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MACHINE LEARNING (ML)-BASED MODELS FOR THE INTELLIGENT DETECTION AND MULTICLASS CLASSIFICATION OF T2DM USING CLINICAL DATA

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Abstract

Type 2 Diabetes Mellitus (T2DM) is one of the most dangerous diseases because of the growing number of cases, the range of serious complications, and the significant costs to the economies. Detecting or classifying T2DM subtypes in the early stages will help improve care and treatment. This research developed and evaluated machine learning (ML) models to detect T2DM intelligently and classify it into subtypes. The data used in this study were obtained from the University of Nigeria Teaching Hospital (UNTH), Enugu, and Parklane Hospital, Enugu State. The data collected from the hospitals comprised 23,300 confirmed cases of T2DM recorded between 2002 and 2024. The data were pre-processed using the Cross-Industry Standard Process for Data Mining (CRISP-DM). The study used seven ML algorithms including Decision Tree (DT), Random Forest (RF), Support Vector Machine (SVM), K-Nearest Neighbour (KNN), Naïve Bayes (NB), Multi-Layer Perceptron (MLP), and Extreme Gradient Boosting (XGBoost). This research classified patients into four categories of T2DM: Mild Age-Related Diabetes (MARD), Mild Obesity-Related Diabetes (MOD), Severe Insulin-Deficient Diabetes (SIDD), Severe Insulin-Resistant Diabetes (SIRD). The performance of the ML models was evaluated using Accuracy, Precision, Recall, F1-score, and Area under Curve (AUC). The results revealed that XGBoost, Random Forest, and SVM recorded the highest accuracy of 98.35%, 98.24%, and 98.20%, respectively. The study concluded that machine learning algorithms can be used to detect and classify T2DM subtypes. Thus, developing an accurate and cost-effective framework for classifying T2DM subtypes has the potential to improve decision-making in managing the disease.

Keywords: Type 2 Diabetes Mellitus, Machine Learning, XGBoost, Random Forest, Diabetes Classification

1. Introduction

Type 2 Diabetes Mellitus (T2DM) is a chronic disease caused by reduced insulin production, decreased cellular response to insulin, and persistent high levels of glucose in the blood, resulting in severe cardiovascular, renal, nerve, and vision complications (Antar et al., 2023; Atun et al., 2022; Poznyak et al., 2020). The rising prevalence of diabetes across the globe presents a significant challenge to healthcare systems worldwide and a burden on the economy, especially in developing countries due to the lack of appropriate diagnostic equipment (Almalki & Khan, 2025; Atun et al., 2022). Recent studies indicate that type 2 diabetes mellitus is a complex syndrome encompassing several phenotypically distinguishable subtypes, including

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Mild Age-Related Diabetes (MARD), Mild Obesity-Related Diabetes (MOD), Severe Insulin-Deficient Diabetes (SIDD), Severe Insulin-Resistant Diabetes (SIRD) with different patterns of progression and treatment response (Agyemang et al., 2023; Baskar et al., 2025; Ordoñez Guillen et al., 2023). Thus, there is a need for an accurate diagnosis for effective treatment of each category of patients.

Artificial Intelligence (AI) and Machine Learning (ML) are disruptive technologies and valuable tools in modern healthcare for diagnosing complex diseases through informed decision-making (Dignum, 2019; Sheikh et al., 2023; Bakker & Korsten, 2021). Various studies have demonstrated that ML can be utilized effectively for the early diagnosis and prediction of diabetes using Decision tree, Random forest, Support vector machine, Artificial Neural Network, and other algorithms (Adua et al., 2021; Ahamed et al., 2022; Chang et al., 2022; Dutta et al., 2022; Howlader et al., 2022). In addition, deep learning algorithms have been successfully applied in the early diagnosis of diabetes by capturing the relationships between clinical and biological variables with enhanced predictive performance (Alex et al., 2022; Alsulami et al., 2024; Wee et al., 2024). Most of the reviewed literatures have unanimously agreed that ML models have greater potential in predicting diabetes mellitus compared to conventional statistical models and provide valuable insights into early interventions and management strategies (Fregoso-Aparicio et al., 2021; Afsaneh et al., 2022; Petridis et al., 2024).

However, most of the previous studies on diabetes prediction employed a binary classification model to distinguish between diabetic and non-diabetic patients without considering the heterogeneity of type 2 diabetes mellitus (Kuo et al., 2020; Shin et al., 2022; Roobini et al., 2023). In addition, many researchers have used datasets collected from developed countries instead of employing local data to predict diabetes in the African population, which lacks adequate resources for healthcare (Kengne & Davies, 2023; Hodgson et al., 2024; Agyemang et al., 2023). Therefore, this study focuses on developing a Machine Learning-based approach to predict type 2 diabetes mellitus using a clinical dataset collected from two hospitals in Nigeria. The study applies Decision tree, Random forest, Support vector machine, K-Nearest Neighbour, Naïve Bayes, Multi-Layer Perceptron, and XGBoost algorithm to classify patients diagnosed with Mild Age-Related Diabetes, Mild Obesity-Related Diabetes, Severe Insulin-Deficient Diabetes, Severe Insulin-Resistant Diabetes, and non-diabetic. Thus, the present study will contribute to the body of knowledge by providing an accurate and effective approach to the early diagnosis of diabetes mellitus and supporting intelligent decision-making in the treatment process (Chang et al., 2023; Nipa et al., 2024; Lee et al., 2025).

2. Research Methodology

The methodology adopted for this research is the Cross-Industry Standard Process for Data Mining (CRISP-DM). This approach ensures a rigorous, systematic, and reproducible workflow that supports high-quality model development for management of T2DM. CRISP-DM follows the following steps in the onion diagram of Figure 1.

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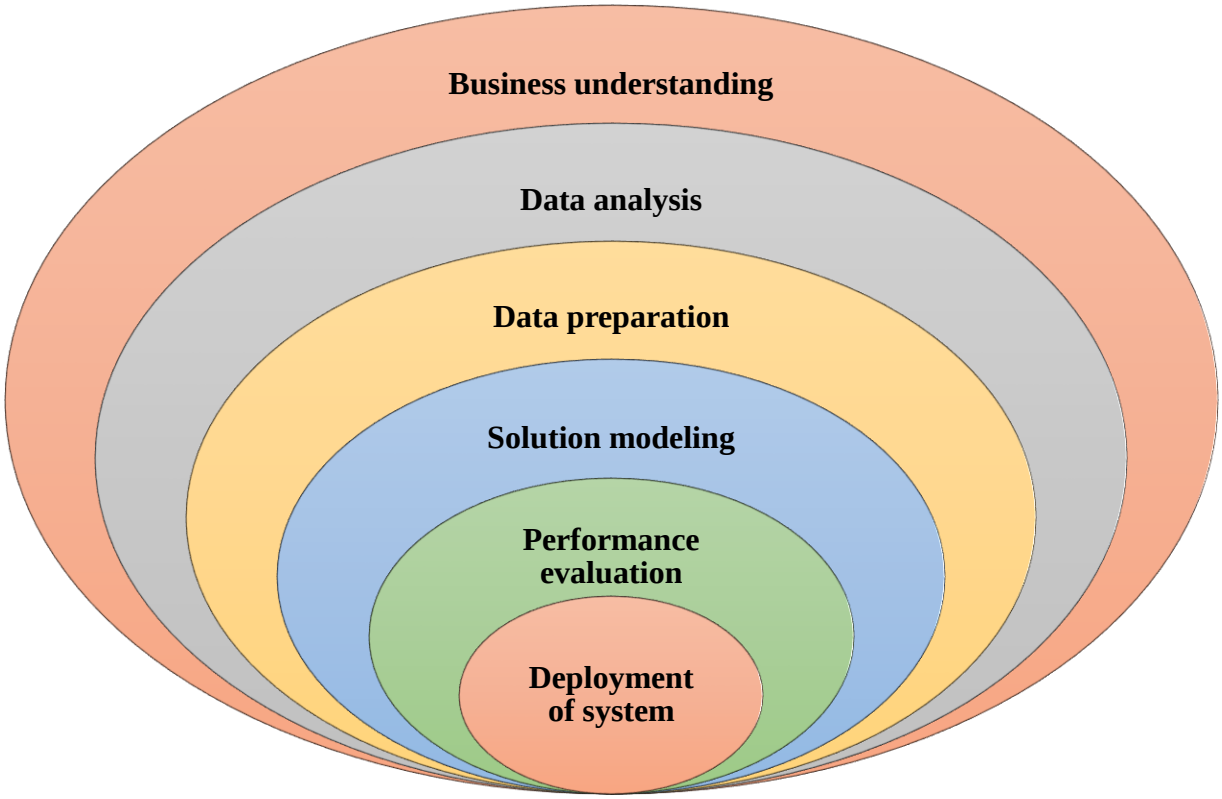


Figure 1: CRISP-DM methodology onion diagram (Elkabalawy *et al*., 2024)

Figure 1 presents the onion diagram of the CRISP-DM methodology and how it applied to this work. The business understanding is the need to solve the processing problem which arises due to the high cost of devices and system currently used in addressing T2DM. Secondly is the lack of solution which facilitates multi T2DM classification in a single diagnostic framework. These presents clear business opportunities for health stakeholder patronage. Data used for this work was analyzation qualitative method to ensure quality and content of actual variables which model the study problem. Data preparation was also applied to handle missing values and ensure data integrity before applying it to develop the proposed solution. Testing was used as the evaluation method before deployment as software into the testbed hospital for management of T2DM.

2.1 Data Collection

The database development was achieved through primary data collection. The data source is the University of Nigeria Teaching Hospital, Ituku, Ozala, Enugu, and Parklane Hospital, G.R.A, Enugu State. The participants in the datasets are men and women aged 19 to 85 years. The population size is 14200 for UNTH and 9100 participants from Parklane. The dataset used in this study was obtained by combining the clinical records from the independent healthcare data sources.

Before the combination, the two datasets were cleaned (attribute mapping, data cleaning, removal of duplicate records, handling of missing values, and standardization of variable names and measurement units were performed), and the attributes were analysed to verify common variables relevant to clinical diagnoses of diabetes. Only attributes that were available in both datasets and considered clinically significant were retained for the merged dataset. The integration of these datasets was carried out to increase the number of patient records available

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for analysis while improving the diversity and generalizability of the proposed T2DM detection. The total population sample size of participants is 23, 300 records of verified diabetes patients in the hospital from 2002 to 2024. For privacy, the actual identification numbers of all patients were changed, and any information that might compromise patients' privacy was not revealed. The resulting dataset contains demographic characteristics, anthropometric measurements, laboratory findings, metabolic indicators, lifestyle factors, and medical history variables that collectively provide sufficient information for accurate diabetes risk assessment and classification. The total number of attributes in the dataset is 23 and are reported in Table 1.

Table 1: Data description

S/N	Attribute	Description
1	Patient_ID	Unique identifier assigned to each patient record.
2	Hospital	The hospital name
3	Class	Target variable indicating the patient's diabetes status
4	Age	Patient's age in years.
5	Sex	Gender of the patient.
6	Career_Type	Occupational category or employment status of the patient.
7	FPG	Fasting Plasma Glucose level (mg/dL).
8	HbA1c	Glycated haemoglobin level indicating long-term blood glucose control (%).
9	Insulin	Fasting insulin concentration.
10	C_Peptide	C-peptide concentration used to assess insulin production.
11	HOMA_IR	Homeostatic Model Assessment of Insulin Resistance.
12	HOMA_B	Homeostatic Model Assessment of Beta-cell function.
13	BMI	Body Mass Index (kg/m^2).
14	Waist	Waist circumference (cm).
15	TG	Triglyceride level.
16	HDL	High-Density Lipoprotein cholesterol level.
17	LDL	Low-Density Lipoprotein cholesterol level.
18	Duration	Duration of diabetes or related symptoms (years).
19	HTN	Hypertension status (Yes/No).
20	Stress_Level	Patient's reported stress level.
21	Sleep_Quality	Quality of sleep reported by the patient.
22	Smoking_Status	Smoking habit of the patient.
23	Alcohol_Consumption	Alcohol consumption status or frequency.

2.3 Proposed Machine Learning Algorithms

This section presents the algorithms of the seven machine learning models trained where their prediction probabilities are used for final diabetes subtype prediction.

Algorithm 1: Decision Tree (DT)

Input: Training dataset (D)
Output: Predicted diabetes class
Load the training dataset.
Select the best splitting attribute using the impurity criterion (e.g., Gini Index or Entropy).
Split the dataset into child nodes.
Repeat the splitting process recursively until a stopping criterion is satisfied.
Construct the decision tree.
Classify each patient record by traversing the tree from the root node to a leaf node.

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Output the predicted diabetes class.
End

Algorithm 2: Random Forest (RF)

Input: Training dataset (D)
Output: Predicted diabetes class
Load the training dataset.
Generate multiple bootstrap samples from the dataset.
Train one decision tree on each bootstrap sample.
Randomly select a subset of features at each node during tree construction.
Predict the diabetes class using each decision tree.
Aggregate the predictions using majority voting.
Output the final predicted diabetes class
End

Algorithm 3: Support Vector Machine (SVM)

Input: Training dataset (D)
Output: Predicted diabetes class
Load the training dataset.
Select the kernel function.
Map the input features into a higher-dimensional feature space.
Determine the optimal separating hyperplane by maximizing the margin.
Classify unseen patient records according to the learned decision boundary.
Output the predicted diabetes class.
End

Algorithm 4: K-Nearest Neighbour (KNN)

Input: Training dataset (D)
Output: Predicted diabetes class
Load the training dataset.
Choose the value of (k).
Compute the distance between the test sample and all training samples.
Select the (k) nearest neighbours.
Count the occurrence of each diabetes class.
Assign the class with the highest frequency.
Output the predicted diabetes class.
End

Algorithm 5: Naïve Bayes (NB)

Input: Training dataset (D)
Output: Predicted diabetes class
Load the training dataset.
Estimate the prior probability of each diabetes class.
Compute the likelihood of each feature for every class.
Apply Bayes' theorem to calculate the posterior probability.
Select the class with the highest posterior probability.
Output the predicted diabetes class.
End

Algorithm 6: MLP

Input: Training dataset (D)
Output: Predicted diabetes class
Load the training dataset.
Initialize network weights and biases.
Perform forward propagation to compute network outputs.

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Calculate the classification error.
Update weights using backpropagation.
Repeat until convergence.
Predict the diabetes class for new patient records.
Output the predicted diabetes class.
End

Algorithm 7 Extreme Gradient Boosting (XGBoost)

Input: Training dataset (D)
Output: Predicted diabetes class
Load the training dataset.
Initialize the prediction model.
Compute residual errors from the current prediction.
Train a new decision tree to minimize the residual errors.
Update the by adding the new tree.
Repeat until the specified number of trees is reached.
Compute the final prediction.
Output the predicted diabetes class.
End

2.3 System implementation

The implementation of the proposed Diabetes Management System was carried out using Python 3.11 in the Google Colaboratory (Google Colab) environment. Google Colab was selected because it provides a cloud-based development platform with high computational capability, pre-installed machine learning libraries, and GPU support for efficient model training and evaluation. The implementation utilized several Python libraries, including NumPy for numerical computation, Pandas for data manipulation and preprocessing, Scikit-learn for implementing conventional machine learning algorithms and performance evaluation, XGBoost for gradient boosting classification, TensorFlow/Keras for the MLP, and Matplotlib and Seaborn for data visualization and performance analysis. The developed models were subsequently integrated into the Diabetes Management System to perform intelligent diagnosis of Type 2 Diabetes Mellitus. Seven supervised machine learning algorithms were independently implemented and evaluated. These algorithms comprised DT, RF, SVM, K-NN, NB, MLP, and XGBoost. Each algorithm was trained using identical training data to ensure a fair comparison. The models were evaluated using Accuracy, Precision, Recall, F1-score, and Area under the Receiver Operating Characteristic Curve (ROC-AUC). Table 2 presents the principal hyper-parameter settings adopted during the implementation of the individual machine learning algorithms.

Table 2: Hyperparameter Configuration of the Machine Learning Models

Model	Hyperparameter	Value
Decision Tree	Criterion	Gini
	Maximum Depth	10
	Minimum Samples Split	2
Random Forest	Number of Trees (n_estimators)	200
	Maximum Depth	20
	Maximum Features	Square Root
Support Vector Machine	Kernel	Radial Basis Function (RBF)
	Regularization Parameter (C)	1.0
	Gamma	Scale

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K-Nearest Neighbour	Number of Neighbours (k)	5
	Distance Metric	Euclidean
Naïve Bayes	Model	Gaussian Naïve Bayes
MLP	Hidden Layers	2
	Neurons	128, 64
	Activation Function	ReLU
	Output Activation	Softmax
	Optimizer	Adam
	Learning Rate	0.001
	Batch Size	32
	Epochs	100
XGBoost	Number of Trees	200
	Learning Rate	0.10
	Maximum Depth	6
	Subsample	0.80
	Column Sample by Tree	0.80

3. System Results

This section presents the training result of the seven ML algorithms trained. The performance was evaluated considering metrics such as precision, recall and f1 score. For the testing, 4660 records data from the four classes of T2DM and also normal class were used to access each model performances. For the MARD class, 698 records were used to test the model, for MOD class, 862 records were used to test it, 1270 records of normal patients without T2DM were used to test the model,764 records of SIDD class were applied to test the model and 1066 records of SIRD were used to test the model. Table 3 presents the result of the DT model.

Table 3: Classification Performance of the Decision Tree Model

Class	**Precision**	**Recall**	**F1-Score**	**Support**
MARD	0.98	0.98	0.98	698
MOD	0.91	0.89	0.90	862
NORMAL	1.00	1.00	1.00	1270
SIDD	1.00	1.00	1.00	764
SIRD	0.92	0.93	0.92	1066
Accuracy	**96.07%**			**4660**

Table 3 presents the result of the DT model training. From the results, it was observed that when 698 records of MARD were applied to test the model, the precision score is 98% for successful classification of MARD. These results implied that the DT was able to report a positive prediction. The recall reported 0.98 which is 98% success rate that the prediction precision is correct. That mean that prediction of MARD was correct with 98% rate. The f1score is the harmonic mean between precision and recall. This record 98% success rate. For the MOD class, 862 records were used to test the model. The precision score is 91%, recall is 89% and f1score reporting 90% classification success rate. In the normal test category, 1270 records were applied to test the model. In the SIDD class, the precision score reported 1.00. the recall and f1-score all recorded 1.00 when 764 records of SIDD were applied to test the mode, while the SIRD when tested with 1066 records reported precision score of 92%, recall of 93%, f1-score of 92%. Finally, the reported accuracy is 96.07%. This result mean that the DT classifier was able to correctly classify the different classes of T2DM with 96.07% success

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rate. Table 4 to Table 9 presents the result of the other models using the same overall sample size of 4660 test data.

Table 4: Classification Performance of the Random Forest Model

Class	Precision	Recall	F1-Score	Support
MARD	0.99	1.00	0.99	698
MOD	0.96	0.95	0.95	862
NORMAL	1.00	1.00	1.00	1270
SIDD	1.00	1.00	1.00	764
SIRD	0.96	0.97	0.97	1066
Accuracy	**98.24%**			**4660**

Table 5: Classification Performance of the Support Vector Machine Model

Class	Precision	Recall	F1-Score	Support
MARD	0.99	1.00	0.99	698
MOD	0.96	0.94	0.95	862
NORMAL	1.00	1.00	1.00	1270
SIDD	1.00	1.00	1.00	764
SIRD	0.96	0.97	0.97	1066
Accuracy	**98.20%**			**4660**

Table 6: Classification Performance of the Naïve Bayes Model

Class	Precision	Recall	F1-Score	Support
MARD	0.98	1.00	0.99	698
MOD	0.95	0.93	0.94	862
NORMAL	1.00	1.00	1.00	1270
SIDD	1.00	1.00	1.00	764
SIRD	0.96	0.97	0.96	1066
Accuracy	**97.88%**			**4660**

Table 7: Classification Performance of the K-Nearest Neighbour Model

Class	Precision	Recall	F1-Score	Support
MARD	0.96	0.99	0.98	698
MOD	0.90	0.92	0.91	862
NORMAL	1.00	1.00	1.00	1270
SIDD	1.00	1.00	1.00	764
SIRD	0.96	0.92	0.94	1066
Accuracy	**96.55%**			**4660**

Table 8: Classification Performance of the Multi-Layer Perceptron Model

Class	Precision	Recall	F1-Score	Support
MARD	0.99	0.99	0.99	698
MOD	0.94	0.91	0.92	862
NORMAL	1.00	1.00	1.00	1270
SIDD	1.00	1.00	1.00	764
SIRD	0.94	0.96	0.95	1066
Accuracy	**97.23%**			**4660**

Table 9: Classification Performance of the XGBoost Model

Class	Precision	Recall	F1-Score	Support
MARD	0.99	1.00	0.99	698
MOD	0.96	0.95	0.95	862
NORMAL	1.00	1.00	1.00	1270
SIDD	1.00	1.00	1.00	764

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SIRD	0.96	0.97	0.97	1066
Accuracy	**98.35%**			**4660**

From the results, XGBoost achieved the highest standalone accuracy (98.35%), followed by Random Forest (98.24%), and Support Vector Machine (98.20%). The remaining models achieved accuracies between 96.07% and 97.88%. Across all models, the NORMAL and SIDD classes were classified almost perfectly, with precision, recall, and F1-scores of 1.00. The MOD and SIRD classes were comparatively more challenging, exhibiting slightly lower performance metrics. Although the stacking ensemble did not surpass XGBoost in overall accuracy, it maintained highly balanced precision, recall, and F1-scores across all diabetes classes, demonstrating its robustness and consistency in multiclass diabetes classification.

In the next part of this work, confusion matrix was used to test each of the T2DM classes and also normal clinical records. First test was reported with the RF model. The confusion matrix result was reported in Figure 2. It was generated when 700 records of MARD class were applied to test the model, 850 MOD class was applied to test the model, 1270 normal records of patient s without T2DM were applied to test the model, 764 records of SIDD were applied to test the model while 1076 records of SIRD was applied to test the model.

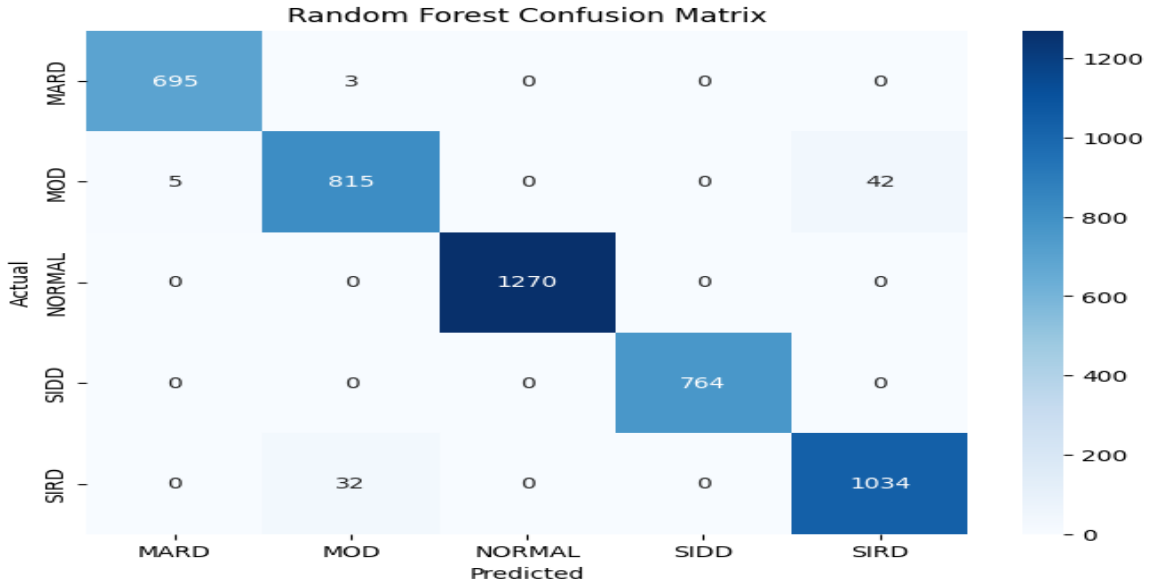


Figure 2: The Confusion matrix of the RF

Figure 2 presents the confusion matrix of the RF model. In the results, it was observed that when 700 records of MARD were applied to test the model, 695 was correctly classified as MARD, while 5 records were misclassified as MOD diabetes. This gives a 99.29% success rate in correct classification of MARD T2DM. When 850 records of MOD class were applied to test the model, 3 records were wrongly classified as MOD, 32 records were also wrongly classified as SIRD. When 1270 records of normal data were applied to test the model, the result recorded 100% success rate as all the record were correctly classified as normal. Similarly, when 764 records were applied to test the model, it reported 100% success rate in classification, while out of the 1076 records which was applied for SIRD classification, 1034 was correctly classified as SIRD, while 42 records were wrongly classified as MOD. Overall, the results showed that the RF classifier recorded very high success rate in correct classification of different classes of T2DM and also patients which are not infected. In Figure 3-8, the result for the other models were reported.

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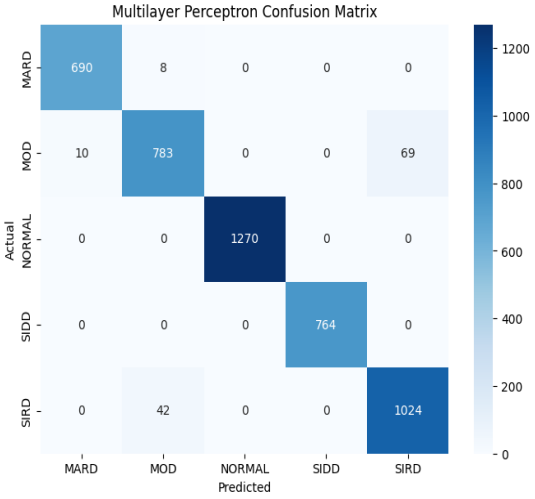


Figure 3: The Confusion matrix of the MLP

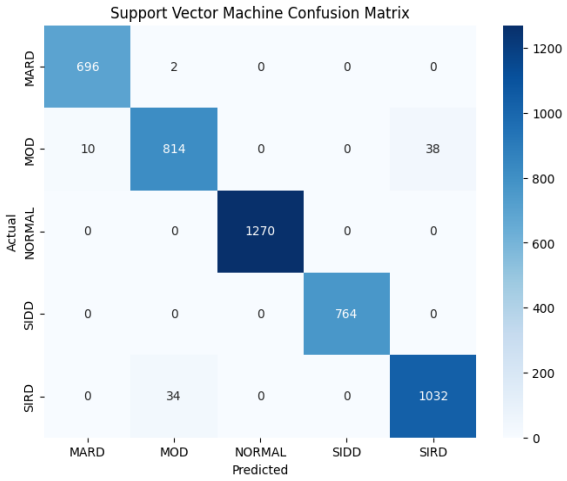


Figure 4: The Confusion matrix of the SVM

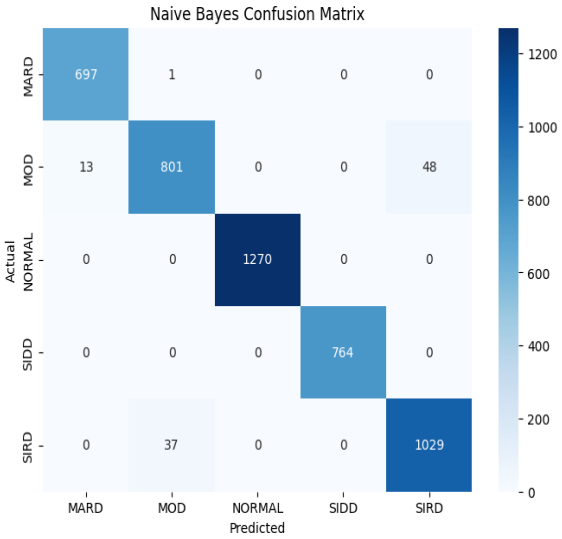


Figure 5: The Confusion matrix of the NB

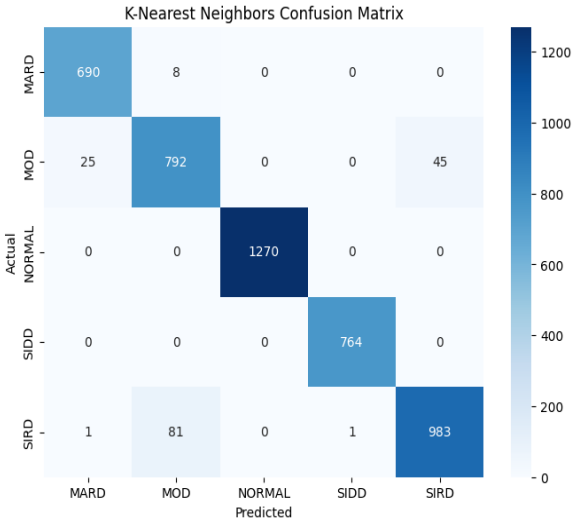


Figure 6: The Confusion matrix of the K-NN

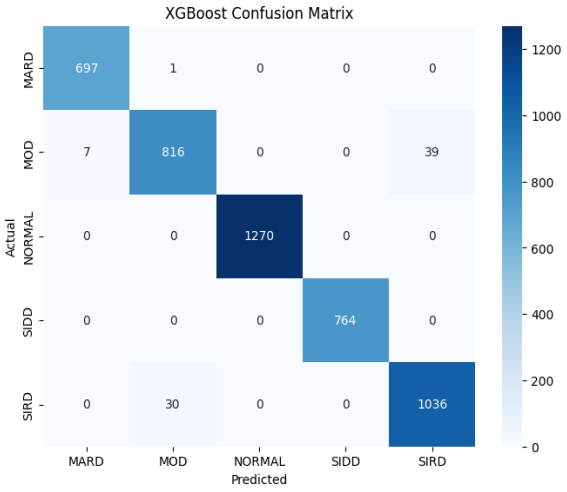


Figure 7: The Confusion matrix of the XGB

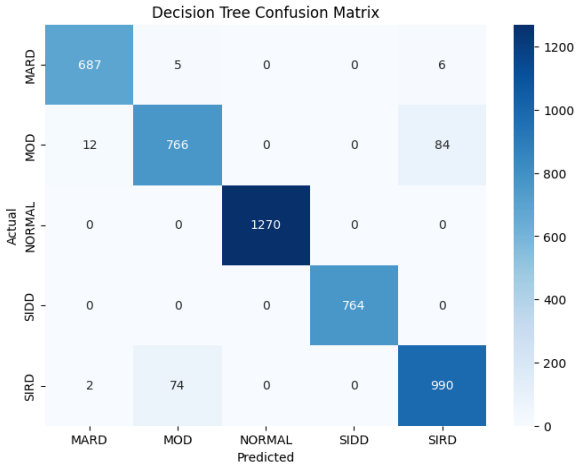


Figure 8: The Confusion matrix of the DT

Overall, the confusion matrix revealed that all the model recorded very high classification success rate on the average above 95% which is good. The confusion matrix has also demonstrated that each of the models have ability to classify the different types of T2DM with high success rate. The results showed that all the model performed most excellent while

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classifying normal and SIDD records. But reported different results on the other classes. These results have demonstrated the success outcome when applying machine learning as a solution to T2DM problem.

3.1 Result comparative analysis

Having trained the models, comparative analysis was applied to identify the most suitable for the development of the ensemble classifier. The comparison considered accuracy and AUC as key metrics. Figure 9 presents the comparative accuracy.

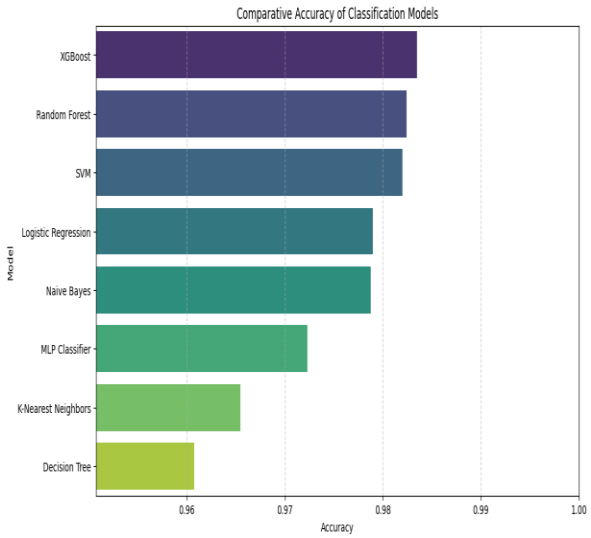


Figure 9: Comparative analysis of the accuracy

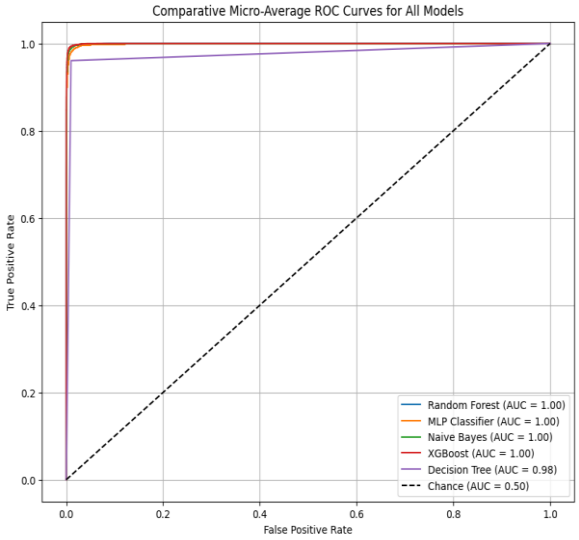


Figure 10: comparative AUC Curve

The Figure 9 compared the accuracy of the seven models trained for the multi classification of the T2DM. From the comparison, it was observed that while all the models reported over 95% success rate, the top three classifiers are the XGB, MLP and SVM respectively. For the AUC analysis which measured the relationship between true positive and false positive, the Figure 10 presents the results.

The Figure 10 compared the AUC and the results showed that the DT recorded the best performance with0.98 success rate, while the other model reported 100% success rate in the correct classification of different T2DM classes. This results further strengthen the justification of the top three models selected in this work for the curation of the ensemble learning model.

4. Conclusion

This study proposed and evaluated a machine learning-based system for the multiclass classification of Type 2 Diabetes Mellitus utilising clinical information extracted from two Nigerian healthcare institutions. Following the CRISP-DM methodology, seven classification algorithms, including DT, RF, SVM, KNN, NB, MLP, and XGBoost, were trained and evaluated using 23,300 patient records containing demographic, anthropometric, lab results, metabolic, lifestyle and medical history data. Experimental results showed that all classification models achieved high accuracy, with all algorithms reporting over 96% accuracy. Of the tested algorithms, XGBoost achieved the highest accuracy of 98.35%, followed by Random Forests and Support Vector Machine at 98.24% and 98.20% respectively, indicating their potential for use in a multiclass diabetes classification task.

The results further showed that machine learning algorithms can be used for differentiating between MARD, MOD, SIDD, SIRD, and the NORMAL class with high precision and recall, with particular strengths in recognising the NORMAL and SIDD categories. Moreover, the

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confusion matrix analysis showed the robustness of the proposed methodology, with potential to support reliable clinical decisions in the diagnosis of Type 2 Diabetes Mellitus. Overall, the study highlighted the potential of applying machine learning-based solutions for the management of diabetes due to their affordability and accuracy, while future studies could explore the use of explainable artificial intelligence techniques, utilise alternative datasets for external validation, and focus on implementing such models in a clinical setting for improved precision and timely management of the disease.

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