Overview

- Intensive Care Units (ICUs) are continually faced with the difficulty of monitoring patients for the development of sepsis (an infection that can accrue while staying in ICU).
- While this challenge is not new and have been around for few years, the recent COVID-19 pandemic has significantly increase its prominence.

Therefore, for an ICU, the ability to predict whether a patient stay in ICU will develop a sepssis or not during their stay in the ICU, is extremely beneficial.

- This is the motivation for developing the machine learning model. There are two main purposes:
- 1. Reducing the risk of health complications.
- 2. Manage the ICU resources (such as bed availability, etc.).
- The training dataset provides list of essential attributes (features) related to: patient characteristics, diagnoses, treatments, services, hospital charges and patients socioeconomic background.

"The main goal is "Predict if a given in ICU would not develop a sepsis (Sepsis Negative / class 0) or will develop sepsis (Sepsis Positive / class 1) during their ICU stay".

Introduction

In this jupyter notebook, there are 3 algorithms including Decision Tree, Random Forest and Logistic Regression each with more than 1 model will be implemented. After each model runs, there is an analysis and justifications will be carefully discussed. This will based on pre-defined criteria and problem context to detect whether the model is efficient or not. Finally, based on the created criteria, context and machine learning performance, the best approach will be chosen to be modified and recommended to be used in practice.

Approach

Import statement

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

In []:
!pip3 install imblearn
```

```
Requirement already satisfied: imblearn in /Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages (0.0)
```

Requirement already satisfied: imbalanced-learn in /Library/Frameworks/Python. framework/Versions/3.9/lib/python3.9/site-packages (from imblearn) (0.9.0)

Requirement already satisfied: scikit-learn>=1.0.1 in /Library/Frameworks/Pyth on.framework/Versions/3.9/lib/python3.9/site-packages (from imbalanced-learn-> imblearn) (1.0.2)

Requirement already satisfied: joblib>=0.11 in /Library/Frameworks/Python.fram ework/Versions/3.9/lib/python3.9/site-packages (from imbalanced-learn->imblear n) (1.0.1)

Requirement already satisfied: scipy>=1.1.0 in /Library/Frameworks/Python.fram ework/Versions/3.9/lib/python3.9/site-packages (from imbalanced-learn->imblear n) (1.7.1)

Requirement already satisfied: numpy>=1.14.6 in /Library/Frameworks/Python.fra mework/Versions/3.9/lib/python3.9/site-packages (from imbalanced-learn->imblea rn) (1.21.1)

Requirement already satisfied: threadpoolctl>=2.0.0 in /Library/Frameworks/Pyt hon.framework/Versions/3.9/lib/python3.9/site-packages (from imbalanced-learn->imblearn) (2.2.0)

Read and convert csv file

```
In []:
    train_dt = pd.read_csv('Paitients_Files_Train.csv')
    test_dt = pd.read_csv('Paitients_Files_Test.csv')
    prediction_dt = pd.read_csv('S3751881_predictions.csv')
```

Exploratory Data Analysis

Training data initial analysis

```
In []:
        # print data frame shape
       print('Train dataset Frame shape: {}'.format(train_dt.shape))
       print('----')
        # save row count
        rowsdf = train dt.shape[0]
        # columns and their types
        print('Data Frame Dtypes')
        train dt.dtypes
       Train dataset Frame shape: (599, 11)
       _____
       Data Frame Dtypes
       TD
                   object
Out[]:
       PRG
                    int.64
       PL
                    int64
       PR
                    int64
       SK
                    int64
                    int64
       M11
                  float64
       BD2
                  float64
       Age
                    int.64
                    int.64
       Insurance
                   object
       Sepssis
       dtype: object
```

train dt.describe()

In []:

Out[]:

	PRG	PL	PR	SK	TS	M11	BD
count	599.000000	599.000000	599.000000	599.000000	599.000000	599.000000	599.00000
mean	3.824708	120.153589	68.732888	20.562604	79.460768	31.920033	0.48118
std	3.362839	32.682364	19.335675	16.017622	116.576176	8.008227	0.33755
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.07800
25%	1.000000	99.000000	64.000000	0.000000	0.000000	27.100000	0.24800
50%	3.000000	116.000000	70.000000	23.000000	36.000000	32.000000	0.38300
75%	6.000000	140.000000	80.000000	32.000000	123.500000	36.550000	0.64700
max	17.000000	198.000000	122.000000	99.000000	846.000000	67.100000	2.42000

- From the description of train data above, we can notice that the mean of PRG and BD2 are pretty far from the mean of other columns Also, SK 's mean is quite far compared to other columns's mean. These differences in the ranges of initial features may provide significant difficulties for many machine learning methods. For example, if one of the attributes has a wide range of values, the distance will be determined by this feature.
- From the min and max of colum Age we can see that the age that have on this medical dataset is from 21-year-old youth to 81-year-old elderly
- Blood Pressure PR and body mass index M11 have some suspicious values (equal 0).
 We need to carefully research about these data insights for applying appropriate preprocessing techniques

```
In []:
          train dt.head()
Out[]:
                       PRG
                             PL
                                  PR
                                      SK
                                           TS
                                               M11
                                                     BD2
                                                           Age
                                                                Insurance
                                                                           Sepssis
           ICU200010
                                               33.6
                                                    0.627
                                                                           Positive
         0
                          6
                            148
                                  72
                                      35
                                                            50
            ICU200011
                             85
                                  66
                                      29
                                               26.6
                                                    0.351
                                                            31
                                                                          Negative
            ICU200012
                             183
                                  64
                                               23.3
                                                    0.672
                                                            32
                                                                           Positive
           ICU200013
                          1
                             89
                                  66
                                      23
                                           94
                                               28.1
                                                     0.167
                                                            21
                                                                          Negative
           ICU200014
                                                                           Positive
                             137
                                  40
                                      35
                                          168
                                               43.1 2.288
                                                            33
In [ ]:
          train dt.info()
         <class 'pandas.core.frame.DataFrame'>
         RangeIndex: 599 entries, 0 to 598
         Data columns (total 11 columns):
                           Non-Null Count Dtype
          #
               Column
          0
               ID
                           599 non-null
                                             object
          1
               PRG
                           599 non-null
                                             int64
          2
               PL
                           599 non-null
                                             int64
          3
               PR
                           599 non-null
                                             int64
```

int64

599 non-null

SK

```
5
            TS
                      599 non-null
                                      int64
                      599 non-null
         6
                                     float64
            M11
        7
            BD2
                      599 non-null float64
        8
            Age
                     599 non-null int64
        9
            Insurance 599 non-null
                                    int64
         10 Sepssis 599 non-null
                                     object
       dtypes: float64(2), int64(7), object(2)
       memory usage: 51.6+ KB
In []:
        train dt.shape
Out[]: (599, 11)
```

 The data shape and all non-null count values from the dataset information can probably tell us that this dataset does not contain any null or nan values - which is pretty clean dataset. However, in order to carefully prepare for the model I will double check each column to make sure there is no null or nan data

Testing data initial analysis

```
In []:
       # print data frame shape
       print('Test dataset Frame shape: {}'.format(test dt.shape))
       print('----')
       # save row count
       rowsdf = test dt.shape[0]
       # columns and their types
       print('Data Frame Dtypes')
       test dt.dtypes
       Test dataset Frame shape: (169, 10)
       _____
       Data Frame Dtypes
       ID
                  object
Out[ ]:
       PRG
                   int64
       PL
                   int64
                    int64
       PR
       SK
                    int64
       TS
                    int64
       M11
                  float64
                  float64
       BD2
                    int64
       Age
                    int64
       Insurance
       dtype: object
In [ ]:
       test dt.describe()
Out[]:
```

	PRG	PL	PR	SK	TS	M11	BD2
count	169.000000	169.000000	169.000000	169.000000	169.000000	169.000000	169.000000
mean	3.917160	123.520710	70.426036	20.443787	81.000000	32.249704	0.438876
std	3.402415	29.259123	19.426805	15.764962	110.720852	7.444886	0.306935
min	0.000000	56.000000	0.000000	0.000000	0.000000	0.000000	0.100000
25%	1.000000	102.000000	62.000000	0.000000	0.000000	27.600000	0.223000
50%	3.000000	120.000000	74.000000	23.000000	0.000000	32.400000	0.343000
75%	6.000000	141.000000	80.000000	32.000000	135.000000	36.600000	0.587000

	PRG	PL	PR	SK	TS	M11	BD2
max	13.000000	199.000000	114.000000	49.000000	540.000000	57.300000	1.698000

- From the description of train data above, we can notice that the mean of PRG and BD2 are pretty far from the mean of other columns Also, SK 's mean is quite far compared to other columns's mean. These differences in the ranges of initial features may provide significant difficulties for many machine learning methods.
- From the min and max of colum Age we can see that the age that have on this medical dataset is from 21-year-old youth to 70-year-old elderly. In the training dataset the maximum age is 81 this would make the prediction of the model might face downgrade in accuracy in test dataset
- Blood Pressure PR and body mass index M11 have some suspicious values (equal 0).
 We need to carefully research about these data insights for applying appropriate preprocessing techniques

```
In [ ]: test_dt.head()
```

Out[]: ID **PRG** PL PR SK TS M11 BD2 Age Insurance **0** ICU200609 109 38 18 120 23.1 0.407 26 1 ICU200610 108 88 19 27.1 0.400 24 1 ICU200611 96 0 0 23.7 0.190 28 1 ICU200612 27.8 0.100 3 1 124 74 36 0 30 1 ICU200613 35.2 0.692 7 150 78 29 126 54 0

```
In [ ]: test_dt.info()
```

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 169 entries, 0 to 168
Data columns (total 10 columns):

#	Column	Non-	-Null Count	Dtype
0	ID	169	non-null	object
1	PRG	169	non-null	int64
2	PL	169	non-null	int64
3	PR	169	non-null	int64
4	SK	169	non-null	int64
5	TS	169	non-null	int64
6	M11	169	non-null	float64
7	BD2	169	non-null	float64
8	Age	169	non-null	int64
9	Insurance	169	non-null	int64
<pre>dtypes: float64(2),</pre>		int64(7),	object(1)	
memory usage: 13.3+			KB	

Prediction Dataset

```
In []:
```

```
print('Prediction dataset Frame shape: {}'.format(prediction_dt.shape))
        print('----')
        # columns and their types
        print('Data Frame Dtypes')
        prediction dt.dtypes
       Prediction dataset Frame shape: (169, 2)
       ______
       Data Frame Dtypes
       ID\t
            object
Out[ ]:
       Sepssis float64
       dtype: object
In [ ]:
        prediction dt.head()
                   ID\t Sepssis
Out[]:
       0 ICU200609\t\t\t\t\t
                          NaN
       1 ICU200610\t\t\t\t\t
                          NaN
       2 ICU200611\t\t\t\t\t
                          NaN
       3 ICU200612\t\t\t\t\t
                          NaN
```

Drop columns

4 ICU200613\t\t\t\t\t

Since we want to drop columns ID and Insurance for training since they do not play a significant in the target column - Sepssis -> We can drop it for better model

```
In [ ]:
         train dt = train dt.drop(['ID', 'Insurance'],axis=1)
         test dt = test dt.drop(['ID', 'Insurance'],axis=1)
```

• Check to make sure if we have successfully dropped out these 2 columns

```
In []:
        print('Train dataset shape {}'.format(train dt.shape))
         print('Test dataset shape {}'.format(test dt.shape))
        Train dataset shape (599, 9)
        Test dataset shape (169, 8)
```

- The number of columns in both datasets reduces 2 from the initial datasets.
- 11 -> 9 and 10 -> 8

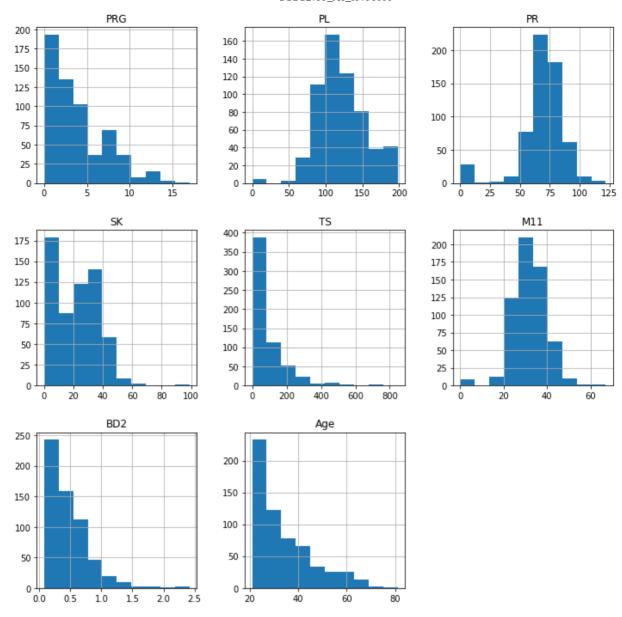
Histogram to see each columns distribution

Training dataset distribution visualization

NaN

```
In []:
         plt.figure()
         train dt.hist(figsize=(12, 12))
         plt.show()
```

<Figure size 432x288 with 0 Axes>

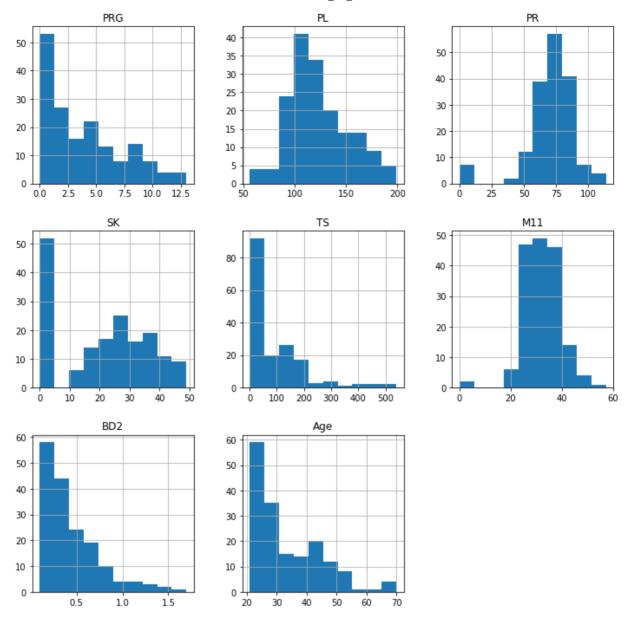


- The historgram shows that columns such as PL , PR , and M11 have a nearly normal distribution.
- Columns such as PRG, SK, TS, BD2, and Age are somehow right skewed.
- Columns PL, M11 and PR have a few suspicious data points with value of 0 which is far from their distribution -> These records can be outliers and are something we must look into carefully in preprocessing process.
- The sample age is biase as we see more youth than elderly people.

Testing dataset distribution visualization

```
plt.figure()
  test_dt.hist(figsize=(12, 12))
  plt.show()
```

<Figure size 432x288 with 0 Axes>



- The historgram shows that columns such as PL, PR and M11 have a nearly normal distribution. Both columns have records with value of 0 just like those on training dataset.
- Columns such as PRG, SK, TS, BD2, and Age are somehow right skewed.
- PR and M11 have some suspicious record with value 0
- Detail on each column will be discussed detailly in the below section -> Although not identical to the training dataset, we can see the testing dataset somehow have quite similar distribution as the training dataset

Prepocessing

Column Age

```
In [ ]: train_dt['Age'].value_counts
```

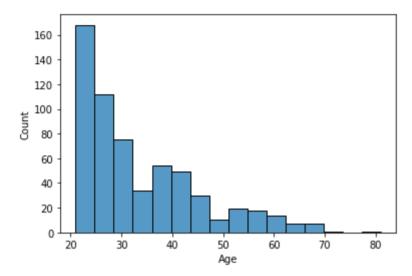
50

Out[]: <bound method IndexOpsMixin.value_counts of 0

```
1
        31
2
        32
3
        21
        33
594
        34
595
        22
596
        46
597
        21
598
        38
Name: Age, Length: 599, dtype: int64>
```

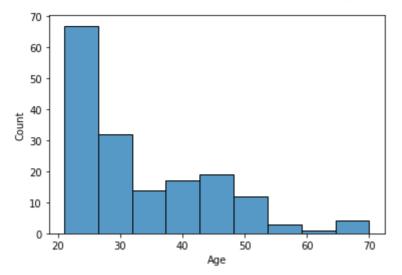
```
In [ ]: sns.histplot(x='Age',data=train_dt)
```

Out[]: <AxesSubplot:xlabel='Age', ylabel='Count'>



- From the distribution of this column in the training dataset, we can see that there is a few records of people above 70 -> These records can be outliers that might cause downgrade to the machine learning model if not appropriately cleaned.
- The dataset has more values on the youth medical record (from 20 to under 40 years old) -> This can cause biase in the result if the test data have more youth than elderly -> The accuracy will be higher than the test set that have more elderly than youth

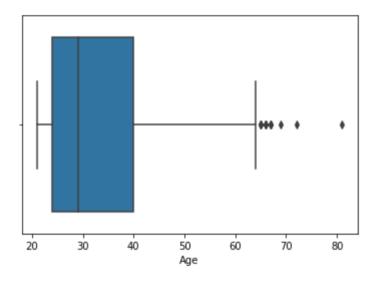
```
In []: sns.histplot(x='Age',data=test_dt)
Out[]: <AxesSubplot:xlabel='Age', ylabel='Count'>
```



Data is biase as the sample size of youth aging in 20 to 30 is more than other age category.

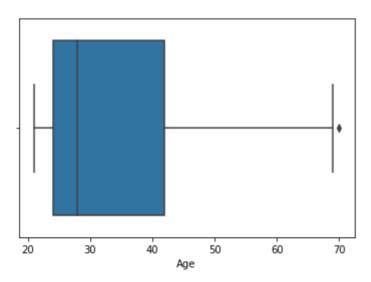
```
In [ ]: sns.boxplot(x='Age',data=train_dt)
```

Out[]: <AxesSubplot:xlabel='Age'>



```
In [ ]: sns.boxplot(x='Age',data=test_dt)
```

Out[]: <AxesSubplot:xlabel='Age'>



```
In []:    null_train_age = train_dt['Age'].isna().sum()
    null_test_age = train_dt['Age'].isna().sum()
    print('Train dataset sum of null values {}'.format(null_train_age))
    print('Test dataset sum of null values {}'.format(null_test_age))
```

Train dataset sum of null values 0 Test dataset sum of null values 0

In []: #Check specific number of record with people who are older than 70 years old
train_dt[train_dt['Age']>70]

```
BD2 Age
Out[]:
              PRG
                    PL PR SK TS M11
                                                      Sepssis
         453
                 2
                   119
                         0
                             0
                                 0
                                    19.6 0.832
                                                 72 Negative
         459
                                                     Negative
                 9 134
                        74
                            33
                                60 25.9 0.460
                                                 81
```

```
In [ ]: test_dt[train_dt['Age']>70].shape[0]
```

/var/folders/qs/m5w6bzsn1fz5jfs1rq4ccsv40000gn/T/ipykernel_61026/1229189570.p y:1: UserWarning: Boolean Series key will be reindexed to match DataFrame inde x.

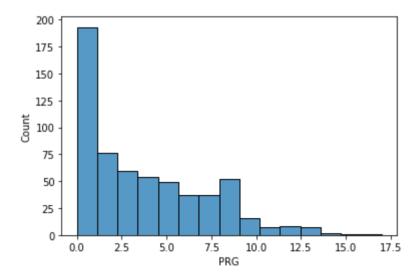
test_dt[train_dt['Age']>70].shape[0]
0

PRG

Out[]:

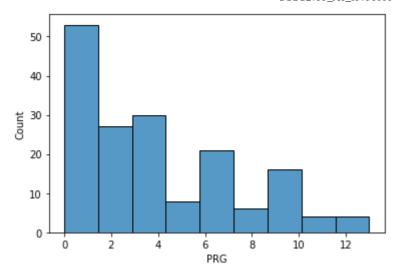
```
In [ ]: sns.histplot(x= 'PRG', data=train_dt)
```

Out[]: <AxesSubplot:xlabel='PRG', ylabel='Count'>



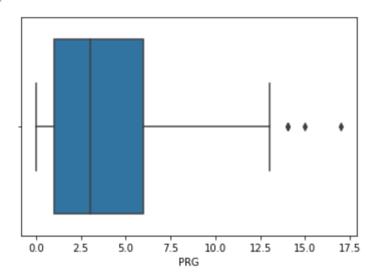
```
In [ ]: sns.histplot(x= 'PRG', data=test_dt)
```

Out[]: <AxesSubplot:xlabel='PRG', ylabel='Count'>



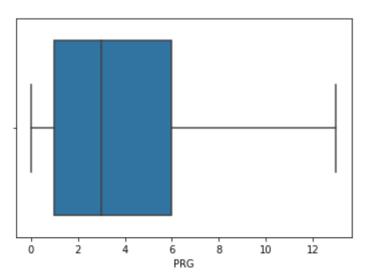
```
In [ ]: sns.boxplot(x='PRG', data= train_dt)
```

Out[]: <AxesSubplot:xlabel='PRG'>



```
In [ ]: sns.boxplot(x='PRG', data= test_dt)
```

Out[]: <AxesSubplot:xlabel='PRG'>



```
In []:
    null_train_prg = train_dt['PRG'].isna().sum()
    null_test_prg = train_dt['PRG'].isna().sum()
```

```
print('Train dataset sum of null values {}'.format(null_train_prg))
print('Test dataset sum of null values {}'.format(null_test_prg))
```

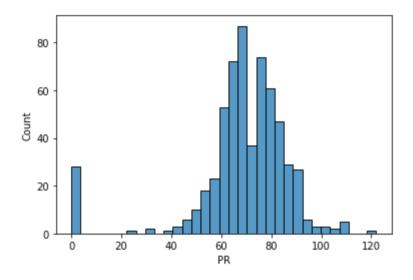
```
Train dataset sum of null values 0 Test dataset sum of null values 0
```

I decided not do perform any outlier's drop as it is still lack of insight to know how the PRG actually affects the Sepssis . Therefore this column is better left original

PR (Blood Pressure)

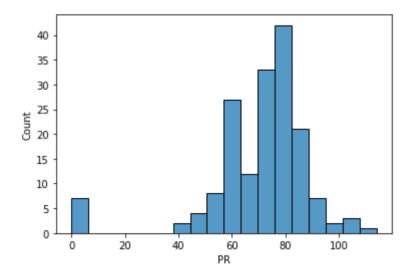
```
In [ ]: sns.histplot(x= 'PR', data=train_dt)
```

Out[]: <AxesSubplot:xlabel='PR', ylabel='Count'>



```
In [ ]: sns.histplot(x= 'PR', data=test_dt)
```

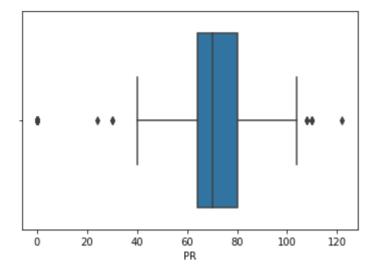
Out[]: <AxesSubplot:xlabel='PR', ylabel='Count'>



- From my observation, in the PR results in both datasets have records with value of 0.
- According to [], researcher reported that it is impossible to have blood pressure equal 0.
 So these values can be seen as impossible value, this can be caused by mistake data entry process. These data must be cleaned before the training process

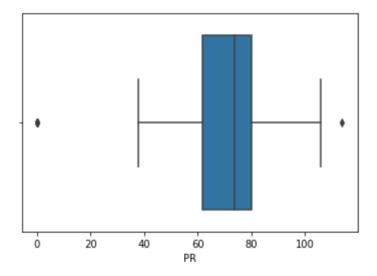
```
In [ ]: sns.boxplot(x='PR',data=train_dt)
```

```
Out[]: <AxesSubplot:xlabel='PR'>
```



```
In [ ]: sns.boxplot(x='PR',data=test_dt)
```

Out[]: <AxesSubplot:xlabel='PR'>



```
In []:
    null_train_pr= train_dt['PR'].isna().sum()
    null_test_pr= test_dt['PR'].isna().sum()

    print('Train dataset sum of null values {}'.format(null_train_pr))
    print('Test dataset sum of null values {}'.format(null_test_pr))
```

Train dataset sum of null values 0 Test dataset sum of null values 0

In here we must check the number of record with value of 0 in both datasets

Sum of record with value of 0 is 7

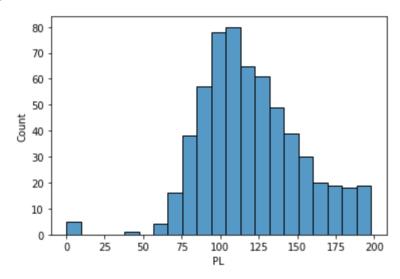
```
In []:
    train_dt['PR'] = train_dt['PR'].replace(0,train_dt['PR'].mean())
    test_dt['PR'] = test_dt['PR'].replace(0,test_dt['PR'].mean())
    # train_dt = train_dt[train_dt['PR']<=120]</pre>
```

• In order to correct both datasets, we want this process to be less complicated as possible. Therefore, mean imputation is brought into usage as mean imputation works well with small numerical (same characteristic to out dataset - with 599 rows only)

PL (Blood Work Result-1 (mu U/ml)

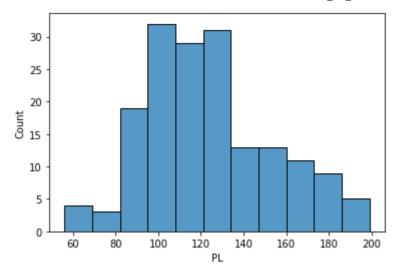
```
In [ ]: sns.histplot(x='PL', data=train_dt)
```

Out[]: <AxesSubplot:xlabel='PL', ylabel='Count'>



```
In [ ]: sns.histplot(x='PL', data=test_dt)
```

Out[]: <AxesSubplot:xlabel='PL', ylabel='Count'>



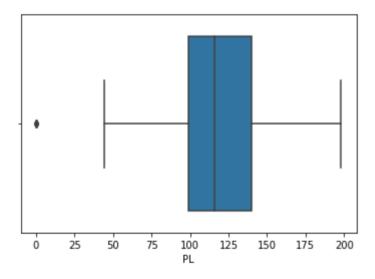
```
In []:
    null_train_pl= train_dt['PL'].isna().sum()
    null_test_pl= test_dt['PL'].isna().sum()

    print('Train dataset PL sum of null values {}'.format(null_train_pl))
    print('Test dataset PL sum of null values {}'.format(null_test_pl))
```

Train dataset PL sum of null values 0 Test dataset PL sum of null values 0

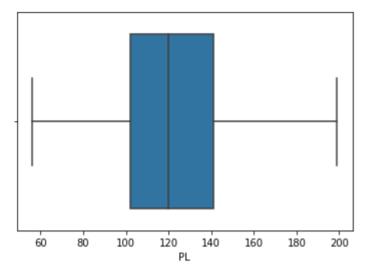
```
In [ ]: sns.boxplot(x='PL',data=train_dt)
```

Out[]: <AxesSubplot:xlabel='PL'>



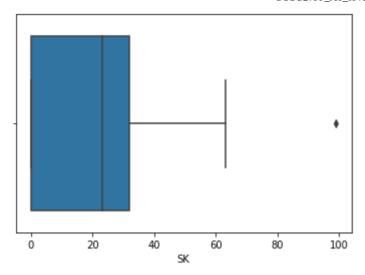
```
In [ ]: sns.boxplot(x='PL',data=test_dt)
```

Out[]: <AxesSubplot:xlabel='PL'>



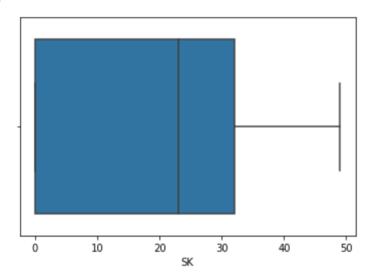
 Only in training dataset have records with value of 0. In this case, these records can be treated as error data, therefore I will replace this one with mean value of the column for better training process

```
In []:
         # Check for null values
         print("Sum of records with value of 0 in train dataset is {}".format(train dt
         print("Sum of records with value of 0 is test dataset {}".format(test dt[test
        Sum of records with value of 0 in train dataset is 5
        Sum of records with value of 0 is test dataset 0
In []:
         train_dt['PL'] = train_dt['PL'].replace(0,train_dt['PL'].mean())
         test dt['PL'] = test dt['PL'].replace(0,test dt['PL'].mean())
In []:
         print(train_dt['PL'].shape)
         print(test dt['PL'].shape)
        (599,)
        (169,)
       SK
In [ ]:
         sns.boxplot(x='SK',data=train_dt)
        <AxesSubplot:xlabel='SK'>
Out[ ]:
```



```
In []: sns.boxplot(x='SK',data=test_dt)
```

Out[]: <AxesSubplot:xlabel='SK'>



 Only the training dataset have one record with SK value > 70. This one can be seen as outlier -> must be deleted for better training process

```
In []:
         null_train_sk= train_dt['SK'].isna().sum()
         null test sk= test dt['SK'].isna().sum()
         print('Train dataset SK sum of null values {}'.format(null_train_sk))
         print('Test dataset SK sum of null values {}'.format(null_test_sk))
        Train dataset SK sum of null values 0
        Test dataset SK sum of null values 0
In [ ]:
         train_dt[train_dt['SK']>70]
                                         BD2 Age
Out[]:
             PRG
                            SK TS M11
                                                   Sepssis
        579
               2 197.0 70.0 99
                                 0 34.7 0.575
                                               62 Positive
In [ ]:
         test_dt[test_dt['SK']>70]
```

```
Out[]: PRG PL PR SK TS M11 BD2 Age
```

```
In []:
         #Remove outlier from both training and testing datasets
         train dt = train dt[train dt['SK']<70]</pre>
         test dt = test dt[test dt['SK']<70]</pre>
In []:
         #Double check
         train dt[train dt['SK']>70]
          PRG PL PR SK TS M11 BD2 Age Sepssis
Out[]:
        TS
In [ ]:
         sns.boxplot(x='TS',data=train dt)
        <AxesSubplot:xlabel='TS'>
Out[ ]:
                    200
                              400
                                       600
                                                 800
In [ ]:
         sns.boxplot(x='TS',data=test_dt)
        <AxesSubplot:xlabel='TS'>
Out[]:
                  100
                         200
                                 300
                                         400
                                                500
                               TS
```

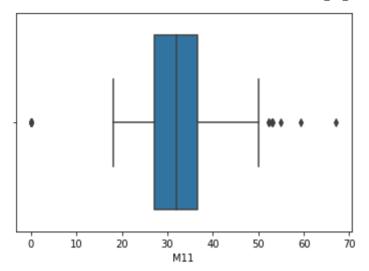
• Many records contain far more values than the normal value range. However, since the

number of rows in the dataset is not large, and I haven't had any insight about which medical type this record represents, Therefore, I will keep these values as they are.

```
In [ ]:
         #Check for null value
         null_train_ts= train_dt['TS'].isna().sum()
         null_test_ts= test_dt['TS'].isna().sum()
         print('Train dataset TS sum of null values {}'.format(null train ts))
         print('Test dataset TS sum of null values {}'.format(null test ts))
        Train dataset TS sum of null values 0
        Test dataset TS sum of null values 0
In [ ]:
         sns.histplot(x='TS', data=train dt)
        <AxesSubplot:xlabel='TS', ylabel='Count'>
Out[ ]:
           300
           250
           200
          150
           100
            50
            0
                                             600
                                   400
                                                      800
                         200
In [ ]:
         sns.histplot(x='TS', data=test dt)
         <AxesSubplot:xlabel='TS', ylabel='Count'>
Out[ ]:
           80
           60
           40
           20
            0
                      100
                              200
                                             400
                                                     500
                                     300
In [ ]:
         print(train dt['TS'].shape)
         print(test dt['TS'].shape)
         (598,)
         (169,)
```

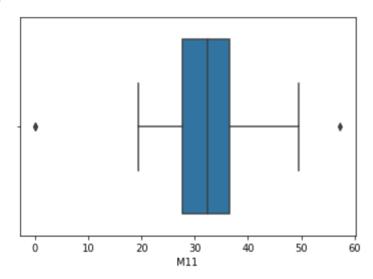
M11 (Body mass index (weight in kg/(height in m)^2)

```
In []:
          sns.histplot(x='M11',data=train_dt)
         <AxesSubplot:xlabel='M11', ylabel='Count'>
Out[]:
           70
           60
           50
           40
           30
           20
           10
                      10
                            20
                                         40
                                               50
                                                      60
                                                             70
                                    M11
In []:
          sns.histplot(x='M11',data=test_dt)
         <AxesSubplot:xlabel='M11', ylabel='Count'>
Out[]:
           30
           25
           20
         ti
8 15
           10
            5
                       10
                              20
                                      30
                                              40
                                                     50
                                                             60
                                    M11
In [ ]:
          sns.boxplot(x='M11',data=train_dt)
         <AxesSubplot:xlabel='M11'>
Out[]:
```



```
In [ ]: sns.boxplot(x='M11',data=test_dt)
```

Out[]: <AxesSubplot:xlabel='M11'>



In both datasets, there are records with a value of 0 for body mass index value.
 According to [], this only happens when people... Therefore, as a normal condition, those records can be seen as probably impossible values. I will replace these values with the mean of the column for both datasets.

```
In [ ]:
    #Check for null values first before performing any data cleaning and transfor
    null_train_mll= train_dt['M11'].isna().sum()
    null_test_mll= test_dt['M11'].isna().sum()

    print('Train dataset M11 sum of null values {}'.format(null_train_ml1))
    print('Test dataset M11 sum of null values {}'.format(null_test_ml1))

Train dataset M11 sum of null values 0

Test dataset M11 sum of null values 0

In [ ]:
    print(train_dt['M11'].shape)
    print(test_dt['M11'].shape)

    (598,)
    (169,)

In [ ]:
```

```
train_dt[train_dt['M11']==0]
```

```
PRG
                          PL
                                           SK
                                                TS
                                                     M11
                                                            BD2
                                                                         Sepssis
Out[]:
                                                                  Age
                              96.000000
             9
                    8
                       125.0
                                             0
                                                 0
                                                      0.0
                                                           0.232
                                                                    54
                                                                         Positive
                                                           0.305
            49
                       105.0
                              68.732888
                                             0
                                                 0
                                                      0.0
                                                                    24
                                                                        Negative
            60
                        84.0
                              68.732888
                                                 0
                                                      0.0
                                                           0.304
                                                                        Negative
            81
                    2
                        74.0
                              68.732888
                                             0
                                                 0
                                                      0.0
                                                           0.102
                                                                    22
                                                                        Negative
                              75.000000
           145
                       102.0
                                           23
                                                      0.0
                                                           0.572
                                                                    21
                                                                        Negative
                                                 0
           371
                       118.0
                              64.000000
                                           23
                                                89
                                                      0.0
                                                           1.731
                                                                        Negative
           426
                        94.0
                              68.732888
                                             0
                                                 0
                                                      0.0
                                                           0.256
                                                                        Negative
           494
                        80.0
                              68.732888
                                                           0.174
                                             0
                                                 0
                                                      0.0
                                                                        Negative
           522
                       114.0
                              68.732888
                                                      0.0
                                                           0.189
                                             0
                                                 0
                                                                    26
                                                                        Negative
```

```
In [ ]: test_dt[test_dt['M11']==0]
```

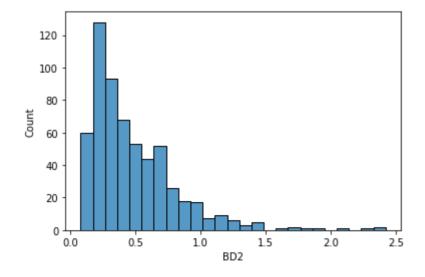
```
Out[ ]:
               PRG
                      PL
                                  PR SK
                                           TS
                                               M11
                                                      BD2
                                                            Age
           85
                     136
                          82.000000
                                        0
                                                0.0
                                                     0.640
                                                              69
                  5
                                            0
          107
                 10
                     115
                          70.426036
                                        0
                                            0
                                                0.0
                                                     0.261
                                                              30
```

```
In [ ]:
    train_dt['M11']=train_dt['M11'].replace(0,train_dt['M11'].mean())
    test_dt['M11']=test_dt['M11'].replace(0,test_dt['M11'].mean())
```

BD2 [Blood Work Result-4 (mu U/ml)]

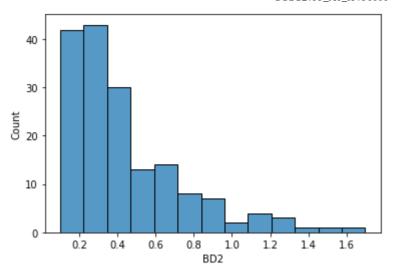
```
In [ ]: sns.histplot(x='BD2', data=train_dt)
```

Out[]: <AxesSubplot:xlabel='BD2', ylabel='Count'>



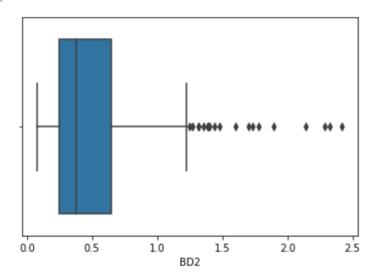
```
In [ ]: sns.histplot(x='BD2', data=test_dt)
```

Out[]: <AxesSubplot:xlabel='BD2', ylabel='Count'>



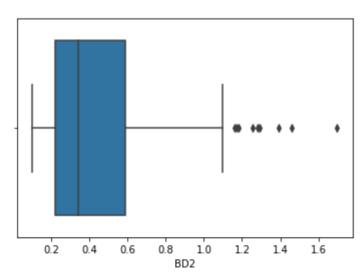
```
In [ ]: sns.boxplot(x='BD2',data=train_dt)
```

Out[]: <AxesSubplot:xlabel='BD2'>



```
In [ ]: sns.boxplot(x='BD2',data=test_dt)
```

Out[]: <AxesSubplot:xlabel='BD2'>



```
In []:    null_train_bd2= train_dt['BD2'].isna().sum()
    null_test_bd2= test_dt['BD2'].isna().sum()
```

```
print('Train dataset BD2 sum of null values {}'.format(null_train_bd2))
print('Test dataset BD2 sum of null values {}'.format(null_test_bd2))
```

```
Train dataset BD2 sum of null values 0
Test dataset BD2 sum of null values 0
```

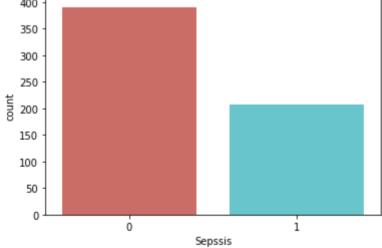
Many records contain far more values than the normal value range. However, since the number of rows in the dataset is not large, and I haven't had any insight about which medical type this record represents, Therefore, I will keep these values as they are.

Explore Target column - Sepssis

Here I will analyse about the target column - Sepssis

• I will convert the value of Sepssis to number before the training process in order to make the binary classification learning process be easier

```
In []:     def convert_binary(x):
          if x == 'Positive':
              return 1
          else:
              return 0
          train_dt['Sepssis'] = train_dt['Sepssis'].apply(convert_binary)
In []:     sns.countplot(x="Sepssis", data=train_dt, palette="hls")
     plt.show()
```



```
In []:
    print(train_dt['Sepssis'].value_counts())

    number_with_sepssis = len(train_dt[train_dt['Sepssis']==1])
    number_no_sepssis = len(train_dt[train_dt['Sepssis']==0])
    percentage_of_sepssis = number_with_sepssis/(number_with_sepssis+number_no_sepsis = number_no_sepsis/(number_with_sepssis+number_no_sepsis = number_no_sepssis/(number_with_sepssis+number_no_sepsis = number_no_sepssis/(number_with_sepssis+number_no_sepsis = number_no_sepssis/(number_with_sepssis+number_no_sepsis = number_no_sepssis = number_with_sepssis+number_no_sepsis = number_no_sepssis = number_with_sepssis = number_with_sep
```

1 207
Name: Sepssis, dtype: int64

```
Percentage of people in ICU develop Sepssis: 34.615
Percentage of people in ICU NOT develop Sepssis: 65.385
Ratio of people develop sepssis / people did not develop sepssis: 1.889
```

As can be seen, our data sets are not balanced. From above values, we can see that the ratio between the patient will develop sepssis during ICU stay (class 0) over people did not develop sepssis is approximately 2 times (~ 1.9) -> This imbalance will lead to the high probability that this dataset will perform well on detecting people without developing sepssis compared to the people will develop sepssis. This dataset is right-skewed to the Negative (or 0) in the diagram

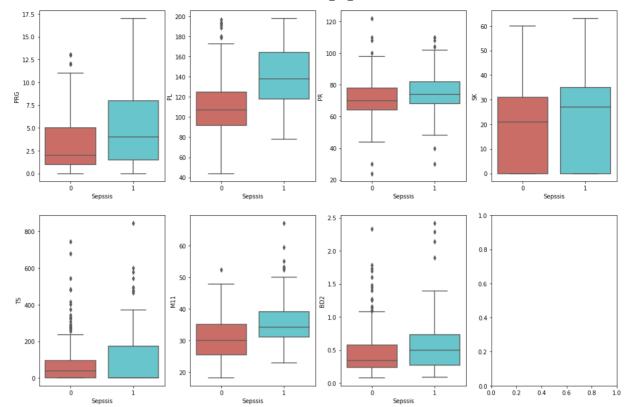
Why balanced the dataset

- Normally when dealing with imbalanced dataset, depending on the purpose of what we are going to predict, that people decide to balance or not balance the dataset. One of the most popular techniques to balance the dataset is resampling. Since the imbalanced dataset might have some impact on the accuracy of the machine learning model. The accuracy will be bias towards the assertive dataset. In this case, the model will be good at predict patient won't develop Sepssis.
- In our case, this bias is not encourage and might cause death for patient if predict wrongly. Since Sepssis is a life-threatening medical emergency, I don't want the model to bias towards 'Negative' class -> It it better to predict patient in ICU will not develop a sepsis to have sepssis, rather than predict patient potentially develop sepssis to not have a sepssis - doctor will ignore them, consequently resulting in death for patient.

Relationship between Age, Sepssis and other features

```
In [ ]:
         # sns.scatterplot(x='PL',y='Age',data=train dt,hue="Sepssis")
         fig, axes = plt.subplots(nrows =2,ncols=4, figsize=(18, 16))
         sns.scatterplot(x='PL',y= 'Age',data=train dt, ax=axes[0,0], hue= 'Sepssis',pe
         sns.scatterplot(x='PR',y='Age',data=train dt,ax=axes[0,1],hue="Sepssis",palet
         sns.scatterplot(x='SK',y='Age',data=train_dt,ax=axes[0,2],hue="Sepssis",palet
         sns.scatterplot(x='BD2',y='Age',data=train_dt,ax=axes[0,3],hue="Sepssis",pale
         sns.scatterplot(x='M11',y='Age',data=train dt,ax=axes[1,0],hue="Sepssis",pale
         sns.scatterplot(x='TS',y='Age',data=train_dt,hue="Sepssis",ax=axes[1,1],palet
         sns.scatterplot(x='PRG',y='Age',data=train_dt,hue="Sepssis",ax=axes[1,2],pale
        <AxesSubplot:xlabel='PRG', ylabel='Age'>
```

```
60
        g 50
                                                                     g 50
                                                                      0.8
                                                                      0.6
        ₽ 50
                                                                      0.4
                                                                      0.2
In []:
         target_col = ['Sepssis']
         features = train dt.columns.tolist()[:-1]
         features
         ['PRG', 'PL', 'PR', 'SK', 'TS', 'M11', 'BD2', 'Age']
Out[]:
In [ ]:
         # for fea in features:
                sns.boxplot(x='Sepssis',y=fea,data=train_dt)
         #
               plt.show()
         fig, axes = plt.subplots(nrows =2,ncols=4, figsize = (18,12) )
         sns.boxplot(x='Sepssis', y =features[0],data=train_dt, ax=axes[0,0],palette="
         sns.boxplot(x='Sepssis', y =features[1],data=train_dt, ax=axes[0,1],palette="
         sns.boxplot(x='Sepssis', y =features[2],data=train_dt, ax=axes[0,2],palette=""
         sns.boxplot(x='Sepssis', y =features[3],data=train_dt, ax=axes[0,3],palette=""
         sns.boxplot(x='Sepssis', y =features[4],data=train_dt, ax=axes[1,0],palette=""
         sns.boxplot(x='Sepssis', y =features[5],data=train_dt, ax=axes[1,1],palette="1
         sns.boxplot(x='Sepssis', y =features[6],data=train_dt, ax=axes[1,2],palette=""
        <AxesSubplot:xlabel='Sepssis', ylabel='BD2'>
Out[ ]:
```



Initial insight

[PL]

- Patient who age from 20 to 30 and PL values that < 125 might not likely to develop a sepssis.
- Patient who age less than 40 and PL values that *>125 could potentially develop a sepssis.
- Overall, there is a clear distinction between the one who develop a sepssis and whom none in features PL. Patient with PL value <120 are less likely to develop a sepssis

[PR]

• Patients who age from 20 to nearly 25 and have a PR (blood pressure) of approximately <70 might not be likely to develop sepsis.

[SK]

- Patient who age from 20 to nearly 27 and have a SK value of approximately <30 might not be likely to develop sepssis
- Patient who age from 48 to nearly 60 and have a SK value of approximately ~20 30 have slight potential to develop sepssis.

[BD2]

- Patient who age from 20 to nearly 28 and have a BD2 value of approximately **<0.4** might not be likely to develop sepssis
- Patient who age 30 -> ~50 and have a BD2 value of approximately >1.0 1.5 might slightly to develop sepssis.

[M11]

Patient who age from 20 to nearly 27 and have a M11 value of approximately <40 might not be likely to develop sepssis. Overall, there is a quite clear distinction between the one who develop a sepssis and whom none in features M11. Patient with higher M11 value have potential to develop sepssis.

[TS and PRG] The scatterplot did not show any significant difference between patient will or will not develop a sepssi in ICU

Correlation Matrix

```
In []: # Check correlation
    from matplotlib.pyplot import figure
        figure(figsize=(8, 6), dpi=80)
        corr=train_dt[features].corr()
        sns.heatmap(corr,cmap="YlGnBu",annot = True)
Out[]: 
Out[]:
```



As can be observed from above correlation graph, the features in the dataset do not depend too much to each other. The highest correlation is just 0.54.

- Age has quite moderate correlation with PRG at 0.54 percentage.
- TS and SK gets correlation of 0.44.
- PL and TS has correlation of 0.34. However, these correlation numbers could not provide any specific insight, expect from the dataset do not relate too much on each other.
 - -> Hence, we are ready to fit the data to machine learning models

Approaches

Import Statement for Models

```
from sklearn.pipeline import make_pipeline
from sklearn.pipeline import Pipeline
from sklearn.ensemble import RandomForestClassifier as rbf
from sklearn.metrics import roc_auc_score
from sklearn.metrics import accuracy_score,make_scorer,precision_score,recall
from sklearn.linear_model import LogisticRegression
from sklearn.preprocessing import StandardScaler
from sklearn.model_selection import RandomizedSearchCV,StratifiedKFold
from sklearn.metrics import fl_score
from sklearn.ensemble import RandomForestClassifier as rbf
from imblearn.under_sampling import RandomUnderSampler
from imblearn.over_sampling import SMOTE
from imblearn.pipeline import Pipeline as imbpipeline
from sklearn.model_selection import train_test_split
```

Split train and test set

```
In [ ]:
         X = train dt[features]
         Y = train dt[target col]
In [ ]:
         X train, X test, Y train, Y test = train test split(X,Y, test size=0.25, rando
                                                              stratify=Y)
In [ ]:
         print(X train.shape)
         print(X test.shape)
         print(Y train.shape)
         print(Y test.shape)
        (448, 8)
         (150, 8)
         (448, 1)
         (150, 1)
In [ ]:
         scaler = StandardScaler()
         scaler.fit(X train)
         X train scaled = scaler.transform(X train)
         X test scaled = scaler.transform(X test)
In []:
         X train=X train.values
         X test=X test.values
         Y train=Y_train.values
         Y_test=Y_test.values
```

Set up evaluation metric

```
from sklearn.metrics import confusion_matrix,precision_score,recall_score
from sklearn.metrics import classification_report
from sklearn.metrics import mean_absolute_error
from sklearn.metrics import mean_squared_error
```

```
from sklearn.model selection import KFold
def evaluation(estimator, X test, Y test, X train, Y train):
       pred train=estimator.predict(X train)
       pred test = estimator.predict(X test)
       # Accuracy, Precision and Recall
       score test 1 = accuracy score(Y test,pred test)*100
       score_test_2 = precision_score(Y_test,pred_test)*100
       score test 3= recall score(Y test,pred test)*100
       score test 4 = f1 score(Y test,pred test)*100
       score test 5 = roc auc score(Y test, pred test)*100
       score test 6 = mean absolute error(Y test,pred test)
       score test 7 = mean squared error(Y test,pred test)
       score_train_1 = accuracy_score(Y_train,pred_train)*100
       score train 2 = precision score(Y train, pred train)*100
       score train 3= recall score(Y train, pred train)*100
       score train 4 = f1 score(Y train, pred train)*100
       score_train_5 = roc_auc_score(Y_train, pred_train)*100
       score train 6 = mean absolute error(Y train, pred train)
       score train 7 = mean squared error(Y train,pred train)
       print("\n")
       print("-----")
       print('Accuracy | Test: %.3f, Train: %.3f, Difference: %.3f' % (score
       print('Precision | Test: %.3f, Train: %.3f, Difference: %.3f' % (sco
       print('Recall | Test: %.3f, Train: %.3f, Difference: %.3f' % (s
       print('F1 score | Test: %.3f, Train: %.3f, Difference: %.3f'% (score
       print('ROC - AUC | Test: %.3f, Train: %.3f, Difference: %.3f'% (sco
       print('MAE
                         Test: %.3f, Train: %.3f, (Test - Train) : %.3f'%
       print('MSE
                         Test: %.3f, Train: %.3f, (Test - Train) : %.3f'%
       print("-----")
       print(classification report(Y test, pred test))
       print("-----")
       # Making the Confusion Matrix
       cm = confusion_matrix(Y_test, pred_test)
       print ("Confusion Matrix:\n",cm)
       group name = ['TP', 'FP', 'FN', 'TN']
       group counts = ["{0:0.0f}".format(value) for value in cm.flatten()]
       group percentages = ["{0:.2%}".format(value) for value in cm.flatten(
       labels = [f'{v1}\n{v2}\n{v3}'  for v1,v2,v3 in zip(group\_name,group\_co)
       labels = np.array(labels).reshape(2,2)
       sns.heatmap(cm,annot = labels, fmt ="",cmap='Greens')
```

Decision Tree

Why Decision Tree

The decision tree receives knowledge in the form of a tree, which can alternatively be
represented as a set of discrete rules to make it easier to understand. The key
advantage of the decision tree classifier is its flexibility in utilizing multiple feature
subsets and decision criteria at various stages of classification. Additionally, a Decision
Tree model is simple to build and does not involve extensive data preparation,
normalization, or scaling.

Notice when using Decision Tree

- The tree is inconsistent when a slight change in the tree's structure results in a substantial change in the structure, resulting in a high variance.
- The tree's algorithms works in top-down manner, directing them from the tree's root to a leaf, based on the results of tests conducted along the journeyare. Therefore this algorithm will search to the deepest section of the tree for the leaf, resulting in increasing complexity of the tree might highly cause to overfitting problem if not justified.

Model 1: Base Model Default Decision Tree

```
In []:
    from sklearn import tree
    dtc = tree.DecisionTreeClassifier(criterion='entropy', max_depth=50, class_we
    dtc = dtc.fit(X_train, Y_train)
```

Model Evaluation

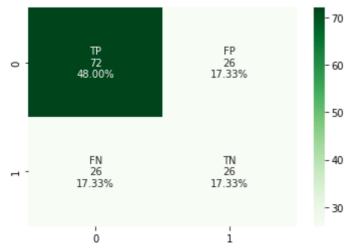
```
In [ ]: evaluation(dtc, X_test, Y_test, X_train, Y_train)
```

```
----- Evaluation metrics -----
Accuracy | Test: 65.333, Train: 100.000, Difference: 34.667
Precision | Test: 50.000, Train: 100.000, Difference: 50.000
            | Test: 50.000, Train: 100.000, Difference: 50.000
          | Test: 50.000, Train: 100.000, Difference: 50.000
ROC - AUC | Test: 61.735, Train: 100.000, Difference: 38.265
           Test: 0.347, Train: 0.000, (Test - Train): 0.347
MAE
           Test: 0.347, Train: 0.000, (Test - Train): 0.347
----- Classification Report -----
             precision
                        recall f1-score
                                            support
          0
                  0.73
                           0.73
                                     0.73
                                                 98
                  0.50
                           0.50
                                     0.50
                                                 52
                                                150
                                     0.65
   accuracy
                                     0.62
                                                150
  macro avg
                  0.62
                           0.62
                  0.65
                           0.65
                                     0.65
                                                150
weighted avg
```

------ Confusion Matrix ------

Confusion Matrix: [[72 26]

[26 26]]



- As mentioned above, the result show that the Decision Tree Algorithm work perfectly
 with the training data with accuracy of 100%, however when it is applied to predict on
 unseen data. The model shown poor result in all metrics.
- With accuracy of 65% on testing set compared to 100% in training set. This model is
 overfitting the issue. In testing data it performed pretty bad although in binary
 classification accuracy does not mean anything, the accuracy gap between testing and
 training datasets should not be too big.
- When we look at other scores which are: F1 (50%), Precision(50%) and recall(50%) on the testing data are around 50% which equal to the probability of a flip of a coin (50-50). This is extremely useless and dangerous for classification problem in health care, especially with Sepssis life-threatening issue. Looking at the cofusion matrix, we can see that it predicts correctly 69 patient who do not develop sepssis. However, among the remain rate, it could not predict many people with sepsiss and will develop sepssis (True Negative). Additionally, patients who had sepssis is but is predicted to not develop sepssis is considerably high with 26 people. In conclusion, it's slightly good at finding patient without a sepssis, but terrible at finding patient who is potentially develop sepssis.
- -> We should use hyperparameter tuning to reduce this overfitting issue.

Model 2: Decision Tree Classifier Hyperparameter Tuning

Why Random CV - Hyperparam tuning

Due to the high variation of the decision tree model, the overfitting problem is likely to occur. GridSearchCV will attempt to discover the ideal parameter that will mitigate this overfitting problem and hence lower the model's variance. KFold will be responsible for selecting one set from each of the n training sets for parameter adjustment. The parameters in this case are the tree's length, min_samples_split, min_weight_fraction_leaf, max_leaf_nodes, max_features('auto','sqrt','log2') and the criterion used to define the tree's split: gini or entropy.

```
In [ ]:
         from sklearn.tree import DecisionTreeClassifier as DTC
         # pipe dtc = Pipeline(['clf', DecisionTreeClassifier(random state =1)])
         pipe dtc = imbpipeline(steps = [
                                         ['decisiontreeclassifier', DTC()]])
         dtc param grid = {
             'decisiontreeclassifier__criterion':['gini','entropy'],
             'decisiontreeclassifier__max_features': ['auto','sqrt','log2', None],
             'decisiontreeclassifier__max_depth': np.arange(1,200,2),
             'decisiontreeclassifier__min_weight_fraction_leaf': np.arange(0,2,0.01),
             'decisiontreeclassifier min samples split':np.arange(1,100,1),
                 'decisiontreeclassifier max leaf nodes': np.arange(1,50,5)
                 # 'decisiontreeclassifier ccp alpha':np.logspace(-5,5,10)
         stratified kfold = StratifiedKFold(n splits=5,
                                                shuffle=True,
                                                random state=1)
         # Perform RandomizedSearchCV
```

Out[]:

```
randomized_search_dtc = RandomizedSearchCV(estimator=pipe_dtc,param_distribut
randomized_search_dtc.fit(X_train,Y_train)
```

```
/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
sklearn/model selection/ validation.py:372: FitFailedWarning:
190 fits failed out of a total of 250.
The score on these train-test partitions for these parameters will be set to n
If these failures are not expected, you can try to debug them by setting error
score='raise'.
Below are more details about the failures:
______
190 fits failed with the following error:
Traceback (most recent call last):
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/sklearn/model_selection/_validation.py", line 680, in _fit_and_score
    estimator.fit(X train, y train, **fit params)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/imblearn/pipeline.py", line 272, in fit
    self._final_estimator.fit(Xt, yt, **fit_params_last_step)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/sklearn/tree/ classes.py", line 937, in fit
    super().fit(
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/sklearn/tree/_classes.py", line 304, in fit
    raise ValueError("min weight fraction leaf must in [0, 0.5]")
ValueError: min weight fraction leaf must in [0, 0.5]
  warnings.warn(some fits failed message, FitFailedWarning)
/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
sklearn/model selection/ search.py:969: UserWarning: One or more of the test s
cores are non-finite: [
                                                   nan 0.12266667
nan
        nan 0.62513485 0.57919573 0.23715121
                                                   nan
 0.11506849
                            nan
                                        nan 0.55250086 0.49205237
                             nan 0.55427365
       nan
                  nan
                                                   nan
                                                              nan
                                        nan 0.
       nan
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                                                              nan
       nan
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                             nan
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                                                   nan
                                                              nan
       nan
                  nan
                                        nan
                                                   nan
                                                              nan
                             nan
       nan 0.51006636 0.12352941 0.
                                                   nan
                                                              nan
 warnings.warn(
RandomizedSearchCV(cv=StratifiedKFold(n splits=5, random state=1, shuffle=Tru
e),
                  estimator=Pipeline(steps=[['decisiontreeclassifier',
                                             DecisionTreeClassifier()]]),
                  n iter=50, n jobs=2,
                  param distributions={'decisiontreeclassifier criterion':
['gini',
'entropy'],
                                       'decisiontreeclassifier max depth': a
                 5, 7, 9, 11, 13, 15, 17, 19, 21, 23,
rray([ 1,
            3,
        27, 29, 31, 33, 35, 37, 39...
       1.32, 1.33, 1.34, 1.35, 1.36, 1.37, 1.38, 1.39, 1.4, 1.41, 1.42,
       1.43, 1.44, 1.45, 1.46, 1.47, 1.48, 1.49, 1.5 , 1.51, 1.52, 1.53,
       1.54, 1.55, 1.56, 1.57, 1.58, 1.59, 1.6 , 1.61, 1.62, 1.63, 1.64,
       1.65, 1.66, 1.67, 1.68, 1.69, 1.7, 1.71, 1.72, 1.73, 1.74, 1.75,
       1.76, 1.77, 1.78, 1.79, 1.8 , 1.81, 1.82, 1.83, 1.84, 1.85, 1.86,
       1.87, 1.88, 1.89, 1.9 , 1.91, 1.92, 1.93, 1.94, 1.95, 1.96, 1.97,
       1.98, 1.99])},
                  scoring=make_scorer(f1_score))
```

```
In []:
    print('Average F1 score of best param:%.3f'%(randomized_search_dtc.best_score
    print('Best parameter using %s'%(randomized_search_dtc.best_params_))
```

Average F1 score of best param:0.625

Best parameter using {'decisiontreeclassifier__min_weight_fraction_leaf': 0.3

1, 'decisiontreeclassifier__min_samples_split': 28, 'decisiontreeclassifier__m ax_leaf_nodes': 6, 'decisiontreeclassifier__max_features': None, 'decisiontree classifier__max_depth': 127, 'decisiontreeclassifier__criterion': 'entropy'}

Model Evaluation

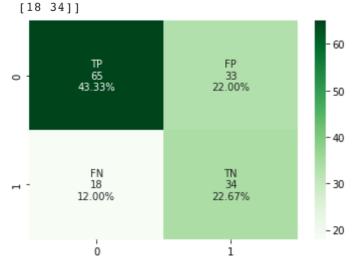
```
In []:
    dtc_hyper = DTC(max_depth=3,criterion= 'entropy',min_weight_fraction_leaf=0.4
    dtc_hyper.fit(X_train,Y_train)
    dtc_pred=dtc_hyper.predict(X_test)
    # random_forest_hyper = rbf(max_depth=192, n_estimators=148,criterion= 'gini'
    # random_forest_hyper.fit(X_train,Y_train)
    evaluation(dtc_hyper,X_test,Y_test,X_train,Y_train)
    tree_feature_importances = dtc_hyper.feature_importances_
    sorted_idx = tree_feature_importances.argsort()
    plt.figure(figsize=(10,10))
    plt.barh(train_dt.columns[sorted_idx], tree_feature_importances[sorted_idx])
    plt.show()
```

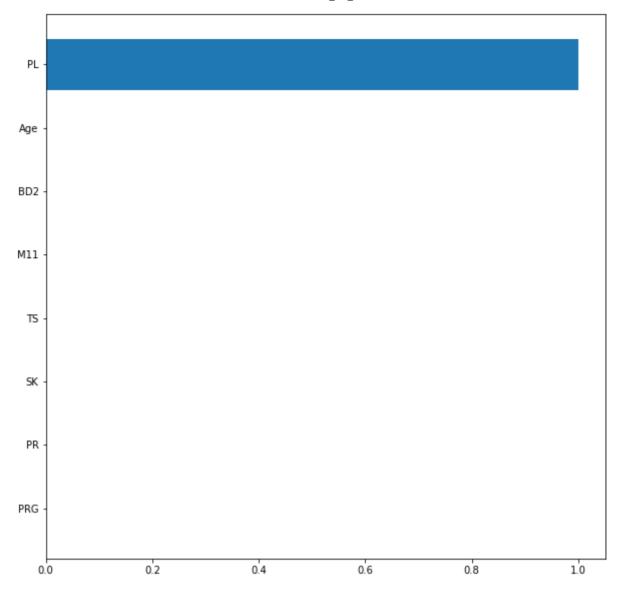
```
----- Evaluation metrics -----
Accuracy | Test: 66.000, Train: 71.652, Difference: 5.652
Precision | Test: 50.746, Train: 56.863, Difference: 6.116
Recall
            Test: 65.385, Train: 74.839, Difference: 9.454
          | Test: 57.143, Train: 64.624, Difference: 7.481
           Test: 65.856, Train: 72.402, Difference: 6.547
ROC - AUC
           | Test: 0.340, Train: 0.283, (Test - Train) : 0.057
MAE
MSE
           Test: 0.340, Train: 0.283, (Test - Train): 0.057
----- Classification Report -----
                        recall f1-score support
             precision
          0
                  0.78
                           0.66
                                     0.72
                                                98
                                     0.57
          1
                  0.51
                           0.65
                                                52
                                     0.66
                                               150
   accuracy
  macro avq
                  0.65
                           0.66
                                     0.64
                                               150
weighted avg
                  0.69
                           0.66
                                     0.67
                                               150
```

----- Confusion Matrix -----

Confusion Matrix:

[[65 33]





- The model does not overfit now, however the performance of accuracy on both dataset is not very high with 65% in testing dataset and 69% in the training set. However, accuracy is not all as we see the model performs slightly better on recall and F1.
- As can be seen from the classification report table, the precision score (50%) and the recall(65%) score are just above average when the model predicts the patient will develop a sepssis in ICU. Resulting in, the f1-score for this class 1 is low as the dataset is right-skewed. On the other hand, the precision for class 0 (0.78) and the recall score (0.66) are higher which leads to the higher value in f1-score for class 0 is 0.72. This means that this Decision tree model does a better job on recognize the fraction of true positive predictions from all positive records in dataset patients who would not develop sepssis and are predicted as not develop sepssis.
- Since patient who have high potential of developing sepssis is important, this reduction can be seen as a slightly good rate since it minimizes the number of patients that would have dead because of wrong prediction. However, looking in detail in confusion matrix, the precision score is just meet the average.
- Precision = 0.5 means that treating 10 patients who are predicted to develop sepssis label "Positive", in half of the cases we'll find patients who do not likely to develop sepssis. Therefore, we must looking at the precision score also to evaluate this model.

Although it might not lead to life-threatening situation, the model does not suitable for ICU as it might lead the hospital to overload situation.

- Despite the fact that we care more about False Negative than False Positive, with the current rate, the hospital can be overlwhelmed in terms of accommodation and staff needed to take care these patients. As when we predict that patient will develop sepssis in ICU, there is a must to apply special treatment to those patient, however it is somehow a redundancy if we are not carefully consider the number of patients who would likely to receive these treatments. There are many other disease that needed to be take cared in the hospital.
- In conclusion, although the Cross Validation in Decision Tree reduce the chance of overfitting and shows significant improvement on recall. This model is not an optimal solution to our problem

It seems that Decision Forest is not a good algorithm for our problem. So we will move to other algorithms - which is also an improvement of Decision Tree in the next section - Random Forest algorithms

Random Forest

Why Random Forest

- Since the Decision Tree algorithm will result in same tree on same dataset despite how many times we run it. Therefore, a new ensemble technique called random forests is applied to inject some randomness. Random Forest Consider that each of the ensemble's classifiers is a decision tree classifier, and the ensemble as a whole is a "forest." Individual decision trees are built by determining the split using a random selection of attributes at each node. In more technical terms, each tree is dependent on the values of a random vector sampled separately and uniformly across the forest. Each tree votes during classification, and the most popular class is returned.
- As with the decision tree, missing data, scaling data, and normalizing data have no effect on the random forest's performance.
- One of the most significant benefits of random forest is its adaptability. It may be used
 for both regression and classification problems, and the relative priority it assigns to the
 input features is easily visible.
- Additionally, Random Forest can make us avoid the biggest problem of machine learning
 which is overfitting. If the forest contains a sufficient number of trees, the classifier will
 avoid overfitting the model.
- On the other hand, because it is a collection of numerous decision trees, the random forest's complexity is very complicated. The prediction time is quite lengthy and costly.

Model 3: Random Forrest Hyperparameter Tuning

Why hyperparameter tuning random forest

- To address the aforementioned issue of the random forest being time consuming and unnecessarily complicated, it is critical to examine the proper number of trees.
 RandomSearchCV plays a part in determining the best number of trees that fits the model as well as the other parameters.
- There are 3 most important parameters that needed to be accessed in the param grid including max_depth, n_estimators, and min_samples_split.
- n_estimators hyperparameter specifies the number of trees the algorithm constructs prior to doing maximum voting or averaging predictions. Resulting in increasing the number of trees improves performance and makes forecasts more stable.
- max_features, which specifies the maximum amount of features considered by random forest when splitting a node.
- min sample leaf. This specifies the smallest number of leafs necessary to separate an internal node.

```
In [ ]:
         from imblearn.combine import SMOTEENN
         from imblearn.under sampling import EditedNearestNeighbours
         pipeline rf = imbpipeline(steps = [
                                         ['randomforestclassifier', rbf()]])
         rf param grid = {
         'randomforestclassifier criterion':['gini','entropy'],
             'randomforestclassifier max features': ['auto', 'sqrt', 'log2'],
             'randomforestclassifier max depth': np.arange(1,250,1),
             'randomforestclassifier n estimators': np.arange(1,200,5),
             'randomforestclassifier__min_weight_fraction_leaf': np.arange(0,5,0.05),
             'randomforestclassifier min samples split':np.arange(1,50,1)
         stratified kfold = StratifiedKFold(n splits=5,
                                                shuffle=True,
                                                random state=1)
         # Perform RandomizedSearchCV
         randomized search rf = RandomizedSearchCV(estimator=pipeline rf,param distrib
         randomized search rf.fit(X train, Y train)
```

```
/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
imblearn/pipeline.py:272: DataConversionWarning: A column-vector y was passed
when a 1d array was expected. Please change the shape of y to (n samples,), fo
r example using ravel().
  self. final estimator.fit(Xt, yt, **fit params last step)
/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
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sklearn/model selection/ validation.py:372: FitFailedWarning:
630 fits failed out of a total of 700.
The score on these train-test partitions for these parameters will be set to n
If these failures are not expected, you can try to debug them by setting error
score='raise'.
Below are more details about the failures:
602 fits failed with the following error:
Traceback (most recent call last):
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/sklearn/model_selection/_validation.py", line 680, in _fit_and_score
    estimator.fit(X train, y train, **fit params)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/imblearn/pipeline.py", line 272, in fit
    self._final_estimator.fit(Xt, yt, **fit_params_last_step)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/sklearn/ensemble/_forest.py", line 450, in fit
    trees = Parallel(
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/joblib/parallel.py", line 1041, in call
    if self.dispatch one batch(iterator):
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/joblib/parallel.py", line 859, in dispatch_one_batch
    self. dispatch(tasks)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/joblib/parallel.py", line 777, in _dispatch
    job = self._backend.apply_async(batch, callback=cb)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/joblib/_parallel_backends.py", line 208, in apply_async
    result = ImmediateResult(func)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/joblib/_parallel_backends.py", line 572, in __init__
    self.results = batch()
```

```
File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/joblib/parallel.py", line 262, in call
    return [func(*args, **kwargs)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/joblib/parallel.py", line 262, in <listcomp>
    return [func(*args, **kwargs)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/sklearn/utils/fixes.py", line 216, in __call__
    return self.function(*args, **kwargs)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/sklearn/ensemble/ forest.py", line 185, in parallel build trees
    tree.fit(X, y, sample weight=curr sample weight, check input=False)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/sklearn/tree/ classes.py", line 937, in fit
    super().fit(
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/sklearn/tree/_classes.py", line 304, in fit
    raise ValueError("min_weight_fraction_leaf must in [0, 0.5]")
ValueError: min weight fraction leaf must in [0, 0.5]
28 fits failed with the following error:
Traceback (most recent call last):
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/sklearn/model selection/ validation.py", line 680, in fit and score
    estimator.fit(X train, y train, **fit params)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/imblearn/pipeline.py", line 272, in fit
    self._final_estimator.fit(Xt, yt, **fit_params_last_step)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/sklearn/ensemble/_forest.py", line 450, in fit
    trees = Parallel(
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/joblib/parallel.py", line 1041, in call
    if self.dispatch one batch(iterator):
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/joblib/parallel.py", line 859, in dispatch_one_batch
    self. dispatch(tasks)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/joblib/parallel.py", line 777, in _dispatch
    job = self._backend.apply_async(batch, callback=cb)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/joblib/_parallel_backends.py", line 208, in apply_async
    result = ImmediateResult(func)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/joblib/_parallel_backends.py", line 572, in __init__
    self.results = batch()
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/joblib/parallel.py", line 262, in call
    return [func(*args, **kwargs)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/joblib/parallel.py", line 262, in <listcomp>
    return [func(*args, **kwargs)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/sklearn/utils/fixes.py", line 216, in __call_
    return self.function(*args, **kwargs)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/sklearn/ensemble/ forest.py", line 185, in parallel build trees
    tree.fit(X, y, sample weight=curr sample weight, check input=False)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/sklearn/tree/_classes.py", line 937, in fit
    super().fit(
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
```

```
ackages/sklearn/tree/_classes.py", line 250, in fit
            raise ValueError(
        ValueError: min samples split must be an integer greater than 1 or a float in
         (0.0, 1.0]; got the integer 1
          warnings.warn(some fits failed message, FitFailedWarning)
        /Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
        sklearn/model selection/ search.py:969: UserWarning: One or more of the test s
        cores are non-finite: [
                                      nan
                                                  nan
                                                             nan
                                                                        nan
                                                                                   nan
        nan
                nan
                           nan
                                      nan 0.5355896
                                                             nan
                                                                        nan
         0.64567555
                           nan
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                                                             nan
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                                                             nan 0.10366245
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                                                  nan
                nan
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                                                             nan
         0.01190476
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                                                  nan 0.41018698
                nan
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                                      nan
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                nan 0.61508621
                                      nan
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                                                  nan
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                nan
                           nan 0.58361054
                                                  nan
                                                             nan
                                                                        nan
                           nan 0.41821588
                nan
                                                  nan
                                                             nan 0.02197802
                nan
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                nan 0.39140882
                                       nan
                                                  nan
                                                             nan
                                                                        nan
                nan
                           nan
                                      nan
                                                  nan 1
          warnings.warn(
        /Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
        imblearn/pipeline.py:272: DataConversionWarning: A column-vector y was passed
         when a 1d array was expected. Please change the shape of y to (n samples,), f
        or example using ravel().
          self. final estimator.fit(Xt, yt, **fit params last step)
        RandomizedSearchCV(cv=7,
                           estimator=Pipeline(steps=[['randomforestclassifier',
                                                       RandomForestClassifier()]]),
                           n iter=100, n jobs=-1,
                           param_distributions={'randomforestclassifier__criterion':
        ['gini',
        'entropy'],
                                                 'randomforestclassifier__max_depth': a
                                    5,
                          3,
                               4,
                                               7,
                                                         9, 10, 11, 12, 13,
        rray([ 1,
                     2,
                                          6,
                                                    8,
                14, 15,
                         16, 17, 18,
                                         19.
                                              20,
                                                    21,
                                                        22, 23, 24,
                27, 28,
                          29, 30, 31, 32, 33, 34, 35, 36, 37, 38,
               3.3 , 3.35 , 3.4 , 3.45 , 3.5 , 3.55 , 3.6 , 3.65 , 3.7 , 3.75 , 3.8 ,
               3.85, 3.9, 3.95, 4., 4.05, 4.1, 4.15, 4.2, 4.25, 4.3, 4.35,
               4.4 , 4.45, 4.5 , 4.55, 4.6 , 4.65, 4.7 , 4.75, 4.8 , 4.85, 4.9 ,
               4.95]),
                                                 'randomforestclassifier n estimator
        s': array([ 1,
                          6, 11, 16, 21,
                                             26, 31, 36, 41, 46, 51, 56, 61,
                          76, 81, 86, 91, 96, 101, 106, 111, 116, 121, 126,
                66, 71,
               131, 136, 141, 146, 151, 156, 161, 166, 171, 176, 181, 186, 191,
               196])},
                           scoring=make scorer(f1 score))
In [ ]:
         print('Average F1 score of best param:%.3f'%(randomized search rf.best score
         print('Best parameter using %s'%(randomized search rf.best params ))
        Average F1 score of best param:0.646
        Best parameter using {'randomforestclassifier__n_estimators': 96, 'randomfores
        tclassifier min weight fraction leaf': 0.0, 'randomforestclassifier min samp
        les_split': 15, 'randomforestclassifier__max_features': 'sqrt', 'randomforestc
```

lassifier max depth': 213, 'randomforestclassifier criterion': 'entropy'}

```
In []: random_forest_hyper = rbf(max_depth=213, n_estimators=96,criterion= 'gini',min')
    random_forest_hyper.fit(X_train,Y_train)
    rf_pred=pipeline_rf.predict(X_test)
    # random_forest_hyper = rbf(max_depth=192, n_estimators=148,criterion= 'gini'
    # random_forest_hyper.fit(X_train,Y_train)
    evaluation(random_forest_hyper,X_test,Y_test,X_train,Y_train)
    tree_feature_importances = random_forest_hyper.feature_importances_
    sorted_idx = tree_feature_importances.argsort()
    plt.figure(figsize=(10,10))
    plt.barh(train_dt.columns[sorted_idx], tree_feature_importances[sorted_idx])
    plt.show()
```

/var/folders/qs/m5w6bzsn1fz5jfs1rq4ccsv40000gn/T/ipykernel_49224/2352307916.p y:3: DataConversionWarning: A column-vector y was passed when a 1d array was e xpected. Please change the shape of y to (n_samples,), for example using ravel ().

random_forest_hyper.fit(X_train,Y_train)

```
----- Evaluation metrics -----
Accuracy | Test: 70.667, Train: 91.741, Difference: 21.074
Precision | Test: 61.111, Train: 93.382, Difference: 32.271
          Test: 42.308, Train: 81.935, Difference: 39.628
          Test: 50.000, Train: 87.285, Difference: 37.285
F1 score
ROC - AUC
          Test: 64.011, Train: 89.432, Difference: 25.421
           Test: 0.293, Train: 0.083, (Test - Train): 0.211
MSE
           Test: 0.293, Train: 0.083, (Test - Train): 0.211
----- Classification Report ------
             precision
                        recall f1-score support
          0
                 0.74
                           0.86
                                    0.79
                                               98
                           0.42
          1
                 0.61
                                    0.50
                                               52
                                    0.71
   accuracy
                                              150
```

0.64

0.71

0.65

0.69

150

150

----- Confusion Matrix -----

0.67

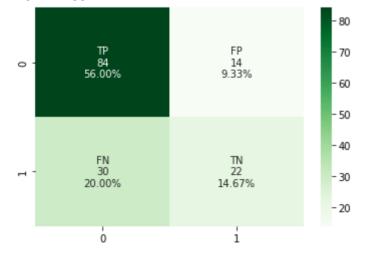
0.69

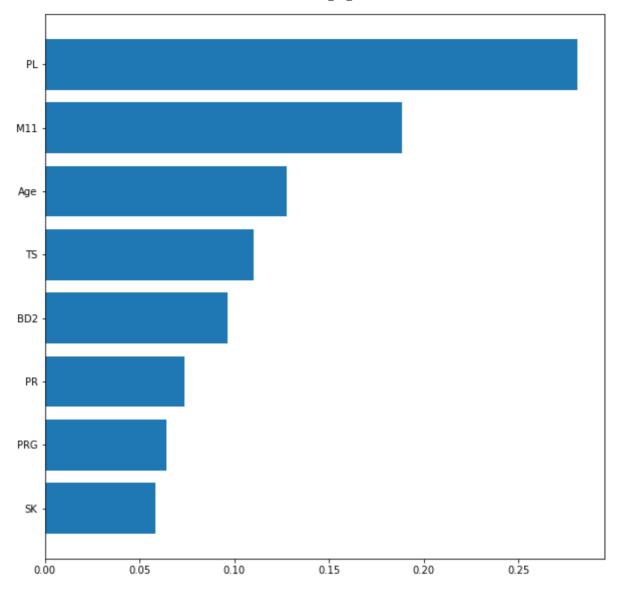
Confusion Matrix:

macro avq

weighted avg

[[84 14] [30 22]]





- From the classification report table, the result shows better score in all metrics. The recall metric is considerably high for class 0 with 0.83. This can be said that the higher the value of the recall is, the better the model at classifying patient without sepssis, but it can't say anything about how many times we had to actually rechecked with patient who actually have a sepssis throughout these searches. The precision score is acceptable in the class 0 with 0.74. This high rate is caused due to the imbalanced dataset (with more 0 labels).
- On the other hand, recall for class 1 is only 0.42, which is below average. As the rate of False Negative is 20% 30 patients are predicted not to develop sepssis when they actually are. We can tell from precision score of 0.61 in class 1 means that half of patient labelled with sepssis, we will find patient would not develop sepssis. Additionally, recall equal to 0.42 can tell that there is a very low chance to detect patient with sepssis. This seems to not helpful in predicting if a patient will develop sepsis in the period of their stay in the ICU. This rate is a not suitable for medical prediction, again especially for extremely dangerous infection.
- Also, in term of machine learning problem, the model is overfit as it perform quite well in the training set but not really good when they acted on unseen data. The gap in all

metric (excluding MAE and MSE) are very high, this can tell that the model is not generalized enough.

Logistic Regression

Why Logistic Regression

- Logistic Regression is a machine learning classification technique. It models the
 dependent variable using a logistic function. The dependent variable is binary in nature,
 implying that there are only two possible classifications. As a result, this algorithm is
 effective for binary classification.
- Logistic regression is simpler to implement, analyze, and train than linear regression.
- It is extremely efficient in classifying unclassified records.
- It can interpret model coefficients as indicators of the significance of particular features.
- Above all of reasons, it is a good fit for our problem as we only classify the target column with 2 values - if a given in ICU would not develop a sepsis (Sepsis Negative / class 0) or will develop sepsis (Sepsis Positive / class 1) during their ICU stay".

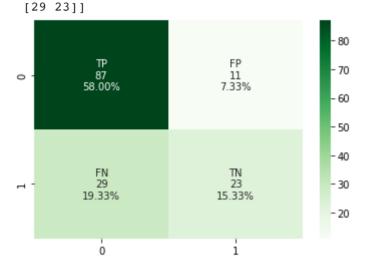
Model 4: Base model Logistic Regression

```
In []:
        model = LogisticRegression(random state=1, penalty='none',
                                 max iter=100
         lr base=model.fit(X train, Y train)
         is grid = False
        /Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
        sklearn/utils/validation.py:993: DataConversionWarning: A column-vector y was
        passed when a 1d array was expected. Please change the shape of y to (n sample
        s, ), for example using ravel().
          y = column or 1d(y, warn=True)
        /Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
        sklearn/linear model/ logistic.py:814: ConvergenceWarning: lbfgs failed to con
        verge (status=1):
        STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.
        Increase the number of iterations (max_iter) or scale the data as shown in:
            https://scikit-learn.org/stable/modules/preprocessing.html
        Please also refer to the documentation for alternative solver options:
            https://scikit-learn.org/stable/modules/linear_model.html#logistic-regress
        ion
          n iter i = check optimize result(
In [ ]:
        evaluation(lr base, X test, Y test, X train, Y train)
         ----- Evaluation metrics -----
        Accuracy | Test: 73.333, Train: 78.795, Difference: 5.461
        Precision | Test: 67.647, Train: 73.077, Difference: 5.430
                    Test: 44.231, Train: 61.290, Difference: 17.060
        Recall
                   | Test: 53.488, Train: 66.667, Difference: 13.178
                   Test: 66.503, Train: 74.672, Difference: 8.169
        ROC - AUC
```

```
MAE
              Test: 0.267, Train: 0.212, (Test - Train): 0.055
            Test: 0.267, Train: 0.212, (Test - Train): 0.055
MSE
      ----- Classification Report ------
              precision
                           recall f1-score
                                               support
           0
                   0.75
                              0.89
                                        0.81
                                                    98
                   0.68
                                        0.53
           1
                             0.44
                                                    52
                                        0.73
                                                   150
    accuracy
                   0.71
                              0.67
                                        0.67
                                                   150
   macro avg
weighted avg
                   0.72
                              0.73
                                        0.72
                                                   150
```

----- Confusion Matrix -------Confusion Matrix:

[[87 11]



- As can be seen in classification report and confusion matrix, the number of patients being clasified accurately at class 0 has an precision 0.75 which is only 0.08 higher than the number of patients being classified at class 1 with 0.68. From the precision score, the precision scores in this model is quite balanced and better than above precision score. However, it is hard to tell that whether this one is good for our purpose is to predict whether patient would or would not develop sepssis during their stay in ICU. Since precision shows quite good ability of our model to differ the "patient would develop sepssis" class from the other, but, unfortunately, it doesn't give an idea of whether we have found all the patient who would develop sepssis.
- Looking into other metrics in detail, recall score for class 0 is high at 0.89 this will determine how many patients at class 0 being classified accurately. The model is good at detecting patients would not develop sepssis during their stay in ICU, supporting with 0.75 in precision tells that 75% of the predictions of class 0 is classified correctly. This is somehow our goal but when we look into the class 1 the model does not perform really well. Since the ultimate goal of our problem is to mitigate both the risk of health complication and staff allocation, above model does not fulfill the first goal. The model performed below average, it failed to predict the classification of patient with positive label, the score is only 0.44 for recall. This is a very low rate to detect correctly patient with high potential to develop sepssis. Looking into the confusion matrix to gain more insight. This low score of recall on class 1 might be caused due to high percentage of False Negative, at 19.33% this rate is unacceptable and it not meet our goal.

- F1 score in class 0 is high which is undoubted as F1 is the harmony of precision and recall. Therefore, the balance recall and precision is the higher f1 is. On the other hand, F1 score for classifying the patient with label 1 are pretty low just a little bit higher than average of 0.53.
- In conclusion, this model is good at correctly classify patient would not likely to develop sepssis but perform poorly on the other label. The False Negative rate is higher, this is the field we will need to carefully consider.

Notice

The class 0 always have higher metric's score in 3 above models as the dataset is imbalanced. I will apply resampling techniques in order to achieve better scores in predicting class 1 for below models. I believe that resampling will make model learn better the class 1

Model 4: Logistic Regression Hyperparameter Tuning with Regularisation + SMOTE

Why applying regularisation

By avoiding the algorithm from overfitting the training dataset, regularization may be used to build models that generalize better to unknown data.

Why applying SMOTE

- SMOTE, or Synthetic Minority Oversampling Technique, is an oversampling technique, however it differs from conventional oversampling in several ways.
- SMOTE is a data augmentation method that generates synthetic data points from the
 original data points. SMOTE can be thought of as a more sophisticated variant of
 oversampling or as a data augmentation method in its own right. The advantage of
 SMOTE is that you are not making duplicates, but rather slightly different synthetic data
 points from the original data points.
- In a conventional oversampling strategy, minority data are reproduced from the population of minority data. While this enhances the data set, it adds no additional information or variety to the machine learning model.
- Most advantage that I bring SMOTE into usage is that we have the ability to adjust algorithm using SMOTE to decrease false negatives while boosting false positives.

Extra: How SMOTE works: SMOTE generates synthetic data using a k-nearest neighbor method. SMOTE begins by selecting random data from the minority class, and then sets the data's k-nearest neighbors. The random data would then be combined with the randomly chosen k-nearest neighbour to create synthetic data.

```
'logis__penalty' : ['l1', 'l2', 'elastic-net'],
         'logis solver': ['newton-cg', 'lbfgs', 'liblinear', 'sag', 'saga'],
     'logis 11 ratio':np.arange(0,1,0.005),
     'logis C':np.arange(0,5,0.01),
 'logis class weight':[dict, 'balanced']}
grid lr hyper smote = RandomizedSearchCV(pipe lr hyper smote,param distributi
grid lr hyper smote.fit(X train, Y train)
/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
sklearn/linear model/ logistic.py:1476: UserWarning: 11 ratio parameter is onl
y used when penalty is 'elasticnet'. Got (penalty=12)
  warnings.warn(
/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
sklearn/linear model/ logistic.py:1476: UserWarning: 11 ratio parameter is onl
y used when penalty is 'elasticnet'. Got (penalty=12)
  warnings.warn(
/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
sklearn/linear model/ logistic.py:1476: UserWarning: 11 ratio parameter is onl
y used when penalty is 'elasticnet'. Got (penalty=12)
  warnings.warn(
/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
sklearn/linear model/ logistic.py:1476: UserWarning: 11 ratio parameter is onl
y used when penalty is 'elasticnet'. Got (penalty=12)
  warnings.warn(
/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
sklearn/linear_model/_logistic.py:1476: UserWarning: l1_ratio parameter is onl
y used when penalty is 'elasticnet'. Got (penalty=12)
  warnings.warn(
/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
sklearn/linear model/ logistic.py:1476: UserWarning: 11 ratio parameter is onl
y used when penalty is 'elasticnet'. Got (penalty=11)
  warnings.warn(
/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
sklearn/linear_model/_logistic.py:1476: UserWarning: 11 ratio parameter is onl
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  warnings.warn(
/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
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sklearn/linear model/ logistic.py:1476: UserWarning: 11 ratio parameter is onl
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  warnings.warn(
/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
sklearn/linear_model/_logistic.py:1476: UserWarning: l1_ratio parameter is onl
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  warnings.warn(
/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
sklearn/linear_model/_logistic.py:1476: UserWarning: l1_ratio parameter is onl
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 warnings.warn(
/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
sklearn/linear model/ logistic.py:1476: UserWarning: 11 ratio parameter is onl
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  warnings.warn(
/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
sklearn/linear_model/_logistic.py:1476: UserWarning: l1_ratio parameter is onl
y used when penalty is 'elasticnet'. Got (penalty=12)
  warnings.warn(
/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
sklearn/linear model/ logistic.py:1476: UserWarning: 11 ratio parameter is onl
y used when penalty is 'elasticnet'. Got (penalty=12)
```

```
warnings.warn(
/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
sklearn/linear model/ logistic.py:1476: UserWarning: 11 ratio parameter is onl
y used when penalty is 'elasticnet'. Got (penalty=12)
  warnings.warn(
/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
sklearn/linear model/ logistic.py:1476: UserWarning: 11 ratio parameter is onl
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  warnings.warn(
/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
sklearn/linear model/ logistic.py:1476: UserWarning: 11 ratio parameter is onl
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  warnings.warn(
/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
sklearn/linear model/ logistic.py:1476: UserWarning: 11 ratio parameter is onl
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  warnings.warn(
/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
sklearn/linear model/ logistic.py:1476: UserWarning: 11 ratio parameter is onl
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 warnings.warn(
/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
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which means the coef did not converge
  warnings.warn(
/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
sklearn/model selection/ validation.py:372: FitFailedWarning:
250 fits failed out of a total of 500.
The score on these train-test partitions for these parameters will be set to n
If these failures are not expected, you can try to debug them by setting error
score='raise'.
Below are more details about the failures:
45 fits failed with the following error:
Traceback (most recent call last):
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/sklearn/model selection/ validation.py", line 680, in fit and score
    estimator.fit(X train, y train, **fit params)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/imblearn/pipeline.py", line 272, in fit
    self._final_estimator.fit(Xt, yt, **fit_params_last_step)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/sklearn/linear model/ logistic.py", line 1461, in fit
    solver = check solver(self.solver, self.penalty, self.dual)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/sklearn/linear_model/_logistic.py", line 447, in _check_solver
    raise ValueError(
ValueError: Solver lbfgs supports only '12' or 'none' penalties, got 11 penalt
30 fits failed with the following error:
Traceback (most recent call last):
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/sklearn/model_selection/_validation.py", line 680, in _fit_and_score
    estimator.fit(X_train, y_train, **fit_params)
```

```
File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/imblearn/pipeline.py", line 272, in fit
    self. final estimator.fit(Xt, yt, **fit params last step)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/sklearn/linear model/ logistic.py", line 1461, in fit
    solver = _check_solver(self.solver, self.penalty, self.dual)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/sklearn/linear model/ logistic.py", line 447, in check solver
    raise ValueError(
ValueError: Solver sag supports only '12' or 'none' penalties, got 11 penalty.
135 fits failed with the following error:
Traceback (most recent call last):
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/sklearn/model_selection/_validation.py", line 680, in _fit_and_score
    estimator.fit(X_train, y_train, **fit_params)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/imblearn/pipeline.py", line 272, in fit
    self. final estimator.fit(Xt, yt, **fit params last step)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/sklearn/linear_model/_logistic.py", line 1461, in fit
    solver = _check_solver(self.solver, self.penalty, self.dual)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/sklearn/linear_model/_logistic.py", line 441, in _check_solver
    raise ValueError(
ValueError: Logistic Regression supports only penalties in ['11', '12', 'elast
icnet', 'none'], got elastic-net.
25 fits failed with the following error:
Traceback (most recent call last):
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/sklearn/model selection/ validation.py", line 680, in fit and score
    estimator.fit(X train, y train, **fit params)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/imblearn/pipeline.py", line 272, in fit
    self._final_estimator.fit(Xt, yt, **fit_params_last_step)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/sklearn/linear_model/_logistic.py", line 1461, in fit
    solver = check solver(self.solver, self.penalty, self.dual)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/sklearn/linear_model/_logistic.py", line 447, in _check_solver
    raise ValueError(
ValueError: Solver newton-cg supports only '12' or 'none' penalties, got 11 pe
nalty.
______
15 fits failed with the following error:
Traceback (most recent call last):
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/sklearn/model selection/ validation.py", line 680, in fit and score
    estimator.fit(X_train, y_train, **fit_params)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/imblearn/pipeline.py", line 272, in fit
    self. final estimator.fit(Xt, yt, **fit params last step)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/sklearn/linear_model/_logistic.py", line 1528, in fit
    self.coef_, self.intercept_, n_iter_ = _fit_liblinear(
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
```

ackages/sklearn/svm/_base.py", line 1150, in _fit_liblinear

```
class weight = compute class weight(class weight, classes=classes , y=y)
          File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
        ackages/sklearn/utils/class weight.py", line 42, in compute class weight
            if class weight is None or len(class weight) == 0:
        TypeError: object of type 'type' has no len()
          warnings.warn(some fits failed message, FitFailedWarning)
        /Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
        sklearn/model selection/ search.py:969: UserWarning: One or more of the test s
        cores are non-finite: [0.67664523 0.68434343
                                                           nan 0.67664523
                                                                                  nan
         0.67664523
         0.6058462 0.60427409 0.60427409
                                                 nan
                                                            nan 0.60427409
                nan 0.60771611
                                                            nan 0.68730648
                                      nan
                                                 nan
         0.6058462
                          nan 0.6058462 0.67664523 0.68920607 0.60427409
         0.68659638
                          nan 0.6058462 0.67664523
         0.67646971
                          nan 0.6058462 0.67664523
                                                            nan
                                                                       nan
                           nan 0.60931451 0.6058462
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                           nan 0.60771611
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          warnings.warn(
        /Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
        sklearn/linear_model/_logistic.py:1476: UserWarning: l1_ratio parameter is onl
        y used when penalty is 'elasticnet'. Got (penalty=12)
          warnings.warn(
        RandomizedSearchCV(cv=StratifiedKFold(n_splits=5, random_state=1, shuffle=Tru
Out[]:
                           estimator=Pipeline(steps=[('smote',
                                                      SMOTE(random_state=1,
                                                            sampling strategy='minorit
        y')),
                                                     ('logis',
                                                      LogisticRegression(max iter=100
        0,
                                                                         random_state=
        1))]),
                           n iter=100.
                           param distributions={'logis C': array([0. , 0.01, 0.02,
        0.03, 0.04, 0.05, 0.06, 0.07, 0.08, 0.09, 0.1,
               0.11, 0.12, 0.13, 0.14, 0....
               0.765, 0.77 , 0.775, 0.78 , 0.785, 0.79 , 0.795, 0.8 , 0.805,
               0.81 , 0.815, 0.82 , 0.825, 0.83 , 0.835, 0.84 , 0.845, 0.85 ,
               0.855, 0.86 , 0.865, 0.87 , 0.875, 0.88 , 0.885, 0.89 , 0.895,
               0.9 , 0.905, 0.91 , 0.915, 0.92 , 0.925, 0.93 , 0.935, 0.94 ,
               0.945, 0.95, 0.955, 0.96, 0.965, 0.97, 0.975, 0.98, 0.985,
               0.99 , 0.995]),
                                                'logis penalty': ['l1', 'l2',
                                                                   'elastic-net'],
                                                 'logis__solver': ['newton-cg', 'lbfg
        s',
                                                                  'liblinear', 'sag',
                                                                  'saga']},
                           scoring=make scorer(f1 score))
In [ ]:
         print('Average F1 score of best param:%.3f'%(grid lr hyper smote.best score )
         print('Best parameter using %s'%(grid lr hyper smote.best params ))
```

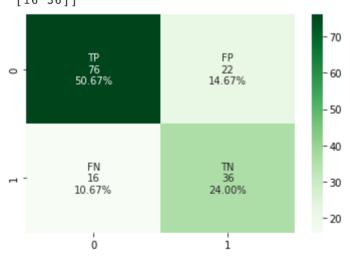
```
Average F1 score of best param:0.694

Best parameter using {'logis_solver': 'liblinear', 'logis_penalty': 'l2', 'logis_l1_ratio': 0.265, 'logis_class_weight': 'balanced', 'logis_C': 3.33}
```

```
----- Evaluation metrics -----
Accuracy | Test: 74.667, Train: 75.893, Difference: 1.226
Precision | Test: 62.069, Train: 63.128, Difference: 1.060
            Test: 69.231, Train: 72.903, Difference: 3.672
          Test: 65.455, Train: 67.665, Difference: 2.210
F1 score
ROC - AUC
           | Test: 73.391, Train: 75.189, Difference: 1.798
           | Test: 0.253, Train: 0.241, (Test - Train): 0.012
           Test: 0.253, Train: 0.241, (Test - Train): 0.012
----- Classification Report -----
             precision
                         recall f1-score
                                            support
          0
                            0.78
                                     0.80
                                                 98
                  0.83
          1
                  0.62
                            0.69
                                     0.65
                                                 52
                                     0.75
                                                150
   accuracy
                                     0.73
  macro avg
                  0.72
                            0.73
                                                150
weighted avg
                  0.75
                            0.75
                                     0.75
                                                150
```

----- Confusion Matrix ------ Confusion Matrix:

[[76 22] [16 36]]



- The average F1_score on cross validation is 0.694 which is the highest F1_score among above F1 score.
- This seems to be a better model. However, until any further determination, we need to perform evaluation on this model.
- It can be said that the gap between recall in class 0 and class 1 is not large only 0.08, with 0.78 and 0.69 respectively. The recall score is calculate by taking True Positive (TP) / (True Positive (TP) + False Negative). This is call True Positive rate and it can tell us that how many patients at specific class being classified correctly. In this case, the recall score for class 0 is higher with 80% of correctly that model

classifies patient who would not develop sepssis -> actually not develop sepssis in their period at ICU. Also, in class 1 the model also classifies moderated number of patient who would likely to develop sepssis -> to actually have sepssis during their stay, with 68%. This rate is moderately acceptable with only the rate of False Negative reduce to only 10.67%. The number of record is 16 compared to around ~29-33 records in above model.

- The precision score is calculated by taking True Positive (TP)/ (True Positive + False Positive). In term of precision score, model has high probability of correct prediction of class 0. However, when it comes to class 1, the precision score is quite low, at 0.62 model does not perform accurately when it predicts the class 1. This low rate can possibly be caused by the increase of False Positive and reduction of True Positive.
- Since we cares about saving and detecting as much patient with high probability to develop sepssis as possible (Detecting positive), the F1 score in this case can be considered the best so far. F1 score is the unit of measurement that only care about positive, and is the harmonic mean between precision and recall. Therefore, this score could not be high if either precision or recall is low. In this case, the model which classifies the patient that would not develop sepssis is well enough, with F1 score for the class 0 is 0.8. Additionally, the precision and recall scores as mentioned above is not considered low (higher than the average at least we do not predict patient just by flipping the coin!).
- The only limitation of this model is that the False Positive rate is still considered high.
- F1 is 0.65 and this is not a really good score. Although me mitigate the number of patient would sepssis that incorrectly predicted, we still need to optimize the ICU's resource, since keeping these patients with low probability of sepssis will overwhelm the human resources in hospital management. We still can have better model

Model 5: Logistic Regression Hyperparameter with Under Sampling

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In [ ]:
         pipeline under = imbpipeline(steps = [
                 ['randomunder', RandomUnderSampler(random state=1)],
                                         ['logis', LogisticRegression(random state=1,m
         stratified kfold = StratifiedKFold(n splits=4,
                                                 shuffle=True,
                                                random state=1)
         logis_param_grid = {
                 'logis tol': np.arange(0,1,0.0001),
             'logis 11 ratio':np.arange(0,2,0.005),
                 'logis__penalty' : ['l1', 'l2', 'elastic-net'],
                 'logis_solver': ['newton-cg', 'lbfgs', 'liblinear', 'sag', 'saga'],
             'logis C':np.arange(0,10,0.005),
         'logis__class_weight':[dict,'balanced']}
         grid under lr = RandomizedSearchCV(pipeline under, param distributions=logis p
         grid under lr.fit(X train, Y train)
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  warnings.warn(
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sklearn/linear model/ logistic.py:1476: UserWarning: 11 ratio parameter is onl
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y used when penalty is 'elasticnet'. Got (penalty=11)
  warnings.warn(
/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
sklearn/model selection/ validation.py:372: FitFailedWarning:
196 fits failed out of a total of 320.
The score on these train-test partitions for these parameters will be set to n
If these failures are not expected, you can try to debug them by setting error
score='raise'.
Below are more details about the failures:
16 fits failed with the following error:
Traceback (most recent call last):
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/sklearn/model_selection/_validation.py", line 680, in _fit_and_score
    estimator.fit(X_train, y_train, **fit_params)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/imblearn/pipeline.py", line 272, in fit
    self. final estimator.fit(Xt, yt, **fit params last step)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
```

ackages/sklearn/linear_model/_logistic.py", line 1461, in fit

solver = _check_solver(self.solver, self.penalty, self.dual)

```
File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/sklearn/linear_model/_logistic.py", line 447, in _check_solver
    raise ValueError(
ValueError: Solver sag supports only '12' or 'none' penalties, got 11 penalty.
128 fits failed with the following error:
Traceback (most recent call last):
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/sklearn/model selection/ validation.py", line 680, in fit and score
    estimator.fit(X train, y train, **fit params)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/imblearn/pipeline.py", line 272, in fit
    self. final estimator.fit(Xt, yt, **fit params last step)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/sklearn/linear_model/_logistic.py", line 1461, in fit
    solver = _check_solver(self.solver, self.penalty, self.dual)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/sklearn/linear model/ logistic.py", line 441, in check solver
    raise ValueError(
ValueError: Logistic Regression supports only penalties in ['11', '12', 'elast
icnet', 'none'], got elastic-net.
______
28 fits failed with the following error:
Traceback (most recent call last):
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/sklearn/model_selection/_validation.py", line 680, in _fit_and_score
    estimator.fit(X train, y train, **fit params)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/imblearn/pipeline.py", line 272, in fit
    self._final_estimator.fit(Xt, yt, **fit_params_last_step)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/sklearn/linear model/ logistic.py", line 1461, in fit
    solver = check solver(self.solver, self.penalty, self.dual)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/sklearn/linear_model/_logistic.py", line 447, in _check_solver
    raise ValueError(
ValueError: Solver newton-cg supports only '12' or 'none' penalties, got 11 pe
nalty.
16 fits failed with the following error:
Traceback (most recent call last):
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/sklearn/model selection/ validation.py", line 680, in fit and score
    estimator.fit(X train, y train, **fit params)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/imblearn/pipeline.py", line 272, in fit
    self._final_estimator.fit(Xt, yt, **fit_params_last_step)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/sklearn/linear_model/_logistic.py", line 1528, in fit
    self.coef_, self.intercept_, n_iter_ = _fit_liblinear(
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/sklearn/svm/_base.py", line 1150, in _fit_liblinear
    class weight = compute class weight(class weight, classes=classes , y=y)
  File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
ackages/sklearn/utils/class weight.py", line 42, in compute class weight
    if class_weight is None or len(class_weight) == 0:
TypeError: object of type 'type' has no len()
```

```
8 fits failed with the following error:
        Traceback (most recent call last):
          File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
        ackages/sklearn/model_selection/_validation.py", line 680, in _fit_and_score
            estimator.fit(X train, y train, **fit params)
          File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
        ackages/imblearn/pipeline.py", line 272, in fit
            self._final_estimator.fit(Xt, yt, **fit_params_last_step)
          File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
        ackages/sklearn/linear model/ logistic.py", line 1461, in fit
            solver = check solver(self.solver, self.penalty, self.dual)
          File "/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-p
        ackages/sklearn/linear_model/_logistic.py", line 447, in _check_solver
            raise ValueError(
        ValueError: Solver lbfgs supports only '12' or 'none' penalties, got 11 penalt
        у.
          warnings.warn(some fits failed message, FitFailedWarning)
        /Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
        sklearn/model selection/ search.py:969: UserWarning: One or more of the test s
        cores are non-finite: [
                                      nan
                                                 nan
                                                            nan
        0.5645457
                nan 0.49730536 0.55097477
                                                 nan
                                                            nan
                                                                       nan
                nan 0.56758947 0.53963625
                                                           nan
                                                                       nan
                          nan 0.56701091
                                               nan
                                                           nan
                                                                       nan
                nan 0.58177612
                                nan 0.3836951
                                                           nan 0.56688829
                          nan 0.66908511
                                                           nan 0.58082303
                                             nan
         0.56663745
                          nan 0.3836951
                                                nan 0.56804339
                nan 0.56921785
                                    nan 0.55097477
                                     nan 0.5645457 0.56701091 0.55097477
                nan 0.66716754
                                                nan 0.55097477 0.56701091
         0.55097477
                          nan 0.56701091
                          nan 0.66910385
                                                nan 0.66910385
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                                                                       nan
                                               nan 0.66506904 0.5645457
         0.56758947
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                nan
                          nanl
          warnings.warn(
        /Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
        sklearn/linear model/ logistic.py:1476: UserWarning: 11 ratio parameter is onl
        y used when penalty is 'elasticnet'. Got (penalty=12)
          warnings.warn(
        RandomizedSearchCV(cv=StratifiedKFold(n splits=4, random state=1, shuffle=Tru
Out[ ]:
        e),
                           estimator=Pipeline(steps=[['nearmiss',
                                                      RandomUnderSampler(random state=
        1)],
                                                     ['logis',
                                                      LogisticRegression(max iter=500,
                                                                         random state=
        1)]]),
                           n iter=80,
                           param_distributions={'logis__C': array([0.000e+00, 5.000e-0
        3, 1.000e-02, ..., 9.985e+00, 9.990e+00,
               9.995e+00]),
                                                'logis__class_weight': [...
               1.845, 1.85 , 1.855, 1.86 , 1.865, 1.87 , 1.875, 1.88 , 1.885,
               1.89 , 1.895, 1.9 , 1.905, 1.91 , 1.915, 1.92 , 1.925, 1.93 ,
               1.935, 1.94 , 1.945, 1.95 , 1.955, 1.96 , 1.965, 1.97 , 1.975,
               1.98 , 1.985, 1.99 , 1.995]),
                                                'logis penalty': ['11', '12',
                                                                   'elastic-net'],
                                                'logis solver': ['newton-cg', 'lbfg
        s',
```

```
'liblinear', 'sag',
                                                                 'saga'],
                                               'logis tol': array([0.000e+00, 1.000e
        -04, 2.000e-04, ..., 9.997e-01, 9.998e-01,
               9.999e-01])},
                          scoring=make scorer(f1 score))
In [ ]:
        print('Average F1 score of best param:%.3f'%(grid under lr.best score ))
        print('Best parameter using %s'%(grid under lr.best params ))
        Average F1 score of best param:0.671
        Best parameter using {'logis tol': 0.482100000000003, 'logis solver': 'new
        ton-cg', 'logis penalty': '12', 'logis 11 ratio': 0.365, 'logis class weigh
        t': <class 'dict'>, 'logis C': 6.95}
In [ ]:
        lr_under = LogisticRegression(solver='newton-cg', penalty='12', 11_ratio=0.36
        pipe lr under = imbpipeline([('under', RandomUnderSampler(random state=1)), (
        pipe lr under.fit(X train,Y train)
        evaluation(pipe lr under, X test, Y test, X train, Y train)
        ----- Evaluation metrics -----
        Accuracy | Test: 74.667, Train: 76.786, Difference: 2.119
        Precision | Test: 62.500, Train: 65.455, Difference: 2.955
                   Test: 67.308, Train: 69.677, Difference: 2.370
        Recall
                   Test: 64.815, Train: 67.500, Difference: 2.685
        F1 score
                  Test: 72.940, Train: 75.112, Difference: 2.172
        MAE
                    | Test: 0.253, Train: 0.232, (Test - Train) : 0.021
                   Test: 0.253, Train: 0.232, (Test - Train): 0.021
        MSE
        ----- Classification Report ------
                     precision
                                 recall f1-score
                                                   support
                   0
                          0.82
                                    0.79
                                              0.80
                                                          98
                          0.62
                                    0.67
                                              0.65
                                                          52
                                              0.75
                                                         150
            accuracy
                          0.72
                                    0.73
                                              0.73
                                                         150
           macro avg
                                              0.75
        weighted avg
                          0.75
                                    0.75
                                                         150
        ----- Confusion Matrix -----
        Confusion Matrix:
         [[77 21]
         [17 35]]
                                   ΕĐ
                                                50
                                                - 30
                11.33%
                                               - 20
```

• The model have all metrics just above average a little bit.

1

0

- It can be said that the gap between recall in class 0 and class 1 is not large only 0.12, with 0.79 and 0.67 respectively. The recall score is calculate by taking True Positive (TP) / (True Positive (TP) + False Negative). This is call True Positive rate and it can tell us that how many patients at specific class being classified correctly. In this case, the recall score for class 0 is higher with 79% of correctly that model classifies patient who would not develop sepssis -> actually not develop sepssis in their period at ICU. Also, in class 1 the model also classifies moderated number of patient who would likely to develop sepssis -> to actually have sepssis during their stay, with 65%. This rate is somehow quite low with only the rate of False Negative reduce to only 11.33%. The number of record is 17 compared to around ~29-33 records in above model.
- The precision score is calculated by taking True Positive (TP)/ (True Positive + False Positive). In term of precision score, model has high probability of correct prediction of class 0. However, when it comes to class 1, the precision score is quite low, at 0.62 model does not perform accurately when it predicts the class 1. This low rate can possibly be caused by the increase of False Positive and reduction of True Positive.

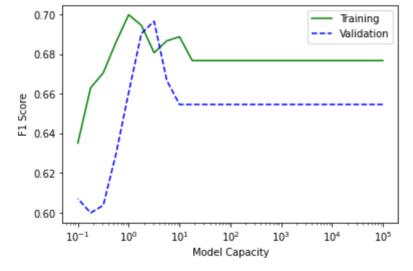
Model 6: Logistic Regression with regulization + SMOTE

```
In []:
         lambda paras = np.logspace(-5, 1, num=25) # establish the lambda values to
         # Then search
         train performace = list()
         valid performace = list()
         for lambda para in lambda paras:
                 clf = LogisticRegression(penalty='12', C =1/lambda_para,
                                      random_state=1, solver='liblinear', max_iter=100
                                      class weight='balanced', tol=0.0001, l1 ratio=0
                                                                         # define pipe
                 pipeline smote lr = imbpipeline(steps =
         [['smote', SMOTE(sampling strategy='minority',random state=1)],
         ['logis', clf]])
             #create a classifier with a different lambda value
                 model =pipeline smote lr.fit(X train, Y train)
                                                                      #train the clas
                 train pred = model.predict(X train)
                 train f1 = f1 score(Y train, train pred) #calculate the train f1-sc
                 val pred = model.predict(X test)
                                                            #calculate the validation
                 val f1 = f1 score(Y test, val pred)
                 train performace.append(train f1)
                 valid performace.append(val f1)
```

```
/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
sklearn/linear_model/_logistic.py:1476: UserWarning: l1_ratio parameter is onl
y used when penalty is 'elasticnet'. Got (penalty=12)
   warnings.warn(
/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
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```
warnings.warn(
/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
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/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
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/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
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sklearn/linear model/ logistic.py:1476: UserWarning: 11 ratio parameter is onl
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  warnings.warn(
/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
sklearn/linear_model/_logistic.py:1476: UserWarning: 11 ratio parameter is onl
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  warnings.warn(
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  warnings.warn(
/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
sklearn/linear model/ logistic.py:1476: UserWarning: 11 ratio parameter is onl
y used when penalty is 'elasticnet'. Got (penalty=12)
  warnings.warn(
/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
```

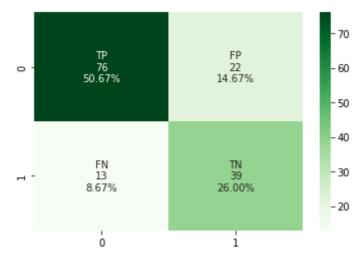
```
warnings.warn(
        /Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
        sklearn/linear model/ logistic.py:1476: UserWarning: 11 ratio parameter is onl
        y used when penalty is 'elasticnet'. Got (penalty=12)
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        /Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
        sklearn/linear model/ logistic.py:1476: UserWarning: 11 ratio parameter is onl
        y used when penalty is 'elasticnet'. Got (penalty=12)
          warnings.warn(
In [ ]:
```



```
In []:
    result = zip(train_performace, valid_performace)
    # print(list(result))
    print('\n'.join('{}: {}'.format(*k) for k in enumerate(result)))

0: (0.6766467065868264, 0.65454545454545)
1: (0.6766467065868264, 0.65454545454545)
2: (0.6766467065868264, 0.65454545454545)
3: (0.6766467065868264, 0.65454545454545)
4: (0.6766467065868264, 0.65454545454545)
5: (0.6766467065868264, 0.65454545454545)
6: (0.6766467065868264, 0.65454545454545)
7: (0.6766467065868264, 0.65454545454545)
8: (0.6766467065868264, 0.65454545454545)
```

```
9: (0.6766467065868264, 0.6545454545454545)
        10: (0.6766467065868264, 0.6545454545454545)
        11: (0.6766467065868264, 0.6545454545454545)
        12: (0.6766467065868264, 0.6545454545454545)
        13: (0.6766467065868264, 0.6545454545454545)
        14: (0.6766467065868264, 0.6545454545454545)
        15: (0.6766467065868264, 0.6545454545454545)
        16: (0.688622754491018, 0.6545454545454545)
        17: (0.6865671641791045, 0.666666666666666)
        18: (0.6805970149253732, 0.6964285714285715)
        19: (0.6943620178041544, 0.6902654867256638)
        20: (0.6997084548104956, 0.6605504587155963)
        21: (0.685878962536023, 0.6296296296296297)
        22: (0.670487106017192, 0.6037735849056604)
        23: (0.6628895184135979, 0.6)
        24: (0.6350974930362117, 0.6071428571428571)
In []:
        clf = LogisticRegression(penalty='12', C = 1.72,
                                 random state=1, solver='liblinear', max iter=1000 ,
                                 class weight='balanced', 11 ratio=0.1, tol=0.0001)
        pipeline smote = imbpipeline(steps =
         [['smote', SMOTE(sampling_strategy='minority',random_state=1)],
         ['logis', clf]])
        model lr = pipeline_smote.fit(X_train, Y_train)
        evaluation(model lr, X test, Y test, X train, Y train)
        /Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
        sklearn/linear model/ logistic.py:1476: UserWarning: 11 ratio parameter is onl
        y used when penalty is 'elasticnet'. Got (penalty=12)
          warnings.warn(
        ----- Evaluation metrics -----
        Accuracy | Test: 76.667, Train: 77.232, Difference: 0.565
        Precision | Test: 63.934, Train: 64.324, Difference: 0.390
        Recall
                   Test: 75.000, Train: 76.774, Difference: 1.774
        F1 score | Test: 69.027, Train: 70.000, Difference: 0.973
        ROC - AUC | Test: 76.276, Train: 77.124, Difference: 0.849
                    | Test: 0.233, Train: 0.228, (Test - Train): 0.006
        MAE
                    | Test: 0.233, Train: 0.228, (Test - Train): 0.006
        MSE
        ----- Classification Report -----
                     precision
                                 recall f1-score
                   0
                          0.85
                                    0.78
                                              0.81
                                                          98
                          0.64
                                    0.75
                                              0.69
                   1
                                                          52
            accuracy
                                              0.77
                                                         150
                          0.75
                                    0.76
                                              0.75
                                                         150
           macro avg
        weighted avg
                          0.78
                                    0.77
                                              0.77
                                                         150
        ----- Confusion Matrix -----
        Confusion Matrix:
         [[76 22]
         [13 39]]
```



In []:

from sklearn.model_selection import cross_val_score,StratifiedKFold
stratifiedKFold(n_splits=5,random_state=1, shuffle=True)
score=cross_val_score(clf,X_train,Y_train,cv=stratifiedkf,scoring='f1')

/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/sklearn/linear_model/_logistic.py:1476: UserWarning: l1_ratio parameter is only used when penalty is 'elasticnet'. Got (penalty=12)

warnings.warn(

/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/sklearn/utils/validation.py:993: DataConversionWarning: A column-vector y was passed when a 1d array was expected. Please change the shape of y to (n_sample s,), for example using ravel().

y = column_or_ld(y, warn=True)

/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/sklearn/linear_model/_logistic.py:1476: UserWarning: l1_ratio parameter is only used when penalty is 'elasticnet'. Got (penalty=12)

warnings.warn(

/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/sklearn/utils/validation.py:993: DataConversionWarning: A column-vector y was passed when a 1d array was expected. Please change the shape of y to (n_sample s,), for example using ravel().

y = column or 1d(y, warn=True)

/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/sklearn/linear_model/_logistic.py:1476: UserWarning: l1_ratio parameter is only used when penalty is 'elasticnet'. Got (penalty=12)

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/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/sklearn/utils/validation.py:993: DataConversionWarning: A column-vector y was passed when a 1d array was expected. Please change the shape of y to (n_sample s,), for example using ravel().

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/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/sklearn/utils/validation.py:993: DataConversionWarning: A column-vector y was passed when a 1d array was expected. Please change the shape of y to (n_sample s,), for example using ravel().

y = column or 1d(y, warn=True)

/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/sklearn/linear_model/_logistic.py:1476: UserWarning: l1_ratio parameter is only used when penalty is 'elasticnet'. Got (penalty=12)

warnings.warn(

/Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/sklearn/utils/validation.py:993: DataConversionWarning: A column-vector y was passed when a 1d array was expected. Please change the shape of y to (n sample

```
s, ), for example using ravel().
    y = column_or_1d(y, warn=True)

In []:
    print("Cross Validation Scores are {}".format(score))
    print("Average Cross Validation score :{}".format(score.mean()))
```

Cross Validation Scores are [0.65714286 0.72972973 0.61538462 0.76470588 0.687 5]

Average Cross Validation score :0.6908926169220286

- The average F1_score on cross validation is 0.69 which is the second highest F1_score among above all F1 scores.
- This model have the F1 score of 0.69 recall of 0.75 precision of 0.64 accuracy of 76.7%. However, until any further determination, we need to perform evaluation on this model.
- Depriving from classification table and confusion matrix, the number of patients being clasified accurately at class 0 has an precision 0.85 which is a high score compared to the number of patients being classified at class 1 by the model only 0.59 above the average a little bit which is not a good model in predicting the patient who needs to stay longer at the hospital.
- It can be said that the gap between recall in class 0 and class 1 is not large only 0.03, with 0.78 and 0.75 respectively. The recall score tells us that the probability of True Positive (TP) predictions from all positive samples in dataset. Model has moderatedly good ability to classify both class 0 and 1, with more than 3/4 correct record. This is call True Positive rate and it can tell us that how many patients at specific class being classified correctly. The decrease in False Negative might leads to the significant improvement in recall score.
- The recall seems to be good enough, now let look at the precision score. The precision score is calculated by taking True Positive (TP)/ (True Positive + False Positive). In this case, the model has high probability of correct prediction of class 0 with score of 0.85 or 85% of correctly differ the patient with "Negative" label on sepssis class from the other. On the other hand, when it comes to class 1, the precision score is pretty lower, at 0.64 or 64%. This can tell that model does not perform accurately when it predicts the class 1. This low rate can possibly be caused by the increase of False Positive and reduction of True Positive.
- Let take the motivation after the model development, we care about "mitigate the risk of health complications, and managing the ICU resources (such as bed availability, etc.)". Since we both want to correctly as much patient with high probability to develop sepssis as possible (Detecting positive) while reduce the resource need to take care of them. In this case, F1 is good unit of measurement that only care about positive, and is the harmonic mean between precision and recall.
- The False Positive which occupies 14.67% to the confusion matrix is an acceptable rate, although not the best, this rate won't put the pressure in ICU resources (such as bed availability, etc.). The model still misclassifies the patients who would not likely to

- develop sepssis (True Label 0) to be likely to develop sepssis (Predicted Label 1). But still, it is better to do the opposite situation.
- Therefore, this score must be considerably higher than average. In this case, the model which classifies the patient that would not develop sepssis is well enough, with F1 score for the class 0 is 0.81. Additionally, the F1 score for class 0 is 0.69, which have been significantly improved ever seen, and is one of the best F1 score of all above.

Ultimate Judgement and Analysis

So far Logistic Regression is the best approach among those models and methods to use in the real world with our problem based on below criteria:

- Logistic Regression is not overfitting easily compared to other model.
- It provides the smallest generalization GAP. With F1 score of 69% in testing dataset and 70% in the training dataset.
- Accruracy is the highest with 76% on testing set, with the smallest different compared to training accuracy of 77.232%.
- False Negative is lowest 8.67%.
- The accuracy when classified the patient in class 1 is the second highest (0.64)
- The ability to detect a class 0 and 1 is nearest to each other, and is considerably high of 75%.

Machine Learning model issue discussion:

From the table below we can say that:

Model	Accuracy Test	Accuracy Train	Diff Accuracy	F1 Test	F1 Train	Diff F1
Decision Tree default	65.33	100	34667	50	100	50
Decision Tree Hyperparameter Tuning	66	71. 652	5652	57.14	64.6	7.5
Random Forest Hyperparameter Tuning	70.67	91.74	21.1	50	87285	37.23
Logistic Regression Base model	73.33	78.8	5.5	53.5	66.7	14.2
Logistic Regression Hyperparameter Tuning with Regulization + SMOTE	74.7	75.9	1226	65.5	67.7	2.2
Logistic Regression Under Sampling Hyperparameter Tuning	75.3	76.8	1.5	65.4	67.9	2.4
Logistic Regression with Regulization and SMOTE - Tuning C	76.7	77.3	0.6	69	70	1

• First I will discuss about the overfitting problem, Decision Tree without Hyperparameter Tuning and Random Forest seems to be overfitted with 100% of accuracy in the training dataset, but perform poorly in the testing dataset around 50%. The other models still have a considerable GAP between the accuracy or F1 score in the testing and training

- dataset > 5%, which is Decision Tree with hyperparameter tuning and base model of logistic regression (without regulization). However, in models with resampling techniques applied in the pipeline with Logistic Regression -> the model seems not to be overfitted. With the application of regularisation in Logistic Regression, the model is prevented from being overfitting as we put penalty in the parameter. This is such an important things to note, as in the base model which is without regularisation we saw a huge generalisation GAP, and the significant higher accuracy on the training dataset.
- According to the dataset, the accuracy of Logistic Regression with Regularisation + SMOTE technique is the highest among those 4 models which is 76.7%. As already mentioned before, the accuracy score is optimal evaluation metrics for this issue, and also this metric is not wisely used to evaluate the imbalanced dataset, however, this also needed to be taken into account in our case. The most important metric we want to notice is F1 score. Among all the models, the Logistic Regression with Regularisation + SMOTE technique have the highest score it is stable in the cross validation process with 0.6908 as a mean for 5-folds. This model is the one that have most generalized characteristic as the GAP of F1 between train and test sets is guite small 0.98.
- According to confusion matrix report of each model, Logisitic Regression with
 regularisation and SMOTE Technique have the best False Negative of 8.47% (patient
 who is likely to develop sepssis but is predicted not to), and considerated low False
 Positive of 14.67%. The model is also good at predicting who is not likely to develop a
 sepssis with nearly 0.8 percentage of accuracy in recall. It can be able to determine how
 many patients at class 0 being classified correctly. While precision of class 0 can also
 tells us that model is good at differ one class 0 from all others.
- Taking context of the problem to this model, we care about 2 factors mitigate the risk and manage the resource of ICU well. In the first purpose, the chosen model is pretty well achieved. As the dataset is imbalanced and many cases is reported not to develop a sepssis during their stay at ICU. The model do it greatest job with 70% to detect the patient who is likely to develop sepssis. The noticeable thing here is the model have the lowest rate of False Negative. Since we more care about the positive detecting, we want to "Predict if a given in ICU would not develop a sepsis (Sepsis Negative / class 0) or will develop sepsis (Sepsis Positive / class 1) during their ICU stay". And Sepssis is a lifethreatening infection, we wants to minimize the rate of False Negative in our model, with good F1 score. In this case, the F1 score of 0.7 or 70% is acceptable.
- In term of resource management for ICU, the model can be able to detect and predict class 0 accurately with presion and recall of 0.85 and 0.78, respectively -> F1 score is 0.81 in the class 0. But at the same time, it is still can detect and predict the patient with class 1 at a moderated rate. Although, the False Positive rate is not the lowest in all above confusion matrix, it is a good rate of 14.67%. This won't put much pressure on the resource since we only incorrectly patient is is not likely to develop sepssis to have sepssis, but not much so the resource spend to check up on them is not much.
- Limitation of chosen model:
- It establishes linear boundaries. Logistic regression requires a linear relationship between the independent variables and the log odds.

- The primary constraint for Logistic Regression is the linear relationship between the dependent and independent variables.
- Algorithms that are more powerful and compact, such as Neural Networks, can easily surpass this one.

Save the model

```
In [ ]:
         import joblib
         # joblib.dump(clf, "./logistic regression.joblib")
         joblib.dump(pipeline smote, "./pipeline smote lr.joblib")
        ['./pipeline smote lr.joblib']
Out[ ]:
In [ ]:
         prediction dt['Sepssis'] = pipeline smote.predict(test dt)
        /Library/Frameworks/Python.framework/Versions/3.9/lib/python3.9/site-packages/
        sklearn/base.py:443: UserWarning: X has feature names, but LogisticRegression
        was fitted without feature names
          warnings.warn(
In [ ]:
         prediction_dt['Sepssis']
               0
Out[]:
               0
               0
               0
        4
               1
        164
        165
               0
        166
               0
        167
        168
        Name: Sepssis, Length: 169, dtype: int64
In [ ]:
         prediction dt['Sepssis']=prediction dt['Sepssis'].replace(0,'Negative')
In []:
         prediction dt['Sepssis']=prediction dt['Sepssis'].replace(1,'Positive')
In [ ]:
         prediction dt.to csv('s38751881 predictions.csv', header=True , index =False)
```

Reference Lists:

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