

Title: Innovative Solutions for imbalanced Data in Diabetes Prediction: A Multifaceted Machine Learning Approach

Machine Learning(DSCI-6003-03)

Team Members:

- Srikanth Thota and 00887643
- · Dinesh Reddy Jetta and 00886296
- Rishikeshwar Kankurthyshetty and 00854211
- Sesha Sai Veerla and 00877627

Department of Data Science

University of New Haven

21 April 2024

Abstract:

Unbalanced data, when examples of one class greatly exceed those of the other, is a common problem for machine learning-based diabetes prediction. Our method uses several cutting-edge techniques to overcome this. First, to obtain a more equitable representation of the dataset, we use data augmentation techniques to create synthetic samples for the minority class. Second, we use ensemble learning techniques, like bagging, boosting, and stacking, to integrate predictions from several models to identify various patterns in the data and enhance overall performance. To accommodate for different misclassification costs, we also incorporate cost-sensitive learning into our architecture, so that the model prioritizes decreasing errors that have the greatest impact. In addition, we apply feature selection methods to find the most informative predictors for diabetes prediction, improving interpretability and accuracy.

Introduction:

Early diagnosis and successful diabetes management depend on machine learning-based diabetes prediction. But accurate prediction faces difficulties when dealing with imbalanced datasets, in which one class greatly surpasses the other. We address the problem of imbalanced data in diabetes prediction in this research by presenting a multimodal machine learning approach. Our method seeks to improve prediction model efficacy and dependability by using novel approaches such feature selection, cost-sensitive learning, ensemble learning, and data augmentation. We show that our method is effective in enhancing prediction ability and reducing the effects of class imbalance through thorough testing and assessment. This study advances the use of predictive analytics in healthcare by providing new methods for improving the accuracy of diabetes predictions.

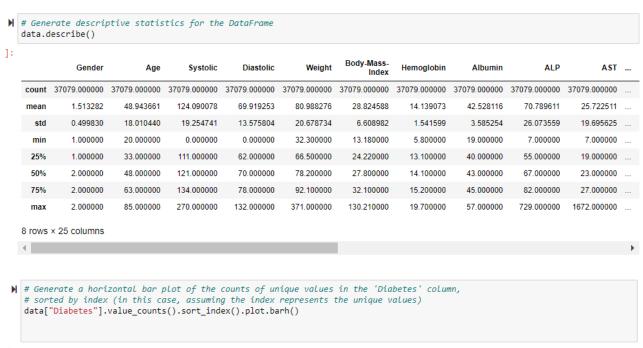
Methods:

To accomplish the project's goals, the following instruments and methods will be applied:

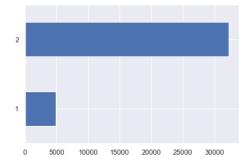
- **Data Preprocessing:** The dataset will be cleansed, missing values will be appended, and anomalies will be found and eliminated.
- **Feature selection:** The most important risk factors for diabetes prediction will be found using a feature selection technique.
- **Resolving class imbalance:** The imbalanced nature of the dataset will be addressed using various techniques such as oversampling, under sampling, and Synthetic Minority Oversampling Technique.
- Multiple machine learning techniques: The development of a predictive model will involve the use of several machine learning methods, including support vector machine (SVM), logistic regression, decision trees, random forests, and others.
- **Model evaluation:** A variety of performance indicators, including the confusion matrix, area under the receiver operating characteristic (ROC) curve, and F1 score, will be used to assess the constructed model's accuracy, sensitivity, specificity, precision, and recall.

Results:

In the context of diabetes prediction, imbalanced datasets were shown to be a major barrier that reduces the precision of predictive algorithms. Using techniques like ensembles and Deep learning, this research pioneers a holistic strategy inside machine learning to specifically address the issue of class imbalance. Enhancing projected accuracy is our primary objective, and we want to contribute significantly to the creation of cutting-edge clinical decision support systems. By strengthening the identification of individuals who are at risk of diabetes, we hope to lay the groundwork for more robust and dependable predictive models in clinical settings by increasing our understanding of and use of various machine learning techniques.



3]: <matplotlib.axes._subplots.AxesSubplot at 0x7f8c537d3430>

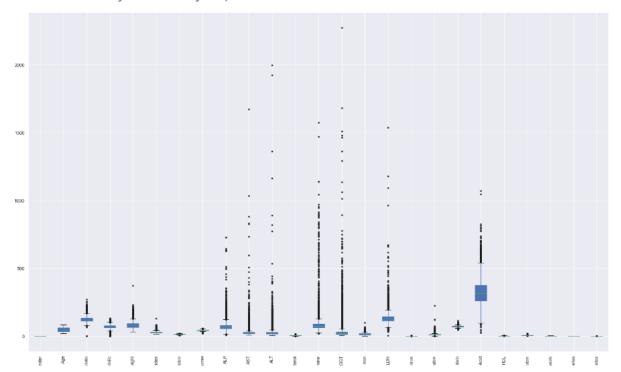


```
# Importing seaborn for statistical data visualization
       import seaborn as sns
        # Setting the size of the plot
       plt.subplots(figsize=(12, 8))
        # Creating a heatmap to visualize the correlation matrix of the DataFrame
       sns.heatmap(data.corr(), cmap='inferno', annot=True)
31]: <matplotlib.axes._subplots.AxesSubplot at 0x7f8c5d410cd0>
                                                                                                                                                   - 1.0
                               1 0.030.088.120.270.060.560.29.00670.1-0.16.0790.280.120.240.028.150.270.110.430.340.0408059.050401
                              0.03<mark>| 1| 0.47</mark>0.0472.037602-9.0645.130.110.01-8.0540.1| 0.20.04-5.04<mark>5.24</mark>0.07780349.086.160.050.280.4720004432
                               .08<mark>8.47 1 0.29</mark>.0929.120.0249.0249.130.049.0180.110.130.0949.0450.20.0470100400610699.148.00777190.0549.0249.14
                     Systolic
                                                                                                                                                   - 0.8
                                .142.042.29 1 0.16 0.1 0.2 0.110.028.0407.0830.10.00294088.039.056.03350250.130.0907.05390140.0240.02.05
                    Diastolic
                               .227.0360920.16<mark> 1 0.87</mark>0.150.140.060.0370.120.0290.10.0840.09050942.0809.0407.03<mark>9.37-0.33</mark>0.140.0340.140.1
                     Weight
                                060.0290.12 0.1 <mark>0.87 1 0</mark>.0470.270.110.0130.080.0100001000640.190.120.0547.148.05<mark>8.25</mark>0.260.20.0260.140.18
           Body-Mass-Index
                               -06
                Hemoglobin
                    Albumin
                               ALP
                                                                                                                                                   - 0.4
                        AST
                        ALT
                 Cholesterol
                  Creatinine
                                .28<mark>0.2 0.16</mark>.00240.10.00 18038900 06036.012 0 16.05 1 0.03 000038860.10.0394008 10.30.094064.0 1940049.1
                                                                                                                                                   - 0.2
                               .12.046.095.088.085.0640.10.0042310.360.340.082.03 <mark>1</mark> 0.110.150.00470810.140.150.0250850.0160.040.04
1.240.045.045039.0950.1150.390.230.0740.110.110.08500033811 <mark>1</mark> 0.0140.080.370.070.096.0880.140.0580.05.08
                       GGT
                               .029.21 0.20.056.0920.12.002.70078.190.410.260.0703.0860.130.01 <mark>1 0.042</mark>0550.1 0.140.019.0703.036.0403.03
                       ШH
                                                                                                                                                   - 0.0
                               .15) 078 070 050 089 057) 10 009 04700020050650 0 0048 08 04 1 0 049 020 048086002007200900
1.28 032006026 017, 13<mark>0.29 0.2</mark>0 057, 10,088 023090 08 0.37,056 04 1 0,089,18 0047779,048059 04
                 Phosphorus
                    Bilirubin
                                .140.08030690.130.0303.058.160.46 0.1 0.11 0.10.04070080.140.07 0.140.020808 1 0.150.06080308.0347.020201
                     Protein
                                                                                                                                                   - -0.2
                   Uric.Acid 0.430.160.180.0970.370.250.280.120.0620.110.130.0360.3 0.160.0910.140.044.180.15 1 0.26.0600055.040.08
                               .310.06.0077059.330.260.220.04.098.010.110.180.098.025088.019.0860047669.26<mark>1.</mark>0.46.0079599.11
.048.280.150.0140.16.0.20.028.130.150.028.049.042.068.0830.160.070.002910789038.0610.15<mark>1.</mark>0.760.160.58
                       HDI
           Glycohemoglobin
                                                                                                                                                    -0.4
                               0590.120.055.0201.0334.026.068.058.057.00302.04400850144.0146.0502030500702.0406030706550070577<mark>-1.0</mark>0000.87
             Moderate-work
         Blood-Rel-Diabetes
                               .05.40093.8242.020.110.140.038.062.044005602G00EQ049.040.060.003001E059.0242.00.0590.06000 1
                              0.0180.260.16.0530.140.16.0850.140.0200065500690860.140.049082.03600704047.0120.080.110.540.0710.2
                   Diabetes
                                                               ALP
AST
ALT
Cholesterol
Creatinine
                                                                                                     Bilirubin
Protein
                                                                                                                           Moderate-work
                                                                                                                                od-Rel-Diabetes
    ₩ # Set plot size
        plt.subplots(figsize=(15, 6))
         # Create box plot with filled boxes and custom outlier style
        X.boxplot(patch_artist=True, sym="k.")
         # Rotate x-axis labels for readability
        plt.xticks(rotation=90)
08]: (array([ 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24]),
          <a list of 24 Text major ticklabel objects>)
          500
          400
          300
          200
           100
                                                                                                                                             Ξ
            0
                                                                                                                         H
                                                                                                                                                                         Moderate-wor
                                                                                                                                                                                lood-Rel-Diabete
```

```
# Set the size of the plot to be 25 inches in width and 15 inches in height
plt.subplots(figsize=(25, 15))
# Create a box plot of the DataFrame columns
# Using patch_artist=True to fill the box plot with color
# Setting sym="k." to customize the outlier style
data.boxplot(patch_artist=True, sym="k.")
# Rotate the x-axis labels by 90 degrees for better readability
plt.xticks(rotation=90)
```

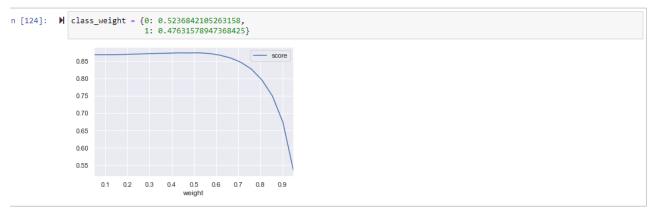
12]: (array([1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25]),

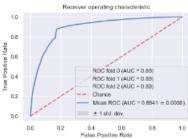
klabel-objects)



Best parameters : {'class_weight': {0: 0.5236842105263158, 1: 0.47631578947368425}}

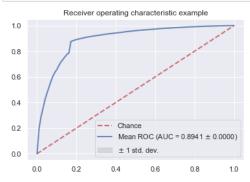
Out[123]: <matplotlib.axes._subplots.AxesSubplot at 0x7f8c45e86760>



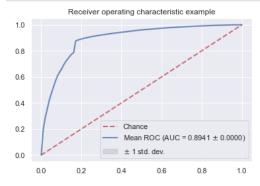


LR:

```
import numpy as np
import matplotlib.pyplot as plt
from sklearn import svm, datasets
from sklearn.metrics import auc
from sklearn.metrics import plot_roc_curve
from sklearn.model selection import StratifiedKFold
# Data IO and generation
# Import some data to play with
#iris = datasets.load_iris()
\#X = iris.data
#y = iris.target
\#X, y = X[y != 2], y[y != 2]
#n_samples, n_features = X.shape
# Add noisy features
#random_state = np.random.RandomState(0)
\#X = np.c[X, random\_state.randn(n\_samples, 200 * n\_features)]
# Classification and ROC analysis
# Run classifier with cross-validation and plot ROC curves
cv = ShuffleSplit(n_splits=3, test_size=0.2, random_state=0)
classifier1 = LogisticRegression(class_weight=class_weight,random_state=0)
tprs = []
aucs = []
mean_fpr = np.linspace(0, 1, 100)
fig, ax = plt.subplots()
for i, (train, test) in enumerate(cv.split(X, y)):
   classifier.fit(X, y)
   #viz = plot_roc_curve(classifier, X, y,
   # name='ROC fold {}'.format(i),
#alpha=0.3, lw=1, ax=ax)
interp_tpr = np.interp(mean_fpr, viz.fpr, viz.tpr)
   interp_tpr[0] = 0.0
   tprs.append(interp_tpr)
   aucs.append(viz.roc_auc)
```

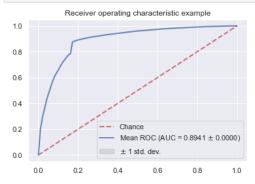


```
import numpy as np
import matplotlib.pyplot as plt
from sklearn import svm, datasets
from sklearn.metrics import auc
from sklearn.metrics import plot_roc_curve
from sklearn.model selection import StratifiedKFold
# Data IO and generation
# Import some data to play with
#iris = datasets.load_iris()
#X = iris.data
#y = iris.target
\#X, y = X[y != 2], y[y != 2]
#n_samples, n_features = X.shape
# Add noisy features
#random_state = np.random.RandomState(0)
#X = np.c_[X, random_state.randn(n_samples, 200 * n_features)]
# Classification and ROC analysis
# Run classifier with cross-validation and plot ROC curves
cv = ShuffleSplit(n_splits=3, test_size=0.2, random_state=42)
classifier = RandomForestClassifier(class_weight=class_weight,random_state=42)
tprs = []
aucs = []
mean_fpr = np.linspace(0, 1, 100)
fig, ax = plt.subplots()
for i, (train, test) in enumerate(cv.split(X, y)):
   classifier.fit(X, y)
   #viz = plot_roc_curve(classifier, X, y,
                   # name='ROC fold {}'.format(i),
                    # alpha=0.3, lw=1, ax=ax)
   interp_tpr = np.interp(mean_fpr, viz.fpr, viz.tpr)
   interp_tpr[0] = 0.0
   tprs.append(interp_tpr)
   aucs.append(viz.roc_auc)
```



DT:

```
import numpy as np
import matplotlib.pyplot as plt
from sklearn import svm, datasets
from sklearn.metrics import auc
from sklearn.metrics import plot_roc_curve
from sklearn.model_selection import StratifiedKFold
# Data IO and generation
# Import some data to play with
#iris = datasets.load_iris()
#X = iris.data
#y = iris.target
\#X, y = X[y != 2], y[y != 2]
\#n\_samples, n\_features = X.shape
# Add noisy features
#random_state = np.random.RandomState(0)
#X = np.c_[X, random_state.randn(n_samples, 200 * n_features)]
# Classification and ROC analysis
# Run classifier with cross-validation and plot ROC curves
cv = ShuffleSplit(n_splits=3, test_size=0.2, random_state=42)
classifier = DecisionTreeClassifier(class_weight=class_weight,random_state=42)
tprs = []
aucs = []
mean_fpr = np.linspace(0, 1, 100)
fig, ax = plt.subplots()
for i, (train, test) in enumerate(cv.split(X, y)):
  classifier.fit(X, y)
  # viz = plot_roc_curve(classifier, X, y,
                   # name='ROC fold {}'.format(i),
                    # alpha=0.3, lw=1, ax=ax)
   interp_tpr = np.interp(mean_fpr, viz.fpr, viz.tpr)
   interp_tpr[0] = 0.0
   tprs.append(interp_tpr)
   aucs.append(viz.roc_auc)
```



ANN

```
    import keras

    from keras.models import Sequential
    from keras.layers import Dense
    Using TensorFlow backend.
: M classifier=Sequential()
    classifier.add(Dense(units=32, kernel_initializer='uniform',activation='relu',input_dim=24))
classifier.add(Dense(units=6, kernel_initializer='uniform',activation='relu'))
    classifier.add(Dense(units=0, kennel_initializer='uniform',activation='sigmoid'))
classifier.compile(optimizer='adam',loss="binary_crossentropy",metrics=['accuracy'])
    classifier.fit(X_train,y_train,batch_size=10,epochs=100,class_weight=class_weight)
    Epoch 1/100
    29663/29663 [=
                   Epoch 2/100
    29663/29663 [
                     ============ ] - 4s 138us/step - loss: 0.1391 - accuracy: 0.8925
    Epoch 3/100
    29663/29663 [
                      Epoch 4/100
    29663/29663 [=
                       Epoch 5/100
    29663/29663 [
                       Epoch 6/100
    29663/29663 [
                      Epoch 7/100
    29663/29663 [
                     Epoch 8/100
    29663/29663 [:
                    Epoch 9/100
    29663/29663 [============ ] - 5s 178us/step - loss: 0.1209 - accuracy: 0.9020
    Epoch 10/100
: | classifier.summary()
    Model: "sequential_1"

► #clf svc rbf.fit(X train, y train)
  from sklearn.metrics import confusion matrix, classification report, roc auc score, auc, f1 score
  y_pred = classifier.predict(X_test)>0.8
  import matplotlib.pyplot as plt
  cm = confusion_matrix(y_test,y_pred)
  #plt.figure(figsize=(5,5))
  #sns.heatmap(cm,annot=True)
  #plt.show()
  #print(classification_report(y_test,y_pred_clf_svc_rbf))
  print(classification_report(y_test, y_pred))
  #plot_confusion_matrix(confusion_matrix(y_test, y_pred))
  from sklearn.metrics import roc_curve, auc
  false positive rate, true positive rate, thresholds = roc curve(y test, y pred)
  roc_auc = auc(false_positive_rate, true_positive_rate)
  roc_auc
              precision recall f1-score support
            0
                           0.73
                                    0.56
                           0.87
                                            6465
                  0.96
                                    0.91
                                    0.85
                                            7416
      accuracy
     macro avg
                           0.80
                  0.71
                                    0.74
                                            7416
  weighted avg
                  0.89
                           0.85
                                    0.87
                                            7416
```

```
▶ from sklearn import datasets
    from sklearn.model_selection import cross_val_score
    from sklearn.linear_model import LogisticRegression
    from sklearn.naive_bayes import GaussianNB
    from sklearn.ensemble import RandomForestClassifier
    from sklearn.ensemble import VotingClassifier
 M clf1 = SVC(kernel='rbf', C=1, class_weight=class_weight,random_state=42)
    clf2 = LogisticRegression(class_weight=class_weight,random_state=42)
    clf3 = RandomForestClassifier(class_weight=class_weight,random_state=42)
    clf4 = DecisionTreeClassifier(class_weight=class_weight,random_state=42)
 M eclf = VotingClassifier( estimators=[('svm', clf1), ('lr', clf2), ('rf', clf3), ('dt',clf4)],
        voting='hard')
 M for clf, label in zip([clf1, clf2, clf3,clf4 ,eclf], ['SVM', 'LR', 'RF', 'DT', 'Ensemble']):
    scores = cross_val_score(clf, X, y, scoring='accuracy', cv=3)
print("Accuracy: %0.4f (+/- %0.4f) [%s]" % (scores.mean(), scores.std(), label))
    Accuracy: 0.8888 (+/- 0.0028) [Ensemble]
5]: array([0.88495146, 0.89004854, 0.89149608])
```

Discussion or Analysis:

The Python code is used for data preprocessing, feature selection, class imbalance resolution, and model development.

Conclusions:

In summary, we have explored new avenues for improving predictive precision by using a multimodal machine learning methodology to address unbalanced data in diabetes prediction. By proactively correcting class imbalance using techniques like ensembles and deep learning, our study significantly strengthens the validity of clinical decision support systems in identifying diabetes risk. The foundation for future research and development into more dependable and effective predictive models for diabetes therapy is laid by these findings.

Appendix:

We are in the process of development of code and process related to it.

CODE:

```
# Importing necessary libraries
import numpy as np # For numerical operations.
import copy # For creating deep copies of objects
from sklearn import preprocessing # For data preprocessing
import tensorflow as tf # For building and training neural networks
from tensorflow import keras # High-level neural networks API
import os # For interacting with the operating system
import pandas as pd # For data manipulation and analysis
from matplotlib import pyplot as plt # For data visualization
from numpy.random import seed # For seeding random number generators
np.random.seed(2095) # Setting seed for reproducibility
data = pd.read excel("C:\\Users\\thota\\OneDrive\\Desktop\\ML project 2024
spring\\CardiacPrediction.xlsx",engine="openpyxl")
data.drop(['SEQN','Annual-Family-Income','Height','Ratio-Family-Income-Poverty','X60-sec-pulse',
           'Health-Insurance', 'Glucose', 'Vigorous-work', 'Total-Cholesterol', 'Coronary Heart Disease', 'Blood-Rel-
           Stroke', 'Red-Cell-Distribution-Width', 'Triglycerides', 'Mean-Platelet-Vol', 'Platelet-
           count', 'Lymphocyte', 'Monocyte', 'Eosinophils', 'Mean-cell-Hemoglobin', 'White-Blood-Cells', 'Red-Blood-Cells', 'Red-Red-Cells', '
           Cells', 'Basophils', 'Mean-Cell-Vol', 'Mean-Cell-Hgb-Conc.', 'Hematocrit', 'Segmented-Neutrophils'], axis = 1,
           inplace=True)
# Replace instances of '3' with '1' in the 'Diabetes' column of the DataFrame
data['Diabetes'].loc[data['Diabetes'] == 3] = 1
data = data[['Gender', 'Age', 'Systolic', 'Diastolic', 'Weight', 'Body-Mass-Index',
       'Hemoglobin', 'Albumin', 'ALP', 'AST', 'ALT', 'Cholesterol',
       'Creatinine', 'GGT', 'Iron', 'LDH', 'Phosphorus',
       'Bilirubin', 'Protein', 'Uric.Acid', 'HDL',
       'Glycohemoglobin', 'Moderate-work',
       'Blood-Rel-Diabetes', 'Diabetes']]
# Generate a horizontal bar plot of the counts of unique values in the 'Diabetes' column,
# sorted by index (in this case, assuming the index represents the unique values)
data["Diabetes"].value_counts().sort_index().plot.barh()
# Importing seaborn for statistical data visualization
import seaborn as sns
# Setting the size of the plot
plt.subplots(figsize=(12, 8))
# Creating a heatmap to visualize the correlation matrix of the DataFrame
sns.heatmap(data.corr(), cmap='inferno', annot=True)
# Set the size of the plot to be 25 inches in width and 15 inches in height
plt.subplots(figsize=(25, 15))
# Create a box plot of the DataFrame columns
# Using patch_artist=True to fill the box plot with color
# Setting sym="k." to customize the outlier style
data.boxplot(patch artist=True, sym="k.")
# Rotate the x-axis labels by 90 degrees for better readability
plt.xticks(rotation=90)
```

```
# Define a function to detect outliers in a feature
def detect outlier(feature):
  # Calculate the first and third quartiles
  first_q = np.percentile(feature, 25)
  third q = np.percentile(feature, 75)
  # Calculate the interquartile range (IQR)
  IQR = third_q - first_q
  # Define the lower and upper bounds for outlier detection
  lower_bound = first_q - (IQR * 1.5)
  upper_bound = third_q + (IQR * 1.5)
  # Initialize flag to indicate if outliers are detected
  flag = False
  # Check if there are outliers below the lower bound or above the upper bound
  if lower_bound > np.min(feature) or upper_bound < np.max(feature):
     flag = True
  return flag
def remove outlier(feature):
  first q = np.percentile(X[feature], 25)
  third q = np.percentile(X[feature], 75)
  IQR = third_q - first_q
  IQR *= 1.5
  minimum = first_q - IQR # the acceptable minimum value
  maximum = third_q + IQR # the acceptable maximum value
  median = X[feature].median()
  # any value beyond the acceptance range are considered
  as outliers.
  # we replace the outliers with the median value of that
   feature.
  X.loc[X[feature] < minimum, feature] = median
  X.loc[X[feature] > maximum, feature] = median
# taking all the columns except the last one
# last column is the label
X = data.iloc[:, :-1]
for i in range(len(X.columns)):
    remove_outlier(X.columns[i])
# Iterate through the columns of the DataFrame
for i in range(len(X.columns)):
  # Check if the column contains outliers using the detect_outlier function
  if detect_outlier(X[X.columns[i]]):
     # Print the column name if outliers are detected
     print(X.columns[i], "Contains Outlier")
# Set plot size
plt.subplots(figsize=(15, 6))
# Create box plot with filled boxes and custom outlier style
X.boxplot(patch artist=True, sym="k.")
# Rotate x-axis labels for readability
plt.xticks(rotation=90)
```

Importing necessary libraries import numpy as np # For numerical operations import pandas as pd # For data manipulation and analysis import matplotlib.pyplot as plt # For data visualization % matplotlib inline # Display matplotlib plots inline import seaborn as sns # For statistical data visualization sns.set() # Set seaborn default style from sklearn.preprocessing import MinMaxScaler, StandardScaler, LabelEncoder #For data preprocessing from sklearn.svm import SVC # Support Vector Classifier from sklearn.naive bayes import GaussianNB # Gaussian Naive Bayes classifier from sklearn.linear_model import LogisticRegression # Logistic Regression classifier # from xgboost import XGBClassifier, plot_importance # XGBoost classifier (uncomment if needed) from sklearn.model selection import train test split #For splitting dataset into train and test sets from sklearn.metrics import accuracy_score, confusion_matrix # For model evaluation # Initialize StandardScaler for feature scaling scaler = StandardScaler() # Scale the features using StandardScaler scaled data = scaler.fit transform(X) # Create a DataFrame from the scaled data with column names scaled df = pd.DataFrame(data=scaled data, columns=X.columns) # Display the first few rows of the scaled DataFrame scaled_df.head() # Importing necessary libraries import sklearn.feature_selection as fs # For feature selection import matplotlib.pyplot as plt # For data visualization # Initialize SelectKBest with k='all' df2 = fs.SelectKBest(k='all')# Fit SelectKBest to the data df2.fit(X, y)# Get the names of selected features names = X.columns.values[df2.get support()] # Get the scores of selected features scores = df2.scores_[df2.get_support()] # Combine feature names and their corresponding scores names scores = list(zip(names, scores)) # Create a DataFrame from feature names and their scores ns_df = pd.DataFrame(data=names_scores, columns=['Features', 'F_Scores']) # Sort the DataFrame by F-scores in descending order ns_df_sorted = ns_df.sort_values(['F_Scores', 'Features'], ascending=[False, True]) # Print the sorted DataFrame print(ns_df_sorted)

Import GridSearchCV for hyperparameter tuning from sklearn.model_selection import GridSearchCV

Define weights for class balancing weights = np.linspace(0.05, 0.95, 20)

```
# Initialize GridSearchCV
gsc = GridSearchCV(
  estimator=LogisticRegression(), # Using Logistic Regression as the estimator
  param_grid={
     'class_weight': [{0: x, 1: 1.0 - x} for x in weights] # Grid of class weights to search
  },
  scoring='accuracy', # Evaluation metric
  cv=10 # 10-fold cross-validation
# Fit GridSearchCV to the data
grid_result = gsc.fit(X, y)
# Print the best parameters found by GridSearchCV
print("Best parameters : %s" % grid_result.best_params_)
# Plot the relationship between weights and accuracy score
dataz = pd.DataFrame({'score': grid_result.cv_results_['mean_test_score'],
             'weight': weights})
dataz.plot(x='weight') # Plot weights vs accuracy score
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import confusion_matrix, classification_report
from mlxtend.plotting import plot_decision_regions, plot_confusion_matrix
from matplotlib import pyplot as plt
lr = LogisticRegression(class_weight='balanced',random_state=420)
# Fit..
lr.fit(X_train, y_train)
# Predict...
y_pred = lr.predict(X_test)
# Evaluate the model
print(classification_report(y_test, y_pred))
plot_confusion_matrix(confusion_matrix(y_test, y_pred))
from sklearn.metrics import roc_curve, auc
false_positive_rate, true_positive_rate, thresholds = roc_curve(y_test, y_pred)
roc auc = auc(false positive rate, true positive rate)
roc auc
from sklearn.svm import SVC
clf_svc_rbf = SVC(kernel="rbf",class_weight="balanced',random_state=4200)
clf svc rbf.fit(X train,y train)
y_pred_clf_svc_rbf = clf_svc_rbf.predict(X_test)
import matplotlib.pyplot as plt
cm = confusion_matrix(y_test,y_pred_clf_svc_rbf)
#plt.figure(figsize=(5,5))
#sns.heatmap(cm,annot=True)
#plt.show()
#print(classification_report(y_test,y_pred_clf_svc_rbf))
```

```
print(classification_report(y_test, y_pred_clf_svc_rbf))
plot_confusion_matrix(confusion_matrix(y_test, y_pred_clf_svc_rbf))
from sklearn.metrics import roc curve, auc
false_positive_rate, true_positive_rate, thresholds = roc_curve(y_test, y_pred_clf_svc_rbf)
roc_auc = auc(false_positive_rate, true_positive_rate)
roc auc
from sklearn.ensemble import RandomForestClassifier
rd = RandomForestClassifier(class_weight='balanced',random_state=4200)
rd.fit(X_train,y_train)
y_pred_rd = rd.predict(X_test)
import matplotlib.pyplot as plt
cm = confusion_matrix(y_test,y_pred_rd)
#plt.figure(figsize=(5,5))
#sns.heatmap(cm,annot=True,linewidths=.3)
#plt.show()
print(classification_report(y_test,y_pred_rd))
plot_confusion_matrix(confusion_matrix(y_test, y_pred_rd))
from sklearn.metrics import roc curve, auc
false positive rate, true positive rate, thresholds = roc curve(y test, y pred rd)
roc_auc = auc(false_positive_rate, true_positive_rate)
roc_auc
SVM:
evaluate a logistic regression model using k-fold cross-validation
from numpy import mean
from numpy import std
from sklearn.model_selection import KFold
from sklearn.model selection import cross val score
from sklearn.model selection import ShuffleSplit
from sklearn.linear model import LogisticRegression
# create dataset
#X, y = make_classification(n_samples=1000, n_features=20, n_informative=15, n_redundant=5, random_state=1)
# prepare the cross-validation procedure
#cv = KFold(n_splits=5, test_size= 0.2, random_state=0)
cv = ShuffleSplit(n_splits=3, test_size=0.2, random_state=42)
# create model
model = SVC(kernel='rbf', C=1, class weight=class weight)
# evaluate model
scores = cross val score(model, X, y, scoring='accuracy', cv=cv, n jobs=-1)
# report performance
print('Accuracy: %.4f (%.4f)' % (mean(scores), std(scores)))
scores
```

```
import numpy as np
import matplotlib.pyplot as plt
from sklearn import svm, datasets
from sklearn.metrics import auc
from sklearn.metrics import plot_roc_curve
from sklearn.model_selection import StratifiedKFold
# Classification and ROC analysis
# Run classifier with cross-validation and plot ROC curves
cv = ShuffleSplit(n_splits=3, test_size=0.2, random_state=42)
classifier = svm.SVC(kernel='rbf', probability=True, class_weight=class_weight,
            random state=42)
tprs = []
aucs = []
mean\_fpr = np.linspace(0, 1, 100)
fig, ax = plt.subplots()
for i, (train, test) in enumerate(cv.split(X, y)):
  classifier.fit(X, y)
  viz = plot_roc_curve(classifier, X, y,
              name='ROC fold { }'.format(i),
              alpha=0.3, lw=1, ax=ax)
  interp tpr = np.interp(mean fpr, viz.fpr, viz.fpr)
  interp tpr[0] = 0.0
  tprs.append(interp_tpr)
  aucs.append(viz.roc_auc)
ax.plot([0, 1], [0, 1], linestyle='--', lw=2, color='r',
    label='Chance', alpha=.8)
mean_tpr = np.mean(tprs, axis=0)
mean\_tpr[-1] = 1.0
mean_auc = auc(mean_fpr, mean_tpr)
std_auc = np.std(aucs)
ax.plot(mean fpr, mean tpr, color='b',
    label=r'Mean ROC (AUC = \%0.4f \text{ pm} \%0.4f)' % (mean auc, std auc),
    lw=2, alpha=.8)
std_tpr = np.std(tprs, axis=0)
tprs_upper = np.minimum(mean_tpr + std_tpr, 1)
tprs_lower = np.maximum(mean_tpr - std_tpr, 0)
ax.fill_between(mean_fpr, tprs_lower, tprs_upper, color='grey', alpha=.2,
         label=r'$\pm$ 1 std. dev.')
ax.set(xlim=[-0.05, 1.05], ylim=[-0.05, 1.05],
    title="Receiver operating characteristic")
ax.legend(loc="lower right")
plt.show()
```

LR:

```
from numpy import mean
from numpy import std
from sklearn.model selection import KFold
from sklearn.model_selection import cross_val_score
from sklearn.model_selection import ShuffleSplit
from sklearn.linear model import LogisticRegression
# create dataset
#X, y = make classification(n samples=1000, n features=20, n informative=15, n redundant=5, random state=1)
# prepare the cross-validation procedure
#cv = KFold(n_splits=5, test_size= 0.2, random_state=0)
cv = ShuffleSplit(n_splits=3, test_size=0.2, random_state=42)
# create model
model = LogisticRegression(class_weight=class_weight)
# evaluate model
scores = cross val score(model, X, y, scoring='accuracy', cv=cv, n jobs=-1)
# report performance
print('Accuracy: %.4f (%.4f)' % (mean(scores), std(scores)))
scores
import numpy as np
import matplotlib.pyplot as plt
from sklearn import svm, datasets
from sklearn.metrics import auc
from sklearn.metrics import plot roc curve
from sklearn.model selection import StratifiedKFold
# Data IO and generation
# Import some data to play with
#iris = datasets.load iris()
#X = iris.data
#y = iris.target
#X, y = X[y != 2], y[y != 2]
#n_samples, n_features = X.shape
# Add noisy features
#random_state = np.random.RandomState(0)
\#X = np.c [X, random state.randn(n samples, 200 * n features)]
# Classification and ROC analysis
# Run classifier with cross-validation and plot ROC curves
cv = ShuffleSplit(n_splits=3, test_size=0.2, random_state=0)
classifier1 = LogisticRegression(class weight=class weight,random state=0)
tprs = \prod
aucs = \Pi
mean\_fpr = np.linspace(0, 1, 100)
fig, ax = plt.subplots()
for i, (train, test) in enumerate(cv.split(X, y)):
  classifier.fit(X, y)
  #viz = plot_roc_curve(classifier, X, y,
            # name='ROC fold { }'.format(i),
             \#alpha=0.3, lw=1, ax=ax)
```

```
interp_tpr = np.interp(mean_fpr, viz.fpr, viz.tpr)
  interp tpr[0] = 0.0
  tprs.append(interp_tpr)
  aucs.append(viz.roc_auc)
ax.plot([0, 1], [0, 1], linestyle='--', lw=2, color='r',
    label='Chance', alpha=.8)
mean tpr = np.mean(tprs, axis=0)
mean_tpr[-1] = 1
mean_auc = auc(mean_fpr, mean_tpr)
std_auc = np.std(aucs)
ax.plot(mean_fpr, mean_tpr, color='b',
    label=r'Mean ROC (AUC = \%0.4f \text{ pm} \%0.4f)' % (mean auc, std auc),
    lw=2, alpha=.8)
std_tpr = np.std(tprs, axis=0)
tprs upper = np.minimum(mean tpr + std tpr, 1)
tprs lower = np.maximum(mean tpr - std tpr, 0)
ax.fill_between(mean_fpr, tprs_lower, tprs_upper, color='grey', alpha=.2,
         label=r'$\pm$ 1 std. dev.')
ax.set(xlim=[-0.05, 1.05], ylim=[-0.05, 1.05],
    title="Receiver operating characteristic example")
ax.legend(loc="lower right")
plt.show()
RF:
from numpy import mean
from numpy import std
from sklearn.model_selection import KFold
from sklearn.model_selection import cross_val_score
from sklearn.model selection import ShuffleSplit
from sklearn.ensemble import RandomForestClassifier
# create dataset
#X, y = make_classification(n_samples=1000, n_features=20, n_informative=15, n_redundant=5, random_state=1)
# prepare the cross-validation procedure
#cv = KFold(n splits=5, test size= 0.2, random state=0)
cv = ShuffleSplit(n_splits=3, test_size=0.2, random_state=42)
# create model
model = RandomForestClassifier(class weight=class weight)
# evaluate model
scores = cross_val_score(model, X, y, scoring='accuracy', cv=cv, n_jobs=-1)
# report performance
print('Accuracy: %.4f (%.4f)' % (mean(scores), std(scores)))
scores
import numpy as np
import matplotlib.pyplot as plt
from sklearn import svm, datasets
from sklearn.metrics import auc
from sklearn.metrics import plot_roc_curve
from sklearn.model_selection import StratifiedKFold
```

Data IO and generation

```
# Import some data to play with
#iris = datasets.load iris()
#X = iris.data
#y = iris.target
#X, y = X[y != 2], y[y != 2]
#n_samples, n_features = X.shape
# Add noisy features
#random_state = np.random.RandomState(0)
\#X = \text{np.c} [X, \text{random state.randn(n samples, } 200 * \text{n features})]
# Classification and ROC analysis
# Run classifier with cross-validation and plot ROC curves
cv = ShuffleSplit(n_splits=3, test_size=0.2, random_state=42)
classifier = RandomForestClassifier(class weight=class weight,random state=42)
tprs = \prod
aucs = \Pi
mean\_fpr = np.linspace(0, 1, 100)
fig, ax = plt.subplots()
for i, (train, test) in enumerate(cv.split(X, y)):
  classifier.fit(X, y)
  #viz = plot_roc_curve(classifier, X, y,
             # name='ROC fold { }'.format(i),
              \# alpha=0.3, lw=1, ax=ax)
  interp tpr = np.interp(mean fpr, viz.fpr, viz.fpr)
  interp tpr[0] = 0.0
  tprs.append(interp_tpr)
  aucs.append(viz.roc_auc)
ax.plot([0, 1], [0, 1], linestyle='--', lw=2, color='r',
     label='Chance', alpha=.8)
mean_tpr = np.mean(tprs, axis=0)
mean\_tpr[-1] = 1.0
mean_auc = auc(mean_fpr, mean_tpr)
std_auc = np.std(aucs)
ax.plot(mean fpr, mean tpr, color='b',
    label=r'Mean ROC (AUC = \%0.4f \text{ pm} \%0.4f)' % (mean auc, std auc),
    lw=2, alpha=.8)
std_tpr = np.std(tprs, axis=0)
tprs_upper = np.minimum(mean_tpr + std_tpr, 1)
tprs lower = np.maximum(mean tpr - std tpr, 0)
ax.fill_between(mean_fpr, tprs_lower, tprs_upper, color='grey', alpha=.2,
         label=r'$\pm$ 1 std. dev.')
ax.set(xlim=[-0.05, 1.05], ylim=[-0.05, 1.05],
    title="Receiver operating characteristic example")
ax.legend(loc="lower right")
plt.show()
```

DT:

```
from numpy import mean
from numpy import std
from sklearn.model_selection import KFold
from sklearn.model_selection import cross_val_score
from sklearn.model selection import ShuffleSplit
from sklearn.tree import DecisionTreeClassifier
# create dataset
#X, y = make_classification(n_samples=1000, n_features=20, n_informative=15, n_redundant=5, random_state=1)
# prepare the cross-validation procedure
#cv = KFold(n_splits=5, test_size= 0.2, random_state=0)
cv = ShuffleSplit(n_splits=3, test_size=0.2, random_state=42)
# create model
model = DecisionTreeClassifier(class weight=class weight)
# evaluate model
scores = cross_val_score(model, X, y, scoring='accuracy', cv=cv, n_jobs=-1)
# report performance
print('Accuracy: %.4f (%.4f)' % (mean(scores), std(scores)))
scores
import numpy as np
import matplotlib.pyplot as plt
from sklearn import svm, datasets
from sklearn.metrics import auc
from sklearn.metrics import plot roc curve
from sklearn.model_selection import StratifiedKFold
# Data IO and generation
# Import some data to play with
#iris = datasets.load_iris()
\#X = iris.data
#y = iris.target
#X, y = X[y != 2], y[y != 2]
\#n samples, n features = X.shape
# Add noisy features
#random state = np.random.RandomState(0)
\#X = np.c [X, random state.randn(n samples, 200 * n features)]
# Classification and ROC analysis
# Run classifier with cross-validation and plot ROC curves
cv = ShuffleSplit(n_splits=3, test_size=0.2, random_state=42)
classifier = DecisionTreeClassifier(class_weight=class_weight,random_state=42)
tprs = []
aucs = \prod
mean\_fpr = np.linspace(0, 1, 100)
fig, ax = plt.subplots()
for i, (train, test) in enumerate(cv.split(X, y)):
  classifier.fit(X, y)
 # viz = plot_roc_curve(classifier, X, y,
```

name='ROC fold { }'.format(i),

```
# alpha=0.3, lw=1, ax=ax)
  interp_tpr = np.interp(mean_fpr, viz.fpr, viz.tpr)
  interp tpr[0] = 0.0
  tprs.append(interp_tpr)
  aucs.append(viz.roc_auc)
ax.plot([0, 1], [0, 1], linestyle='--', lw=2, color='r',
     label='Chance', alpha=.8)
mean_tpr = np.mean(tprs, axis=0)
mean tpr[-1] = 1.0
mean_auc = auc(mean_fpr, mean_tpr)
std_auc = np.std(aucs)
ax.plot(mean_fpr, mean_tpr, color='b',
     label=r'Mean ROC (\overline{AUC} = \%0.4f \pm\$ \%0.4f)' % (mean_auc, std_auc),
     lw=2, alpha=.8)
std_tpr = np.std(tprs, axis=0)
tprs upper = np.minimum(mean tpr + std tpr, 1)
tprs lower = np.maximum(mean tpr - std tpr, 0)
ax.fill_between(mean_fpr, tprs_lower, tprs_upper, color='grey', alpha=.2,
          label=r'$\pm$ 1 std. dev.')
ax.set(xlim=[-0.05, 1.05], ylim=[-0.05, 1.05],
    title="Receiver operating characteristic example")
ax.legend(loc="lower right")
plt.show()
ANN:
import keras
from keras.models import Sequential
from keras.layers import Dense
#clf_svc_rbf.fit(X_train,y_train)
from sklearn.metrics import confusion_matrix,classification_report,roc_auc_score,auc,f1_score
y_pred = classifier.predict(X_test) > 0.8
import matplotlib.pyplot as plt
cm = confusion_matrix(y_test,y_pred)
#plt.figure(figsize=(5,5))
#sns.heatmap(cm,annot=True)
#plt.show()
#print(classification_report(y_test,y_pred_clf_svc_rbf))
print(classification_report(y_test, y_pred))
#plot_confusion_matrix(confusion_matrix(y_test, y_pred))
from sklearn.metrics import roc_curve, auc
false_positive_rate, true_positive_rate, thresholds = roc_curve(y_test, y_pred)
roc_auc = auc(false_positive_rate, true_positive_rate)
roc_auc
```

```
from sklearn import datasets
from sklearn.model selection import cross val score
from sklearn.linear_model import LogisticRegression
from sklearn.naive_bayes import GaussianNB
from sklearn.ensemble import RandomForestClassifier
from sklearn.ensemble import VotingClassifier
clf1 = SVC(kernel='rbf', C=1, class weight=class weight,random state=42)
clf2 = LogisticRegression(class_weight=class_weight,random_state=42)
clf3 = RandomForestClassifier(class_weight=class_weight,random_state=42)
clf4 = DecisionTreeClassifier(class_weight=class_weight,random_state=42)
#clf5 = Sequential()
eclf = VotingClassifier( estimators=[('svm', clf1), ('lr', clf2), ('rf', clf3), ('dt',clf4)],
   voting='hard')
for clf, label in zip([clf1, clf2, clf3,clf4,eclf], ['SVM', 'LR', 'RF','DT', 'Ensemble']):
  scores = cross_val_score(clf, X, y, scoring='accuracy', cv=3)
print("Accuracy: %0.4f (+/- %0.4f) [%s]" % (scores.mean(), scores.std(), label))
scores
```