## ML logistic regression xgboost

## May 8, 2024

```
[1]: import pandas as pd
     pd.set_option('display.max_columns', None)
     pd.set_option('display.max_rows', None)
     pd.set_option('display.max_colwidth', None)
     import numpy as np
     # from functools import reduce
     from IPython.display import display
     #Preprocessing
     from sklearn.model_selection import cross_val_predict
     from sklearn.model selection import StratifiedKFold
     from sklearn import preprocessing
     from sklearn.pipeline import Pipeline
     from sklearn.compose import ColumnTransformer
     from sklearn import preprocessing
     from sklearn.preprocessing import MinMaxScaler
     from sklearn.preprocessing import StandardScaler
     from imblearn.over_sampling import RandomOverSampler
     from imblearn.under_sampling import RandomUnderSampler
     #Imputation
     # import miceforest as mf
     # import random
     # import sklearn.neighbors._base
     # import sys
     # sys.modules['sklearn.neighbors.base'] = sklearn.neighbors._base
     # from missingpy import MissForest
     # from sklearn.impute import KNNImputer
     from sklearn.preprocessing import OneHotEncoder
     from sklearn.utils import resample
     from sklearn.impute import SimpleImputer
     from sklearn.experimental import enable_iterative_imputer
     #Modeling
```

```
from sklearn.model_selection import train_test_split, GridSearchCV,u

StratifiedKFold, KFold

from sklearn.linear_model import LogisticRegression, LogisticRegressionCV

from sklearn import datasets

import xgboost as xgb

#Metrics

from sklearn.metrics import accuracy_score, precision_score, recall_score,u

of1_score, confusion_matrix, mean_squared_error, r2_score,u

oprecision_recall_curve, auc, roc_auc_score

from sklearn.model_selection import cross_val_score

#Visualizations

import matplotlib.pyplot as plt

import seaborn as sns

import shap

from xgboost import plot_importance
```

/opt/conda/lib/python3.11/site-packages/tqdm/auto.py:21: TqdmWarning: IProgress
not found. Please update jupyter and ipywidgets. See
https://ipywidgets.readthedocs.io/en/stable/user\_install.html
from .autonotebook import tqdm as notebook\_tqdm

```
[2]: #Function for creating our confusion matrices
     def conf_matrix(y_test, y_predicted):
       cm = confusion_matrix(y_test, y_predicted)
      plt.figure(figsize=(15,10))
      plt.clf()
      plt.imshow(cm, interpolation='nearest', cmap=plt.cm.Wistia)
      classNames = ['Negative', 'Positive']
       plt.title('Confusion Matrix', fontsize=14)
      plt.ylabel('True label', fontsize=14)
      plt.xlabel('Predicted label', fontsize=14)
       tick_marks = np.arange(len(classNames))
      plt.xticks(tick marks, classNames, rotation=45,fontsize=14)
      plt.yticks(tick_marks, classNames,fontsize=14)
       s = [['TN','FP'], ['FN', 'TP']]
       for i in range(2):
           for j in range(2):
             plt.text(j, i, str(s[i][j]) + " = " + str(cm[i][j]), fontsize=20, u
      horizontalalignment="center") # Adjust text font size and alignment
      plt.show()
```

```
[3]: #Read in the data

df = pd.read_csv("../data/AR_cleaned_ISB_aging_new_merge_fi_wgcna.csv")
```

```
[7]: #Look at all the columns we have
      df.columns
 [7]: Index(['public_client_id', 'sex', 'age', 'merge_fi', 'MElightcyan',
             'MEgreenyellow', 'MEpurple', 'MEblue', 'MEbrown', 'MEgreen',
             'MEmidnightblue', 'MEcyan', 'MEtan', 'MEyellow', 'MEblack', 'MEmagenta',
             'MEred', 'MEsalmon', 'MEpink', 'MEturquoise', 'MEgrey',
             'MEturquoise_prots', 'MEblue_prots', 'MEbrown_prots', 'MEgrey_prots',
             'A/G RATIO', 'ALAT (SGPT)', 'ALBUMIN', 'ALKALINE PHOSPHATASE',
             'ARACHIDONIC ACID', 'ASAT (SGOT)', 'BILIRUBIN, TOTAL',
             'BUN/CREAT RATIO', 'CALCIUM', 'CARBON DIOXIDE (CO2)', 'CHLORIDE',
             'CHOLESTEROL, TOTAL', 'CREATININE ENZ, SER', 'CRP HIGH SENSITIVITY',
             'DHA', 'DPA', 'EPA', 'FERRITIN', 'GFR, MDRD', 'GFR, MDRD, AFRICAN AM',
             'GGT', 'GLOBULIN', 'GLUCOSE', 'GLYCOHEMOGLOBIN A1C', 'HDL CHOL DIRECT',
             'HDL PARTICLE NUMBER', 'HOMA-IR', 'HOMOCYSTEINE, SERUM', 'INSULIN',
             'LDL PARTICLE NUMBER', 'LDL SMALL', 'LDL-CHOL CALCULATION', 'LDL_SIZE',
             'LINOLEIC_ACID', 'LPIR_SCORE', 'OMEGA-3 INDEX', 'OMEGA-6/OMEGA-3 RATIO',
             'OMEGA_3_TOTAL', 'OMEGA_6_TOTAL', 'POTASSIUM', 'PROTEIN, TOTAL SERUM',
             'SODIUM', 'TRIGLYCERIDES', 'Triglyceride HDL Ratio', 'UREA NITROGEN',
             'URIC ACID', 'VITAMIN D, 25-OH TOT', 'race_black or african-american',
             'race_east asian', 'race_hispanic latino or spanish origin',
             'race_other', 'race_south asian', 'race_white'],
            dtype='object')
 []: print(df.shape) #Number of rows, number of columns
      df.head() #First 5 rows of the df
 [8]: df = df.set_index('public_client_id')
 []: df.head()
 [7]: ### Outcome Definition
[65]: df.merge_fi.max()
[65]: 0.426865672
[66]: df.merge_fi.min()
[66]: 0.054545455
[10]: #Define the cutoff value as the top quartile
      cutoff = df['merge_fi'].quantile(0.75)
      print("Cutoff value:", cutoff)
```

Cutoff value: 0.241414141

```
[11]: \#Create a new binary feature (merge_fi_class) using the top quartile as the
       ⇔"positive" class
      df['merge_fi_class'] = (df['merge_fi'] > cutoff).astype(int)
[69]: merge_cats = df['merge_fi_class'].value_counts()
      print(merge_cats)
     merge_fi_class
     0
          577
          192
     1
     Name: count, dtype: int64
[12]: df = df.drop(['merge_fi'], axis=1)
[13]: #Define our categorical and numerical columns
      categorical_chosen_features = ['sex', 'race_other', 'race_black or_
       ⇔african-american', 'race_east asian', 'race_hispanic latino or spanish⊔
       →origin', 'race_south asian', 'race_white']
      cols_to_drop = ['merge_fi_class','sex','race_other', 'race_black or_
       ⇔african-american', 'race_east asian', 'race_hispanic latino or spanish⊔
       →origin', 'race_south asian', 'race_white']
      numerical_chosen_features = df.drop(cols_to_drop, axis = 1).columns.tolist()
      print("Number of categorical features:", len(categorical_chosen_features))
      print("Number of numerical features:",len(numerical_chosen_features))
     Number of categorical features: 7
     Number of numerical features: 69
[14]: #Set our target variable
      y_col = ["merge_fi_class"]
      ## separate X and Y
      y = df[y_col]
      X = df.drop(y_col, axis=1)
      class_names = np.unique(y)
      print("unique labels from y: ", class_names)
     unique labels from y: [0 1]
[15]: #Split our data into training and testing (80/20 split)
      #https://scikit-learn.org/stable/modules/generated/sklearn.model_selection.
       \hookrightarrow train\_test\_split.html
```

```
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2,_
 →random_state=42, stratify = y)
columns = X_train.columns
#Randomly oversample the minority class
\#https://imbalanced-learn.org/stable/references/generated/imblearn.
→over_sampling.RandomOverSampler.html
oversample = RandomOverSampler(random_state=42)
os_data_X, os_data_y = oversample.fit_resample(X_train, y_train)
#Set our X train and y train using the oversampled data
X_train = os_data_X
y_train = os_data_y
## Control the balance of positive and negative weights, useful for unbalanced
 →classes. A typical value to consider: sum(negative instances) / sum(positive
⇔instances)
ratio = ( np.size(os_data_y) - np.sum(os_data_y) ) / np.sum(os_data_y)
print("The ratio of negatives/positives is the the value of scale_pos_weight:__

¬", ratio)
```

The ratio of negatives/positives is the the value of scale\_pos\_weight: merge\_fi\_class 1.0 dtype: float64

The behavior of DataFrame.sum with axis=None is deprecated, in a future version this will reduce over both axes and return a scalar. To retain the old behavior, pass axis=0 (or do not pass axis)

The behavior of DataFrame.sum with axis=None is deprecated, in a future version this will reduce over both axes and return a scalar. To retain the old behavior, pass axis=0 (or do not pass axis)

```
#Iterative Imputer
      #IterativeImputer(max_iter = 10, random_state=r_seed)
      # Hotcoder_pipe = Pipeline([
      # ('imputer', SimpleImputer(strateqy='mean')),
      # ('onehot', OneHotEncoder(handle_unknown='ignore'))
      # 7)
      categorical pipe = Pipeline([
        ('imputer', SimpleImputer(strategy='constant',fill_value=0))
      1)
     numerical_pipe = Pipeline([
        ('imputer', SimpleImputer(strategy='mean')),
        ('scaler', MinMaxScaler())
     ])
[17]: preprocessor = ColumnTransformer([('cat', categorical_pipe, __
       ⇔categorical_chosen_features),('num', numerical_pipe,⊔
       →numerical_chosen_features)])
      # Fit on and transform our training data
      X_train_v1 = preprocessor.fit_transform(X_train)
      # Transform the test data
      X_test_v1 = preprocessor.transform(X_test)
      # Names of our features
      feature_names = np.r_[categorical_chosen_features, numerical_chosen_features]
      # Create pandas versions of our train and test data
      X_train_v2 = pd.DataFrame(X_train_v1, columns=feature_names)
      X_test_v2 = pd.DataFrame(X_test_v1, columns=feature_names)
 []: X_train_v2.head(10)
 []: y_train.head()
 []: X_test_v2.head()
[77]: # Logistic Regression
      model_lr = LogisticRegression(max_iter = 200)
      model_lr.fit(X_train_v1, y_train)
      predictions_lr = model_lr.predict(X_test_v1)
      y_proba = model_lr.predict_proba(X_test_v1)[:, 1]
```

```
precision, recall, _ = precision_recall_curve(y_test, y_proba)
pr_auc = auc(recall, precision)
roc_auc = roc_auc_score(y_test, y_proba)

accuracy_lr = accuracy_score(y_test, predictions_lr)
precision_lr = precision_score(y_test, predictions_lr, average='binary')
recall_lr = recall_score(y_test, predictions_lr, average='binary')
f1_lr = f1_score(y_test, predictions_lr, average='binary')

print("PR AUC:", pr_auc)
print("ROC AUC:", roc_auc)
print("Accuracy Logistic Regression:", accuracy_lr)
print("Precision LR:", precision_lr)
print("Recall LR:", recall_lr)
print("F1 Score LR:", f1_lr)
```

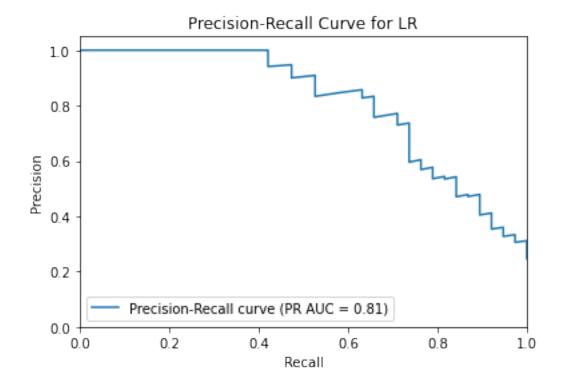
A column-vector y was passed when a 1d array was expected. Please change the shape of y to (n\_samples, ), for example using ravel().

PR AUC: 0.8099659799883311 ROC AUC: 0.8883847549909256

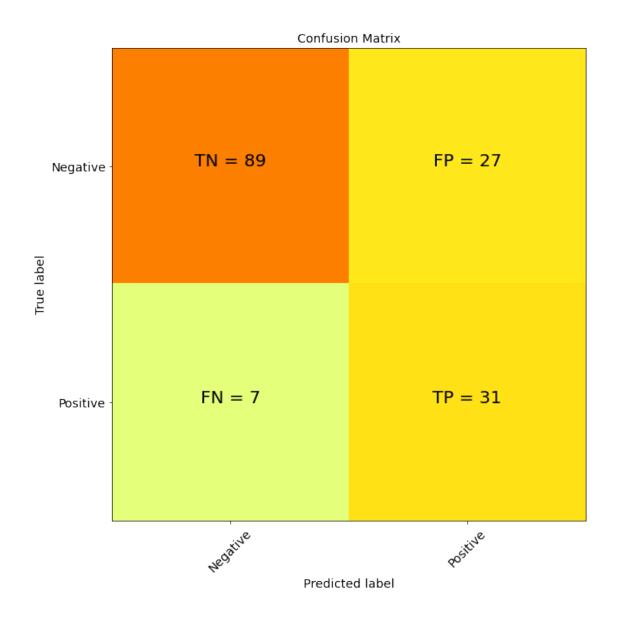
Accuracy Logistic Regression: 0.7792207792207793

Precision LR: 0.5344827586206896 Recall LR: 0.8157894736842105 F1 Score LR: 0.645833333333333

```
[78]: |y_proba = model_lr.predict_proba(X_test_v1)[:, 1]
      # Compute precision-recall curve
      precision, recall, _ = precision_recall_curve(y_test, y_proba)
      # Compute area under the curve (AUC) for precision-recall curve
      auc_score = auc(recall, precision)
      # Plot precision-recall curve
      plt.figure()
      plt.plot(recall, precision, label='Precision-Recall curve (PR AUC = %0.2f)' %
       →auc_score)
      plt.xlabel('Recall')
      plt.ylabel('Precision')
      plt.ylim([0.0, 1.05])
      plt.xlim([0.0, 1.0])
      plt.title('Precision-Recall Curve for LR')
      plt.legend(loc="lower left")
      plt.show()
```







```
[80]: # Logistic Regression + Lasso
model_lasso = LogisticRegression(penalty='l1', solver='liblinear') #Lasso

model_lasso.fit(X_train_v1, y_train)

predictions_lasso = model_lasso.predict(X_test_v1)
y_proba = model_lasso.predict_proba(X_test_v1)[:, 1]

precision, recall, _ = precision_recall_curve(y_test, y_proba)
pr_auc = auc(recall, precision)
roc_auc = roc_auc_score(y_test, y_proba)
```

```
accuracy_lasso = accuracy_score(y_test, predictions_lasso)
precision_lasso = precision_score(y_test, predictions_lasso, average='binary')
recall_lasso = recall_score(y_test, predictions_lasso, average='binary')
f1_lasso = f1_score(y_test, predictions_lasso, average='binary')

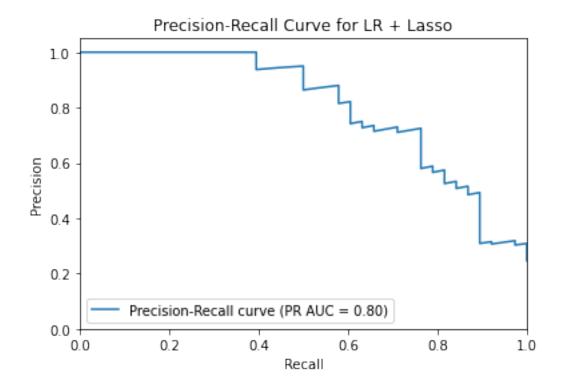
print("PR AUC:", pr_auc)
print("ROC AUC:", roc_auc)
print("Accuracy LR + Lasso:", accuracy_lasso)
print("Precision LR + Lasso:", precision_lasso)
print("Recall LR + Lasso:", recall_lasso)
print("F1 Score LR + Lasso:", f1_lasso)
```

A column-vector y was passed when a 1d array was expected. Please change the shape of y to (n\_samples, ), for example using ravel().

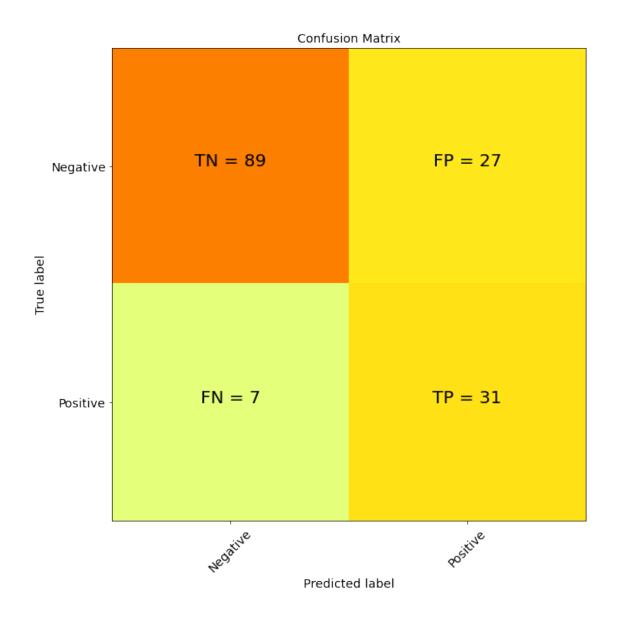
PR AUC: 0.8025563981672981 ROC AUC: 0.8788566243194192 Accuracy LR + Lasso: 0.7792207792207793 Precision LR + Lasso: 0.5344827586206896

Recall LR + Lasso: 0.8157894736842105 F1 Score LR + Lasso: 0.64583333333333334

```
[81]: y_proba = model_lasso.predict_proba(X_test_v1)[:, 1]
      # Compute precision-recall curve
      precision, recall, _ = precision_recall_curve(y_test, y_proba)
      # Compute area under the curve (AUC) for precision-recall curve
      auc_score = auc(recall, precision)
      # Plot precision-recall curve
      plt.figure()
      plt.plot(recall, precision, label='Precision-Recall curve (PR AUC = %0.2f)' %
       ⇒auc_score)
      plt.xlabel('Recall')
      plt.ylabel('Precision')
      plt.ylim([0.0, 1.05])
      plt.xlim([0.0, 1.0])
      plt.title('Precision-Recall Curve for LR + Lasso')
      plt.legend(loc="lower left")
      plt.show()
```



[82]: conf\_matrix(y\_test,predictions\_lasso)



```
# Plot top 20 features with highest coefficients

plt.figure(figsize=(10, 6))

plt.barh(top_20_features['Feature'], top_20_features['Coefficient'],

color='skyblue')

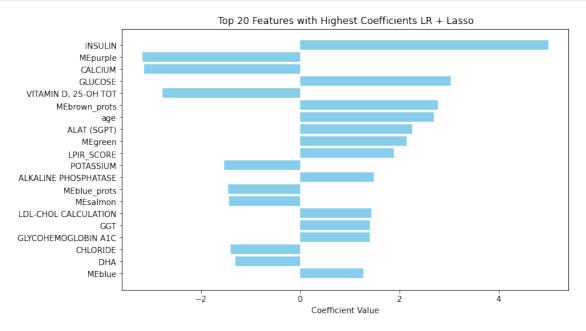
plt.xlabel('Coefficient Value')

plt.title('Top 20 Features with Highest Coefficients LR + Lasso')

plt.gca().invert_yaxis() # Invert y-axis to have the highest coefficient atu

the top

plt.show()
```



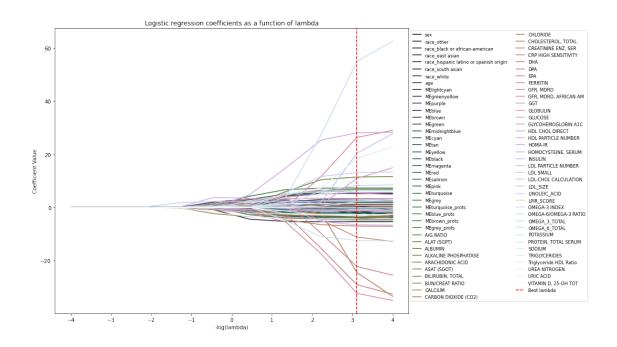
A column-vector y was passed when a 1d array was expected. Please change the shape of y to (n\_samples, ), for example using ravel().

```
Best C: 1291.5496650148827
Best Lambda (1/C): 0.0007742636826811277
```

```
[19]: best_log_lambda = -np.log10(best_lambda)
print(best_log_lambda)
```

## 3.111111111111107

```
[43]: coefs = np.array(model_lasso_cv.coefs_paths_[1]) # Extract coefficients for_
      ⇔each fold and C value
      mean_coefs = coefs.mean(axis=0) # Average over folds
      log_lambdas = -np.log10(1/model_lasso_cv.Cs_) # Convert Cs to log(lambda)
      sns.set_palette("cubehelix", len(mean_coefs[0]))
      if mean_coefs.shape[1] == len(X_train_v2.columns) + 1:
          intercept = mean_coefs[:, 0] # Assuming intercept is the first column
         mean_coefs = mean_coefs[:, 1:] # Exclude intercept from feature plotting
      # Plotting
      plt.figure(figsize=(15, 10))
      for i in range(mean coefs.shape[1]):
         plt.plot(log_lambdas, mean_coefs[:, i], label=X_train_v2.columns[i])
      plt.xlabel('-log(lambda)')
      plt.ylabel('Coefficient Value')
      plt.title('Logistic regression coefficients as a function of lambda')
      plt.axvline(x=3.11, color='r', linestyle='--', label='Best lambda')
      plt.legend(loc='upper left', bbox_to_anchor=(1, 1), fontsize='small', ncol=2)
      plt.subplots_adjust(right=0.75)
      plt.show()
```



	Feature	Coefficient
66	OMEGA_3_TOTAL	56.593112
55	HOMA-IR	28.001241
47	GFR, MDRD	26.602995
60	LDL-CHOL CALCULATION	18.857735
71	TRIGLYCERIDES	17.447133
62	LINOLEIC_ACID	12.813691
33	ARACHIDONIC ACID	11.174032
53	HDL CHOL DIRECT	10.131622
27	MEbrown_prots	7.248614
29	A/G RATIO	6.617513
64	OMEGA-3 INDEX	6.556852
65	OMEGA-6/OMEGA-3 RATIO	6.226713
30	ALAT (SGPT)	6.165542
73	UREA NITROGEN	5.975897
50	GLOBULIN	5.461354
52	GLYCOHEMOGLOBIN A1C	5.246357

16	MEtan	5.155505
11	MEblue	4.885962
49	GGT	3.098656
14	MEmidnightblue	3.051615
20	MEred	2.398454
63	LPIR_SCORE	2.263707
58	LDL PARTICLE NUMBER	2.233395
13	MEgreen	
69	PROTEIN, TOTAL SERUM	
7	age	1.874785
70	SODIUM	1.508980
28	MEgrey_prots	
32	ALKALINE PHOSPHATASE	1.017224
0		0.693096
51	Sex	
	GLUCOSE	0.622748
3	race_east asian	0.620176
18	MEblack	0.596864
9	MEgreenyellow	0.041012
15	MEcyan	-0.028067
46	FERRITIN	-0.036754
74	URIC ACID	-0.183745
23	MEturquoise	-0.403068
61	LDL_SIZE	
19	MEmagenta	-1.014681
54	HDL PARTICLE NUMBER	-1.081329
6	race_white	-1.185684
4	<pre>race_hispanic latino or spanish origin</pre>	-1.278450
35	BILIRUBIN, TOTAL	-1.292727
1	race_other	-1.305965
56	HOMOCYSTEINE, SERUM	-1.313993
21	MEsalmon	-1.358560
5	race_south asian	-1.680073
24	MEgrey	-1.885325
17	MEyellow	-2.106742
2	race_black or african-american	
68	POTASSIUM	
72	Triglyceride HDL Ratio	
42		
38	3 .	-2.998552
	CRP HIGH SENSITIVITY	-2.998552 -3.293459
	CRP HIGH SENSITIVITY CARBON DIOXIDE (CO2)	-3.293459
8	CRP HIGH SENSITIVITY CARBON DIOXIDE (CO2) MElightcyan	-3.293459 -3.328864
8 36	CRP HIGH SENSITIVITY CARBON DIOXIDE (CO2)  MElightcyan BUN/CREAT RATIO	-3.293459 -3.328864 -3.373633
8 36 12	CRP HIGH SENSITIVITY CARBON DIOXIDE (CO2) MElightcyan BUN/CREAT RATIO MEbrown	-3.293459 -3.328864 -3.373633 -3.400190
8 36 12 25	CRP HIGH SENSITIVITY CARBON DIOXIDE (CO2)  MElightcyan BUN/CREAT RATIO  MEbrown MEturquoise_prots	-3.293459 -3.328864 -3.373633 -3.400190 -3.543526
8 36 12 25 31	CRP HIGH SENSITIVITY CARBON DIOXIDE (CO2)  MElightcyan BUN/CREAT RATIO  MEbrown MEturquoise_prots ALBUMIN	-3.293459 -3.328864 -3.373633 -3.400190 -3.543526 -3.671142
8 36 12 25 31 22	CRP HIGH SENSITIVITY CARBON DIOXIDE (CO2)  MElightcyan BUN/CREAT RATIO  MEbrown MEturquoise_prots ALBUMIN MEpink	-3.293459 -3.328864 -3.373633 -3.400190 -3.543526 -3.671142 -3.757524
8 36 12 25 31 22 59	CRP HIGH SENSITIVITY CARBON DIOXIDE (CO2)  MElightcyan BUN/CREAT RATIO  MEbrown MEturquoise_prots ALBUMIN  MEpink LDL SMALL	-3.293459 -3.328864 -3.373633 -3.400190 -3.543526 -3.671142 -3.757524 -4.243272
8 36 12 25 31 22	CRP HIGH SENSITIVITY CARBON DIOXIDE (CO2)  MElightcyan BUN/CREAT RATIO  MEbrown MEturquoise_prots ALBUMIN MEpink	-3.293459 -3.328864 -3.373633 -3.400190 -3.543526 -3.671142 -3.757524 -4.243272

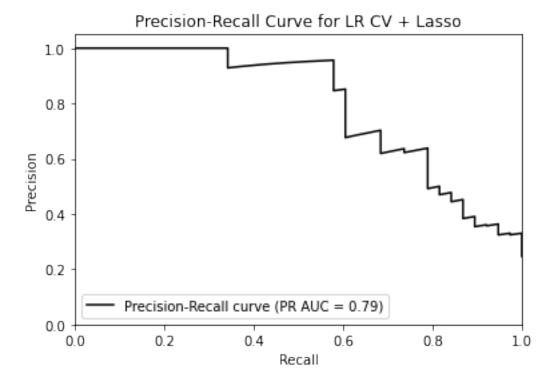
```
VITAMIN D, 25-OH TOT
     75
                                                   -4.735864
                                    ASAT (SGOT)
     34
                                                   -4.871669
     10
                                       MEpurple
                                                   -5.158355
                                        INSULIN
     57
                                                   -6.736506
     41
                            CREATININE ENZ, SER
                                                   -6.856152
     44
                                            DPA
                                                  -11.089019
     67
                                  OMEGA_6_TOTAL
                                                  -12.116757
     45
                                            EPA
                                                  -22.290040
                             CHOLESTEROL, TOTAL
                                                  -22.729687
     40
     43
                                                  -29.073188
                                            DHA
     48
                          GFR, MDRD, AFRICAN AM
                                                  -32.460891
[41]: predictions_lasso_cv = model_lasso_cv.predict(X_test_v1)
      y_proba = model_lasso_cv.predict_proba(X_test_v1)[:, 1]
      precision, recall, _ = precision_recall_curve(y_test, y_proba)
      pr_auc_cv = auc(recall, precision)
      roc_auc_cv = roc_auc_score(y_test, y_proba)
      accuracy_lasso_cv = accuracy_score(y_test, predictions_lasso_cv)
      precision_lasso_cv = precision_score(y_test, predictions_lasso_cv,_
       ⇔average='binary')
      recall_lasso_cv = recall_score(y_test, predictions_lasso_cv, average='binary')
      f1_lasso_cv = f1_score(y_test, predictions_lasso_cv, average='binary')
      print("PR AUC LassoCV:", pr_auc_cv)
      print("ROC AUC LassoCV:", roc auc cv)
      print("Accuracy LR + LassoCV:", accuracy lasso cv)
      print("Precision LR + LassoCV:", precision lasso cv)
      print("Recall LR + LassoCV:", recall_lasso_cv)
      print("F1 Score LR + LassoCV:", f1_lasso_cv)
     PR AUC LassoCV: 0.7925301036437941
     ROC AUC LassoCV: 0.8756805807622504
     Accuracy LR + LassoCV: 0.7987012987012987
     Precision LR + LassoCV: 0.5660377358490566
     Recall LR + LassoCV: 0.7894736842105263
     F1 Score LR + LassoCV: 0.6593406593406593
[43]: # Plot precision-recall curve
      plt.figure()
      plt.plot(recall, precision, label='Precision-Recall curve (PR AUC = %0.2f)' %
       →pr_auc_cv)
      plt.xlabel('Recall')
      plt.ylabel('Precision')
      plt.ylim([0.0, 1.05])
```

CHLORIDE

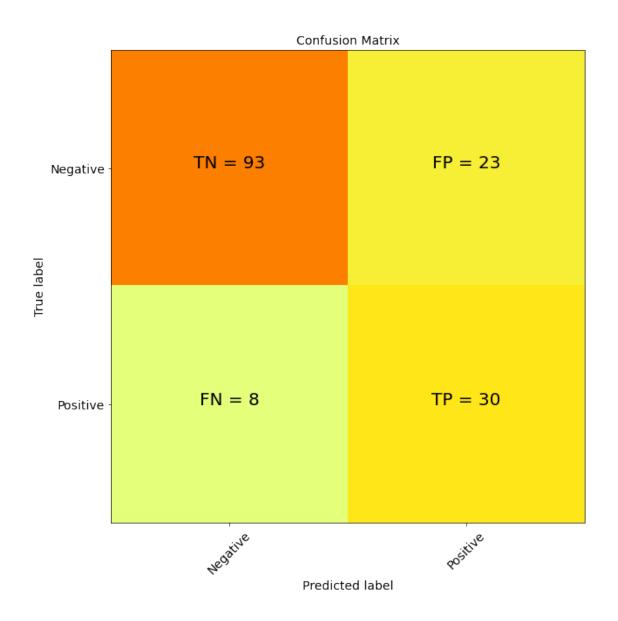
-4.530840

39

```
plt.xlim([0.0, 1.0])
plt.title('Precision-Recall Curve for LR CV + Lasso')
plt.legend(loc="lower left")
plt.show()
```



```
[44]: conf_matrix(y_test,predictions_lasso_cv)
```



```
[84]: # Logistic Regression + Ridge
model_ridge = LogisticRegression(penalty='12', solver='liblinear') #Ridge

model_ridge.fit(X_train_v1, y_train)

predictions_ridge = model_ridge.predict(X_test_v1)
y_proba_ridge = model_ridge.predict_proba(X_test_v1)[:, 1]

precision, recall, _ = precision_recall_curve(y_test, y_proba_ridge)
pr_auc_ridge = auc(recall, precision)
roc_auc_ridge = roc_auc_score(y_test, y_proba_ridge)
```

```
accuracy_ridge = accuracy_score(y_test, predictions_ridge)
precision_ridge = precision_score(y_test, predictions_ridge, average='binary')
recall_ridge = recall_score(y_test, predictions_ridge, average='binary')
f1_ridge = f1_score(y_test, predictions_ridge, average='binary')

print("PR AUC Ridge:", pr_auc_ridge)
print("ROC AUC Ridge:", roc_auc_ridge)
print("Accuracy LR + Ridge:", accuracy_ridge)
print("Precision LR + Ridge:", precision_ridge)
print("Recall LR + Ridge:", recall_ridge)
print("F1 Score LR + Ridge:", f1_ridge)
```

PR AUC Ridge: 0.8090447827152129

ROC AUC Ridge: 0.889065335753176

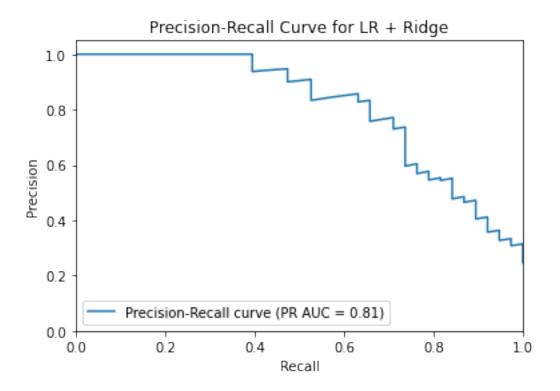
Accuracy LR + Ridge: 0.7857142857142857

Precision LR + Ridge: 0.5423728813559322

Recall LR + Ridge: 0.8421052631578947

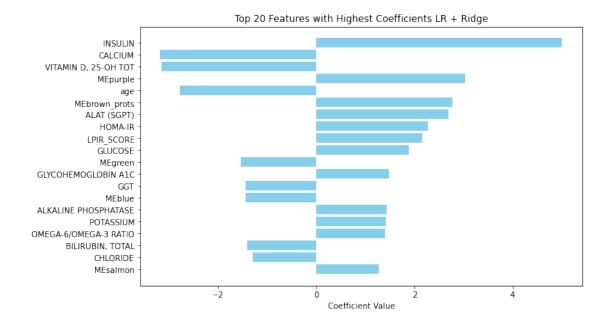
F1 Score LR + Ridge: 0.6597938144329897

A column-vector y was passed when a 1d array was expected. Please change the shape of y to (n\_samples, ), for example using ravel().

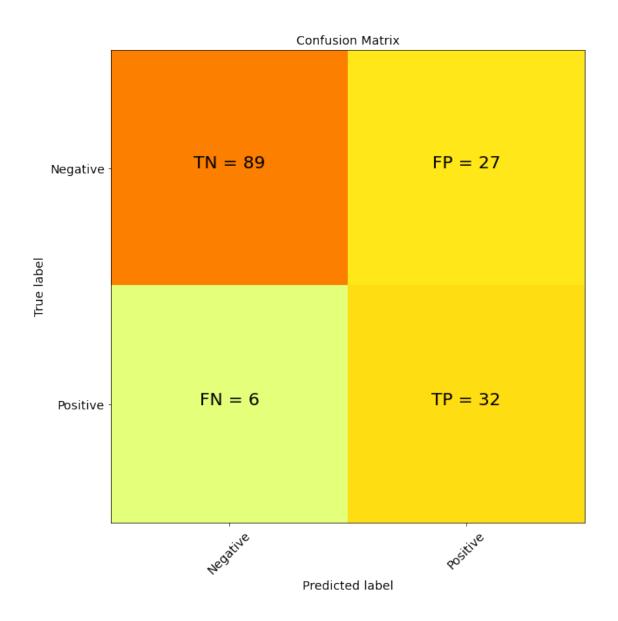


```
[86]: coefficients_ridge = model_ridge.coef_[0]
      feature_names_ridge = X_train_v2.columns
      coefficients_df_ridge = pd.DataFrame({'Feature': feature_names_ridge,__

¬'Coefficient': coefficients_ridge})
      # Sort DataFrame by absolute value of coefficients
      coefficients_df_ridge['Abs_Coefficient'] = ___
       ⇔abs(coefficients_df_ridge['Coefficient'])
      coefficients_df_ridge = coefficients_df_ridge.sort_values(by='Abs_Coefficient',_
       →ascending=False)
      top_20_features_ridge = coefficients_df_ridge.head(20)
      # Plot top 20 features with highest coefficients
      plt.figure(figsize=(10, 6))
      plt.barh(top_20_features_ridge['Feature'], top_20_features['Coefficient'],__
       ⇔color='skyblue')
      plt.xlabel('Coefficient Value')
      plt.title('Top 20 Features with Highest Coefficients LR + Ridge')
      plt.gca().invert_yaxis() # Invert y-axis to have the highest coefficient at_
       \hookrightarrow the top
      plt.show()
```



[87]: conf\_matrix(y\_test,predictions\_ridge)



```
[88]: model_xgb = xgb.XGBClassifier()
    model_xgb.fit(X_train_v1, y_train)

    y_pred_xgb = model_xgb.predict(X_test_v1)
    y_proba_xgb = model_xgb.predict_proba(X_test_v1)[:, 1]

[89]: precision, recall, _ = precision_recall_curve(y_test, y_proba_xgb)
    pr_auc = auc(recall, precision)
    roc_auc = roc_auc_score(y_test, y_proba_xgb)

    accuracy_xgb = accuracy_score(y_test, y_pred_xgb)
```

```
precision_xgb = precision_score(y_test, y_pred_xgb, average='binary')
recall_xgb = recall_score(y_test, y_pred_xgb, average='binary')
f1_xgb = f1_score(y_test, y_pred_xgb, average='binary')

print("PR AUC:", pr_auc)
print("ROC AUC:", roc_auc)
print("Accuracy XGB:", accuracy_xgb)
print("Precision XGB:", precision_xgb)
print("Recall XGB:", recall_xgb)
print("F1 Score XGB:", f1_xgb)
```

PR AUC: 0.8241714305543074

ROC AUC: 0.9235480943738656

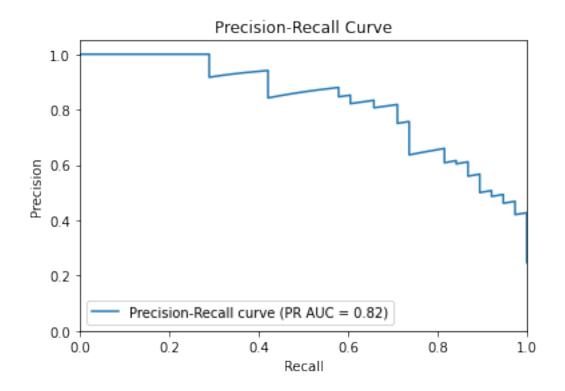
Accuracy XGB: 0.8311688311688312

Precision XGB: 0.6363636363636364

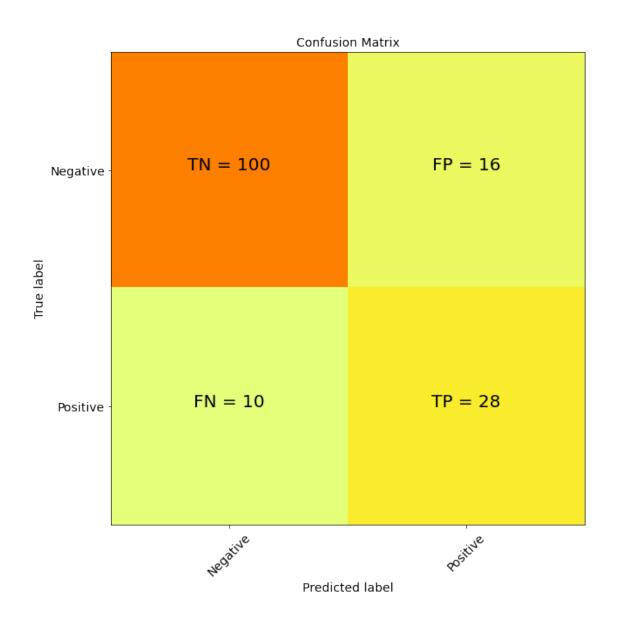
Recall XGB: 0.7368421052631579

F1 Score XGB: 0.6829268292682927

```
[90]: |y_proba = model_xgb.predict_proba(X_test_v1)[:, 1]
      # Compute precision-recall curve
      precision, recall, _ = precision_recall_curve(y_test, y_proba)
      # Compute area under the curve (AUC) for precision-recall curve
      auc score = auc(recall, precision)
      # Plot precision-recall curve
      plt.figure()
      plt.plot(recall, precision, label='Precision-Recall curve (PR AUC = %0.2f)' %
      ⇒auc_score)
      plt.xlabel('Recall')
      plt.ylabel('Precision')
      plt.ylim([0.0, 1.05])
     plt.xlim([0.0, 1.0])
      plt.title('Precision-Recall Curve')
      plt.legend(loc="lower left")
      plt.show()
```



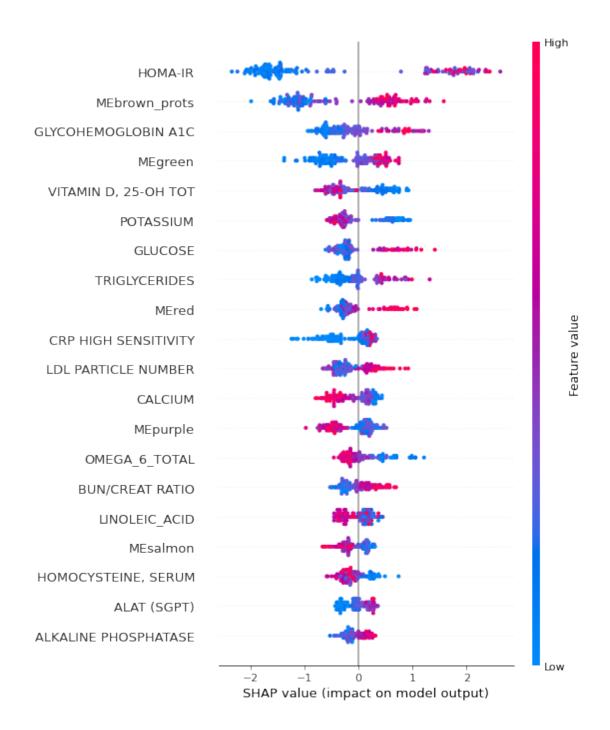
[91]: conf\_matrix(y\_test,y\_pred\_xgb)

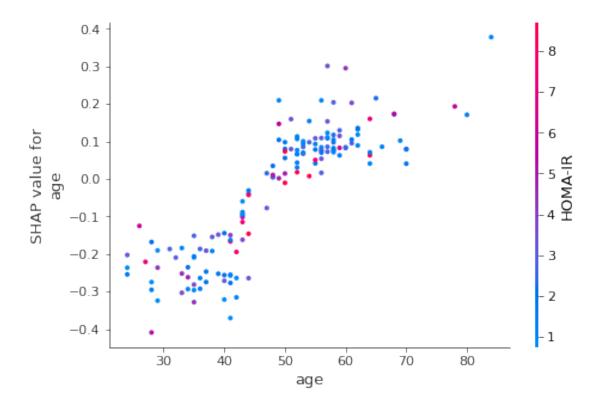


```
[92]: columns_sel = X_train_v2.columns
X_test_v3 = X_test_v2[columns_sel]

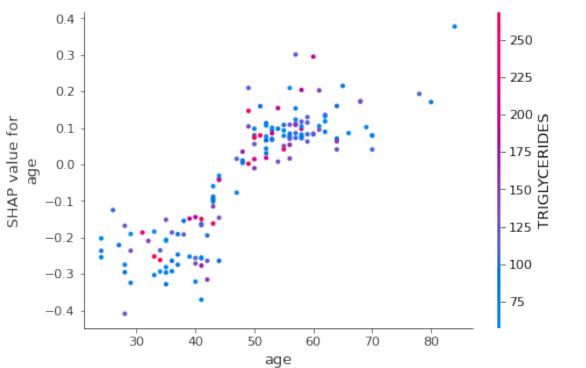
[93]: explainer = shap.TreeExplainer(model_xgb)
    shap_values = explainer.shap_values(X_test_v3)

[94]: shap.summary_plot(shap_values, X_test_v3, max_display=20, show = False)
    plt.show()
```

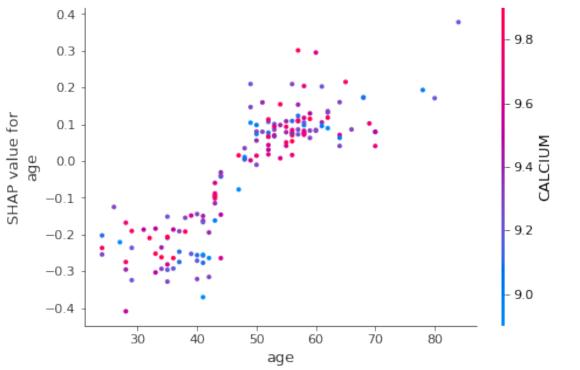




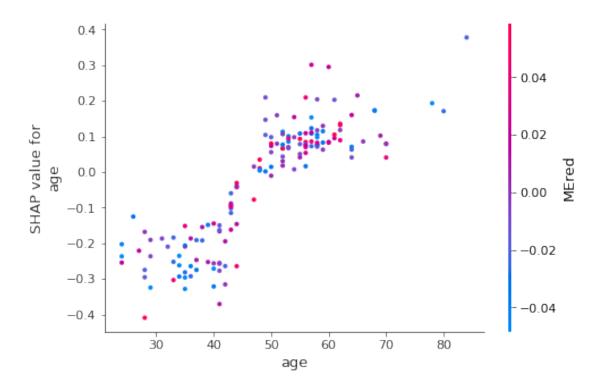




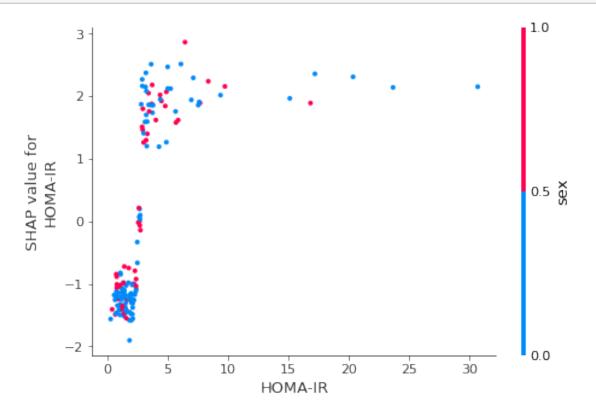
[92]: shap.dependence\_plot("age", shap\_values, X\_test\_v4, interaction\_index="CALCIUM")

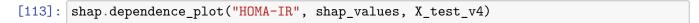


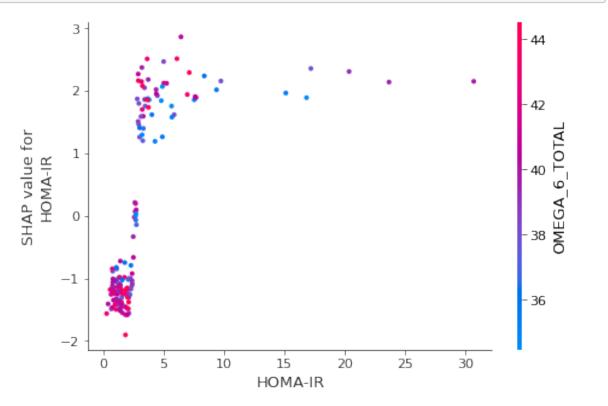
[100]: shap.dependence\_plot("age", shap\_values, X\_test\_v4, interaction\_index="MEred")



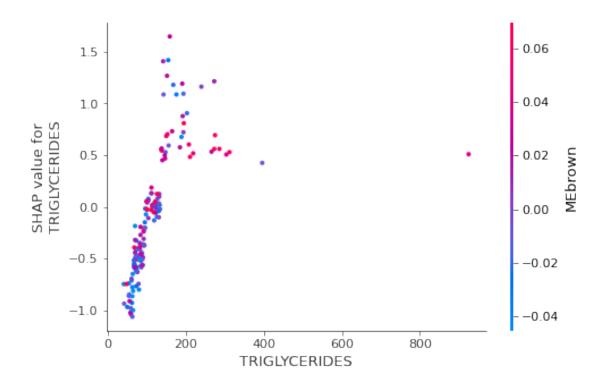
[111]: shap.dependence\_plot("HOMA-IR", shap\_values, X\_test\_v4, interaction\_index="sex")







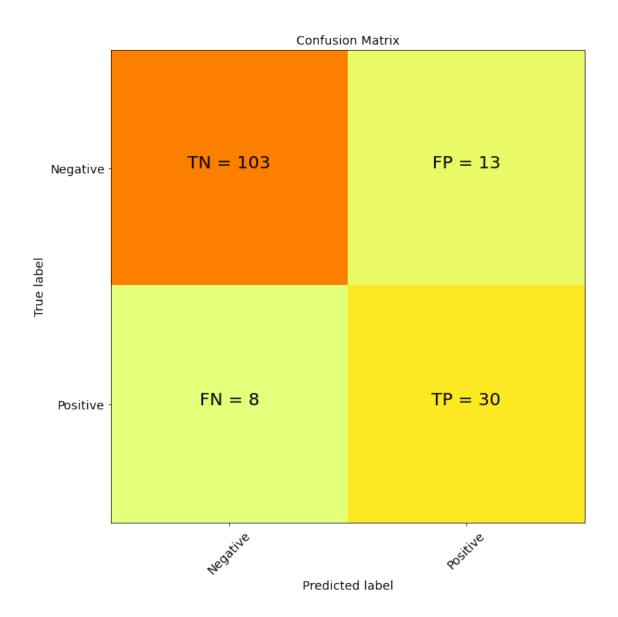
[114]: shap.dependence\_plot("TRIGLYCERIDES", shap\_values, X\_test\_v4)



```
[59]: # hyperparameter tuning and k-fold cross-validation
      xgb_hyper = xgb.XGBClassifier()
      param_grid = {
          'n_estimators': [100, 200, 300],
          'max_depth': [3, 4, 5],
          'learning_rate': [0.1, 0.01, 0.001],
      }
      #Straitifed K-fold preserves the percentage of samples for each class
      #https://scikit-learn.org/stable/modules/generated/sklearn.model_selection.
       \hookrightarrow Stratified KFold.html
      kfold = StratifiedKFold(n_splits=10, shuffle=True, random_state=42)
      grid_search = GridSearchCV(estimator=xgb_hyper, param_grid=param_grid,__
       ⇒scoring='accuracy', cv=kfold)
      grid_result = grid_search.fit(X_train_v1, y_train)
      print("Best Parameters: ", grid_result.best_params_)
      xgb_best_model = grid_result.best_estimator_
```

[61]: conf\_matrix(y\_test,xgb\_pred\_best\_model)

Precision XGB Best Model: 0.6976744186046512 Recall XGB Best Model: 0.7894736842105263 F1 Score XGB Best Model: 0.7407407407407



```
[56]: #Manually adjust threshold
def adjust_threshold(X_test, threshold, model):
    probs = model.predict_proba(X_test)[:, 1]
    y_pred = (probs >= threshold).astype(int)

    precision = precision_score(y_test, y_pred, average='binary')
    recall = recall_score(y_test, y_pred, average='binary')
    f1 = f1_score(y_test, y_pred, average='binary')

    print("Precision:", precision)
    print("Recall:", recall)
    print("F1 Score:", f1)
```

```
new_preds = adjust_threshold(X_test= X_test_v1, threshold=0.4, u omodel=model_lasso_cv)
```

Precision: 0.5

Recall: 0.7894736842105263 F1 Score: 0.6122448979591837

[]: