#### In [200]:

```
# here we are importing the all necessary packages
from imblearn.under sampling import RandomUnderSampler
import numpy as np
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
%matplotlib inline
import plotly.offline as py
py.init_notebook_mode(connected=True)
import plotly.graph_objs as go
import plotly.tools as tls
import os
import gc
import pandas as pd
import matplotlib.pyplot as plt
import time
import warnings
import numpy as np
from sklearn.ensemble import RandomForestClassifier
warnings.filterwarnings("ignore")
from sklearn import model_selection
from sklearn.linear_model import LogisticRegression
from scipy import stats
from sklearn.feature_extraction.text import CountVectorizer
from sklearn.preprocessing import StandardScaler
from sklearn.model_selection import train_test_split
from imblearn.over sampling import SMOTE
from sklearn.metrics import accuracy_score,precision_score,recall_score,f1_score
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
from imblearn.pipeline import Pipeline
from sklearn.model_selection import train_test_split
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LogisticRegression
from sklearn.model selection import cross val score
from sklearn.model selection import GridSearchCV
from sklearn.metrics import confusion matrix
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import RandomForestClassifier
import lightgbm as lgb
from sklearn.svm import SVC
# using one hot encoding
from sklearn.preprocessing import OneHotEncoder
from sklearn import metrics
from sklearn.feature_selection import SelectKBest
from sklearn.feature selection import chi2
from sklearn import metrics
import tensorflow
from tensorflow.keras.models import Sequential
from tensorflow.keras.layers import Dense
from tensorflow.keras.models import Model
```

#### In [201]:

```
# code for printing the confusion matrix
#https://gist.github.com/shaypal5/94c53d765083101efc0240d776a23823i
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
def print_confusion_matrix(confusion_matrix, class_names, figsize = (10,7), fontsize=14):
   df_cm = pd.DataFrame(
        confusion matrix, index=class names, columns=class names,
   fig = plt.figure(figsize=figsize)
        heatmap = sns.heatmap(df_cm, annot=True, fmt="d")
   except ValueError:
        raise ValueError("Confusion matrix values must be integers.")
   heatmap.yaxis.set_ticklabels(heatmap.yaxis.get_ticklabels(), rotation=0, ha='right', fo
   heatmap.xaxis.set_ticklabels(heatmap.xaxis.get_ticklabels(), rotation=0, ha='right', fo
   plt.ylabel('True label')
   plt.xlabel('Predicted label')
```

#### In [202]:

```
# reading the data using pandas
data=pd.read_csv('/content/drive/My Drive/Artificial engineering/diabetic_data.csv')
print("Number of data points:",data.shape[0])

condition = data['readmitted']=='<30'
data['readmitted'] = np.where(condition,1,0)</pre>
```

Number of data points: 101766

```
In [203]:
```

```
# splitting inot x and y
y=data['readmitted']
X=data.drop(columns=['readmitted'])
```

#### In [204]:

```
# printing the data columns
data.columns
```

#### Out[204]:

```
Index(['encounter_id', 'patient_nbr', 'race', 'gender', 'age', 'weight',
       'admission_type_id', 'discharge_disposition_id', 'admission_source_i
d',
       'time_in_hospital', 'payer_code', 'medical_specialty',
       'num_lab_procedures', 'num_procedures', 'num_medications',
       'number_outpatient', 'number_emergency', 'number_inpatient', 'diag_
1',
       'diag_2', 'diag_3', 'number_diagnoses', 'max_glu_serum', 'A1Cresult',
       'metformin', 'repaglinide', 'nateglinide', 'chlorpropamide',
       'glimepiride', 'acetohexamide', 'glipizide', 'glyburide', 'tolbutamid
е',
       'pioglitazone', 'rosiglitazone', 'acarbose', 'miglitol', 'troglitazon
e',
       'tolazamide', 'examide', 'citoglipton', 'insulin',
       'glyburide-metformin', 'glipizide-metformin',
       'glimepiride-pioglitazone', 'metformin-rosiglitazone',
       'metformin-pioglitazone', 'change', 'diabetesMed', 'readmitted'],
      dtype='object')
```

## In [205]:

# # printing the data types data.dtypes

### Out[205]:

040[205].	
encounter_id	int64
patient nbr	int64
race	object
gender	object
age	object
weight	object
admission_type_id	int64
discharge_disposition_id	int64
admission_source_id	int64
time_in_hospital	int64
payer_code	object
medical_specialty	object
num_lab_procedures	int64
num_procedures	int64
num_medications	int64
number_outpatient	int64
number_emergency	int64
number_inpatient	int64
diag_1	object
diag_2	object
diag_3	object
number_diagnoses	int64
max_glu_serum	object
A1Cresult	object
metformin	object
repaglinide	object
nateglinide	object
chlorpropamide	object
glimepiride	object
acetohexamide	object
glipizide	object
glyburide	object
tolbutamide	object
	_
pioglitazone	object
rosiglitazone	object
acarbose	object
miglitol	object
troglitazone	object
tolazamide	object
examide	object
citoglipton	object
insulin	object
glyburide-metformin	object
glipizide-metformin	object
glimepiride-pioglitazone	object
metformin-rosiglitazone	object
metformin-pioglitazone	object
change	object
diabetesMed	object
readmitted	int64
dtype: object	

## In [206]:

```
# splitting
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.33, stratify=y)
```

#### In [207]:

```
# taking all categroical data and convert into one hot encoding
enc = OneHotEncoder(handle_unknown='ignore')
enc.fit(X_train['race'].values.reshape(-1,1))
X_train_race=enc.transform(X_train['race'].values.reshape(-1,1))
X_test_race=enc.transform(X_test['race'].values.reshape(-1,1))
enc.fit(X_train['gender'].values.reshape(-1,1))
X_train_gender=enc.transform(X_train['gender'].values.reshape(-1,1))
X_test_gender=enc.transform(X_test['gender'].values.reshape(-1,1))
enc.fit(X_train['age'].values.reshape(-1,1))
X_train_age=enc.transform(X_train['age'].values.reshape(-1,1))
X_test_age=enc.transform(X_test['age'].values.reshape(-1,1))
enc.fit(X_train['weight'].values.reshape(-1,1))
X_train_weight=enc.transform(X_train['weight'].values.reshape(-1,1))
X_test_weight=enc.transform(X_test['weight'].values.reshape(-1,1))
enc.fit(X_train['payer_code'].values.reshape(-1,1))
X_train_payer_code=enc.transform(X_train['payer_code'].values.reshape(-1,1))
X_test_payer_code=enc.transform(X_test['payer_code'].values.reshape(-1,1))
enc.fit(X_train['medical_specialty'].values.reshape(-1,1))
X_train_medical_specialty=enc.transform(X_train['medical_specialty'].values.reshape(-1,1))
X_test_medical_specialty=enc.transform(X_test['medical_specialty'].values.reshape(-1,1))
enc.fit(X_train['diag_1'].values.reshape(-1,1))
X_train_diag_1=enc.transform(X_train['diag_1'].values.reshape(-1,1))
X_test_diag_1=enc.transform(X_test['diag_1'].values.reshape(-1,1))
enc.fit(X_train['diag_2'].values.reshape(-1,1))
X_train_diag_2=enc.transform(X_train['diag_2'].values.reshape(-1,1))
X_test_diag_2=enc.transform(X_test['diag_2'].values.reshape(-1,1))
enc.fit(X_train['diag_3'].values.reshape(-1,1))
X_train_diag_3=enc.transform(X_train['diag_3'].values.reshape(-1,1))
X_test_diag_3=enc.transform(X_test['diag_3'].values.reshape(-1,1))
enc.fit(X_train['max_glu_serum'].values.reshape(-1,1))
X_train_max_glu_serum=enc.transform(X_train['max_glu_serum'].values.reshape(-1,1))
X_test_max_glu_serum=enc.transform(X_test['max_glu_serum'].values.reshape(-1,1))
enc.fit(X_train['A1Cresult'].values.reshape(-1,1))
X_train_A1Cresult=enc.transform(X_train['A1Cresult'].values.reshape(-1,1))
X_test_A1Cresult=enc.transform(X_test['A1Cresult'].values.reshape(-1,1))
enc.fit(X_train['metformin'].values.reshape(-1,1))
X_train_metformin=enc.transform(X_train['metformin'].values.reshape(-1,1))
X_test_metformin=enc.transform(X_test['metformin'].values.reshape(-1,1))
enc.fit(X_train['metformin'].values.reshape(-1,1))
X_train_metformin=enc.transform(X_train['metformin'].values.reshape(-1,1))
X_test_metformin=enc.transform(X_test['metformin'].values.reshape(-1,1))
enc.fit(X_train['repaglinide'].values.reshape(-1,1))
X_train_repaglinide=enc.transform(X_train['repaglinide'].values.reshape(-1,1))
X_test_repaglinide=enc.transform(X_test['repaglinide'].values.reshape(-1,1))
enc.fit(X_train['nateglinide'].values.reshape(-1,1))
X_train_nateglinide=enc.transform(X_train['nateglinide'].values.reshape(-1,1))
X_test_nateglinide=enc.transform(X_test['nateglinide'].values.reshape(-1,1))
enc.fit(X_train['chlorpropamide'].values.reshape(-1,1))
X_train_chlorpropamide=enc.transform(X_train['chlorpropamide'].values.reshape(-1,1))
X_test_chlorpropamide=enc.transform(X_test['chlorpropamide'].values.reshape(-1,1))
enc.fit(X_train['glimepiride'].values.reshape(-1,1))
X_train_glimepiride=enc.transform(X_train['glimepiride'].values.reshape(-1,1))
X_test_glimepiride=enc.transform(X_test['glimepiride'].values.reshape(-1,1))
enc.fit(X train['acetohexamide'].values.reshape(-1,1))
X_train_acetohexamide=enc.transform(X_train['acetohexamide'].values.reshape(-1,1))
X_test_acetohexamide=enc.transform(X_test['acetohexamide'].values.reshape(-1,1))
enc.fit(X_train['glipizide'].values.reshape(-1,1))
X train glipizide=enc.transform(X train['glipizide'].values.reshape(-1,1))
X_test_glipizide=enc.transform(X_test['glipizide'].values.reshape(-1,1))
```

```
enc.fit(X_train['glyburide'].values.reshape(-1,1))
X_train_glyburide=enc.transform(X_train['glyburide'].values.reshape(-1,1))
X_test_glyburide=enc.transform(X_test['glyburide'].values.reshape(-1,1))
enc.fit(X_train['tolbutamide'].values.reshape(-1,1))
X_train_tolbutamide=enc.transform(X_train['tolbutamide'].values.reshape(-1,1))
X_test_tolbutamide=enc.transform(X_test['tolbutamide'].values.reshape(-1,1))
enc.fit(X_train['pioglitazone'].values.reshape(-1,1))
X_train_pioglitazone=enc.transform(X_train['pioglitazone'].values.reshape(-1,1))
X_test_pioglitazone=enc.transform(X_test['pioglitazone'].values.reshape(-1,1))
enc.fit(X_train['rosiglitazone'].values.reshape(-1,1))
X_train_rosiglitazone=enc.transform(X_train['rosiglitazone'].values.reshape(-1,1))
X_test_rosiglitazone=enc.transform(X_test['rosiglitazone'].values.reshape(-1,1))
enc.fit(X_train['acarbose'].values.reshape(-1,1))
X_train_acarbose=enc.transform(X_train['acarbose'].values.reshape(-1,1))
X_test_acarbose=enc.transform(X_test['acarbose'].values.reshape(-1,1))
enc.fit(X_train['miglitol'].values.reshape(-1,1))
X_train_miglitol=enc.transform(X_train['miglitol'].values.reshape(-1,1))
X_test_miglitol=enc.transform(X_test['miglitol'].values.reshape(-1,1))
enc.fit(X_train['troglitazone'].values.reshape(-1,1))
X_train_troglitazone=enc.transform(X_train['troglitazone'].values.reshape(-1,1))
X_test_troglitazone=enc.transform(X_test['troglitazone'].values.reshape(-1,1))
enc.fit(X_train['tolazamide'].values.reshape(-1,1))
X_train_tolazamide=enc.transform(X_train['tolazamide'].values.reshape(-1,1))
X_test_tolazamide=enc.transform(X_test['tolazamide'].values.reshape(-1,1))
enc.fit(X_train['examide'].values.reshape(-1,1))
X_train_examide=enc.transform(X_train['examide'].values.reshape(-1,1))
X test examide=enc.transform(X test['examide'].values.reshape(-1,1))
enc.fit(X_train['citoglipton'].values.reshape(-1,1))
X_train_citoglipton=enc.transform(X_train['citoglipton'].values.reshape(-1,1))
X_test_citoglipton=enc.transform(X_test['citoglipton'].values.reshape(-1,1))
enc.fit(X_train['insulin'].values.reshape(-1,1))
X_train_insulin=enc.transform(X_train['insulin'].values.reshape(-1,1))
X_test_insulin=enc.transform(X_test['insulin'].values.reshape(-1,1))
enc.fit(X_train['glyburide-metformin'].values.reshape(-1,1))
X_train_glyburide_metformin=enc.transform(X_train['glyburide-metformin'].values.reshape(-1,
X_test_glyburide_metformin=enc.transform(X_test['glyburide-metformin'].values.reshape(-1,1)
enc.fit(X_train['glipizide-metformin'].values.reshape(-1,1))
X_train_glipizide_metformin=enc.transform(X_train['glipizide-metformin'].values.reshape(-1,
X_test_glipizide_metformin=enc.transform(X_test['glipizide-metformin'].values.reshape(-1,1)
enc.fit(X_train['metformin-rosiglitazone'].values.reshape(-1,1))
X_train_metformin_rosiglitazone=enc.transform(X_train['metformin-rosiglitazone'].values.res
X_test_metformin_rosiglitazone=enc.transform(X_test['metformin-rosiglitazone'].values.resha
enc.fit(X_train['glimepiride-pioglitazone'].values.reshape(-1,1))
X_train_glimepiride_pioglitazone=enc.transform(X_train['glimepiride-pioglitazone'].values.r
X test glimepiride pioglitazone=enc.transform(X test['glimepiride-pioglitazone'].values.res
enc.fit(X_train['metformin-rosiglitazone'].values.reshape(-1,1))
X_train_metformin_rosiglitazone=enc.transform(X_train['metformin-rosiglitazone'].values.res
X_test_metformin_rosiglitazone=enc.transform(X_test['metformin-rosiglitazone'].values.resha
enc.fit(X_train['metformin-pioglitazone'].values.reshape(-1,1))
X_train_metformin_pioglitazone=enc.transform(X_train['metformin-pioglitazone'].values.resha
X_test_metformin_pioglitazone=enc.transform(X_test['metformin-pioglitazone'].values.reshape
enc.fit(X_train['change'].values.reshape(-1,1))
X_train_change=enc.transform(X_train['change'].values.reshape(-1,1))
X_test_change=enc.transform(X_test['change'].values.reshape(-1,1))
enc.fit(X_train['diabetesMed'].values.reshape(-1,1))
X_train_diabetesMed=enc.transform(X_train['diabetesMed'].values.reshape(-1,1))
X_test_diabetesMed=enc.transform(X_test['diabetesMed'].values.reshape(-1,1))
enc.fit(X_train['admission_type_id'].values.reshape(-1,1))
X_train_admission_type_id=enc.transform(X_train['admission_type_id'].values.reshape(-1,1))
X_test_admission_type_id=enc.transform(X_test['admission_type_id'].values.reshape(-1,1))
enc.fit(X_train['discharge_disposition_id'].values.reshape(-1,1))
```

```
X_train_discharge_disposition_id=enc.transform(X_train['discharge_disposition_id'].values.r
X_test_discharge_disposition_id=enc.transform(X_test['discharge_disposition_id'].values.res
enc.fit(X_train['admission_source_id'].values.reshape(-1,1))
X_train_admission_source_id=enc.transform(X_train['admission_source_id'].values.reshape(-1,
X_test_admission_source_id=enc.transform(X_test['admission_source_id'].values.reshape(-1,1)
```

#### In [208]:

```
# normalising the numerical data
from sklearn.preprocessing import Normalizer
normalizer = Normalizer()
normalizer.fit(X train['patient nbr'].values.reshape(1,-1))
X_train_patient_nbr = normalizer.transform(X_train['patient_nbr'].values.reshape(1,-1))
X_test_patient_nbr = normalizer.transform(X_test['patient_nbr'].values.reshape(1,-1))
normalizer.fit(X_train['time_in_hospital'].values.reshape(1,-1))
X_train_time_in_hospital = normalizer.transform(X_train['time_in_hospital'].values.reshape(
X_test_time_in_hospital = normalizer.transform(X_test['time_in_hospital'].values.reshape(1,
normalizer.fit(X_train['num_lab_procedures'].values.reshape(1,-1))
X_train_num_lab_procedures = normalizer.transform(X_train['num_lab_procedures'].values.resh
X_test_num_lab_procedures = normalizer.transform(X_test['num_lab_procedures'].values.reshap
normalizer.fit(X_train['num_procedures'].values.reshape(1,-1))
X_train_num_procedures = normalizer.transform(X_train['num_procedures'].values.reshape(1,-1
X_test_num_procedures = normalizer.transform(X_test['num_procedures'].values.reshape(1,-1))
normalizer.fit(X_train['num_medications'].values.reshape(1,-1))
X_train_num_medications = normalizer.transform(X_train['num_medications'].values.reshape(1,
X_test_num_medications = normalizer.transform(X_test['num_medications'].values.reshape(1,-1
normalizer.fit(X_train['number_outpatient'].values.reshape(1,-1))
X_train_number_outpatient = normalizer.transform(X_train['number_outpatient'].values.reshap
X_test_number_outpatient = normalizer.transform(X_test['number_outpatient'].values.reshape(
normalizer.fit(X_train['number_emergency'].values.reshape(1,-1))
X_train_number_emergency = normalizer.transform(X_train['number_emergency'].values.reshape(
X_test_number_emergency = normalizer.transform(X_test['number_emergency'].values.reshape(1,
normalizer.fit(X_train['number_inpatient'].values.reshape(1,-1))
X_train_number_inpatient = normalizer.transform(X_train['number_inpatient'].values.reshape(
X_test_number_inpatient = normalizer.transform(X_test['number_inpatient'].values.reshape(1,
normalizer.fit(X_train['number_diagnoses'].values.reshape(1,-1))
X_train_number_diagnoses = normalizer.transform(X_train['number_diagnoses'].values.reshape(
X_test_number_diagnoses = normalizer.transform(X_test['number_diagnoses'].values.reshape(1,
X_train_patient_nbr = X_train_patient_nbr.reshape(-1,1)
X_test_patient_nbr =X_test_patient_nbr.reshape(-1,1)
X_train_time_in_hospital =X_train_time_in_hospital.reshape(-1,1)
X_test_time_in_hospital =X_test_time_in_hospital.reshape(-1,1)
X_train_num_lab_procedures = X_train_num_lab_procedures.reshape(-1,1)
X_test_num_lab_procedures = X_test_num_lab_procedures.reshape(-1,1)
X_train_num_procedures = X_train_num_procedures.reshape(-1,1)
X_test_num_procedures = X_test_num_procedures.reshape(-1,1)
X_train_num_medications = X_train_num_medications.reshape(-1,1)
X_test_num_medications = X_test_num_medications.reshape(-1,1)
X_train_number_outpatient =X_train_number_outpatient.reshape(-1,1)
X_test_number_outpatient = X_test_number_outpatient.reshape(-1,1)
X_train_number_emergency =X_train_number_emergency.reshape(-1,1)
X_test_number_emergency =X_test_number_emergency.reshape(-1,1)
X_train_number_inpatient =X_train_number_inpatient.reshape(-1,1)
X_test_number_inpatient = X_test_number_inpatient.reshape(-1,1)
X_train_number_diagnoses = X_train_number_diagnoses.reshape(-1,1)
X_test_number_diagnoses =X_test_number_diagnoses.reshape(-1,1)
```

#### In [209]:

```
# stacking
from scipy.sparse import hstack
X_train = hstack((X_train_race,X_train_gender,X_train_age,X_train_weight,X_train_payer_code
X_test = hstack((X_test_race,X_test_gender,X_test_age,X_test_weight,X_test_payer_code,X_test_age,X_test_weight,X_test_payer_code,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test_age,X_test
```

#### In [210]:

```
#https://stackoverflow.com/a/45386397/13693423
# function to select k best features which returns new dataset
def select_features(X_train, y_train, X_test):
    fs = SelectKBest(score_func=chi2, k=150)
    fs.fit(X_train, y_train)
    X_train_fs = fs.transform(X_train)
    X_test_fs = fs.transform(X_test)
    return X_train_fs, X_test_fs, fs
```

#### In [211]:

```
# to get the best features
from sklearn.feature_selection import SelectKBest
from sklearn.feature_selection import chi2
X_train_fs, X_test_fs, fs = select_features(X_train, y_train, X_test)
```

#### In [212]:

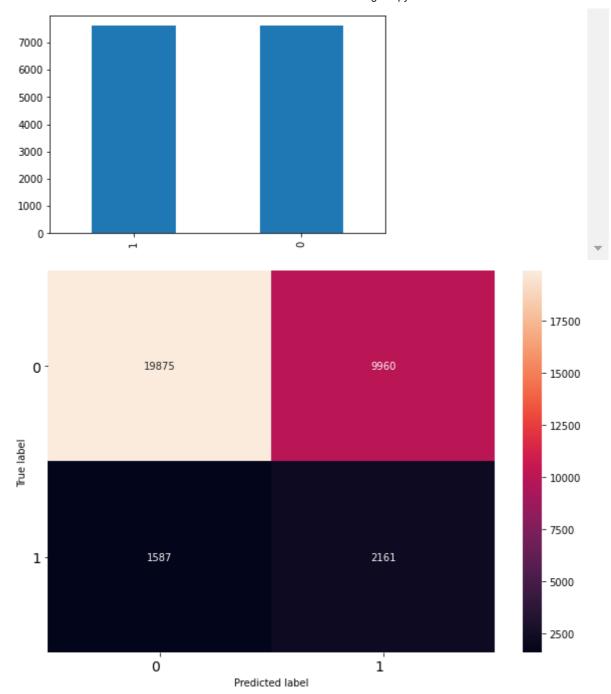
```
# selecting important features
X_train_fs=X_train_fs.toarray()
X_test_fs=X_test_fs.toarray()
```

## Logistic regression

#### In [213]:

```
from sklearn.model_selection import train_test_split
from sklearn.model_selection import train_test_split
from sklearn.linear model import LogisticRegression
from sklearn.model_selection import cross_val_score
from sklearn.model_selection import GridSearchCV
from sklearn.metrics import confusion_matrix
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import RandomForestClassifier
# function to try on different sets of ratio for smote
# here upsampling is done for imbalanced data
under = RandomUnderSampler()
X_train_fs, y_train = under.fit_resample(X_train_fs, y_train.ravel())
#here bar plot shows equal distribution after upsampling
pd.Series(y_train).value_counts().plot.bar()
# here the scaling is done x train
scaler = StandardScaler()
X_train_fs=scaler.fit_transform(X_train_fs)
X_test_fs=scaler.transform(X_test_fs)
# here using cross validation and gridsearch to determine the best hyperparameter
logit = LogisticRegression()
param_grid = {'C': [0.001, 0.01, 0.1, 1, 10, 100, 1000] }
clf = GridSearchCV(logit, param_grid,scoring='roc_auc',cv=5,n_jobs=-1)
clf.fit(X_train_fs,y_train)
# selecting the best model and printing the confusion matrix
logit =clf.best_estimator_
logit_pred = logit.predict(X_test_fs)
logit_pred_train=logit.predict(X_train_fs)
print_confusion_matrix(confusion_matrix(y_test,logit_pred),['0','1'])
print("Logistic regression")
print("Test confusion matrix")
# printing the accuracy preicison, recall, f1-score from logistic regression
fpr, tpr, thresholds = metrics.roc curve(y test,logit pred)
print('auc is {0:.2f}'.format(metrics.auc(fpr, tpr)))
log_auc=format(metrics.auc(fpr, tpr))
log_f1_score=format(f1_score(y_test, logit_pred))
print("Accuracy is {0:.2f}".format(accuracy_score(y_test, logit_pred)))
print("Precision is {0:.2f}".format(precision_score(y_test, logit_pred)))
print("Recall is {0:.2f}".format(recall score(y test, logit pred)))
print("f1-score is {0:.2f}".format(f1 score(y test, logit pred)))
```

```
Logistic regression
Test confusion matrix
auc is 0.62
Accuracy is 0.66
Precision is 0.18
Recall is 0.58
f1-score is 0.27
```

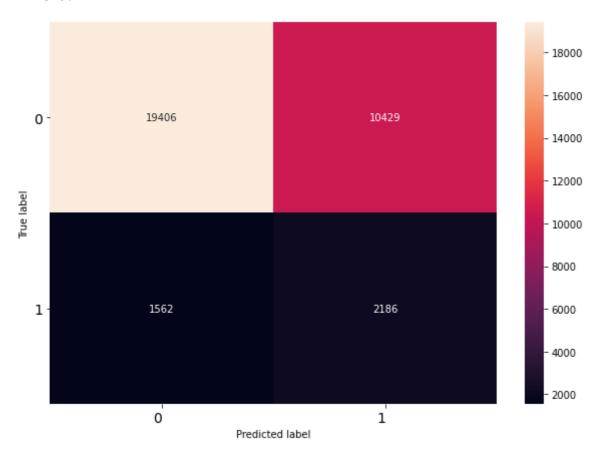


## **Decision tree**

#### In [214]:

```
# decison tree
# here using cross validation and gridsearch to determine the best hyperparameter
parameters = {'max_depth': [1, 5, 10, 50], 'min_samples_split': [5, 10, 100, 500]}
dtree = DecisionTreeClassifier()
clf = GridSearchCV(dtree,parameters,scoring='roc_auc',cv=5,n_jobs=-1)
clf.fit(X_train_fs,y_train)
   # selecting the best model and printing the confusion matrix
dtree =clf.best_estimator_
dtree.fit(X_train_fs,y_train)
dtree pred = dtree.predict(X test fs)
print_confusion_matrix(confusion_matrix(y_test,dtree_pred),['0','1'])
print("Decision tree")
print("Test confusion matrix")
   # printing the accuracy preicison, recall, f1-score from logistic regression
fpr, tpr, thresholds = metrics.roc_curve(y_test,dtree_pred)
print('auc is {0:.2f}'.format(metrics.auc(fpr, tpr)))
decision_auc=format(metrics.auc(fpr, tpr))
decision_f1=format(f1_score(y_test, dtree_pred))
print("Accuracy is {0:.2f}".format(accuracy_score(y_test, dtree_pred)))
print("Precision is {0:.2f}".format(precision_score(y_test, dtree_pred)))
print("Recall is {0:.2f}".format(recall_score(y_test, dtree_pred)))
print("f1 is {0:.2f}".format(f1_score(y_test, dtree_pred)))
```

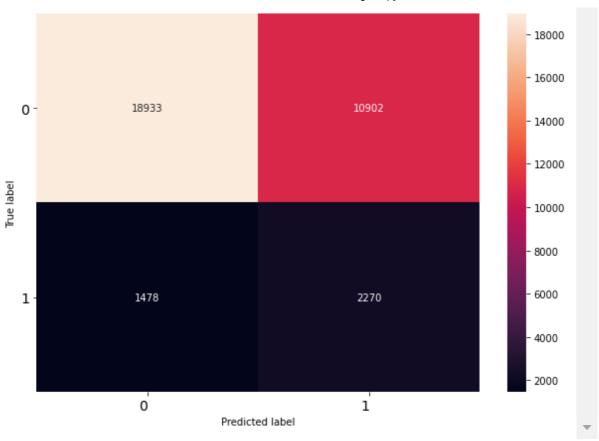
Decision tree
Test confusion matrix
auc is 0.62
Accuracy is 0.64
Precision is 0.17
Recall is 0.58
f1 is 0.27



# **Random forest**

#### In [215]:

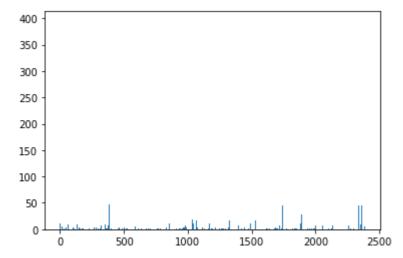
```
# doing hyperparameter tuning for random forest
rm = RandomForestClassifier()
params={'n_estimators':[5,10,25,50,100,300,500],'n_estimators': [10, 25], 'max_features': [
 'max depth': [10, 50,75,100, None], 'bootstrap': [True, False]}
model_rf=GridSearchCV(rm,param_grid=params,cv=5,scoring='roc_auc',n_jobs=-1,verbose=1)
model_rf.fit(X_train_fs, y_train)
rm =model_rf.best_estimator_
rm.fit(X_train_fs,y_train)
rm_prd = rm.predict(X_test_fs)
# selecting the best model and printing the confusion matrix
print confusion matrix(confusion matrix(y test,rm prd),['0','1'])
print("random forest")
print("Test confusion matrix")
# printing the accuracy preicison, recall, f1-score from logistic regression
fpr, tpr, thresholds = metrics.roc_curve(y_test,rm_prd)
print('auc is {0:.2f}'.format(metrics.auc(fpr, tpr)))
print("Accuracy is {0:.2f}".format(accuracy_score(y_test, rm_prd)))
print("Precision is {0:.2f}".format(precision_score(y_test, rm_prd)))
print("Recall is {0:.2f}".format(recall_score(y_test, rm_prd)))
print("f1score is {0:.2f}".format(f1_score(y_test, rm_prd)))
rm_auc=format(metrics.auc(fpr, tpr))
rm_f1=format(f1_score(y_test, rm_prd))
Fitting 5 folds for each of 40 candidates, totalling 200 fits
```



## feature importance

#### In [216]:

```
# feature importance plot
from matplotlib import pyplot
#for i in range(len(fs.scores_)):
# print('Feature %d: %f' % (i, fs.scores_[i]))
# plot the scores
pyplot.bar([i for i in range(len(fs.scores_))], fs.scores_)
pyplot.show()
```



# predicting the probability of the model using the decision tree and random forest

#### In [217]:

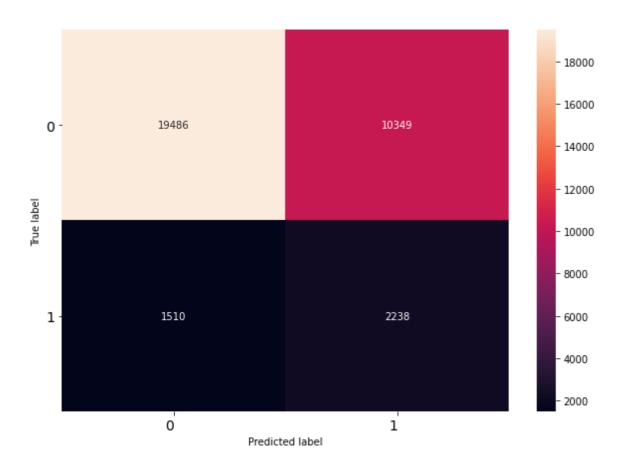
```
# in the believe function i wrote the code for weighted average with markdown
from sklearn.model_selection import train_test_split
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LogisticRegression
from sklearn.model_selection import cross_val_score
from sklearn.model selection import GridSearchCV
from sklearn.metrics import confusion matrix
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import RandomForestClassifier
import lightgbm as lgb
from sklearn.calibration import CalibratedClassifierCV
# function to do weighted average
# used decision tree
decision = DecisionTreeClassifier()
param_grid = {'max_depth': [1, 5, 10, 50], 'min_samples_split': [5, 10, 100, 500]}
clf = GridSearchCV(decision, param_grid,scoring='roc_auc',cv=5,n_jobs=-1)
clf.fit(X_train_fs,y_train)
decision =clf.best estimator
sig_clf = CalibratedClassifierCV(decision, method="sigmoid")
sig_clf.fit(X_train_fs, y_train)
    # used calibrated classifer to get the probability using decision tree
predict_y_decision = sig_clf.predict_proba(X_test_fs)
    # used random forest classifier
rm = RandomForestClassifier()
params={'n_estimators':[5,10,25,50,100,300,500],'n_estimators': [10, 25], 'max_features': [
     'max_depth': [10, 50,75,100, None], 'bootstrap': [True, False]}
model_rf=GridSearchCV(rm,param_grid=params,cv=5,scoring='roc_auc',n_jobs=-1,verbose=1)
model_rf.fit(X_train_fs, y_train)
rm =model_rf.best_estimator_
sig_clf = CalibratedClassifierCV(rm, method="sigmoid")
sig_clf.fit(X_train_fs, y_train)
    # used calibrated classifer to get the correct probability predicitons
predict_y_rm = sig_clf.predict_proba(X_test_fs)
one,two=predict_y_decision,predict_y_rm
z=[]
    # added the probability of both the predictions
for i in range(len(one)):
  z.append([one[i][0]+two[i][0],one[i][1]+two[i][1]])
predicted=[]
# using argmax got the output and checked for the answer
for i in range(len(z)):
  predicted.append(np.argmax(z[i]))
print confusion matrix(confusion matrix(y test,predicted),['0','1'])
print("combined accuracy")
print("Test confusion matrix")
# printing the accuracy preicison, recall, f1-score from logistic regression
fpr, tpr, thresholds = metrics.roc curve(y test,predicted)
print('auc is {0:.2f}'.format(metrics.auc(fpr, tpr)))
print("Precision is {0:.2f}".format(precision_score(y_test,predicted)))
print("Recall is {0:.2f}".format(recall_score(y_test,predicted)))
print("f1score is {0:.2f}".format(f1_score(y_test,predicted)))
avgweight_auc=format(metrics.auc(fpr, tpr))
avgweight_f1=format(f1_score(y_test,predicted))
```

Fitting 5 folds for each of 40 candidates, totalling 200 fits

```
[Parallel(n_jobs=-1)]: Using backend LokyBackend with 2 concurrent workers.
[Parallel(n_jobs=-1)]: Done 64 tasks | elapsed: 17.8s
```

[Parallel(n\_jobs=-1)]: Done 200 out of 200 | elapsed: 1.3min finished

combined accuracy
Test confusion matrix
auc is 0.63
Precision is 0.18
Recall is 0.60
f1score is 0.27



#### In [219]:

```
from prettytable import PrettyTable
#If you get a ModuleNotFoundError error , install prettytable using: pip3 install prettytab
x = PrettyTable()
x.field_names = ["Vectorizer", "Model", "f1-score", "TEST AUC"]
x.add_row(["ONE HOT ENCODING", "LOGISTIC REGRESSION", round(float(log_f1_score), 2), round(float
x.add_row(["ONE HOT ENCODING", "DECISION TREE", round(float(decision_f1), 2), round(float(decis
x.add_row(["ONE HOT ENCODING", "RANDOM FOREST", round(float(rm_f1), 2), round(float(rm_auc), 2)]
x.add_row(["ONE HOT ENCODING", "COMBINED DECISION TREE RANDOM FOREST", round(float(avgweight_print(x))
```

+	+	-+-		-+	
+   Vectorizer AUC	Model	l	f1-score	Τ	EST
+	+	-+-		-+	
+					
ONE HOT ENCODING	LOGISTIC REGRESSION		0.27		0.6
2					
ONE HOT ENCODING	DECISION TREE	1	0.27	1	0.6
2	,	'		'	
ONE HOT ENCODING	RANDOM FOREST	1	0.27	1	0.6
o l	MANDON TOKEST	ı	0.27	1	0.0
L ONE HOT ENCODING	COMPTNED DECTETON THEE DANDOM CORECT	1	0 27		0.0
	COMBINED DECISION TREE RANDOM FOREST	ı	0.27	ı	0.6
3					
+	+	-+-		-+	
+					

## predicting using deep learning

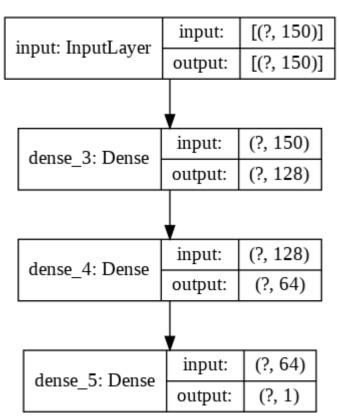
#### In [ ]:

```
# simple deep learning model
k = tensorflow.keras.initializers.he_uniform(seed=None)
inputlayer=Input(shape=(X_test_fs.shape[1]),name='input')
dense=Dense(128,activation='relu',kernel_initializer=k)(inputlayer)
dense1=Dense(64,activation='relu',kernel_initializer=k)(dense)
output=Dense(1, activation='sigmoid',kernel_initializer=k)(dense1)
model=Model(inputs=inputlayer,outputs=output)
opt = tensorflow.keras.optimizers.Adam(learning_rate=0.001)
model.compile(loss='binary_crossentropy', optimizer=opt, metrics=['accuracy',tensorflow.ker
```

#### In [ ]:

```
# plt of the model simple dl model
from tensorflow.keras.utils import plot_model
plot_model(model, to_file='model_plot.png', show_shapes=True, show_layer_names=True)
```

#### Out[210]:



#### In [ ]:

Epoch 1/5

```
model= model.fit(X_train_fs,y_train,validation_data=(X_test_fs, y_test), epochs=5)
```

```
476/476 [============ ] - 6s 12ms/step - loss: 0.6718 - acc
uracy: 0.5989 - auc_1: 0.6413 - val_loss: 0.7363 - val_accuracy: 0.5803 - va
l_auc_1: 0.6565
Epoch 2/5
uracy: 0.6452 - auc 1: 0.7015 - val loss: 0.6711 - val accuracy: 0.6526 - va
l_auc_1: 0.6557
Epoch 3/5
476/476 [============== ] - 5s 11ms/step - loss: 0.6116 - acc
uracy: 0.6595 - auc_1: 0.7203 - val_loss: 0.6524 - val_accuracy: 0.6608 - va
l_auc_1: 0.6534
Epoch 4/5
476/476 [============ ] - 5s 11ms/step - loss: 0.5998 - acc
uracy: 0.6705 - auc_1: 0.7351 - val_loss: 0.6924 - val_accuracy: 0.6127 - va
l_auc_1: 0.6535
Epoch 5/5
476/476 [============= - - 5s 11ms/step - loss: 0.5868 - acc
uracy: 0.6817 - auc_1: 0.7508 - val_loss: 0.7127 - val_accuracy: 0.6150 - va
l_auc_1: 0.6522
```

#### Out[211]:

<tensorflow.python.keras.callbacks.History at 0x7f28b2fe17f0>

## plot of the history

#### In [ ]:

```
# printing the plot of accuracy and loss and auc
it=model.history
import matplotlib.pyplot as plt
training_loss = it['loss']
test_loss = it['val_loss']
# Create count of the number of epochs
epoch_count = range(1, len(training_loss) + 1)
# Visualize loss history
plt.plot(epoch count, training loss, 'r--')
plt.plot(epoch_count, test_loss, 'b-')
plt.legend(['Training Loss', 'Test Loss'])
plt.xlabel('Epoch')
plt.ylabel('Loss')
plt.title("PLOT OF LOSS ")
plt.show();
training_accuracy = it['auc']
test_accuracy = it['val_auc']
# Create count of the number of epochs
epoch_count = range(1, len(training_accuracy) + 1)
# Visualize loss history
plt.plot(epoch_count, training_accuracy, 'r--')
plt.plot(epoch_count, test_accuracy, 'b-')
plt.legend(['Training AUC', 'Test AUC'])
plt.xlabel('Epoch')
plt.ylabel('accuracy')
plt.title("PLOT OF AUC ")
plt.show()
training_accuracy1 = it['accuracy']
test_accuracy1 = it['val_accuracy']
# Create count of the number of epochs
epoch_count = range(1, len(training_accuracy1) + 1)
# Visualize loss history
plt.plot(epoch_count, training_accuracy1, 'r--')
plt.plot(epoch_count, test_accuracy1, 'b-')
plt.legend(['Training ACCURACY', 'Test ACCURACY'])
plt.xlabel('Epoch')
plt.ylabel('accuracy')
plt.title("PLOT OF ACCURACY")
plt.show();
```

