  90.0 %
              precision    recall  f1-score   support

           0       0.90      0.95      0.92        37
           1       0.90      0.83      0.86        23

    accuracy                           0.90        60
   macro avg       0.90      0.89      0.89        60
weighted avg       0.90      0.90      0.90        60
```



Best Model to Choose

Models	Accuracy	Recall
Logistic Regression	82%	81%
Random Forest	85%	83%
Gradient Boosting	90%	89%

Based on both accuracy and recall score, **Gradient Boosting** outperformed other algorithms. The reason for considering recall score here is, the data and prediction to be made about heart failure and in such case less False Negatives is to be predicted and to calculate it with proportion I have used **Recall Score**.

Future Scope

- Ahead while revisiting the model again, I have plans to do more in-depth analysis of the data.
- To add additional derived features to the data based on analysis.
- Can try different classifiers to train the model and also few ensemble methods as well to see any improvement.