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Comparative Performance Analysis of Selected Machine Learning Algorithms for Predicting Type 2 Diabetes Using Non-Invasive Method

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ABSTRACT

Diabetes mellitus, a chronic metabolic disorder characterised by elevated blood glucose levels, is a global health concern. Non-invasive techniques for predicting Type 2 diabetes are less burdensome than invasive methods, yet developing a machine learning model on non-invasive data remains underexplored. This study evaluated six classification algorithms namely Logistic Regression (LR), Naïve Bayes (NB), Support Vector Machine (SVM), Decision Tree (DT), XGBoost (XGB), and CATBoost (CATB) on non-invasive datasets using Percentage Accuracy, AUC, recall, precision, F1 score, kappa, and MCC as metrics. The datasets were obtained from the LAUTECH Teaching Hospital, Ogbomoso, Mainspring Hospital, and State Specialist Hospital, Akure. Results showed that CATB was the most effective, with a Percentage Accuracy of 90.60%, while NB had the lowest performance with a Percentage Accuracy of 73.05% on the data. This study offered important insights into using machine learning for diabetes prediction by highlighting the promise of non-invasive techniques for early Type 2 diabetes screening and the efficiency of CATB in predictive performance.

INTRODUCTION

Diabetes is a chronic disease that occurs when the body does not produce enough insulin or when body cells cannot effectively utilize the insulin produced (Ogunniyi *et al*., 2024). The primary types of diabetes include Type 1 diabetes (T1D), Type 2 diabetes (T2D), and Gestational diabetes (GD), along with rarer forms such as double diabetes and other atypical types (Olamoyegun *et al*., 2020). T2D accounts for over 90% of diabetes cases worldwide, with its prevalence rising almost yearly (Ogunniyi *et al*, 2024; Garg and Duggal, 2022). This has significant health and economic impacts on the global population, either directly or indirectly (Tinajero and Malik, 2021). Early detection is crucial in curbing the increasing prevalence of T2D, as late diagnosis can lead to severe complications such as hearing and vision impairments, cardiovascular diseases, kidney disease, skin disorders, neuropathy, blindness, and lower-extremity amputation (Matoori, 2022).

The most common method of detecting diabetes through invasive techniques has several drawbacks, including mild pain from blood sample collection, the need for technical knowledge to perform self-tests, and the financial burden of frequent testing (Gusev, 2022). To address these challenges, non-invasive methods for detecting T2D have recently gained traction. In a non-invasive approach, a blood sample is not involved, which automatically eliminates the pains associated with invasive techniques (Mohanram and Edward, 2021). The development of non-invasive methods for T2D detection offers new hope, particularly for individuals in developing countries, where diabetes prevalence is rising most rapidly (Ogunniyi *et al*., 2021). Machine learning (ML), a subset of artificial intelligence, analyses complex data, identifies patterns, and predicts outcomes based on historical datasets. It has emerged as a powerful tool for disease prediction (Ihme *et al*., 2022). ML can predict T2D using non-invasive parameters such as demographics, lifestyle factors, and anthropometric measurements. Several such machine learning algorithms for the prediction of T2D have been developed and used for prediction on different datasets in several works (Deberneh and Kim, 2021; Ismail *et al*., 2022; Lu *et al*, 2022; Suryadevara, 2023). Depending on the problem being solved, the following machine learning algorithms are commonly used in the prediction of T2D: Naive Bayes, K-Nearest Neighbours (KNN), Random Forest (RF), Logistic Regression (LR), Decision Tree (DT), Support Vector Machine (SVM), Extreme Gradient Boosting (XGBoost), LightGBM, and Categorical Boosting (CATBoost)(Suryadevara, 2023; Ogunniyi *et al*., 2024).

ML algorithms often exhibit varying performance depending on the dataset and implementation environment. As a result, determining the most suitable ML algorithm for a given problem requires empirical evaluation. Thus, comparing the performance of selected ML algorithms on the dataset used in this study is a necessary step. This study aims to provide insights into the comparative performance of these ML algorithms, offering guidance to researchers and ML engineers in selecting the most appropriate algorithm for similar predictive tasks.

RELATED WORKS

Savitesh *et al* (2022) developed an ML model that uses six ML algorithms, which include XGBoost, RF, Gradient Boosting (GB), SVM, DT and Extra Tree Classifier (ETC) via a non-invasive technique to predict children and adolescents who have early-onset diabetes. Based on haemoglobin A1C (HbA1C) readings, the researchers classified 26,567 people in India between the ages of 5 and 19 into normal and pre-diabetic categories. The prediction Percentage Accuracy of six machine learning models was assessed after taking into account eight features, namely: age, gender, height, weight, tricep skinfold thickness (TSFT), subscapular skinfold thick- ness (SSFT), mid-upper arm circumference (MUAC) and waist cir- cumference (WC)). With the largest area under the receiver operator curve (AUC) and a cross-validation (10-fold) score of 90.13%, the XGBoost classifier was determined to be the best model. The created model was incorporated into an automated pre-diabetes prediction screening tool, offering a real-time solution that might potentially stop the course of the illness. The study underlines the value of early intervention to lessen the impacts of pre-diabetes in children and demonstrates the potential of ML in this area.

Nistal-Nuño, (2022) compared the predictive performance of XGBoost, Bayesian Network (BN), and Naïve Bayes network (NB) on the Medical Information Mart for Intensive Care III (MIMIC-III) dataset. The dataset of 9893 ,consisting of physico-demographic, diagnosis/procedure and physiological measurements, was used to assess the Percentage Accuracy, discrimination, and calibration of machine learning models. The results revealed that XGBoost achieved the best performance with an area under the receiver operating characteristic (AUROC) of 0.919, outperforming BN (0.905), NB (0.864), and conventional systems maximum of 0.814 for serial SOFA. These findings highlight the potential of ML models, particularly XGBoost, to enhance patient monitoring and outcome predictions in the Medical Intensive Care Unit (MICU), warranting further investigation in future studies.

Rady *et al* (2021) used seven (7) ML algorithms to develop predictive models for diabetes using a dataset of 521 records. The ML algorithms used are Logistic Regression (LR), Support Vector Machine (SVM), Random Forest (RF), Decision Tree (DT), Adaptive boosting classifier, K-Nearest Neighbour (KNN), and Naïve Bayes (NB). The result of the work revealed that RF performed better than others with a Percentage Accuracy of 98%. Khanam and Foo (2021) compared the performance of six (6) machine learning algorithms using the Pima Indian Diabetes dataset, containing 768 records. The ML algorithms used were LR, KNN, SVM, NB, DT and RF. The LR and SVM perform best for diabetes prediction. In addition to the six ML algorithms, a Neural Network (NN) model was also developed and the Percentage Accuracy obtained is 88.6%, which is higher than the six ML algorithms. This outcome indicates the efficiency of ML and NN approaches in the prediction of diabetes.

Ahamed *et al.* (2022) developed predictive models for diabetes using three (3) algorithms, namely: ANN, RF and K- means clustering techniques. Principal component analysis was employed to select risk factors, with Body Mass Index (BMI) and glucose level having a strong correlation with a high risk of diabetes. The ANN achieved a Percentage Accuracy of 75.7%, above the other two algorithms. The work indicated the potential of the ANN in making clinical decisions regarding diabetes detection and treatment. Gupta *et al*. (2022) compared Deep Learning (DL) and Quantum Machine Learning (QML) for predicting Type 2 Diabetes (T2D) using the PIMA Indian Diabetes dataset. It also discussed the development of a prognostic tool to reduce the mortality associated with diabetes. Both DL and QML models were developed using the collected dataset. Results indicated that the DL model outperformed the QML model with an Accuracy of 0.95, while QML has an Accuracy of 0.86.

In the related works, several models were developed using different ML algorithms on different sources of data, with different outcomes. It then means that there is no particular model that can claim superiority over other models, because of their diverse performance on different data sources. This work also sought to compare the performance of some selected ML algorithms on a non-invasive dataset collected from LAUTECH Teaching Hospital, Ogbomoso, Mainspring Hospital, Ogbomoso and State Specialist Hospital, Akure.

METHODOLOGY

An experimental approach was used in this work. The data collection, preprocessing operations, model formulation, training and testing of the model, and implementation tools are as discussed.

Data Collection

This study utilised datasets from LAUTECH Teaching Hospital (8.15150N, 4.25259E), Mainspring Hospital (8.13333N, 4.26667E), Irewolede Community (8.08333N, 4.18333E) in Ogbomoso, and State General Hospital, Akure (7.10615W, 4.84665E), all in Nigeria. The dataset used in the work consisted of two hundred and fifty-two (252) instances and the following risk factors (independent variables): Body Mass Index (BMI), waist circumference, age in years, and whether the patient does regular exercise. (Exercise), Marital status, Gender, Family History of Diabetes Mellitus, whether the patient has a family history of Hypertension, and the outcome(dependent variable) is labelled Class as presented in Table 1.

Table 1: Characteristics of the Non-invasive Dataset Used

S/N	Column	Description	Type
1	BMI (kg/m^2)	Body Mass Index of a Patient	Quantitative
2	Waist	The Waist Circumference of the patient	Quantitative
3	Age (years)	How old is the patient in years	Quantitative
4	Exercise	Whether the patient does regular exercise or not	Nominal
5	Marital status	Whether a patient is married or not	Nominal
6	Gender	The Gender of a patient	Nominal
7	FHD	Whether the patient has a family history of Diabetes Mellitus	Nominal
8	FHH	Whether the patient has a family history of hypertension	Nominal
9	Class	The class indicates whether there is a presence of diabetes or an absence of diabetes.	Nominal

Preprocessing Operations

The data preprocessing stage is vital for raw data for machine learning algorithms. It involves some operations such as risk factor selection, handling missing data, and encoding categorical features. Risk factors that contribute to the risk of type 2 diabetes were identified through consultation with medical experts at the LAUTECH Teaching Hospital, Ogbomoso. A typical ML challenge was missing data, which was substituted with either the mode or the mean, depending on the type of variable. Non-numeric values, Diabetic' and 'Non-Diabetic', were encoded as 1 and 0 for language compatibility, and nominal independent variables were converted accordingly.

Model formulation

The following variables were used for model formulation: BMI=X_1, Waist=X_2, Age=X_3, Exercise=X_4, Marital status=X_5, Gender=X_6, FHD=X_7, FHH=X_8.

The Formulation of a predictive model for diabetes Type 2 using the Logistic Regression algorithm.

The logistic regression equation is equation (1):

$$P(DiabetesOutcome = 1 \mid X_1, X_2, X_3, X_4, X_5, X_6, X_7, X_8) = \frac{1}{1 + \exp(-z)} \tag{1}$$

The linear combination (z) is calculated with equation (2)

$$z = b_0 + b_1 * X_1 + b_2 * X_2 + b_3 * X_3 + b_4 * X_4 + b_5 * X_5 + b_6 * X_6 + b_7 * X_7 + b_8 * X_8 \tag{2}$$

Where: b_n is the intercept term (bias), and n = 0..8.

Formulation of the predictive model with Naïve Bayes algorithm

The following were used in equation (3).

P(Y) is the target variable's prior probability (the likelihood of having type 2 diabetes). (Xi|Y) denotes the likelihood of predictor characteristics Xi given Y (the likelihood of observing Xi given Y). The chance of observing Xi regardless of the target variable is P(Xi), which is the marginal probability of the predictor attributes Xi. The needed probabilities from the training data were used to estimate the prediction using Naive Bayes, and the values of the predictor attributes for a particular person were entered to get the posterior probability of them having type 2 diabetes (Y=1).

The formula to compute posterior probability was given in equation (3).

$$P(Y|X_1,X_2,X_3,X_4,X_5,X_6,X_7,X_8) = \frac{P(Y).X_1|Y.X_2|Y.X_3|Y.X_4|Y.X_5|Y.X_6|Y.X_7|Y.X_8|Y}{P(X_1).P(X_2).P(X_3).P(X_4).P(X_5).P(X_6).P(X_7).P(X_8)} \quad (3)$$

The Formulation of a predictive model for diabetes type 2 using the Support Vector Machine (SVM) algorithm.

Formulation of a model with Support Vector Machine on Radial Basis Function

To use the radial basis function (RBF) kernel with SVM for the target variable outcome and the predictors' attributes, an SVM expression was formulated. The selection of the RBF kernel was done using the trial-and-error method. The SVM expression with the RBF kernel is equation (4):

$$minimize\ \frac{1}{2}\|w\|^2 + C\sum_{i=1}^{n}\xi_i \quad (4)$$

$$y_i(\langle w, \phi(x_i)\rangle + b) \geq 1 - \xi_i$$

$$\xi_i \geq 0$$

Where:

W is the weight vector of the hyperplane.

C is the regularisation parameter that balances the margin maximisation and the training error.

N is the number of data points in the training set.

y_i is the target variable outcome for data point I (y_i =1 or -1 for binary classification).

$\langle w, \phi(x_i)\rangle$ Represent the inner product of the weight vector and the transformed feature vector

$\phi(x_i)$ Using the RBF kernel.

b is the bias term of the hyperplane.

ξ_i is the slack variable that allows some data points to be misclassified or fall within the margin.

The transformation $\phi(x_i)$ using the RBF kernel is given in equation (5):

$$\phi(x_i) = e^{\left(-\frac{\|x_i - c\|^2}{2\sigma^2}\right)} \quad (5)$$

Where,

C is a support vector that represents the centre of the RBF kernel.

σ is the kernel width, which determines the spread of the kernel function.

The Gradient Descent method was used to determine the optimal value for the regularization parameter C.

Formulation of predictive models for Type 2 diabetes using the Decision Tree

The techniques of Entropy and Information Gain were used in the formulation of a predictive model. Their equations were given in (6) and (7), respectively.

$$E(S) = \sum_{I=1}^{C} -P_i log_2 P_i \tag{6}$$

Where:

P_i is the probability of a class. In this work, there are two classes: diabetic and non-diabetic.

c is the total number of classes. In this work, c is 2. S is the subset of the training dataset.

$$Information\ Gain = E(Y) - E(Y|X) \tag{7}$$

Where:

E(Y) is the Entropy of the full dataset

E(Y|X) is the Entropy of the dataset given some features, X1 to X8.

The following steps were followed to carry out the splitting of the tree.

1. Input the dataset
2. Compute the parent entropy of the dataset using equation (6).
3. Calculate the information gain for each feature variable using its probability value.
   i. Compute the entropy for each of the feature variables for each class
   ii. Calculate the weighted average of the entropy of each node
   iii. Select the feature that has the highest information gain and then split the node based on that feature.
   iv. Compare the node depth with max_depth via the GridSearchCV technique.
4. Repeat 3. i-iii until the max_depth is reached.

Formulation of predictive model using Extreme Gradient Boosting (XGBoost) Algorithm

Equations (8), (9) and (10) were used to formulate the predictive model using the dataset collected in this work based on the flowchart in Figure 1.

$$R.E = (y_i - M_0) \tag{8}$$

$$S.S = \frac{(S.R^2)}{(N + \lambda)} \tag{9}$$

$$N.P = Previous\ Prediction + eta * Output \tag{10}$$

Where, y_i is the target value for each of the records in the dataset, and M_0 is the predicted value.

S.R is the sum of residual error, N is the total number of records in the dataset, ƛ is a parameter which is set to 0, eta >=0, and the output is the weighted average of each of the branches in the decision tree.

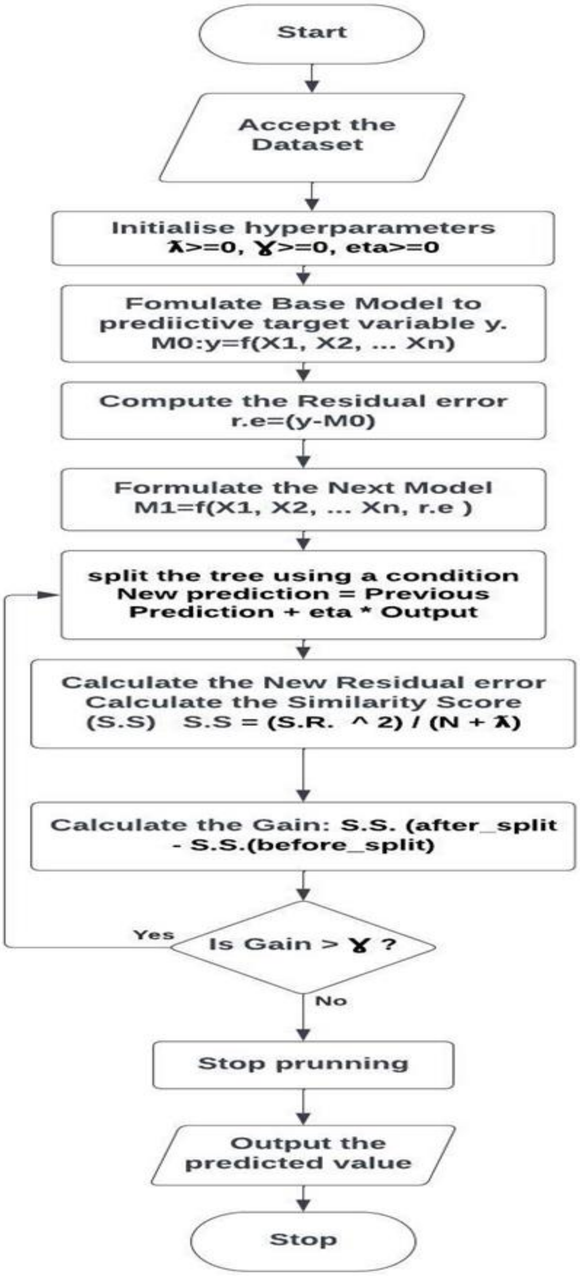

Figure 1: Flowchart for XGBoost algorithm

The Formulation of a predictive model for a non-invasive dataset with the CATBoost Algorithm

Equations (11), (12), (13), and (14) were used in the formulation of the models based on the CATBoost algorithm:

1. The model was initialized with a constant value:

$$F_0(x) = \arg\min_{\gamma} \sum_{i=1}^{n} L(y_i, \gamma) \qquad (11)$$

2. For m=1 to M:

3. The pseudo-residuals were computed using:

4. $r_{im} = -\left[\frac{\partial L(y_i, F(x_i))}{\partial F(x_i)}\right]_{F(x)=F_{m-1}(x)} \, for\ i = 1, \dots, n.$ (12)

5. The base learner (e.g., tree) $h_m(x)$ was fit to pseudo-residuals, i.e., train it using the training set $\{(x_i, r_{im})\}_{i=1}^{n}$

6. A multiplier γ_m was computed by solving the following one-dimensional optimisation problem in equation (13):

$$\gamma_m = -\arg\min_{\gamma} \sum_{i=1}^{n} L(y_i, F_{m-1}(x_i) + \gamma h_m(x_i)) \tag{13}$$

7. The model was updated using equation (14):

$$F_m(x) = F_{m-1}(x) + \gamma_m h_m(x) \tag{14}$$

8. The predicted value was outputted: $F_M(x)$.

The hyperparameter tuning was done using Grid Search techniques.

Training and Testing

The datasets used were split into training and testing datasets in the ratio of 4:1, respectively. The 80% was used for training, while the 20% was used for testing the developed models.

Performance metrics

Table 2 is the confusion matrix, and the table's parameters are interpreted as follows:

True Positive (TP): These are the correctly predicted positive values, which means that the value of the actual class is "1" and the value of the predicted class is also "1".

True Negative (TN): These are the correctly predicted negative values, which means that the actual class is "0" and the value of the predicted class is "0".

False Positive (FP): When the actual class is "0" and the predicted class is "1".

False Negative (FN): When the actual class is "1" but the predicted class is "0".

From the values of the confusion matrix, the following metrics were used to evaluate the models of this work further:

a. **Percentage Accuracy:** This is the most intuitive performance measure and it is simply a ratio of correctly predicted observations to the total observations, multiplied by 100. Equation (15) is the percentage Accuracy.

$$\text{Percentage Accuracy} = \frac{\text{TP} + \text{TN}}{\text{TP} + \text{FP} + \text{FN} + \text{TN}} * 100 \tag{15}$$

b. **Precision**: Precision is the ratio of correctly predicted positive observations to the total predicted positive observations. Equation (16) was used to calculate Precision.

$$\text{Precision} = \frac{\text{TP}}{\text{TP} + \text{FP}} \qquad (16)$$

Table 2: Confusion Matrix

		Actual Values	
		POSITIVE	**NEGATIVE**
PREDICTED VALUES	POSITIVE	TP	FP
	NEGATIVE	FN	TN

c. **Recall** (Sensitivity): Recall is the ratio of correctly predicted positive observations to all observations in the actual class. Equation (17) was used to calculate the recall of the model.

$$\text{Recall} = \frac{\text{TP}}{\text{TP+FN}} \qquad (17)$$

d. **F1 Score**: The F1 Score is the weighted average of Precision and Recall. Therefore, this score takes both FP and FN into account. Equation (18) was used to calculate the F1 score.

$$\text{F1 Score} = 2 * \frac{\text{Recall} * \text{Precision}}{\text{Recall} + \text{Precision}} \qquad (18)$$

e. **Matthews Correlation Coefficient:** MCC determines the classification's quality, which is divided into two categories. The MCC value offered a binary correlation coefficient between the expected and detected classifications. MCC's formula is given in equation (19), according to the Confusion Matrix.

$$MCC = \frac{TP\ X\ TN - FP\ X\ FN}{(TP + FP)(TP + FN)(TN + FP)(TN + FN)} \qquad (19)$$

f. **Kappa Statistic:** Cohen's Kappa is another name for the Kappa Statistic. In reality, it is used to measure a variable's ability to reproduce itself. In equation (20), the formula is explained in detail.

$$K = \frac{P_O - P_e}{1\ - P_e} = 1 - \frac{1 - P_o}{1 - P_e} \qquad (20)$$

Here, P_o = Observed Agreement and P_e = Expected Agreement.

Implementation tools

The models for this work were implemented using Python due to its rich libraries and built-in functions that supported the six machine learning algorithms used. Likewise, the programming and testing of the models were performed on an AMD Ryzen 5 2500U with Radeon Vega Mobile Gfx, 2 GHz, 4 cores, and 16 GB of RAM running on the Ubuntu operating system.

RESULTS AND DISCUSSIONS

The summary of the result of the model evaluation is presented in Table 3. The result indicated that the model with the CATBoost algorithm outperformed other models with a Percentage Accuracy of 90.60% and an AUC value of 0.9032. Other metrics further support the Percentage Accuracy and AUC value, because their values were higher than the values of other models. This supports the assertion given by (Modak and Jha, 2024; Jerith *et al*., 2024; and Liu *et al*., 2023) that the CATBoost algorithm performs better than other existing ML algorithms in recent times. With this revelation, it is a good decision to always consider the CATBoost algorithm first in the prediction of T2D and other similar tasks.

The XGBoost model has a percentage accuracy of 85.47% and an AUC value of 0.8416. All the other metrics, except recall, also supported the position of the percentage accuracy and AUC in the XGBoost model. This implies that XGBoost is next to the CATBoost in terms of performance in this work. This observation about the XGBoost is similar to the results obtained from (Qiu *et al*., 2024). The percentage accuracy of the Decision Tree is 79.76% and the AUC value of 0.7105. This performance by the Decision Tree shows that its performance is good, although it is less than that of CATBoost and XGBoost models, although less than that of the CATBoost and XGBoost. Its recall of 0.5523 also indicated that it could identify True positives to a reasonable degree. Logistic Regression's Percentage Accuracy is lower than that of Decision Tree at 77.01%, whereas Recall was very poor at 0.0939-the obvious indicator that it has failed to identify the most true positives. Its precision (0.4417) is not bad, and the low recall coupled with a low F1 score (0.1532) signifies that it has not been able to cope with balancing false positives and false negatives. Thus, this makes Logistic Regression an unsuitable technique for this problem. The Naïve Bayes has a recall close to an average of 0.4971, precision (0.4208) and modest Percentage Accuracy (73.05%). This model was able to identify more true positives than Logistic Regression, but the value of false positives worsened the case and made it less reliable.

Table 3: Summary of Results of all the Models with the Non-invasive Dataset

S/N	Model	Percentage Accuracy (%)	AUC	Recall	Precision	F1	Kappa	MCC
1	LR	77.01	0.7254	0.0939	0.4417	0.1532	0.0831	0.1167
2	NB	73.05	0.6724	0.4971	0.4208	0.4490	0.2751	0.2802
3	SVM	75.27	0.0000	0.1427	0.3514	0.1851	0.0871	0.1079
4	DT	79.76	0.7105	0.5523	0.5702	0.5506	0.4221	0.4287
5	XGBoost	85.47	0.8416	0.5523	0.7566	0.6287	0.5418	0.5583
6	CatBoost	90.60	0.9032	0.6591	0.9073	0.7622	0.7054	0.7203

SVM did not do well in this analysis. It has a Percentage Accuracy of 75.27% and an AUC of 0.0000. This could mean that the AUC was inappropriate for the model or that there were problems with how the model was evaluated: wrong calculation of the metrics or imbalance handling. This requires further research to discover what leads to that value. Its recall (0.1427) and F1 score (0.1851) are among the lowest, showing its complete ineffectiveness in predicting Type 2 Diabetes in this particular case.

CONCLUSION

This work is a comparative analysis of six different machine-learning algorithms. Using a non-invasive dataset, the following machine learning classification techniques were utilised to create models for this work: Logistic Regression (LR), Naïve Bayes (NB), Support Vector Machine (SVM), Decision Tree (DT), Extreme Gradient Boosting (XGBoost), and CATBoost. While Naïve Bayes and Logistic Regression demonstrated the lowest performance in the developed models, the CATBoost algorithm outperformed the rest. The CATBoost is the number one choice of ML algorithm when it comes to the prediction of T2D in recent times. Thisalgorithm can be used to develop a predictive system that can detect the risk of T2D in an individual. This system can be used to enhance healthcare facilities in countries where the doctor-to-patient ratio is higher than the WHO-prescribed ratio of 1:600 (Wonodi *et al*., 2021).

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