

In [1]:

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

from sklearn.ensemble import RandomForestClassifier
from sklearn.svm import SVC
from xgboost import XGBClassifier

from sklearn.metrics import accuracy_score
from sklearn.metrics import confusion_matrix, f1_score, recall_score, precision
from sklearn.model_selection import cross_val_predict
from sklearn.model_selection import cross_val_score

from sklearn.metrics import classification_report
from sklearn.model_selection import train_test_split

from sklearn.feature_selection import SelectPercentile
from sklearn.feature_selection import chi2, f_classif
from mlxtend .plotting import plot_confusion_matrix
from sklearn.metrics import mean_absolute_error, r2_score, mean_squared_error
from sklearn.feature_selection import RFE
warnings.filterwarnings('ignore')
```

In [2]:

```
data=pd.read_csv(r"C:\Users\DELL\Downloads\archive\diabetes_binary_health_ir
```

In [3]:

data

	Diabetes_binary	HighBP	HighChol	CholCheck	BMI	Smoker	Stroke	HeartDis
0	0.0	0	1.0	1	15.0	1.0	0.0	0.0
1	1.0	1	0.0	1	28.0	0.0	0.0	1.0
2	1.0	1	1.0	1	33.0	0.0	0.0	0.0
3	1.0	0	1.0	1	29.0	0.0	1.0	1.0
4	0.0	0	0.0	1	24.0	1.0	0.0	0.0
...	...	...	...	...	...	...	...	...
236373	1.0	1	1.0	1	21.0	0.0	0.0	0.0
236374	0.0	1	0.0	1	25.0	1.0	0.0	0.0
236375	0.0	0	1.0	1	31.0	0.0	0.0	0.0
236376	0.0	1	0.0	1	24.0	0.0	0.0	0.0
236377	0.0	0	1.0	1	32.0	0.0	0.0	0.0

236378 rows × 22 columns

In [4]:

data.head()

	Diabetes_binary	HighBP	HighChol	CholCheck	BMI	Smoker	Stroke	HeartDisease
0	0.0	0	1.0	1	15.0	1.0	0.0	0.0
1	1.0	1	0.0	1	28.0	0.0	0.0	1.0
2	1.0	1	1.0	1	33.0	0.0	0.0	0.0
3	1.0	0	1.0	1	29.0	0.0	1.0	1.0
4	0.0	0	0.0	1	24.0	1.0	0.0	0.0

5 rows × 22 columns

```
In [5]: data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 236378 entries, 0 to 236377
Data columns (total 22 columns):
#   Column                                Non-Null Count  Dtype
---  -
0   Diabetes_binary                       236378 non-null float64
1   HighBP                               236378 non-null int64
2   HighChol                             236378 non-null float64
3   CholCheck                            236378 non-null int64
4   BMI                                   236378 non-null float64
5   Smoker                               236378 non-null float64
6   Stroke                               236378 non-null float64
7   HeartDiseaseorAttack                 236378 non-null float64
8   PhysActivity                         236378 non-null int64
9   Fruits                               236378 non-null int64
10  Veggies                              236378 non-null int64
11  HvyAlcoholConsump                    236378 non-null int64
12  AnyHealthcare                        236378 non-null int64
13  NoDocbcCost                          236378 non-null float64
14  GenHlth                              236378 non-null float64
15  MentHlth                             236378 non-null float64
16  PhysHlth                             236378 non-null float64
17  DiffWalk                             236378 non-null float64
18  Sex                                   236378 non-null int64
19  Age                                   236378 non-null int64
20  Education                            236378 non-null float64
21  Income                               236378 non-null float64
dtypes: float64(13), int64(9)
memory usage: 39.7 MB
```

```
In [6]: data.describe()
```

	Diabetes_binary	HighBP	HighChol	CholCheck	BMI	Sn
count	236378.000000	236378.000000	236378.000000	236378.000000	236378.000000	236378.0
mean	0.142010	0.418558	0.402059	0.963347	28.953579	0.411997
std	0.349061	0.493324	0.490315	0.187909	6.552055	0.492196
min	0.000000	0.000000	0.000000	0.000000	12.000000	0.000000
25%	0.000000	0.000000	0.000000	1.000000	24.000000	0.000000
50%	0.000000	0.000000	0.000000	1.000000	28.000000	0.000000
75%	0.000000	1.000000	1.000000	1.000000	32.000000	1.000000
max	1.000000	1.000000	1.000000	1.000000	99.000000	1.000000

8 rows × 22 columns

```
In [7]: data["Diabetes_binary"] = data["Diabetes_binary"].astype(int)
data["HighBP"] = data["HighBP"].astype(int)
data["HighChol"] = data["HighChol"].astype(int)
data["CholCheck"] = data["CholCheck"].astype(int)
data["BMI"] = data["BMI"].astype(int)
data["Smoker"] = data["Smoker"].astype(int)
data["Stroke"] = data["Stroke"].astype(int)
data["HeartDiseaseorAttack"] = data["HeartDiseaseorAttack"].astype(int)
data["PhysActivity"] = data["PhysActivity"].astype(int)
data["Fruits"] = data["Fruits"].astype(int)
data["Veggies"] = data["Veggies"].astype(int)
data["HvyAlcoholConsump"] = data["HvyAlcoholConsump"].astype(int)
data["AnyHealthcare"] = data["AnyHealthcare"].astype(int)
data["NoDocbcCost"] = data["NoDocbcCost"].astype(int)
data["GenHlth"] = data["GenHlth"].astype(int)
data["MentHlth"] = data["MentHlth"].astype(int)
data["PhysHlth"] = data["PhysHlth"].astype(int)
data["DiffWalk"] = data["DiffWalk"].astype(int)
data["Sex"] = data["Sex"].astype(int)
data["Age"] = data["Age"].astype(int)
data["Education"] = data["Education"].astype(int)
data["Income"] = data["Income"].astype(int)
```

```
In [8]: data.info()

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 236378 entries, 0 to 236377
Data columns (total 22 columns):
 #   Column                Non-Null Count  Dtype  
---  -
 0   Diabetes_binary        236378 non-null  int32  
 1   HighBP                 236378 non-null  int32  
 2   HighChol               236378 non-null  int32  
 3   CholCheck              236378 non-null  int32  
 4   BMI                    236378 non-null  int32  
 5   Smoker                 236378 non-null  int32  
 6   Stroke                 236378 non-null  int32  
 7   HeartDiseaseorAttack   236378 non-null  int32  
 8   PhysActivity           236378 non-null  int32  
 9   Fruits                 236378 non-null  int32  
10  Veggies                 236378 non-null  int32  
11  HvyAlcoholConsump      236378 non-null  int32  
12  AnyHealthcare           236378 non-null  int32  
13  NoDocbcCost             236378 non-null  int32  
14  GenHlth                236378 non-null  int32  
15  MentHlth                236378 non-null  int32  
16  PhysHlth                236378 non-null  int32  
17  DiffWalk                236378 non-null  int32  
18  Sex                     236378 non-null  int32  
19  Age                     236378 non-null  int32  
20  Education               236378 non-null  int32  
21  Income                  236378 non-null  int32  
dtypes: int32(22)
memory usage: 19.8 MB
```

```
In [9]: data.shape

(236378, 22)
```

```
In [10]: data.isnull().sum()

Diabetes_binary      0
HighBP               0
HighChol             0
CholCheck            0
BMI                 0
Smoker              0
Stroke              0
HeartDiseaseorAttack 0
PhysActivity         0
Fruits              0
Veggies             0
HvyAlcoholConsump    0
AnyHealthcare        0
NoDocbcCost          0
GenHlth             0
MentHlth            0
PhysHlth            0
DiffWalk            0
Sex                 0
Age                 0
Education            0
Income              0
dtype: int64
```

```
In [11]: #checking for any duplicated data from all the dataset
data.drop_duplicates(inplace=True)
```

```
In [12]: data.shape

(223243, 22)
```

```
In [13]: #outlier detection
from sklearn.ensemble import IsolationForest
model=IsolationForest()
model.fit(data)
data['anomaly']=model.predict(data)
```

In [14]:

data

	Diabetes_binary	HighBP	HighChol	CholCheck	BMI	Smoker	Stroke	HeartDis
0	0	0	1	1	15	1	0	0
1	1	1	0	1	28	0	0	1
2	1	1	1	1	33	0	0	0
3	1	0	1	1	29	0	1	1
4	0	0	0	1	24	1	0	0
...	...	...	...	...	...	...	...	...
236373	1	1	1	1	21	0	0	0
236374	0	1	0	1	25	1	0	0
236375	0	0	1	1	31	0	0	0
236376	0	1	0	1	24	0	0	0
236377	0	0	1	1	32	0	0	0

223243 rows × 23 columns

In [15]:

#checking the outliers that have been detected

data[data['anomaly']==-1]

	Diabetes_binary	HighBP	HighChol	CholCheck	BMI	Smoker	Stroke	HeartDis
0	0	0	1	1	15	1	0	0
1	1	1	0	1	28	0	0	1
3	1	0	1	1	29	0	1	1
4	0	0	0	1	24	1	0	0
5	0	1	0	1	40	1	0	0
...	...	...	...	...	...	...	...	...
236364	0	0	0	1	37	0	0	0
236369	1	1	1	1	33	0	0	0
236371	0	1	1	0	21	0	0	0
236373	1	1	1	1	21	0	0	0
236374	0	1	0	1	25	1	0	0

68533 rows × 23 columns

In [16]:

data[data['anomaly']==-1].shape

(68533, 23)

In [17]:

# we have to remove the outliers(anomalies)detected

data.drop(data[data['anomaly']==-1].index,inplace=True)

```
In [18]: data.shape

(154710, 23)
```

```
In [19]: data
```

	Diabetes_binary	HighBP	HighChol	CholCheck	BMI	Smoker	Stroke	HeartDis
2	1	1	1	1	33	0	0	0
8	0	1	1	1	30	0	0	0
9	0	1	1	1	36	1	0	0
11	1	1	1	1	30	0	0	0
14	0	1	1	1	27	1	0	0
...	...	...	...	...	...	...	...	...
236370	0	0	0	1	19	0	0	0
236372	0	0	0	1	29	0	0	0
236375	0	0	1	1	31	0	0	0
236376	0	1	0	1	24	0	0	0
236377	0	0	1	1	32	0	0	0

154710 rows x 23 columns

```
In [20]: # now we have to remove the column 'anomaly ' that has been created for the
data.drop(columns=['anomaly'],inplace=True)
```

```
In [21]: data.shape

(154710, 22)
```

## Scaling the data

```
In [22]: x=data.drop(['Diabetes_binary'],axis=1)
y=data['Diabetes_binary']
```

```
In [23]: from sklearn.preprocessing import StandardScaler
scaler=StandardScaler()
scaler.fit(x)
```

```
StandardScaler
StandardScaler()
r()
```



```
In [24]: scaled_features=scaler.transform(x)
x=pd.DataFrame(scaled_features,columns=data.columns[1:])
x.head(10)
```

	HighBP	HighChol	CholCheck	BMI	Smoker	Stroke	HeartDiseaseorAttack	I
0	1.321513	1.318273	0.122084	0.810077	-0.760388	-0.089448	-0.171712	(
1	1.321513	1.318273	0.122084	0.287202	-0.760388	-0.089448	-0.171712	-
2	1.321513	1.318273	0.122084	1.332953	1.315118	-0.089448	-0.171712	-
3	1.321513	1.318273	0.122084	0.287202	-0.760388	-0.089448	-0.171712	-
4	1.321513	1.318273	0.122084	-0.235673	1.315118	-0.089448	-0.171712	-
5	1.321513	1.318273	0.122084	1.158661	1.315118	-0.089448	-0.171712	(
6	1.321513	1.318273	0.122084	0.287202	-0.760388	-0.089448	-0.171712	(
7	-0.756708	-0.758568	0.122084	0.461494	-0.760388	-0.089448	-0.171712	(
8	1.321513	1.318273	0.122084	0.810077	-0.760388	-0.089448	-0.171712	-
9	-0.756708	-0.758568	0.122084	0.461494	1.315118	-0.089448	-0.171712	(

10 rows x 21 columns

```
In [25]: #Splitting the data
x_train,x_test,y_train,y_test=train_test_split(x,y,test_size=0.35,random_sta
```

```
In [26]: from sklearn.neighbors import KNeighborsClassifier
knn=KNeighborsClassifier(n_neighbors=5)
knn.fit(x_train,y_train)
```

▼ KNeighborsClassifier

KNeighborsClassifi  
er()

```
In [27]: y_pred = knn.predict(x_test)
```

```
In [28]: print(x_test.dtypes)
```

```
HighBP          float64
HighChol        float64
CholCheck       float64
BMI             float64
Smoker          float64
Stroke          float64
HeartDiseaseorAttack float64
PhysActivity     float64
Fruits          float64
Veggies         float64
HvyAlcoholConsump float64
AnyHealthcare   float64
NoDocbcCost     float64
GenHlth         float64
MentHlth        float64
PhysHlth        float64
DiffWalk        float64
Sex             float64
Age            float64
Education       float64
Income          float64
dtype: object
```

```
In [29]: !pip install --upgrade scikit-learn
```

```
Requirement already satisfied: scikit-learn in c:\users\dell\anaconda3\lib\site-packages (1.3.2)
Requirement already satisfied: numpy<2.0,>=1.17.3 in c:\users\dell\anaconda3\lib\site-packages (1.24.3)
Requirement already satisfied: scipy>=1.5.0 in c:\users\dell\anaconda3\lib\site-packages (from scikit-learn) (1.10.1)
Requirement already satisfied: joblib>=1.1.1 in c:\users\dell\anaconda3\lib\site-packages (from scikit-learn) (1.3.2)
Requirement already satisfied: threadpoolctl>=2.0.0 in c:\users\dell\anaconda3\lib\site-packages (from scikit-learn) (3.1.0)
```

```
In [30]: y_pred
```

```
array([0, 0, 0, ..., 0, 0, 0])
```

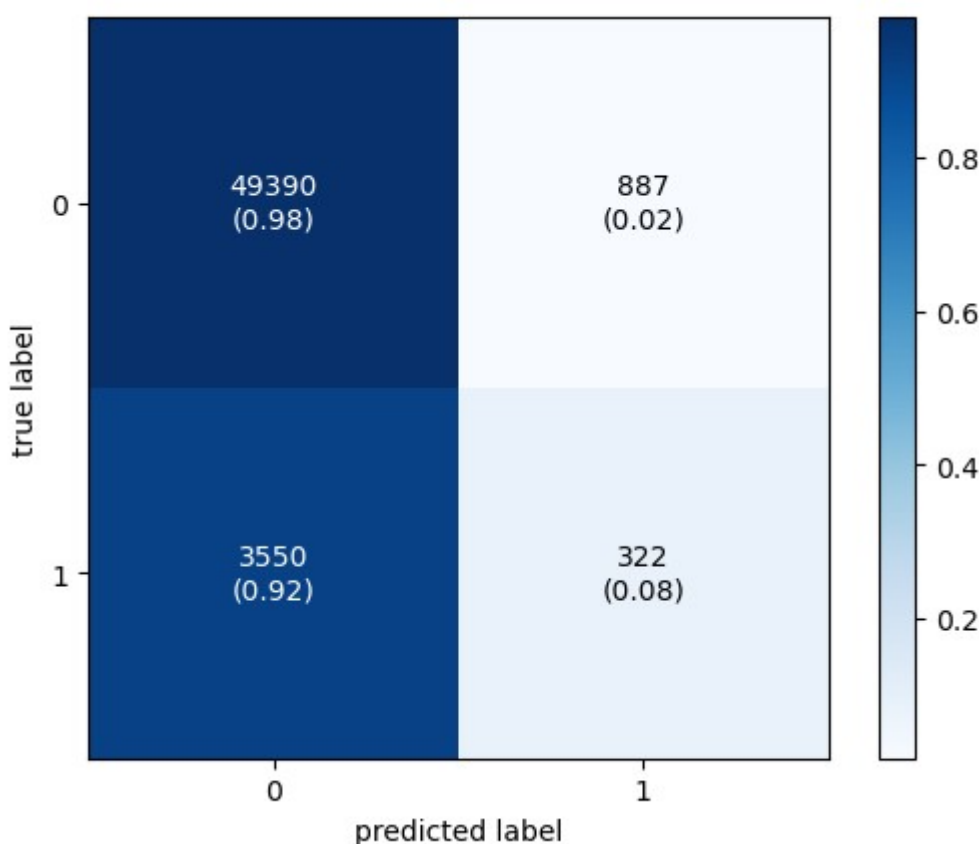
```
In [31]: data['Diabetes_binary'].value_counts()
```

```
0    143556
1     11154
Name: Diabetes_binary, dtype: int64
```

```
In [32]: print(classification_report(y_test,y_pred))
```

	precision	recall	f1-score	support
0	0.93	0.98	0.96	50277
1	0.27	0.08	0.13	3872
accuracy			0.92	54149
macro avg	0.60	0.53	0.54	54149
weighted avg	0.89	0.92	0.90	54149

```
In [33]: cm1=confusion_matrix(y_test,y_pred)
plot_confusion_matrix(conf_mat=cm1,show_absolute=True,show_normed=True,color
plt.show())
```



### Addressing Imbalanced Data for Improved Diabetes Prediction

One of the challenges in predicting diabetes using machine learning models is class imbalance, which means that the number of individuals with diabetes is significantly lower compared to those without diabetes. This imbalance can lead to skewed model predictions, favoring the majority class and underestimating the true risk of diabetes for individuals in the minority class.

To address this issue, we will employ a combined technique known as SMOTE

- SMOTE (Synthetic Minority Oversampling Technique): This technique artificially generates synthetic data points in the minority class by generating synthetic samples based on the existing minority class data. It helps to balance the class distribution and provides the model with more information about the minority class.

to improved predictions.

- ENN (Edited Nearest Neighbors): This technique removes noisy data points from the training set. This helps eliminate misclassified data that could lead to a cleaner and more accurate representation of the underlying class structure.

Combined effect of SMOTE + ENN: By combining SMOTE and ENN, we achieve

- Increased representation of the minority class: SMOTE generates synthetic samples, increasing the number of data points in the minority class and providing the model with a more balanced dataset.
- Enhanced data quality: ENN removes noisy data points from both classes, resulting in a cleaner and more consistent training set. This improves the model's ability to learn the true relationship between the features and the target variable, leading to more accurate and reliable predictions.

Overall, the combination of SMOTE and ENN is a powerful technique for addressing class imbalance and improving the accuracy of diabetes prediction models. By balancing the class distribution and enhancing data quality, these techniques ensure that the model learns from a representative and high-quality dataset, leading to more reliable and accurate predictions for individuals with and without diabetes.

```
In [34]: from imblearn.combine import SMOTEENN
sm=SMOTEENN()
x_resampled,y_resampled = sm.fit_resample(x,y)
```

```
In [35]: xre_train,xre_test,yre_train,yre_test = train_test_split(x_resampled, y_resampled,
```

```
In [36]: knn_smote = KNeighborsClassifier(n_neighbors = 5)
knn_smote.fit(xre_train,yre_train)
```

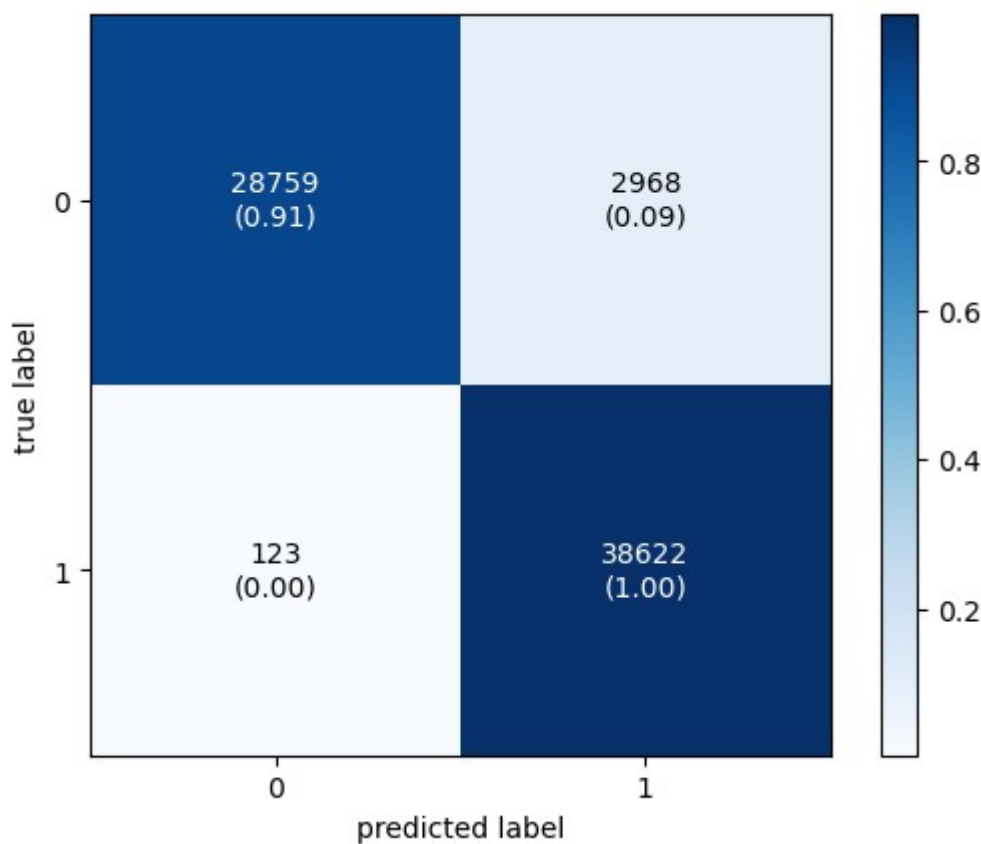
```
▼ KNeighborsClassifier
KNeighborsClassifi
er()
```

```
In [37]: yre_pred = knn_smote.predict(xre_test)
```

```
In [38]: print(classification_report(yre_test,yre_pred))
```

	precision	recall	f1-score	support
0	1.00	0.91	0.95	31727
1	0.93	1.00	0.96	38745
accuracy			0.96	70472
macro avg	0.96	0.95	0.96	70472
weighted avg	0.96	0.96	0.96	70472

```
In [39]: cm1=confusion_matrix(yre_test,yre_pred)
plot_confusion_matrix(conf_mat=cm1,show_absolute=True,show_normed=True,color
plt.show())
```



## Modeling(RF,SVM,&XGB)

### RANDOM FOREST(RF)

```
In [40]: rf = RandomForestClassifier(n_estimators=100, max_features=16 , max_depth=16)
rf.fit(xre_train,yre_train)
```

```
RandomForestClassifier
RandomForestClassifier(max_depth=16, max_f
eatures=16)
```

```
In [41]: print(rf.score(xre_train, yre_train))
print(rf.score(xre_test, yre_test))
```

```
0.949985404300866
0.9390396185719151
```

```
In [42]: y_pred_train_rf = rf.predict(xre_train)
acc_train_rf = accuracy_score(yre_train, y_pred_train_rf)

y_pred_test_rf = rf.predict(xre_test)
acc_test_rf = accuracy_score(yre_test, y_pred_test_rf)
print(acc_train_rf)
print(acc_test_rf)

0.949985404300866
0.9390396185719151
```

```
In [43]: print(classification_report(yre_test, y_pred_test_rf))
```

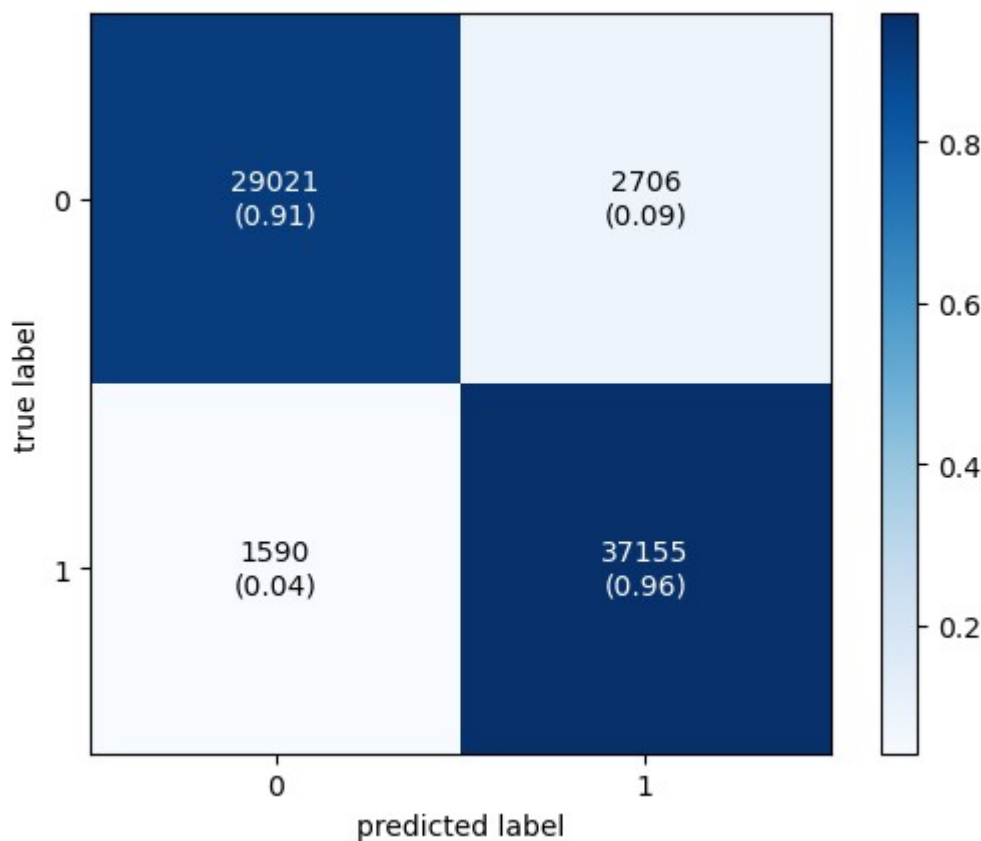
	precision	recall	f1-score	support
0	0.95	0.91	0.93	31727
1	0.93	0.96	0.95	38745
accuracy			0.94	70472
macro avg	0.94	0.94	0.94	70472
weighted avg	0.94	0.94	0.94	70472

```
In [44]: print('Precision: %.3f' % precision_score(yre_test, y_pred_test_rf, average="
print('Recall: %.3f' % recall_score(yre_test, y_pred_test_rf, average="micro"
print('F-measure: %.3f' % f1_score(yre_test, y_pred_test_rf, average="micro")

Precision: 0.939
Recall: 0.939
F-measure: 0.939
```

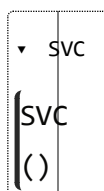
```
In [45]: cm1 = confusion_matrix(yre_test,y_pred_test_rf)
plot_confusion_matrix(conf_mat=cm1,show_absolute=True,
                      show_normed=True,
                      colorbar=True)

plt.show()
```



## Support Vector Machine (SVM)

```
In [46]: svm = SVC(C=1.0, kernel='rbf', gamma='scale')
svm.fit(xre_train, yre_train)
```



```
In [47]: print(svm.score(xre_train, yre_train))
print(svm.score(xre_test, yre_test))
```

```
0.8822917680256884
0.8807185832671132
```

```
In [48]: y_pred_train_svm = svm.predict(xre_train)
acc_train_svm = accuracy_score(yre_train, y_pred_train_svm)

y_pred_test_svm = svm.predict(xre_test)
acc_test_svm = accuracy_score(yre_test, y_pred_test_svm)
print(acc_train_svm)
print(acc_test_svm)

0.8822917680256884
0.8807185832671132
```

```
In [49]: print(classification_report(yre_test, y_pred_test_svm))
```

	precision	recall	f1-score	support
0	0.90	0.82	0.86	31727
1	0.86	0.93	0.90	38745
accuracy			0.88	70472
macro avg	0.88	0.88	0.88	70472
weighted avg	0.88	0.88	0.88	70472

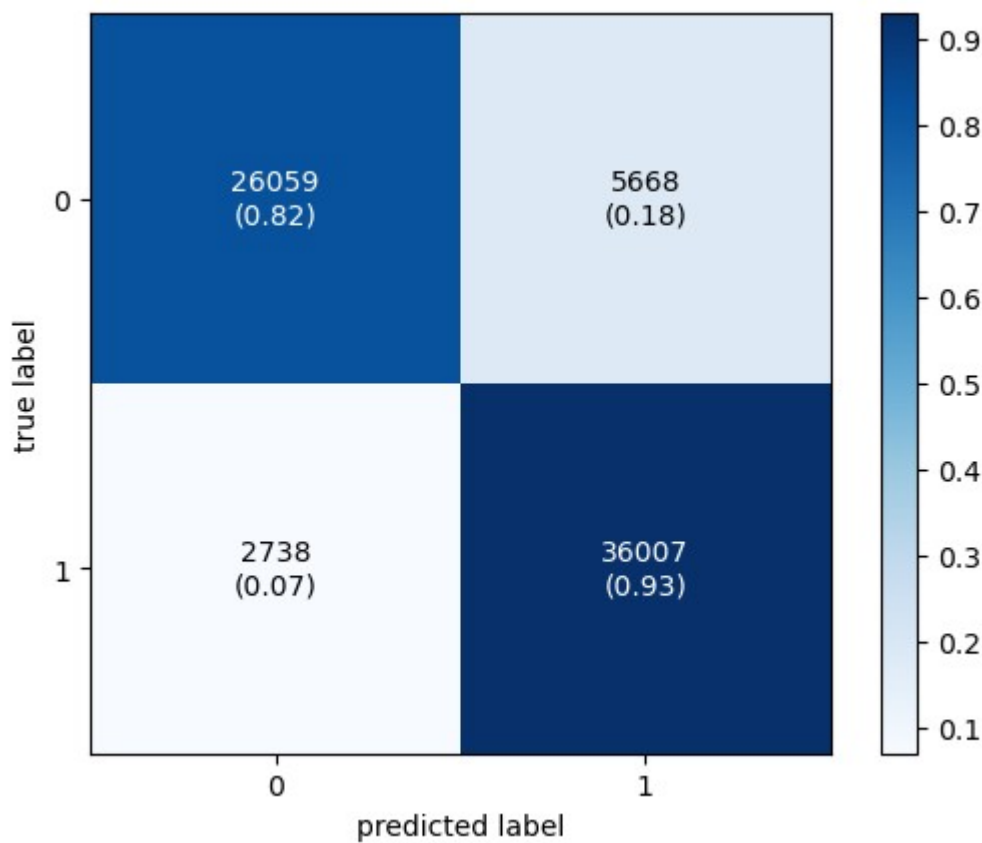
```
In [50]: print('Precision: %.3f' % precision_score(yre_test, y_pred_test_svm,average=
print('Recall: %.3f' % recall_score(yre_test, y_pred_test_svm,average="micro
print('F-measure: %.3f' % f1_score(yre_test, y_pred_test_svm,average="micro"

Precision: 0.881
Recall: 0.881
F-measure: 0.881
```



```
In [51]: # calculating and plotting the confusion matrix
cm1 = confusion_matrix(yre_test,y_pred_test_svm)
plot_confusion_matrix(conf_mat=cm1,show_absolute=True,
                      show_normed=True,
                      colorbar=True)

plt.show()
```



## Extreme Gradient Boosting (XGB)

In [52]:

```
xgb=XGBClassifier(max_depth=20)
xgb.fit(xre_train,yre_train)
```

```

XGBClassifier
XGBClassifier(base_score=None, booster=None, callbacks=None,
               colsample_bylevel=None, colsample_bynode=None,
               colsample_bytree=None, device=None, early_stoppin
ng_rounds=None,
               enable_categorical=False, eval_metric=None, feat
ure_types=None,
               gamma=None, grow_policy=None, importance_type=No
ne,
```

In [53]:

```
print(xgb.score(xre_train,yre_train))
print(xgb.score(xre_test,yre_test))
```

```
0.999787146054296
0.9682285162901578
```

In [55]:

```
y_pred_train_xgb = xgb.predict(xre_train)
acc_train_xgb = accuracy_score(yre_train,y_pred_train_xgb)
y_pred_test_xgb=xgb.predict(xre_test)
acc_test_xgb = accuracy_score(yre_test,y_pred_test_xgb)
print(acc_train_xgb)
print(acc_test_xgb)
```

```
0.999787146054296
0.9682285162901578
```

```
In [56]: print(classification_report(yre_test,y_pred_test_xgb))
```

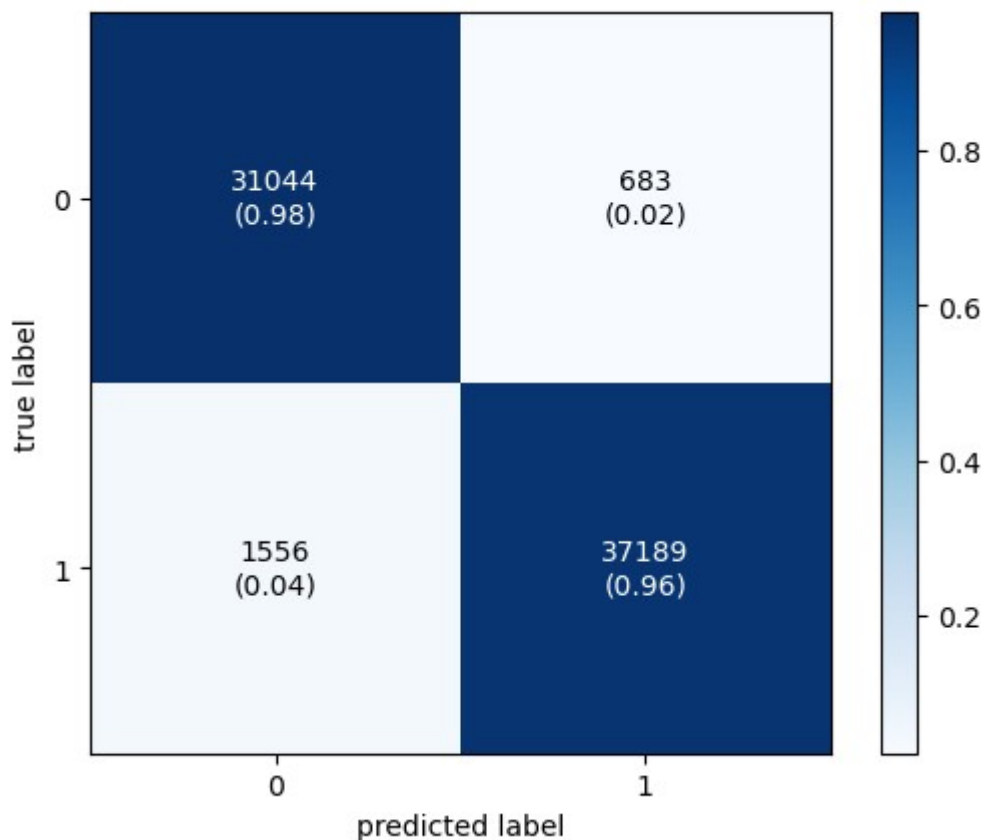
	precision	recall	f1-score	support
0	0.95	0.98	0.97	31727
1	0.98	0.96	0.97	38745
accuracy			0.97	70472
macro avg	0.97	0.97	0.97	70472
weighted avg	0.97	0.97	0.97	70472

```
In [57]: print('Precision: %.3f' % precision_score(yre_test, y_pred_test_xgb,average=
print('Recall: %.3f' % recall_score(yre_test, y_pred_test_xgb,average="micro
print('F-measure: %.3f' % f1_score(yre_test, y_pred_test_xgb,average="micro"
```

```
Precision: 0.968
Recall: 0.968
F-measure: 0.968
```

```
In [58]: # calculating and plotting the confusion matrix
cm1 = confusion_matrix(yre_test,y_pred_test_xgb)
plot_confusion_matrix(conf_mat=cm1,show_absolute=True,
                      show_normed=True,
                      colorbar=True)

plt.show()
```



In [ ]: