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1 Intro to AI and Machine Learning M505 Group (C)

1.1 Predicting Heart Failure Using Machine Learning

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2 Business Problem Understanding

2.1 Introduction

In a healthy heart, oxygen-rich blood is pumped from the left ventricle through the body into the organs, supplying oxygen and nutrients to the organs.After feeding the organs, the oxygen-poor blood returns from the body to the right side of the heart, where it is carried to the lungs. In the lungs, the blood is so rich in oxygen that it can be pumped back into the body through the left ventricle.

Heart failure is the weakening of the pumping function of the heart. Usually, either the right side of the heart (right heart failure) or the left side of the heart (left heart failure) is affected. As heart failure progresses, both halves of the heart can be affected (global heart failure). Heart failure can also be chronic or acute in nature. Chronic heart failure is more common than sudden and unexpected acute heart failure. Acute heart failure can occur suddenly in the context of acute cardiovascular catastrophe and / or decompensation of heart failure.

Cardiovascular disease is the world's leading cause of death, killing an estimated 17.9 million people each year and accounting for 31% of all deaths worldwide.

2.1.1 What is the aim of this notebook?

I was hired by a company that performs Stent placement and Angioplasty. In this notebook I will build a ML pipeline model that predicts ”Heart Failure” according to the dataset that we have.

3 Data Collection

[1]:
```python
from google.colab import drive
drive.mount('/content/drive')
```

```
Drive already mounted at /content/drive; to attempt to forcibly remount, call
drive.mount("/content/drive", force_remount=True).
```

[2]:
```
!pip install catboost
```

```
Requirement already satisfied: catboost in /usr/local/lib/python3.7/dist-
packages (1.0.4)
Requirement already satisfied: matplotlib in /usr/local/lib/python3.7/dist-
packages (from catboost) (3.2.2)
Requirement already satisfied: scipy in /usr/local/lib/python3.7/dist-packages
(from catboost) (1.4.1)
Requirement already satisfied: plotly in /usr/local/lib/python3.7/dist-packages
(from catboost) (5.5.0)
Requirement already satisfied: numpy>=1.16.0 in /usr/local/lib/python3.7/dist-
packages (from catboost) (1.21.5)
Requirement already satisfied: six in /usr/local/lib/python3.7/dist-packages
(from catboost) (1.15.0)
Requirement already satisfied: pandas>=0.24.0 in /usr/local/lib/python3.7/dist-
packages (from catboost) (1.3.5)
Requirement already satisfied: graphviz in /usr/local/lib/python3.7/dist-
packages (from catboost) (0.10.1)
Requirement already satisfied: pytz>=2017.3 in /usr/local/lib/python3.7/dist-
packages (from pandas>=0.24.0->catboost) (2018.9)
Requirement already satisfied: python-dateutil>=2.7.3 in
/usr/local/lib/python3.7/dist-packages (from pandas>=0.24.0->catboost) (2.8.2)
Requirement already satisfied: cycler>=0.10 in /usr/local/lib/python3.7/dist-
packages (from matplotlib->catboost) (0.11.0)
Requirement already satisfied: kiwisolver>=1.0.1 in
/usr/local/lib/python3.7/dist-packages (from matplotlib->catboost) (1.4.0)
Requirement already satisfied: pyparsing!=2.0.4,!=2.1.2,!=2.1.6,>=2.0.1 in
/usr/local/lib/python3.7/dist-packages (from matplotlib->catboost) (3.0.7)
Requirement already satisfied: typing-extensions in
/usr/local/lib/python3.7/dist-packages (from
kiwisolver>=1.0.1->matplotlib->catboost) (3.10.0.2)
Requirement already satisfied: tenacity>=6.2.0 in /usr/local/lib/python3.7/dist-
packages (from plotly->catboost) (8.0.1)
```

3.1 Importing Libraries

```
[18]: import warnings
      warnings.filterwarnings("ignore")                                    ␣
       ↪#Because we will use not Sckit Model

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

      from sklearn.neighbors import KNeighborsClassifier
      from sklearn.model_selection import train_test_split
      from sklearn import svm
      from sklearn.tree import DecisionTreeClassifier
      from sklearn import metrics
      from sklearn.preprocessing import StandardScaler
      from collections import Counter
      from imblearn.over_sampling import SMOTE
```

3.2 Loading the dataset

```
[6]: df = pd.read_csv ("heart_failure_clinical_records_dataset.csv")
     df = df.set_index("age")
     df
```

```
[6]:       anaemia  creatinine_phosphokinase  diabetes  ejection_fraction  \
     age
     75.0        0                       582         0                 20
     55.0        0                      7861         0                 38
     65.0        0                       146         0                 20
     50.0        1                       111         0                 20
     65.0        1                       160         1                 20
     …        …                       …         …                 …
     62.0        0                        61         1                 38
     55.0        0                      1820         0                 38
     45.0        0                      2060         1                 60
     45.0        0                      2413         0                 38
     50.0        0                       196         0                 45

           high_blood_pressure  platelets  serum_creatinine  serum_sodium  sex  \
     age
     75.0                    1  265000.00               1.9           130    1
     55.0                    0  263358.03               1.1           136    1
     65.0                    0  162000.00               1.3           129    1
```

```
50.0                        0  210000.00                 1.9           137    1
65.0                        0  327000.00                 2.7           116    0
…                        …         …                  …            …  …
62.0                        1  155000.00                 1.1           143    1
55.0                        0  270000.00                 1.2           139    0
45.0                        0  742000.00                 0.8           138    0
45.0                        0  140000.00                 1.4           140    1
50.0                        0  395000.00                 1.6           136    1

      smoking  time  DEATH_EVENT
age
75.0        0     4            1
55.0        0     6            1
65.0        1     7            1
50.0        0     7            1
65.0        0     8            1
…        …    …          …
62.0        1   270            0
55.0        0   271            0
45.0        0   278            0
45.0        1   280            0
50.0        1   285            0

[299 rows x 12 columns]
```

3.3 Data Overview

Age: Age of the patient in years

Anaemia: Desease that occurs because of low hemoglobin or lack of red cells (0:Reduced or 1:Normal)

creatinine_phosphokinase: It is a phosphocreatine kinase in our dataset it is level in blood measured in (mcg/L)

Diabetes: Desease that caused by high level of sugar in the blood. In our dataset if the patient has it (0:No or 1:Yes)

ejection_fraction: Percentage of blood leaving the heart at each contraction (percentage)

high_blood_pressure: It is a medical termin called hypertension. In our dataset if the patient has it (0:No or 1:Yes)

platelets: Platelets are very large cells in the bone of a human. In our dataset measured in (kiloplatelets/mL)

serum_creatinine: It is a diagnostic test to evaluate performance of kidneys. In our dataset measured in (mg/dL)

serum_sodium: An amount of sodium in patients blood. In our dataset measured in (mEq/L) sex: Biological sex of the patient (0:Female or 1:Male)

smoking: If the patient is a smoker (0:No or 1: Yes)

time: It is amount of visits that patient performed in months

death_event: If the patient with according results survived or not. (0:No or 1:Yes)

As we can understand from 'Data Overview' all columns that we have are the complex reasons according to which 'Death Event' has value '0' or '1'.

In this pipeline 'Death Event' is going to be my target label and I will analyze other columns to understand how they can affect my results. I will be checking null values, identifying data types and separating it to 'Train' and 'Test' sets

3.4 Checking Null Values

[5]:
```
print(df.isnull().sum())
```

```
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
```

The data that we are using has no null values.

3.5 Getting more detailed look

[6]:
```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Float64Index: 299 entries, 75.0 to 50.0
Data columns (total 12 columns):
 #   Column                    Non-Null Count  Dtype
---  ------                    --------------  -----
 0   anaemia                   299 non-null    int64
 1   creatinine_phosphokinase  299 non-null    int64
 2   diabetes                  299 non-null    int64
 3   ejection_fraction         299 non-null    int64
 4   high_blood_pressure       299 non-null    int64
 5   platelets                 299 non-null    float64
 6   serum_creatinine          299 non-null    float64
 7   serum_sodium              299 non-null    int64
 8   sex                       299 non-null    int64
 9   smoking                   299 non-null    int64
 10  time                      299 non-null    int64
 11  DEATH_EVENT               299 non-null    int64
dtypes: float64(2), int64(10)
memory usage: 30.4 KB
```

By running this code I took a detailed look on a count of null values and understood data types that we have : #dtypes: float64(2), int64(10)

In addition, the dataset that I am using has no categorical values.

3.6 Splitting data into 'Train' and 'Test' datasets

[11]:
```python
df_train, df_test = train_test_split(df, random_state=2)
print("df_train:", df_train.shape)
print("df_test:", df_test.shape)
print("Test and Train Datasets are ready")
```

```
df_train: (224, 12)
df_test: (75, 12)
Test and Train Datasets are ready
```

First of all, I decided to split 'Training' and 'Test' datasets in order to not touch 'Test' dataset consequently to not affect prediction results.

In some cases, it is necessary to work with 'Test' dataset as well like to clean null values or to drop some unnecessary columns, however in my case all columns are relevant and my dataset looks clean.

First, I divided my dataset to 'df_train' and 'df_test' to explain splitting process more precisely. I set a random state in order to reproduce my problem the same way every time it runs.

3.6.1 Dropping the Target Label

[12]:
```python
X_train = df_train.drop('DEATH_EVENT',axis=1)
Y_train = df_train['DEATH_EVENT']

X_Test = df_test.drop('DEATH_EVENT',axis=1)
Y_Test = df_test['DEATH_EVENT']

print(X_train)
print(Y_train)
```

```
      anaemia  creatinine_phosphokinase  diabetes  ejection_fraction  \
age
72.0        1                       943         0                 25
49.0        0                       972         1                 35
55.0        1                      2794         0                 35
75.0        0                       582         1                 30
50.0        1                      1051         1                 30
…         …                       …        …                 …
60.0        1                        47         0                 20
68.0        1                       220         0                 35
85.0        0                      5882         0                 35
82.0        1                       379         0                 50
65.0        0                       582         1                 40

      high_blood_pressure  platelets  serum_creatinine  serum_sodium  sex  \
age
72.0                    1  338000.00              1.70           139    1
49.0                    1  268000.00              0.80           130    0
55.0                    1  141000.00              1.00           140    1
75.0                    1  263358.03              1.83           134    0
50.0                    0  232000.00              0.70           136    0
…                     …        …                 …            …   …
60.0                    0  204000.00              0.70           139    1
68.0                    1  289000.00              0.90           140    1
85.0                    0  243000.00              1.00           132    1
82.0                    0   47000.00              1.30           136    1
65.0                    0  270000.00              1.00           138    0

      smoking  time
age
72.0        1   111
49.0        0   187
55.0        0   206
75.0        0    23
50.0        0   246
…         …   …
60.0        1    73
68.0        1    20
85.0        1    72
82.0        0    13
65.0        0   140

[224 rows x 11 columns]
age
72.0    1
49.0    0
55.0    0
75.0    1
```

```
50.0     0
        ..
60.0     1
68.0     1
85.0     1
82.0     1
65.0     0
Name: DEATH_EVENT, Length: 224, dtype: int64
```

In this section I divided 'df_train' and 'df_test' to 'x' and 'y' variables.

4 Data Exploration

4.1 Checking the correlation

[19]:
```
df.corr().style.background_gradient(cmap='coolwarm').set_precision(2)
```

[19]:
```
<pandas.io.formats.style.Styler at 0x7f1238a277f0>
```

I made a correlation between columns using a 'heatmap'. Heatmap is a tool used to visualize 2-dimensional format data using color variance. Color variations help to understand the magnitude better than visually analyzing each column and checking the relations by comparing them.

4.1.1 Checking correlation with Target

[10]:
```
corr = df.corr()
corr[abs(corr['DEATH_EVENT']) > 0.1]['DEATH_EVENT']
```

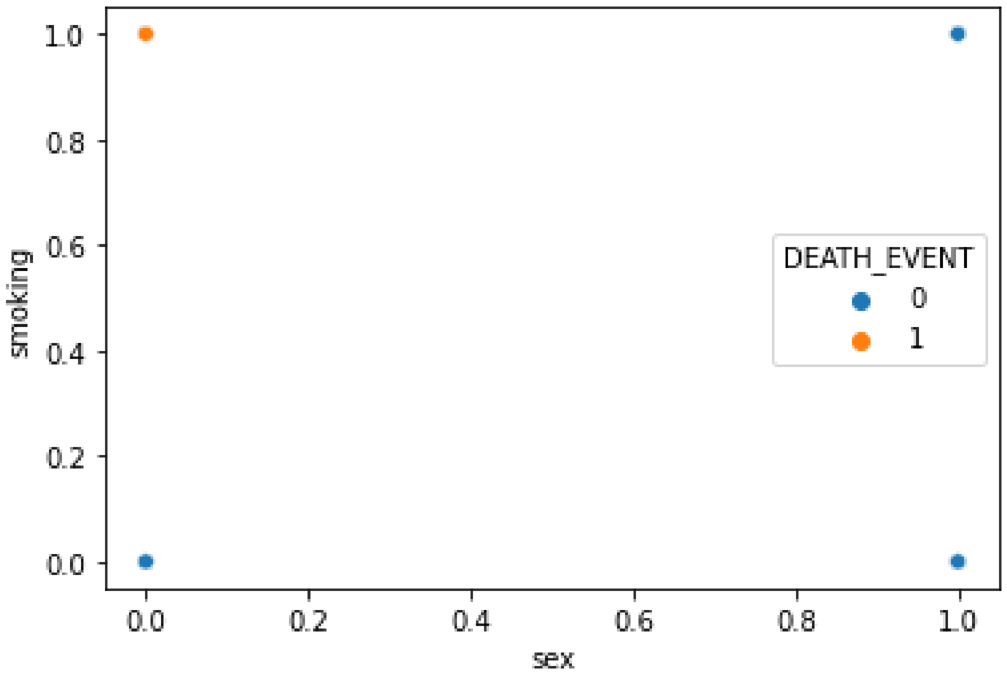
[10]:
```
ejection_fraction   -0.268603
serum_creatinine     0.294278
serum_sodium        -0.195204
time                -0.526964
DEATH_EVENT          1.000000
Name: DEATH_EVENT, dtype: float64
```

The main reason I used a heatmap is to understand correlation of other columns with my Target Label.

By running this code, we can see the columns that has more relations to the 'Death Event' column. They might interact with Target and lower the performance; thus, I will try results after dropping the most related ones.

4.1.2 Visualazing most correlated columns

```
[11]: sns.scatterplot(data=df, x='sex', y='smoking', hue='DEATH_EVENT')
      plt.show()
```

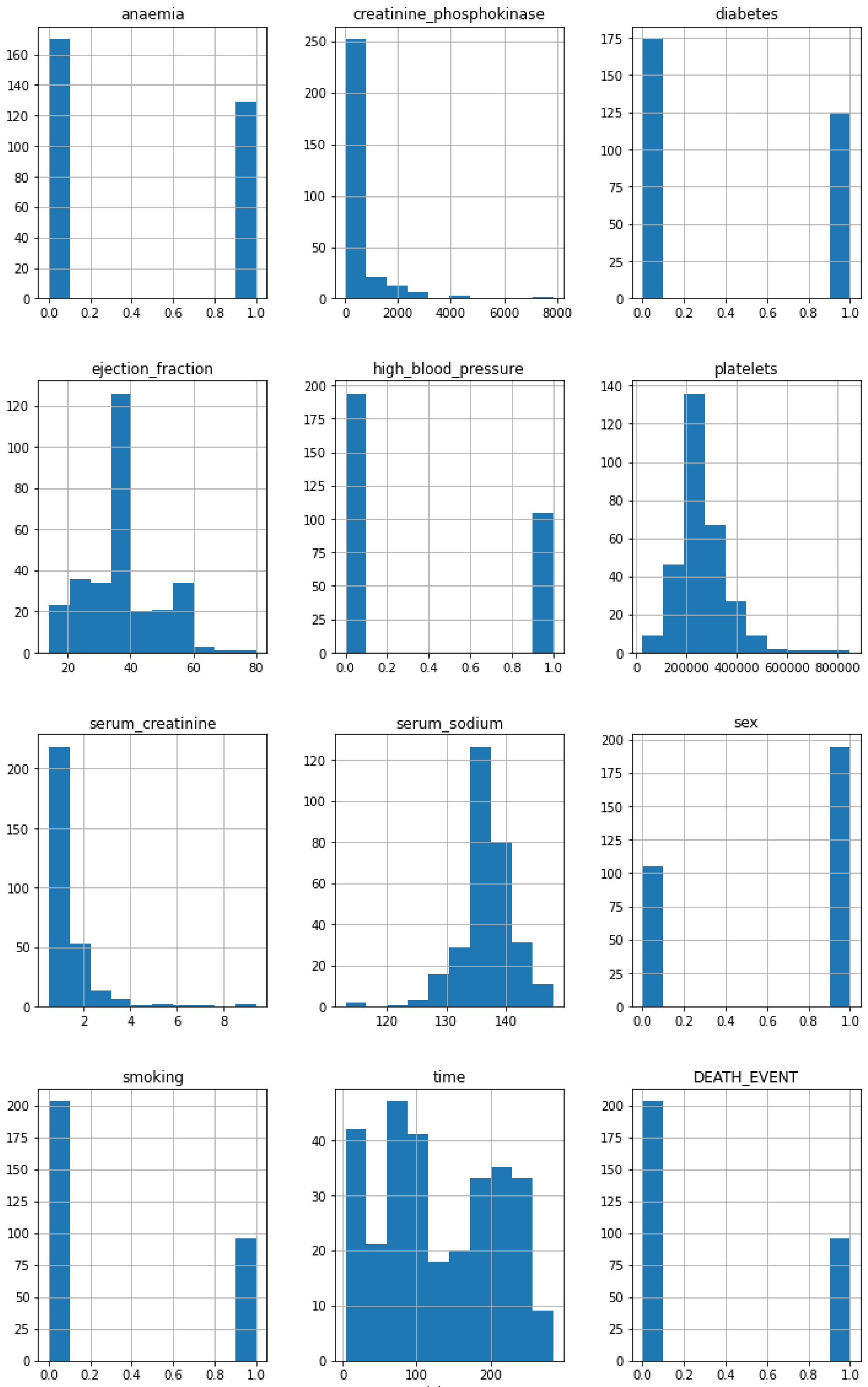


As I mentioned before other columns might have a stronger correlation as column 'sex' and 'smoking' for example, however we do not need to do anything about it because they are not correlated with Target.

4.2 Plot histogram to represent the distribution of data

```
[12]: fig = plt.figure(figsize = (12,20))
      ax = fig.gca()
      df.hist(ax = ax)
```

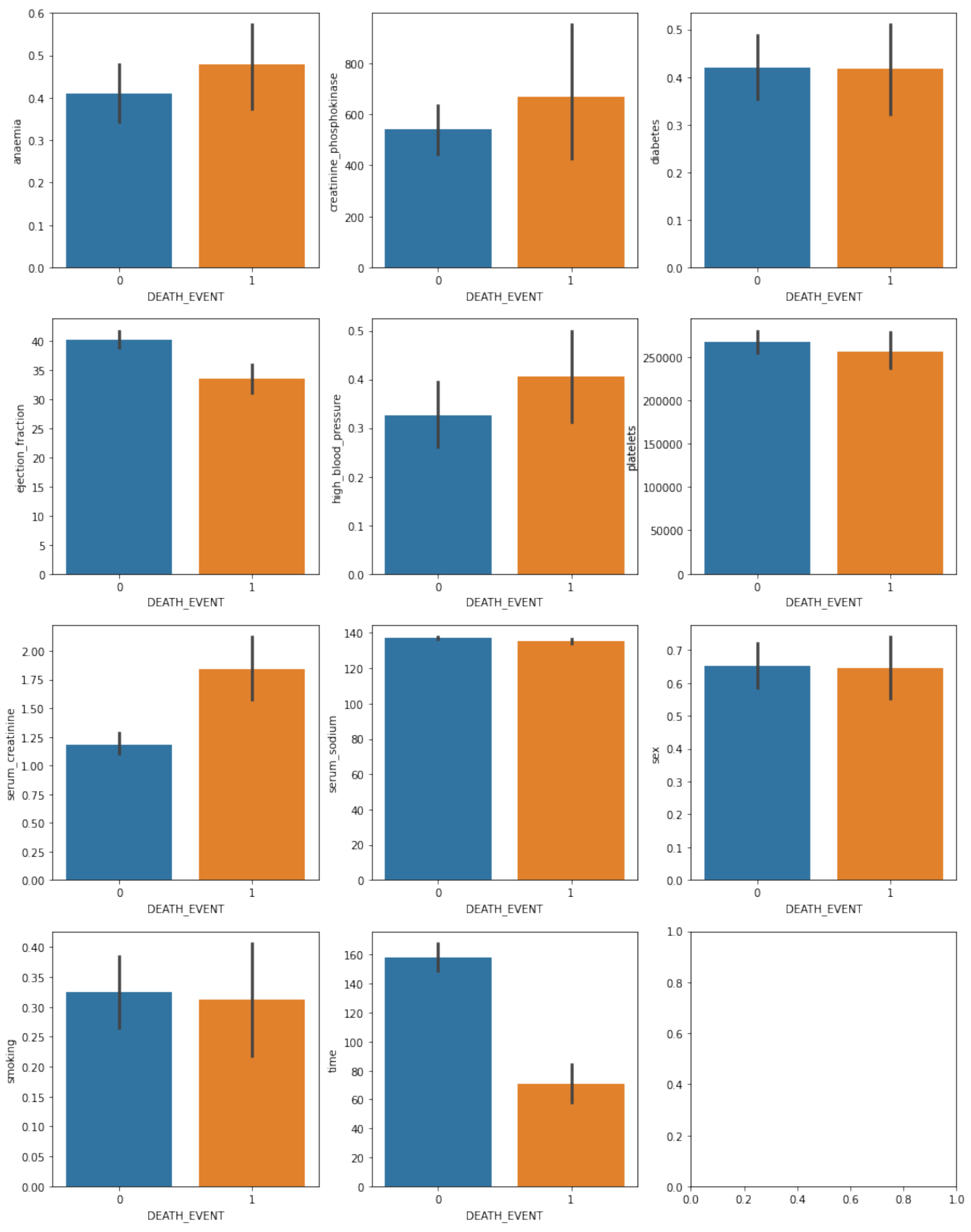
```
[12]: array([[<matplotlib.axes._subplots.AxesSubplot object at 0x7f933dc061d0>,
              <matplotlib.axes._subplots.AxesSubplot object at 0x7f933db48a50>,
              <matplotlib.axes._subplots.AxesSubplot object at 0x7f933db11190>],
             [<matplotlib.axes._subplots.AxesSubplot object at 0x7f933dc16e50>,
              <matplotlib.axes._subplots.AxesSubplot object at 0x7f933da83050>,
              <matplotlib.axes._subplots.AxesSubplot object at 0x7f933da38610>],
             [<matplotlib.axes._subplots.AxesSubplot object at 0x7f933da6fc10>,
              <matplotlib.axes._subplots.AxesSubplot object at 0x7f933d9b3250>,
              <matplotlib.axes._subplots.AxesSubplot object at 0x7f933d9bd750>],
             [<matplotlib.axes._subplots.AxesSubplot object at 0x7f933d974dd0>,
              <matplotlib.axes._subplots.AxesSubplot object at 0x7f933d965490>,
              <matplotlib.axes._subplots.AxesSubplot object at 0x7f933d91da90>]],
            dtype=object)
```


anaemia
creatinine_phosphokinase
diabetes
ejection_fraction
high_blood_pressure
platelets
serum_creatinine
serum_sodium
sex
smoking
time
DEATH_EVENT

4.2.1 Plot graph count values of each classes on target colunms

[13]:
```
fig, ax = plt.subplots(4,3, figsize = (15,20))
sns.barplot(data = df, y ="anaemia", x="DEATH_EVENT", ax=ax[0,0])
sns.barplot(data = df, y ="creatinine_phosphokinase", x="DEATH_EVENT",␣
↪ax=ax[0,1])
sns.barplot(data = df, y ="diabetes", x="DEATH_EVENT", ax=ax[0,2])
sns.barplot(data = df, y ="ejection_fraction", x="DEATH_EVENT", ax=ax[1,0])
sns.barplot(data = df, y ="high_blood_pressure", x="DEATH_EVENT", ax=ax[1,1])
sns.barplot(data = df, y ="platelets", x="DEATH_EVENT", ax=ax[1,2])
sns.barplot(data = df, y ="serum_creatinine", x="DEATH_EVENT", ax=ax[2,0])
sns.barplot(data = df, y ="serum_sodium", x="DEATH_EVENT", ax=ax[2,1])
sns.barplot(data = df, y ="sex", x="DEATH_EVENT", ax=ax[2,2])
sns.barplot(data = df, y ="smoking", x="DEATH_EVENT", ax=ax[3,0])
sns.barplot(data = df, y ="time", x="DEATH_EVENT", ax=ax[3,1])
```

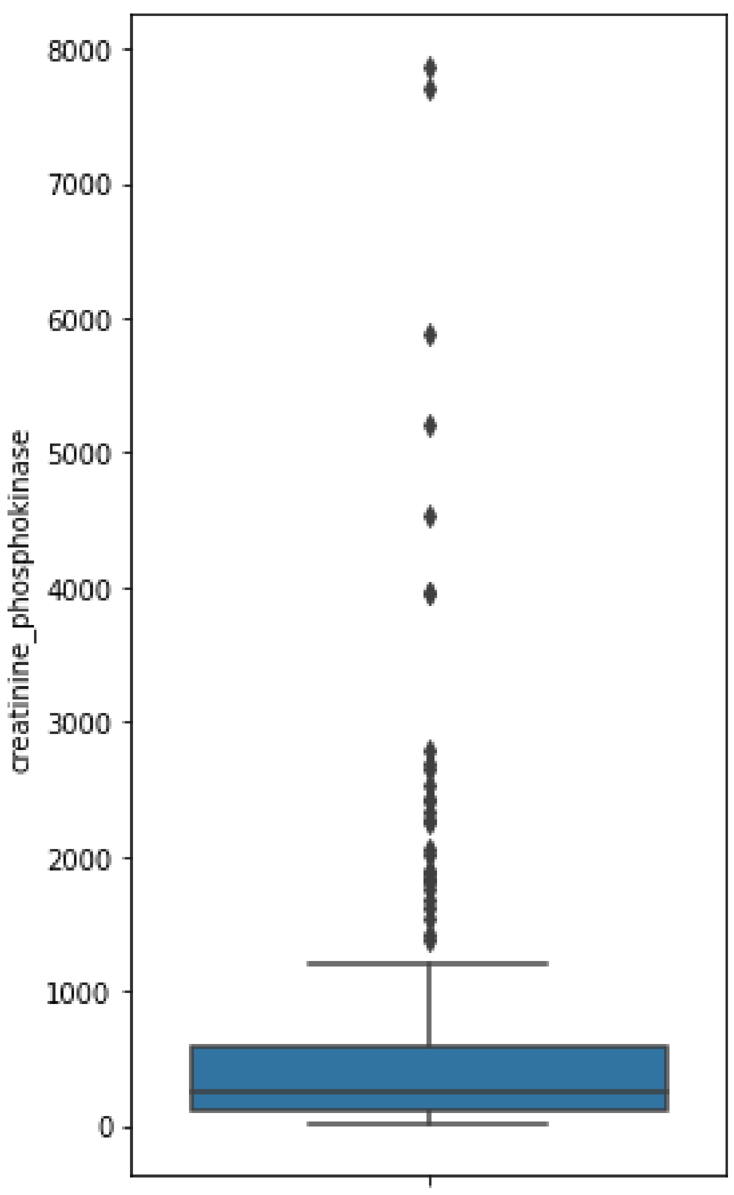
[13]:
```
<matplotlib.axes._subplots.AxesSubplot at 0x7f933d36b250>
```


anaemia
creatinine_phosphokinase
diabetes
ejection_fraction
high_blood_pressure
platelets
serum_creatinine
serum_sodium
sex
smoking
time
DEATH_EVENT
0
1

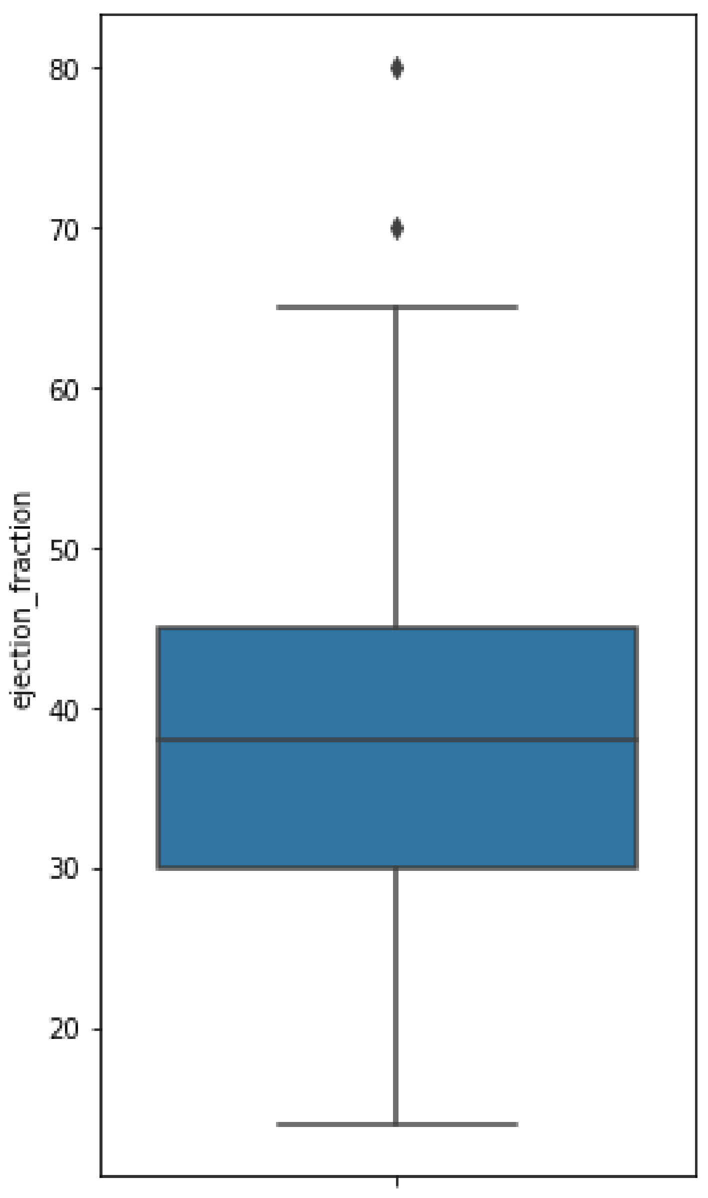
4.3 Outliers Detection

[14]:
```
plt.figure(figsize = (4,8))
sns.boxplot(y = df.creatinine_phosphokinase)

plt.figure(figsize = (4,8))
sns.boxplot(y = df.ejection_fraction)

plt.figure(figsize = (4,8))
sns.boxplot(y = df.platelets)

plt.figure(figsize = (4,8))
sns.boxplot(y = df.serum_creatinine)

plt.figure(figsize = (4,8))
sns.boxplot(y = df.serum_sodium)
```

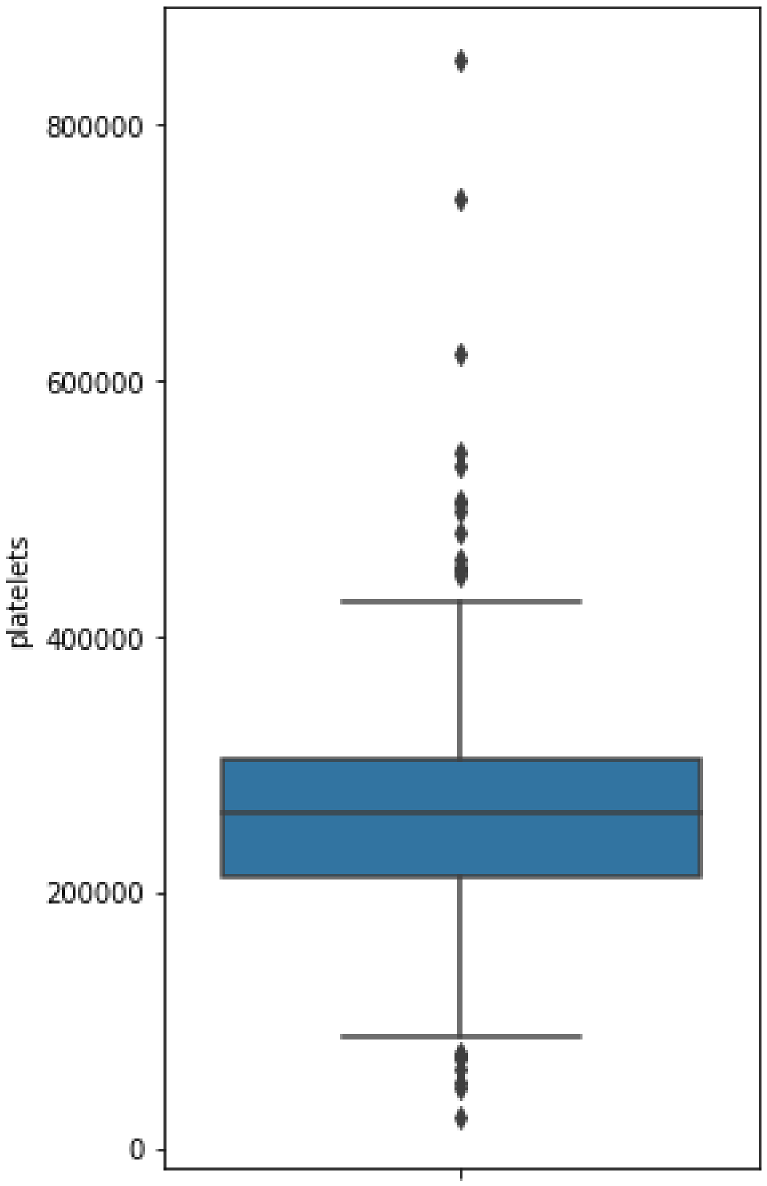
[14]:
```
<matplotlib.axes._subplots.AxesSubplot at 0x7f933cfd2dd0>
```



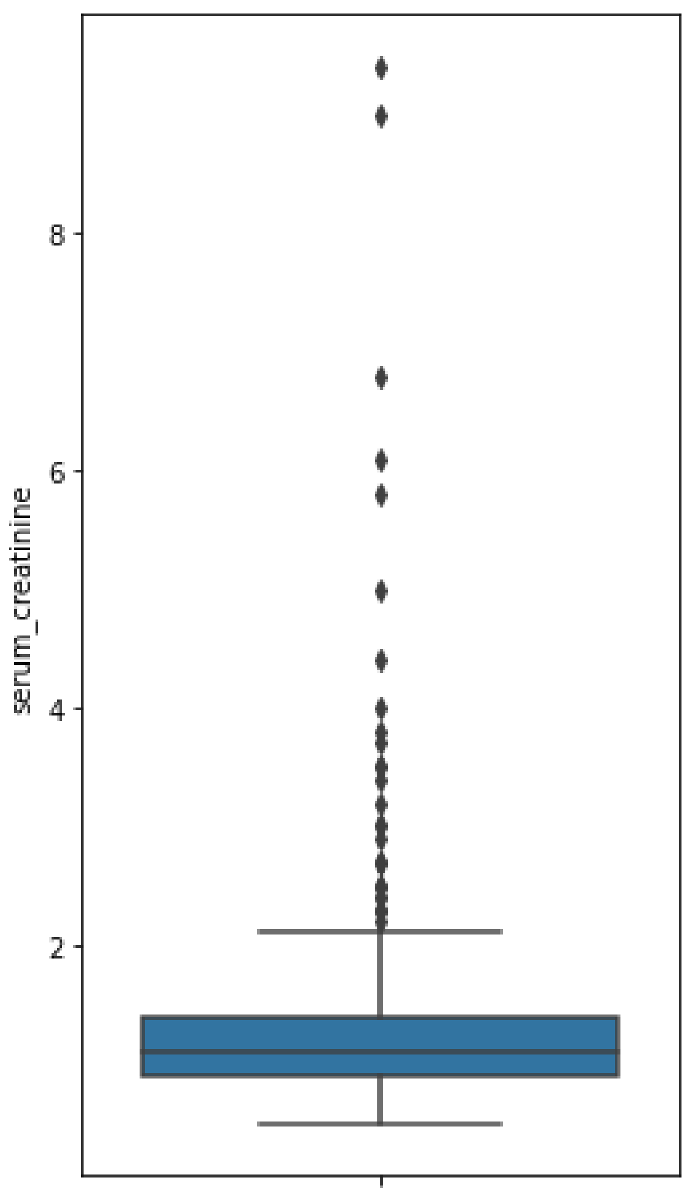
creatinine_phosphokinase
8000
7000
6000
5000
4000
3000
2000
1000
0

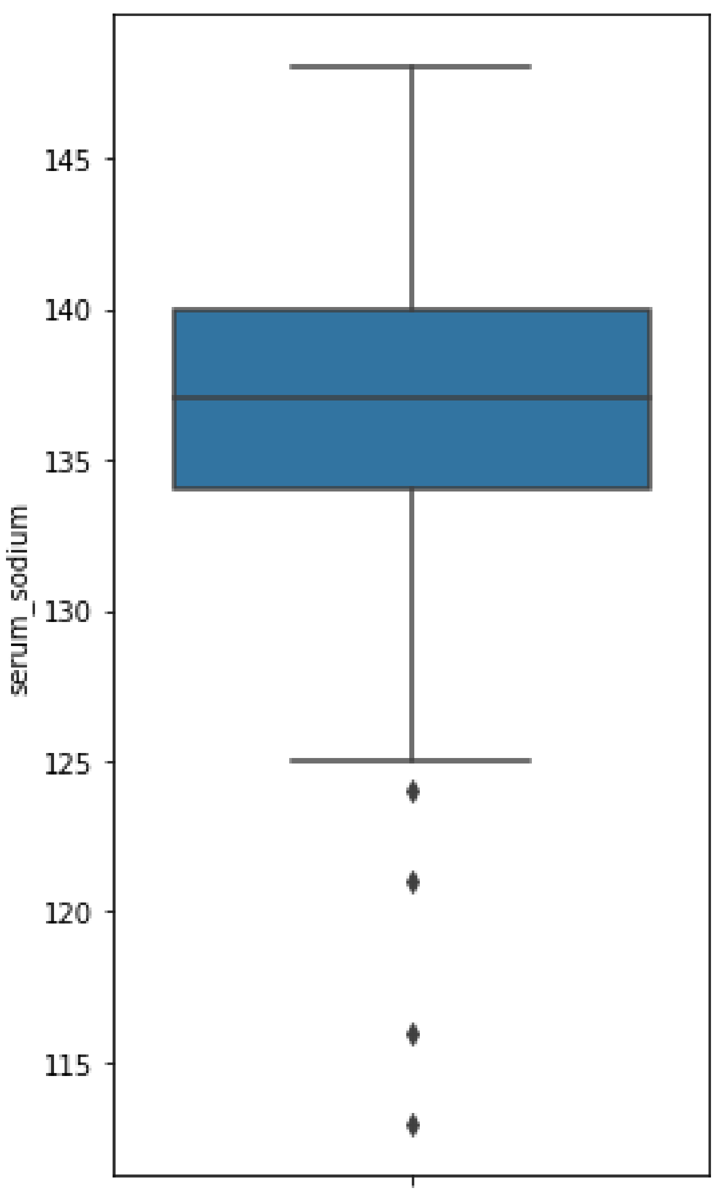


80
70
60
50
40
30
20
ejection_fraction



800000
600000
400000
200000
0
platelets


serum_creatinine
2
4
6
8



I plot 4 columns to visualize outliers. Lower and Upper skirts that we see in our graph shows us minimum and maximum mean values range.

Data points that we see below and above those skirts are outliers.

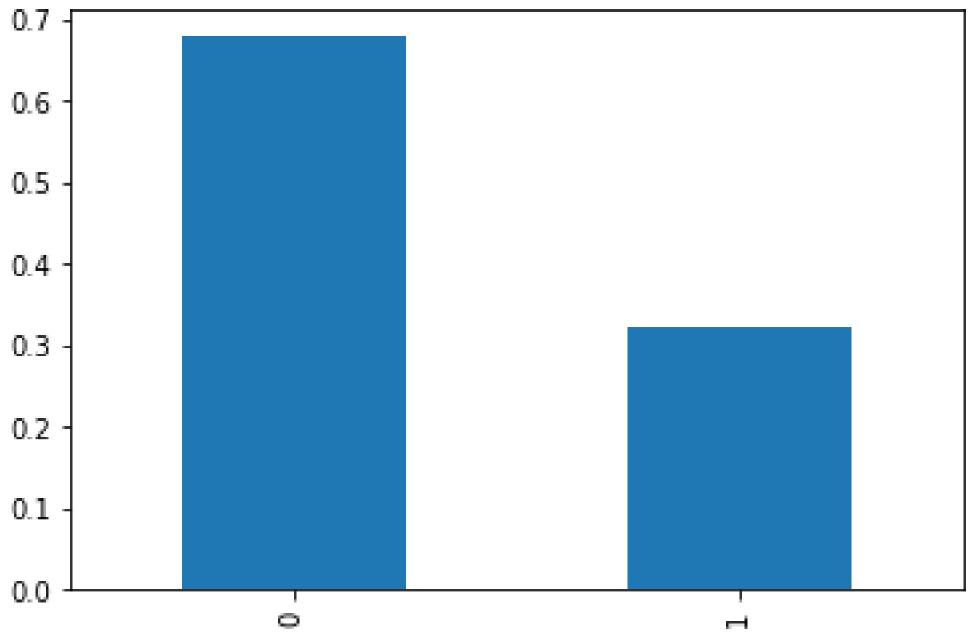
However not everything that falls within a range is an outlier. All the values that we have in those columns are real life data points which were recorded from patients. They help us to predict our 'Target Label'. Let's take a look at the most obvious outlier in 'Platelets' column that looks completely unnecessary, however patients with kidney disfunction may have this result. For this reason, I decided to keep all outliers.

5 4. Feature Engineering

5.1 Checking Imbalanced Data

[8]:
```
df["DEATH_EVENT"].value_counts(normalize=True).plot(kind='bar')
```

[8]:
```
<AxesSubplot:>
```



As we can see classes in our target label are imbalanced. I decided not to plot all the columns with imbalanced classes that have '0' and '1' values such as 'smoking', 'sex', 'diabetes', however I will print the shape of resampled 'x' and 'y' to show the difference. The main question is why Oversampling?

The answer is because there are 2 techniques to deal with imbalanced classes : 'Oversampling' and 'Undersampling'.

In my case my dataset consists of 12 columns and 299 rows and decreasing number of samples may lead to low performance, thus I decided to oversample the classes.

5.1.1 Value Count Before Oversampling

[16]:
```
unique,count = np.unique(Y_train,return_counts=True)
Y_train_count = (unique,count)
Y_train_count
```

```
[16]: (array([0, 1]), array([149,  75]))
```

To explain imbalance between '0' and '1' classes in our Target Label I decided to apply 'count' function to see the count of variables in each class. I will use 'count' function after Oversampling as well to show the difference.

5.1.2 Oversampling Using SMOTE

```
[14]: sm = SMOTE()
      X_train_resampled,Y_train_resampled = sm.fit_resample(X_train, Y_train)
      print("Smote Oversampled")
```

```
Smote Oversampled
```

First of all, we have to understand how Smote works. By using 'Smote' method we simply add artificial rows to our dataset to deal with class imbalances. It might not be useful in our case because we might have inconsistence between actual 'Y' and 'Y' predicted. I will check it in further steps.

5.1.3 Value Count After Oversampling

```
[18]: unique,count=np.unique(Y_train_resampled,return_counts=True)
      Y_train_resampled_smote_value_count = (unique,count)
      Y_train_resampled_smote_value_count
```

```
[18]: (array([0, 1]), array([149, 149]))
```

After using the count I can see that classes in my target label are balanced.

5.1.4 Printing Shape

```
[19]: print(X_train_resampled)
```

```
     anaemia  creatinine_phosphokinase  diabetes  ejection_fraction  \
0          1                       943         0                 25
1          0                       972         1                 35
2          1                      2794         0                 35
3          0                       582         1                 30
4          1                      1051         1                 30
..       …                        …       …                  …
293        0                        98         0                 47
294        1                       410         0                 17
295        0                       441         0                 28
296        1                       863         0                 27
297        1                       121         0                 30
```

```
     high_blood_pressure      platelets  serum_creatinine  serum_sodium  sex  \
0                      1  338000.000000          1.700000           139    1
1                      1  268000.000000          0.800000           130    0
2                      1  141000.000000          1.000000           140    1
3                      1  263358.030000          1.830000           134    0
4                      0  232000.000000          0.700000           136    0
..                   …             …               …            …   …
293                    1  189876.110438          1.000000           139    0
294                    0  133969.856758          2.915657           134    1
295                    0  264592.866289          1.356211           135    0
296                    0  134557.553425          1.116027           137    1
297                    0  393295.892109          1.142009           138    0

     smoking  time
0          1   111
1          0   187
2          0   206
3          0    23
4          0   246
..       …   …
293        0    27
294        0    26
295        0   139
296        0    10
297        0    78

[298 rows x 11 columns]
```

X_train_resampled has more rows of artificial data now. Before Smote I had 299 rows in my dataset.

6 Data Scaling

[15]:
```python
std = StandardScaler()
X_train_resampled = std.fit_transform(X_train_resampled)
X_Test = std.transform(X_Test)

print("Data has been scaled")
```

```
Data has been scaled
```

I scaled the data in order to put all the values within a range of '0' and '1'.Data needs to be scaled when using methods based on measures of how far apart data points, like support vector machines, or SVM or k-nearest neighbors, or KNN and etc.

7 Model Training

Before I start Model Training, I need to clarify that the dataset that I use requires Classification methods, because we need to classify the Target 'Death Event' into '0' and '1'.

I use precision as a scoring method because I need to understand how precise my model is predicting both classes. In addition, I will use a cross validation and 'cv' is a number of cross validation model has to try for each hyperparameters.

7.1 KNN

[21]:
```
parameters_grid = {
    "n_neighbors": [11, 33, 55, 77, 99, 111],
    "metric": ["minkowski","manhattan", "euclidean"]
}
model_1 = sklearn.model_selection.GridSearchCV(sklearn.neighbors.
 ↪KNeighborsClassifier(),
                                                parameters_grid,␣
 ↪scoring="precision", cv=5)
model_1.fit(X_train_resampled, Y_train_resampled)
print("Precision of best KNN classfier = {:.2f}".format(model_1.best_score_))
print("Best found hyperparameters of KNN classifier = {}".format(model_1.
 ↪best_params_))
```

```
Precision of best KNN classfier = 0.79
Best found hyperparameters of KNN classifier = {'metric': 'manhattan',
'n_neighbors': 11}
```

I decided to use grid parameters for KNN and to check the score with the hyperparameters that I set. For this reason I will use 'Grid Search' to get the best hyperparameters.More detailed about KNN: The nearest neighbor algorithm, often abbreviated as knn, is a data classification approach that estimates the probability that a data point will be a member of one or another group, depending on which group the data point is closest to.

The Nearest Neighbor Method is an example of the "lazy learner" algorithm. That is, do not build a model using the training set until the dataset is requested.

More about hyperparameters :
n_neighbors = Number of data points we want to take as a neighbouring ones. For example : If we set this parameter to '3', it means that the alghoritm will analyse 3 nearest neigbours and as we increase number of neighbouring points it checks more points.

metric = Metrics that we want to you use as our hyperparameter. In my case I used

"minkowski" - The default metric of KNN.

"manhattan" and

"euclidean"

7.2 SVM

[22]:
```
parameters_grid = {
    "kernel": ["linear", "poly"],
    "C": [0.01, 1, 10]
}
model_2 = sklearn.model_selection.GridSearchCV(sklearn.svm.SVC(),␣
 ↪parameters_grid, scoring = "precision", cv=4)
model_2.fit(X_train_resampled, Y_train_resampled)
print("Precision of best SVM classfier = {:.2f}".format(model_2.best_score_))
print("Best found hyperparameters of SVM classifier = {}".format(model_2.
 ↪best_params_))
```

```
Precision of best SVM classfier = 0.78
Best found hyperparameters of SVM classifier = {'C': 1, 'kernel': 'linear'}
```

More detailed about Support Vector Machine :

This is a set of similar ”supervised learning” type algorithms used for classification and regression analysis tasks. This method belongs to a family of linear classifiers. The main idea of the support vector method is to transform the original vector into a higher dimensional space and find the separated hyperplane with the largest gap in this space. Two parallel hyperplanes are constructed on either side of the hyperplane that separates the classes.

More about hyperparameters :
”kernel” = Kernel functions are a machine learning method that can transform an element into a new linear separable space when it is not linearly separable. Such a space is called a correction space. All consistent samples have a larger dimension of corresponding space, so the main problem is finding it. For this reason I chose ”linear” kernel and ”poly”

In order to find the best match between them. Another hyperparameter is :

”C” = The C parameter tells SVM optimization how much to avoid misclassification of each training sample. For large C values, the optimizer chooses a hyperplane with a small margin if the hyperplane is good at classifying all training points correctly. Conversely, if the value of C is very small, the optimizer will look for a larger margin to separate the hyperplane, even if the hyperplane misclassifies more points. If the value of C is very small, you need to get a misclassified example, even if the training data is linearly separable.

7.3 Decision Tree

[26]:
```
parameters_grid = {
    "criterion": ["gini", "entropy"],
    "max_depth": range(11, 55, 77),
    "min_samples_split": range(5, 10, 20)

}
model_3 = sklearn.model_selection.GridSearchCV(sklearn.tree.
 ↪DecisionTreeClassifier(),
                                                                  parameters_grid,␣
 ↪scoring="precision", cv=5)
model_3.fit(X_train_resampled, Y_train_resampled)
print("Precision of best decision tree classfier = {:.2f}".format(model_3.
 ↪best_score_))
print("Best found hyperparameters of decision tree classfier = {}".
 ↪format(model_3.best_params_))
```

```
Precision of best decision tree classfier = 0.76
Best found hyperparameters of decision tree classfier = {'criterion': 'entropy',
'max_depth': 11, 'min_samples_split': 5}
```

More detailed about Decision Tree Clasifier :
A decision tree is a classifier built on the basis of "if, then" decision rules arranged in a tree-like hierarchy. The decision tree is based on the process of recursively splitting an initial set of objects into a subset associated with a predefined class. Partitioning is done using decision rules that check attribute values according to specific criteria.They are built on supervised learning. A set of observations with predefined class labels is used as the training dataset.

More detailed about Hyperparameters :
"criterion" = Quality of split in Decision Tree Alghiritm is one of the most important factors. Criterion basically measures quality of a split in a Decision Tree Classifier. Default is 'giny'

"max_depth" = It is a maximum depth of the tree. If this isn't certain withinside the Decision Tree, the nodes can be improved till all leaf nodes are natural or till all leaf nodes include much less than min_samples_split.

"min_samples_split" = Is the minimum amount of samples that is required to split the node. If the sample size of an internal node is smaller than min_samples_split, then that node is a leaf node.

7.4 CatBoost

[31]:
```
parameters_grid = {
    "max_leaves": [16,32,64],
    "learning_rate": [0.01, 0.1]
}
model_4 = sklearn.model_selection.GridSearchCV(CatBoostClassifier(verbose=0),␣
 ↪parameters_grid, scoring="precision", cv=5)
model_4.fit(X_train_resampled, Y_train_resampled)
print("Precision of best decision tree classfier = {:.2f}".format(model_4.
 ↪best_score_))
print("Best found hyperparameters of decision tree classfier = {}".
 ↪format(model_4.best_params_))
```

```
Precision of best decision tree classfier = 0.86
Best found hyperparameters of decision tree classfier = {'learning_rate': 0.01,
'max_leaves': 64}
```

More detailed about Hyperparameters:
"Learning_Rate" = It affects the total training time.
The lower the value, the more iterations required for training. For this reason, we have to choose a value based on our performance expectations. I will provide more detailed explanation of CatBoost Model in Model Assessment part.

8 Model Assesment

Now lets print a confusion matrix of all models to understand the score for both of the classes

Now a little about Confusion Matrix :

The confusion matrix is a way of summarizing the work of a classification algorithm. If each class has an odd number of observations, or if the dataset contains more than one class, the accuracy of the classification alone can be misleading. Computing the confusion matrix gives you a better idea of what the classification model is doing correctly and what error it is causing.

8.1 Using KNN

[39]:
```
Y_predicted = model_1.predict(X_Test)
precision = sklearn.metrics.precision_score(Y_Test, Y_predicted)
cm = sklearn.metrics.confusion_matrix(Y_Test, Y_predicted)
precision, recall, f1, support = sklearn.metrics.
 ↪precision_recall_fscore_support(Y_Test, Y_predicted)
print("Accuracy =", accuracy)
print("Precision =", precision)
print("Recall =", recall)
print("F1-Score =", f1)
print("Confusion Matrix:\n", cm)
```

```
Precision = [0.83928571 0.63157895]
Recall = [0.87037037 0.57142857]
F1-Score = [0.85454545 0.6       ]
Confusion Matrix:
 [[47  7]
 [ 9 12]]
```

8.2 Using SVM

[40]:
```
Y_predicted = model_2.predict(X_Test)
precision = sklearn.metrics.precision_score(Y_Test, Y_predicted)
cm = sklearn.metrics.confusion_matrix(Y_Test, Y_predicted)
precision, recall, f1, support = sklearn.metrics.
 ↪precision_recall_fscore_support(Y_Test, Y_predicted)
print("Precision =", precision)
print("Recall =", recall)
print("F1-Score =", f1)
print("Confusion Matrix:\n", cm)
```

```
Precision = [0.8627451  0.58333333]
Recall = [0.81481481 0.66666667]
F1-Score = [0.83809524 0.62222222]
Confusion Matrix:
 [[44 10]
 [ 7 14]]
```

8.3 Using Decision Tree

[41]:
```
Y_predicted = model_3.predict(X_Test)
precision = sklearn.metrics.precision_score(Y_Test, Y_predicted)
cm = sklearn.metrics.confusion_matrix(Y_Test, Y_predicted)
precision, recall, f1, support = sklearn.metrics.
 ↪precision_recall_fscore_support(Y_Test, Y_predicted)
print("Precision =", precision)
print("Recall =", recall)
print("F1-Score =", f1)
print("Confusion Matrix:\n", cm)
```

```
Precision = [0.86792453 0.63636364]
Recall = [0.85185185 0.66666667]
F1-Score = [0.85981308 0.65116279]
Confusion Matrix:
 [[46  8]
 [ 7 14]]
```

8.4 Using CatBoost

[42]:
```
Y_predicted = model_4.predict(X_Test)
precision = sklearn.metrics.precision_score(Y_Test, Y_predicted)
cm = sklearn.metrics.confusion_matrix(Y_Test, Y_predicted)
precision, recall, f1, support = sklearn.metrics.
 ↪precision_recall_fscore_support(Y_Test, Y_predicted)
print("Precision =", precision)
print("Recall =", recall)
print("F1-Score =", f1)
print("Confusion Matrix:\n", cm)
```

```
Precision = [0.94545455 0.9       ]
Recall = [0.96296296 0.85714286]
F1-Score = [0.95412844 0.87804878]
```

```
Confusion Matrix:
 [[52  2]
 [ 3 18]]
```

Now we can see that model 4 'CatBoost Classifier' has the best score overall. Now what is CatBoost Classifier?

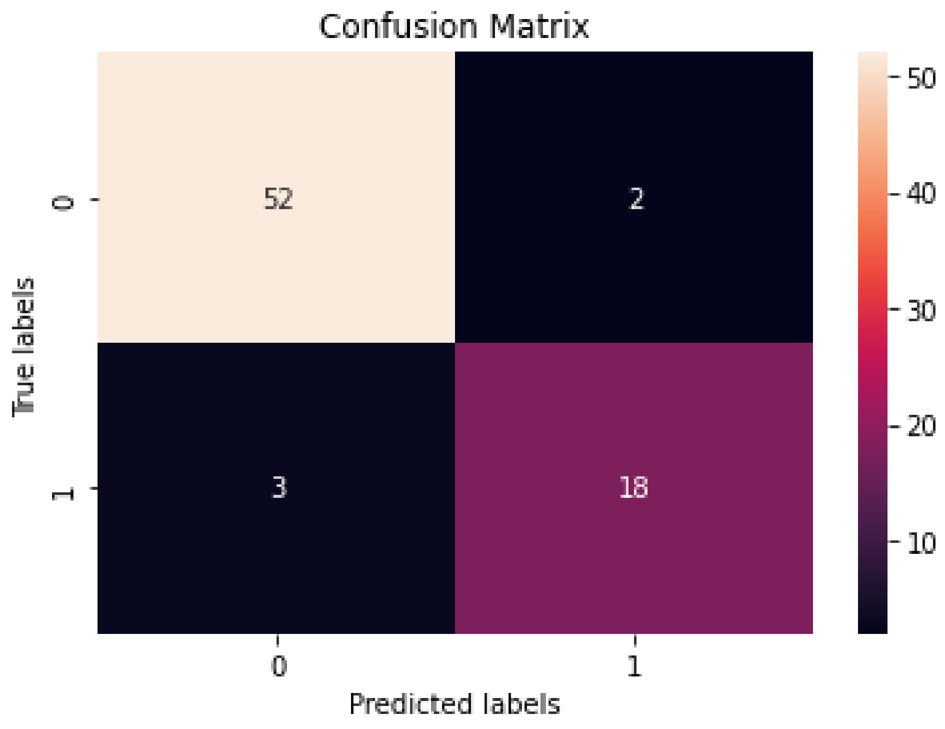
CatBoost is an open source machine learning library created by the Russian search giant Yandex in 2017, and is a variation of the Boosting algorithm family. CatBoost, Boost, and Light GBL are collectively known as the three main GBTD artifacts, which are improved implementations within the GBTD XGBoost algorithm widely used in the industry. LightGBM effectively increases the efficiency of GBDT calculations. Yandex CatBoost is known as a better algorithm than Boost and Light GBL in terms of algorithm accuracy.

Why Catboost?

After trying XGBoost I decided to try a Catboost and got better results. Catboost is a simply more developed version of XGBoost alghoritm which I tried before and had not bad scores.

8.5 Visualisation of Final Confusion Matrix

[37]:
```python
ax= plt.subplot()
sns.heatmap(cm, annot=True, fmt='g', ax=ax);

# labels, title and ticks
ax.set_xlabel('Predicted labels');ax.set_ylabel('True labels');
ax.set_title('Confusion Matrix');
ax.xaxis.set_ticklabels(['0','1']); ax.yaxis.set_ticklabels(['0','1']);
```



```
[38]: target_names = ['0','1']
      print("Report model\n")
      print(sklearn.metrics.classification_report(Y_Test, Y_predicted,␣
       ↪target_names=target_names))
```

```
Report model

              precision    recall  f1-score   support

           0       0.95      0.96      0.95        54
           1       0.90      0.86      0.88        21

    accuracy                           0.93        75
   macro avg       0.92      0.91      0.92        75
weighted avg       0.93      0.93      0.93        75
```

9 Conclusion

After trying four different models I can conclude that 'CatBoostClassifier' had the best performance overall. During the studies I tried other models that I did not include to this work such as: XGBoost Classifier and Naive Bayes, however after printing the confusion matrix results I noticed lack of precision in both classes. As we can see from confusion matrixes of other models that I used, imbalanced precision was the main problem that I had. XGBoost Classifier had really similar scores as well and as I mentioned before that was the main reason why I used CatBoost.

Morover studies showed that when not taking into account 'serum_creatinine' column overall performance of Model raise

- Without serum_creatinine column

  Precision 97 91

  Recall 96 89

  F-1 Score 96 93

```
[ ]:
```