Prediction of Metabolic Disease Using Various Multilevel Classification Algorithms and Their Analysis

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***Abstract*—In recent years, multilevel classification algorithms have gained much attention due to their ability to handle complex classification problems. This study provides a metabolic syndrome prediction model using multi-layer classification algorithms. The model is based on a dataset containing medical records of patients. In order to determine which multi-level classification algorithms performed best at detecting the existence or absence of a metabolic syndrome, the study examined SVM, decision trees, and random forests. The suggested approach has potential applications in the early identification and prevention of metabolic syndrome, a substantial risk factor for cardiovascular disease and diabetes.**

Keywords— Machine Learning; Classification; Multi level classification; Metabolic Syndrome; Prediction system

I. INTRODUCTION

Classification is one of the most widely studied and applied tasks in machine learning and data mining. To predict a label or category for a given input using a set of features is the objective of classification. Many real-world classification problems, however, can be more complex and hierarchical in nature.

Multilevel classification algorithms have been proposed to address these complex classification problems by leveraging the hierarchical structure of the labels. By exploiting the hierarchical structure of the labels, multilevel classification algorithms can improve the accuracy and interpretability of the classification task.

Multilevel classification algorithms have drawn more attention in recent years, and numerous distinct strategies have been put out. These techniques can be categorized into two categories: Hierarchical-to-flat and flat-to-hierarchical. For instance, in bio-informatics, multilevel classification algorithms have been used to predict protein function and identify functional modules in protein-protein interaction networks. In medical diagnosis, multilevel classification algorithms have been used to predict the risk of diseases such as diabetes [8] and cardiovascular disease. In image recognition, multilevel classification algorithms have been used to recognize objects at different levels of abstraction. [6][3]

II. LITERATURE SURVEY

Multi-level classification is a type of machine learning algorithm that assigns multiple labels to an input object or observation. In multi-level classification, each label represents a distinct level, with the highest level of classification being the most general and the lowest level being the most specific. As multiple levels are assigned so it makes multi-level classification more complex and challenging than normal classification, as it requires algorithms that can effectively learn and manage multiple levels of abstraction and granularity. Multi-level classification algorithms must be able to produce structured and hierarchical output, which can be challenging to interpret and analyze. Finally, multi-level classification often requires more data and more complex algorithms than normal classification, as it must learn and manage multiple levels of abstraction and granularity. This can make it more computationally expensive and time-consuming than normal classification. [9][10]

The time taken for multi-level classification can change depending on a number of variables, including the dataset's size, algorithm complexity, number of classification levels, and resources available. In general, multi-level classification can be more time-consuming than normal classification, as it involves assigning multiple labels to each input object, with each label representing a different level of classification. Optimization algorithms can be applied to multi-level classification to increase the classification model's efficacy and accuracy. Optimization algorithms are employed to identify the model's ideal parameter values that maximize performance metric or minimize loss function, such as accuracy or F_1 score. [2]

Multi-level classification algorithms' effectiveness when used on large datasets depends on a number of variables, including the algorithm's complexity, the size as well as the complexity of the dataset, and the available computer resources. In general, multi-level classification algorithms

can face scalability challenges when dealing with large datasets, as they need to assign multiple labels to each input object, with each label representing a different level of classification. This can increase the training time and memory requirements of the algorithm, making it more challenging to process large datasets. However, there are several techniques that are able to enhance multi-level classification algorithms' efficiency when applied to large datasets. One such method is feature selection, which lowers the problem's dimension and increases the algorithm's efficiency by selecting a subset of the most insightful features from the information being provided. Furthermore, deep learning architectures that can be scaled up to handle large datasets, like convolutional neural network architectures and recurrent neural networks, have demonstrated promising results in multi-level classification tasks. These architectures are able to recognize long-term connections between the input features and the many layers of labels as well as complicated representations of the input data. [7]

Multilevel classification has 3 methods. These are Problem transformation, adapted algorithm and ensemble.

A. Problem Transformation :

The multilevel problem is split into one or more standard single-label problems using problem transformation techniques. The transformed problems are then solved using standard single-label classification algorithms. Common problem transformation includes binary relevance.

Binary relevance is a method that transforms the multilevel problem into multiple binary classification problems. A single class in the hierarchy corresponds to each binary classification task. The transformed problems are then solved using standard binary classification algorithms.

Adapted Algorithm :

The methods to adapt single-label algorithms generally to directly handle multi-labeled data. This method is built on the notion of directly handling multi-labeled data by changing existing single-label algorithms. One example of an adapted algorithm is the hierarchical classifier. The hierarchical classifier is a modified version of the decision tree algorithm that can handle multi-labeled data directly.

B. Ensemble:

Ensemble approaches to enhance the performance of multilevel categorization, use numerous models. The most common ensemble approach is hierarchical ensemble. In hierarchical ensembles, multiple models are trained on different levels of the hierarchy. The output of each model is used as input for the next model in the hierarchy. The final output is obtained by combining the outputs of all models.

Consider, for instance, the issue of classifying images of objects into categories such as vehicles, animals, and buildings. This is a multilevel classification problem because the categories are organized in a hierarchical structure. To solve this problem using hierarchical ensemble, the approach would involve training multiple models on different levels of the hierarchy, such as vehicle vs non-vehicle, animal vs non-animal, and building vs non-building. Another ensemble approach is flat ensemble. In a flat ensemble, multiple models are to be trained on the same level of the hierarchy. The final output is obtained by combining the outputs of all models. [4]

Decision Tree Algorithm:

Decision tree, a sophisticated machine learning technique can be utilized for both classification and regression tasks. This is a well-liked tool for analyzing complex data and forecasting based on a collection of features or attributes. The method creates a structure that resembles a tree, with each node denoting a feature or attribute and each branch denoting a potential value or decision based on that feature. Recursively dividing the input into the classes or values of the target variable is how the decision tree algorithm functions. This is accomplished by choosing the most advantageous feature to divide the data at each node according to a standard that maximises information gain or minimises impurity in the resulting subsets. The most commonly used criterion for splitting the data is the entropy or information gain, with which the randomness or ambiguity in the data is measured. The entropy is calculated as the total of all class probabilities or values multiplied by the logarithm of the inverse of the probability. A lower entropy indicates a higher degree of purity or homogeneity in the resulting subsets. Once the best feature is selected, the data is partitioned into two or more subsets, one for each possible value or decision based on that feature. A stopping requirement, such as reaching a maximum depth or a minimum number of observations per leaf node, is then fulfilled, and the procedure is then repeated recursively for each subset. In comparison to other machine learning algorithms, decision trees have a number of benefits, such as being straightforward to understand and explain, being able to handle both categorical and continuous variables, and being robust to outliers and missing values. The flexibility of decision trees to handle categorical and continuous data is one of their key advantages. The primary drawbacks is the potential for over fitting, which happens when the tree is overly complex and fits the training data too closely, resulting in subpar performance on new and untried data. This can be mitigated by using techniques such as pruning, regularization, and ensemble methods, such as random forests and gradient boosting, which combine multiple decision trees to improve their accuracy and stability. Another limitation of decision trees is their lack of robustness to small changes in the data or the tree structure, which may affect the accuracy and stability of the predictions. This can be addressed by using techniques such as bagging and boosting, which introduce randomness and diversity into the decision tree algorithm to improve its robustness and stability.

Logistic regression is a statistical model used to analyze data that contains a binary outcome variable. It is a powerful tool for predicting the probability of a certain outcome given a set of predictor variables. This model has several advantages over different methods of classification, including decision trees and support vector machines. It is

easy to interpret, provides a probabilistic estimate of the outcome, and can handle both categorical and continuous data predictor variables. However, it also has some limitations, such as the assumption of linearity between the predictor variables and the log-odds of the outcome, the assumption of independence between observations, and the possibility of overfitting when there are many predictor factors compared to observations.

XGBoost is a highly efficient and scalable machine learning library that uses distributed gradient boosting to train models. It employs an ensemble learning approach, combining multiple weak models to generate a more robust prediction. Known for its ability to handle large datasets and deliver modern proficiency in problems like classification and regression, One of its key strengths is its ability to effectively manage missing values in real-world data without the need for extensive pre-processing. Additionally, XGBoost supports parallel processing, enabling rapid training on large datasets. XGBoost employs an ensemble learning technique that combines the predictions of various weak models. It has gained popularity as a result of its capacity to manage big datasets and provide cutting-edge results in various machine learning applications.[1]

Random Forest, a popular machine learning algorithm, is used for regression and classification analysis. Multiple decision trees are combined using an ensemble learning technique to create a more precise forecast. Using several subsets of the data and various sets of features, Random Forest builds multiple decision trees. After then, the computer integrates the findings from each decision tree to create a final prediction. Each decision tree is built independently, and the algorithm selects a random subset of the data to train the model. This technique is known as bagging or bootstrap aggregating. Random Forest builds decision trees using the same splitting criteria as the decision tree algorithm. Random Forest has the capacity to manage high-dimensional data with a very small sample size is one of its key advantages. Random Forest can also handle nonlinear decision boundaries and works well with both binary and multi-class classification problems. It is also less prone to overfitting than other machine learning algorithms due to the use of multiple decision trees. The algorithm can be computationally expensive, particularly when working with big datasets. It may also be difficult to interpret the results of the model, as the decision trees are combined to produce the final prediction. In addition, Random Forest may not perform well in cases where the dataset has a lot of noise or outliers.

Support Vector Machine (SVM), a supervised learning technique that can handle both regression and classification tasks. It is primarily utilized in machine learning for categorization issues, though. Finding the ideal decision boundary, or hyperplane, to categorise the n-dimensional space and make it easier to assign subsequent data points to the correct category is the fundamental objective of the SVM method. The Support Vector Machine (SVM), as its name suggests, chooses the extreme vectors that aid in the creation of the hyperplane. SVMs come in both linear and non-linear varieties. Using a single straight line, a dataset can be divided into two classes using linearly separable data, which is the case for linear SVM. Non-linear SVM, on the other hand, is used for non-linearly separable data, where the dataset cannot be classified by using a straight line. In such cases, the Non-linear SVM classifier is utilized to classify the data. The quantity of features in the dataset affects how the Support Vector Machine (SVM) algorithm shapes the hyperplane. The objective is to construct a hyperplane with the highest margin, or the largest space between data points.[5]

K-nearest neighbours (KNN) is a widely used supervised machine learning algorithm that can be applied to both classification and regression problems. The algorithm operates on the principle of proximity, classifying new data points by comparing them to their K-nearest neighbours. The value of K is a crucial hyper parameter that determines how many neighbors are taken into account during classification. KNN is known to perform well when there is a large amount of training data and a small number of classes. However, the KNN algorithm has some limitations. It requires a significant amount of memory to store training data, which makes it computationally expensive for larger datasets. Furthermore, it becomes less effective for high-dimensional data as the computation time increases with the number of dimensions. Furthermore, the choice of distance metric can significantly impact its performance, and thus, the algorithm is sensitive to it.

III. Problem Statement

Globally, the pervasiveness of metabolic illnesses like diabetes, hypertension, and obesity is rising quickly. Early detection and accurate prediction of metabolic diseases can help prevent complications and improve treatment outcomes. However, existing prediction models often rely on single-level classification methods, which may limit their accuracy and applicability. In this case, two target values were taken, which are gender and metabolic sign. The goal is to develop a multilevel classification model which predicts the risk of metabolic diseases based on demographic and clinical variables, with a particular focus on gender differences. Specifically, the researchers will investigate the performance of the model in predicting metabolic disease risk for males and females, as well as for individuals with and without a previous diagnosis of a metabolic disease. The model will be trained on a large dataset of patient records and validated using appropriate metrics to ensure its reliability and generalizability. The final objective of this is to progress towards creating a reliable tool that can assist healthcare providers in early identification of metabolic disease risk and prompt intervention to prevent disease progression.

IV. Proposed Model

The suggested model is designed upon a large dataset of metabolic disease data. First the dataset was loaded in the model. Then the data preprocessing have done. Here the null values are removed by two processes, either removing the rows having null values, or replacing the null values with the median of that particular column. Then the target columns are separated from the labels and categorical columns are changed to numerical columns using one hot

encoding and label encoding. Then the exploratory data analysis have done by plotting graphs and pie charts. Next the fitting and training of the model have done using various multi level classification algorithms like logistic regression, XGBoost, random forest classifier, support vector machine and K-Neighbours classifier. Then we have found their confusion matrix and accuracy. Based on the accuracy the best model for the data set would be predicted.

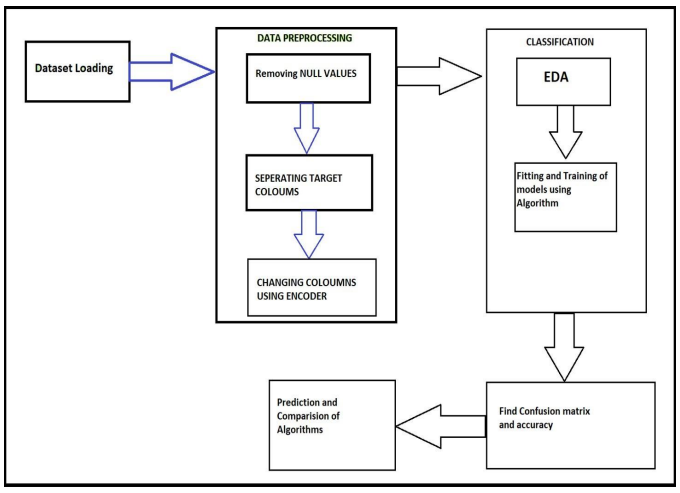

Fig. 1. Proposed Model

V. EXPERIMENTAL SETUP

To meet the hardware needs, a core i5 8th generation processor, 1.10 GB of RAM, and a 30 GB hard drive were used. To meet the software requirements, the most recent version of Windows software, Python programming language, Jupyter notebook, Seaborn library, pandas library, and NumPy library were used. As input CSV file is given and the output will come.

VI. IMPLEMENTATION

First the dataset is loaded and its parameters are displayed.

	seqn	Age	Sex	Marital	Income	Race	WaistCirc	BMI	Albuminuria	UrAlbCr	UricAcid	BloodGlucose	HDL	Triglycerides	MetabolicSyndrome
0	62161	22	Male	Single	8200.0	White	81.0	23.3	0	3.88	4.9	92	41	84	No MetSyn
1	62164	44	Female	Married	4500.0	White	80.1	23.2	0	8.55	4.5	82	28	56	No MetSyn
2	62169	21	Male	Single	800.0	Asian	69.6	20.1	0	5.07	5.4	107	43	78	No MetSyn
3	62172	43	Female	Single	2000.0	Black	120.4	33.3	0	5.22	5.0	104	73	141	No MetSyn
4	62177	51	Male	Married	NaN	Asian	81.1	20.1	0	8.13	5.0	95	43	126	No MetSyn

Fig. 2. Parameters of the dataset

Then, the null values from the columns are deducted. Two target values are taken for implementing multi-level classification, making the model more versatile and accurate.

```
y1=df[["Sex"]]
y2=df[["MetabolicSyndrome"]]
```

Fig. 3. The two target columns

Now the graphs and pie charts of different parameters of the data set would be plotted. These visualizations will aid in understanding the actual condition of the parameters that are responsible for the model's performance.

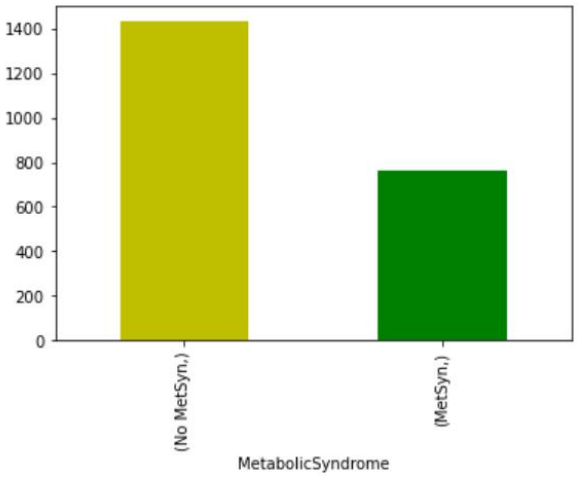

Fig. 4. Graphical representation of metabolic and non-metabolic sign

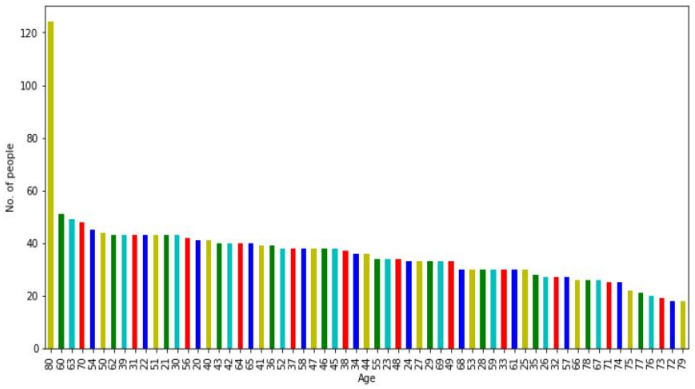

Fig. 5. Graphical representation of Age vs. Number of people

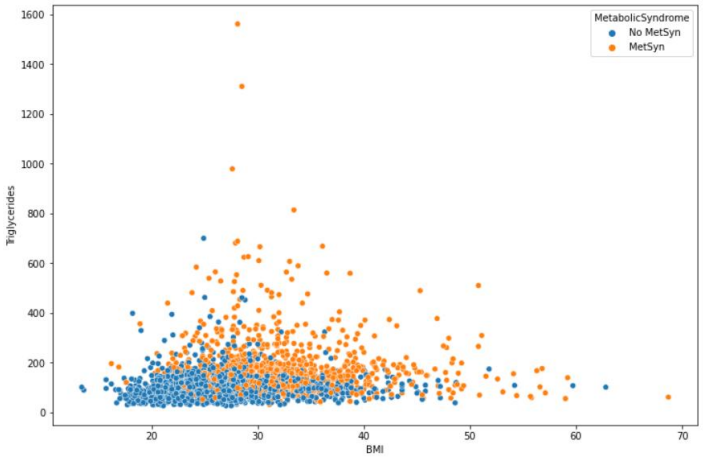

Fig. 6. Graphical representation of BMI vs. Triglycerides

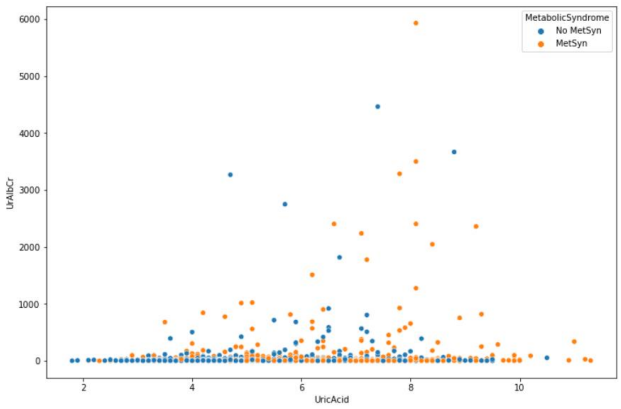

Fig. 7. Graphical representation of UricAcid vs. UrAlbCr

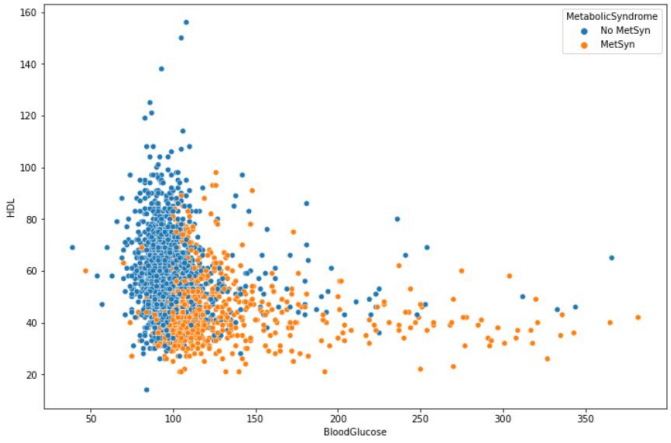

Fig. 8. Graphical representation of BloodGlucose vs. HDL

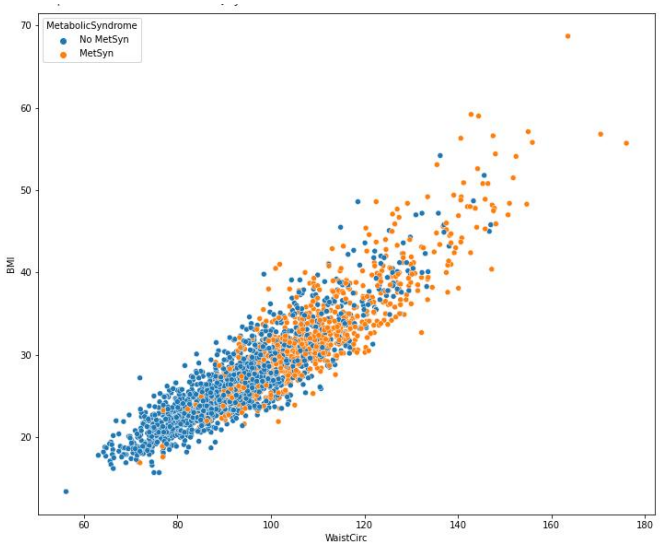

Fig. 9. Graphical representation of WaistCirc vs. BMI

In the process of implementation it was obsserved that some parameters are not in the numeric form. So they need to be converted into numeric form using OneHotEncoder. Next, all the algorithms required for analysis will be imported.

```
from sklearn.svm import SVC
from sklearn.naive_bayes import MultinomialNB
from sklearn.linear_model import LogisticRegression
from sklearn.ensemble import RandomForestClassifier
from sklearn.neighbors import KNeighborsClassifier
from sklearn.linear_model import SGDClassifier
from sklearn.metrics import roc_auc_score, roc_curve
import time
from sklearn.metrics import confusion_matrix, classification_report
```

Fig. 10. Importing required libraries and modules

Previously, it was mentioned that two target columns, "MetSyn or No MetSyn" and "Male or Female," were taken. So the logistic regression, XGBoost, random forest, SVM and K-Neighbours algorithm are applied to these two parameters.

```
[[1029  115]
 [ 201  409]]
[[252  37]
 [ 34 116]]
              precision    recall  f1-score   support

           0       0.84      0.90      0.87      1144
           1       0.78      0.67      0.72       610

    accuracy                           0.82      1754
   macro avg       0.81      0.78      0.79      1754
weighted avg       0.82      0.82      0.82      1754

              precision    recall  f1-score   support

           0       0.88      0.87      0.88       289
           1       0.76      0.77      0.77       150

    accuracy                           0.84       439
   macro avg       0.82      0.82      0.82       439
weighted avg       0.84      0.84      0.84       439
```

Fig. 11. Logistic Regression on Metabolic and non metabolic sign

```
[[724 174]
 [168 688]]
[[167  50]
 [ 55 167]]
              precision    recall  f1-score   support

      Female       0.81      0.81      0.81       898
        Male       0.80      0.80      0.80       856

    accuracy                           0.81      1754
   macro avg       0.80      0.80      0.80      1754
weighted avg       0.81      0.81      0.81      1754

              precision    recall  f1-score   support

      Female       0.75      0.77      0.76       217
        Male       0.77      0.75      0.76       222

    accuracy                           0.76       439
   macro avg       0.76      0.76      0.76       439
weighted avg       0.76      0.76      0.76       439
```

Fig. 12. Logistic Regression on male and female patients

```
[[1144    0]
 [   0  610]]
[[259  30]
 [ 32 118]]
              precision    recall  f1-score   support

           0       1.00      1.00      1.00      1144
           1       1.00      1.00      1.00       610

    accuracy                           1.00      1754
   macro avg       1.00      1.00      1.00      1754
weighted avg       1.00      1.00      1.00      1754

              precision    recall  f1-score   support

           0       0.89      0.90      0.89       289
           1       0.80      0.79      0.79       150

    accuracy                           0.86       439
   macro avg       0.84      0.84      0.84       439
weighted avg       0.86      0.86      0.86       439
```

Fig. 13. XGBoost on Metabolic and non metabolic sign

```
[[898   0]
 [  0 856]]
[[158  59]
 [ 54 168]]
              precision    recall  f1-score   support

      Female       1.00      1.00      1.00       898
        Male       1.00      1.00      1.00       856

    accuracy                           1.00      1754
   macro avg       1.00      1.00      1.00      1754
weighted avg       1.00      1.00      1.00      1754

              precision    recall  f1-score   support

      Female       0.75      0.73      0.74       217
        Male       0.74      0.76      0.75       222

    accuracy                           0.74       439
   macro avg       0.74      0.74      0.74       439
weighted avg       0.74      0.74      0.74       439
```

```
[[898   0]
 [  0 856]]
[[167  50]
 [ 42 180]]
              precision    recall  f1-score   support

           0       1.00      1.00      1.00       898
           1       1.00      1.00      1.00       856

    accuracy                           1.00      1754
   macro avg       1.00      1.00      1.00      1754
weighted avg       1.00      1.00      1.00      1754

              precision    recall  f1-score   support

           0       0.80      0.77      0.78       217
           1       0.78      0.81      0.80       222

    accuracy                           0.79       439
   macro avg       0.79      0.79      0.79       439
weighted avg       0.79      0.79      0.79       439
```

Fig. 14. XGBoost on male and female patients

```
[[1078   66]
 [ 169  441]]
[[255  34]
 [ 37 113]]
              precision    recall  f1-score   support

           0       0.86      0.94      0.90      1144
           1       0.87      0.72      0.79       610

    accuracy                           0.87      1754
   macro avg       0.87      0.83      0.85      1754
weighted avg       0.87      0.87      0.86      1754

              precision    recall  f1-score   support

           0       0.87      0.88      0.88       289
           1       0.77      0.75      0.76       150

    accuracy                           0.84       439
   macro avg       0.82      0.82      0.82       439
weighted avg       0.84      0.84      0.84       439
```

Fig. 17. SVM on Metabolic and non metabolic sign

```
[[1144    0]
 [   0  610]]
[[263  26]
 [ 33 117]]
              precision    recall  f1-score   support

           0       1.00      1.00      1.00      1144
           1       1.00      1.00      1.00       610

    accuracy                           1.00      1754
   macro avg       1.00      1.00      1.00      1754
weighted avg       1.00      1.00      1.00      1754

              precision    recall  f1-score   support

           0       0.89      0.91      0.90       289
           1       0.82      0.78      0.80       150
```

Fig. 15. Random Forest on Metabolic and non metabolic sign

```
[[752 146]
 [116 740]]
[[163  54]
 [ 57 165]]
              precision    recall  f1-score   support

      Female       0.87      0.84      0.85       898
        Male       0.84      0.86      0.85       856

    accuracy                           0.85      1754
   macro avg       0.85      0.85      0.85      1754
weighted avg       0.85      0.85      0.85      1754

              precision    recall  f1-score   support

      Female       0.74      0.75      0.75       217
        Male       0.75      0.74      0.75       222

    accuracy                           0.75       439
   macro avg       0.75      0.75      0.75       439
weighted avg       0.75      0.75      0.75       439
```

Fig. 18. SVM on male and female patients

```
[[1036  108]
 [ 171  439]]
[[251  38]
 [ 51  99]]
              precision    recall  f1-score   support

           0       0.86      0.91      0.88      1144
           1       0.80      0.72      0.76       610

    accuracy                           0.84      1754
   macro avg       0.83      0.81      0.82      1754
weighted avg       0.84      0.84      0.84      1754

              precision    recall  f1-score   support

           0       0.83      0.87      0.85       289
           1       0.72      0.66      0.69       150

    accuracy                           0.80       439
   macro avg       0.78      0.76      0.77       439
weighted avg       0.79      0.80      0.79       439
```

Fig. 19. K-N on Metabolic and non metabolic sign

```
[[717 181]
 [152 704]]
[[140  77]
 [ 71 151]]
              precision    recall  f1-score   support

      Female       0.83      0.80      0.81       898
        Male       0.80      0.82      0.81       856

    accuracy                           0.81      1754
   macro avg       0.81      0.81      0.81      1754
weighted avg       0.81      0.81      0.81      1754

              precision    recall  f1-score   support

      Female       0.66      0.65      0.65       217
        Male       0.66      0.68      0.67       222

    accuracy                           0.66       439
   macro avg       0.66      0.66      0.66       439
weighted avg       0.66      0.66      0.66       439
```

Fig. 20. K-N on male and female patients

VII. RESULT AND ANALYSIS

The authors applied multilevel classification algorithms to this model. Two target columns, sex and metabolic syndrome, were used in the analysis. It was observed that the XGBoost algorithm achieved the highest accuracy of about 90% for both target values. XGBoost is known for its effectiveness, precision, and viability, as it combines tree learning methods and linear model solvers. Its ability to perform parallel computation on a single machine contributes to its speed. Additionally, the authors compared the performance of different algorithms on this specific dataset and found that their model achieved impressive accuracy, indicating that it is highly optimized.

TABLE- 1

Algorithms	***Logistic Regression***	***XG-Boost***	***Random Forest***	***SVM***	***K-N***
Metabolic sign	0.84	0.86	0.87	0.84	0.80
Male Female	0.76	0.79	0.74	0.75	0.66

Accuracy Score

VIII. CONCLUSION

The development of a metabolic disease prediction model using multilevel classification has the potential to significantly impact the field of healthcare by providing accurate and early detection of metabolic diseases. The proposed model leverages a comprehensive dataset, advanced feature engineering techniques, and multiple classification algorithms to predict metabolic disease risk based on demographic and clinical variables, with a particular focus on gender differences. The project demonstrates the implementation of all the algorithms, which significantly improve the accuracy of metabolic disease prediction models. The XGBoost algorithm is found to be the best for the model. The model achieved high levels of accuracy (approximately 90%), precision, recall, and F1-score, the crucial metrics in clinical decision-making. In future work, efforts will be made to increase the accuracy of the model and implement it into a user-friendly web application.

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