A Data-Driven Approach to Diabetes Prediction Using Machine Learning

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Abstract: As the prevalence of health-threatening diseases and mortality rates continue to increase, medical decision support systems have demonstrated their effectiveness in enhancing the efficiency of healthcare providers and aiding clinical decision-making. Diabetes is a significant contributor to global mortality, characterized by high blood glucose levels that can lead to severe complications in various organs. The International Diabetes Federation (IDF) reports that approximately 386 million individuals are currently living with diabetes, a figure projected to rise to 662 million by 2038. This paper presents a clinical prediction model for diabetes utilizing machine learning (ML) techniques. We explore widely used classifiers, including Logistic Regression (LR) and XGBoost, and compare their performance. Additionally, we implement deep learning (DL) approaches, specifically a fully convolutional neural network (DNN), for diabetes prediction. The models were assessed using the publicly available Kaggle database, with prediction performance analysed through Precision, Recall, AUC, accuracy, and F1 metrics. Overall prediction efficiency was evaluated based on accuracy and its macro-average across DL, LR, and XGBoost. The results indicated that XGBoost achieved an accuracy of 93.78%, while LR and DL models recorded accuracies of 89.85% and 98.15%, respectively. The findings suggest that XGBoost outperforms both deep learning and LR methods in predicting diabetes.

Keywords: Large-scale feature optimization, Diabetes mellitus, Feature selection, XGBoost, Deep FM (Deep Factorization Machine).

I. INTRODUCTION

The World Health Organization (WHO) reports that around 1.6 million individuals die from diabetes each year. When the pancreas fails to produce sufficient insulin, glucose cannot be utilized by cells, leading to elevated blood sugar levels, [1]. This condition, known as hyperglycaemia, is characterized by symptoms such as extreme hunger, intense thirst, and frequent urination. Diabetes mellitus is a complex metabolic disorder with various underlying causes, defined by persistent hyperglycaemia and disruptions in carbohydrate, lipid, and protein metabolism due to either inadequate insulin secretion, impaired insulin action, or a combination of both. It is a chronic condition resulting from sustained high blood sugar levels. Approximately 10-15% of the global population is affected by Type 2 diabetes, and the prevalence continues to rise, [2]. Uncontrolled blood sugar levels can result in serious complications, including cardiovascular disease, kidney failure, stroke, and nerve damage. There is currently no cure for diabetes, which remains one of the leading causes of mortality worldwide, contributing to countless deaths each year. Currently, around 463 million people aged 20-79 are living with diabetes, and projections suggest this figure could reach 700 million by 2045, [3].

Numerous studies indicate that deep learning techniques tend to outperform other methodologies, exhibiting lower classification error rates. Deep learning is particularly effective at processing large datasets and addressing complex problems with relative ease. In addition to deep learning, various machine learning and bio-inspired computing methods are now employed for medical predictions. For example, research in 2019 utilized logistic models for diabetes prediction. Recently, Lee developed an enhanced XGBoost algorithm based on feature combinations, achieving an accuracy of 80.2%. Another study evaluated a diabetes dataset using nine different classification algorithms, revealing that XGBoost performed exceptionally well, nearing 100% accuracy, and significantly surpassed other machine learning and deep learning techniques in early diabetes detection [4].

This research focuses on improving the performance of the XGBoost model and comparing its effectiveness with eight conventional machine learning models, such as logistic regression (LR), decision trees (DT), random forests (RF), gradient-boosted decision trees (GBDT), AdaBoost, and neural networks (NN).

II. LITERATURE REVIEW

Kalisir and Dogantekin introduced the LDA-MWSVM system for diabetes diagnosis, integrating feature extraction and dimensionality reduction through Linear Discriminant Analysis (LDA) with classification using the Morlet Wavelet Support Vector Machine (MWSVM). Plis et al. examined various classification methods, such as support vector machines (SVM) and logistic regression, to predict hypoglycaemia 30 minutes in advance, achieving an accuracy of 23%. Ju young et al. used SVM and logistic regression to predict Type 2 diabetes (T2D) based on 499 single nucleotide polymorphisms (SNPs) from 87 associated genes. Deja et al [5]. employed a differential sequencing model to analyse fluctuations in patients' blood glucose levels and insulin dosages, which assisted physicians in treatment decisions. Wright et al. applied the CSPADE algorithm for sequence searching to uncover temporal relationships between medication prescriptions, enabling them to forecast future patient medications. However, many of these studies did not optimize their hyperparameters. Lagani and colleagues focused on various diabetes-related complications, including cardiovascular diseases (CVD), hypoglycaemia, ketoacidosis, microalbuminuria, proteinuria, neuropathy, and retinopathy [6]. Their research aimed to identify the most significant clinical parameters for these complications by utilizing a range of predictive models developed through data mining and machine learning techniques. Additionally, another study utilized drug purchase records and administrative data to implement temporal data mining methods, enhancing the assessment of risks related to diabetic complications [7].

III. METHODS

1.1. Datasets

The diabetes dataset used in this study was obtained from a publicly accessible Kaggle repository and consists of electronic medical records for 100,000 patients. It contains both medical and demographic details, along with each patient's diabetes diagnosis (positive or negative). Key attributes include age, gender, weight, body mass index (BMI), hypertension, cardiovascular disease, and blood glucose levels, as illustrated in Table 1 and Figure 1.

Table 1: Overview of Features

Feature	**Description**
Age	Age is a crucial factor since diabetes is more commonly observed in older adults.
Gender	Gender refers to an individual's biological sex, which can influence diabetes risk. The dataset shows a distribution of 59% female and 41% male.
Weight	Weight affects individuals because it can lead to either insulin resistance or an increased sensitivity to insulin, impacting diabetes development.
High Blood Pressure	Hypertension refers to persistently elevated blood pressure, represented as 0 (no hypertension) or 1 (hypertension).
Glucose Level	Blood glucose refers to the concentration of glucose present in the bloodstream.

	Elevated levels are a key indicator of diabetes.
BMI	The Body Mass Index (BMI) is a standard measure to evaluate body weight status, helping to determine overall health. It is calculated using the formula: BMI = weight (kg) / height (m^2). A higher BMI correlates with a higher risk of diabetes. BMI ranges are: underweight (<18.8), normal (18.8-25.3), overweight (24-29), and obese (≥32). Values in the dataset range from 10.16 to 71.65.
HbA1c Level	The HbA1c test provides an indication of average blood sugar levels over the previous two to three months. Higher values indicate increased diabetes risk, with a level above 6.5% generally signalling diabetes presence.

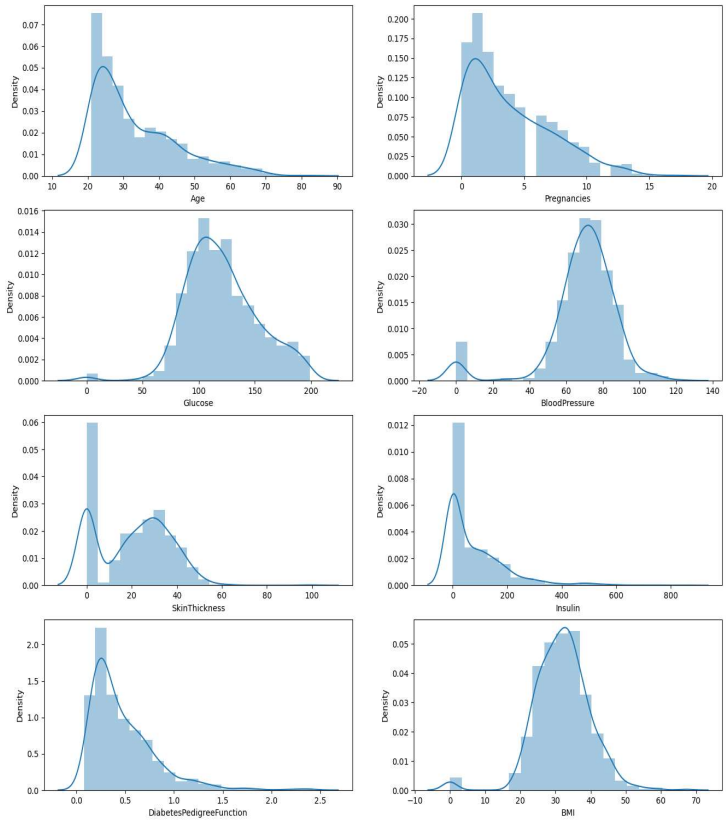

Figure 1: Distribution Patterns and Analysis

1.2. Data Preprocessing

1.2.1. Feature Analysis and Data Visualization

Before data preprocessing, data mining techniques and feature analysis are performed to understand the distribution of the data and the interactions between various features. This is achieved through a combination of visualization techniques and statistical methods, allowing for a comprehensive exploration of the dataset [8]. One frequently utilized technique in this context is correlation analysis, which assesses the strength of relationships between different variables. This is done by calculating correlation coefficients, which quantify the degree of association between the variables. The results of this analysis are often presented in heat maps, providing a clear visual representation of the correlations and enabling easier identification of patterns and relationships within the data. These analyses enhance comprehension of the data and inform subsequent modelling and feature selection, as illustrated in Figure 2.

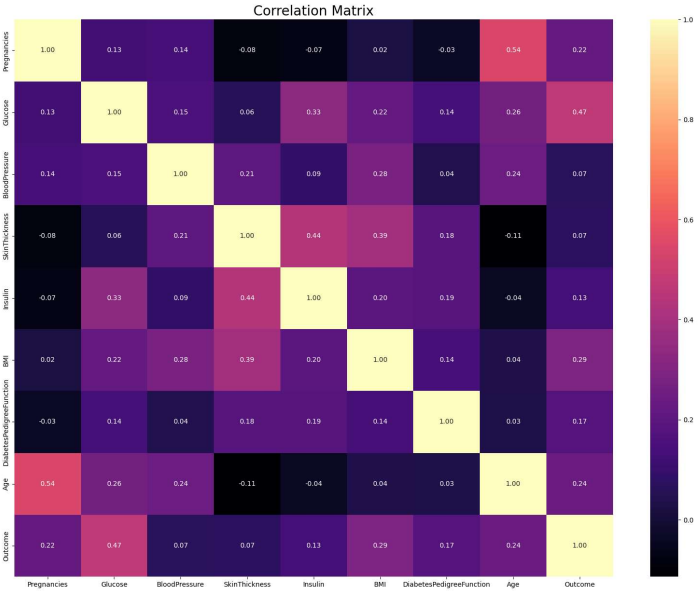

Figure 2: Feature Correlation Analysis

Blood glucose levels and HbA1c levels demonstrated a moderately strong correlation with diabetes, with correlation coefficients of 0.42 and 0.44, respectively. Among the characteristic variables, the highest correlation was observed between BMI and age, indicating a certain linear relationship; however, this correlation is not very strong. Therefore, in the processing of experimental data, the influence of the correlation between these two variables can be disregarded, as shown in Figure 3.

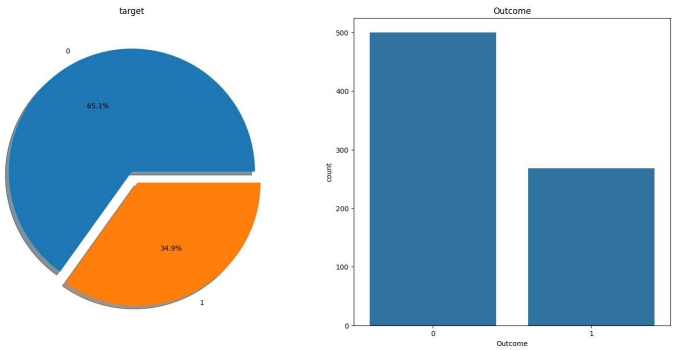

Figure 3: Overview of Relationships in Diabetes Data

1.2.2. Data Preprocessing

1.2.2.1. Data Cleaning

Handling Missing Values: Missing values can be addressed by replacing them with means, medians, or modes, or through interpolation methods.

Handling Outliers: Outliers can be identified and managed using statistical or model-based approaches, including truncation, deletion, or replacement.

Handling Duplicate Values: Duplicate samples or features should be removed to prevent negative impacts on model training.

In this dataset, there were no missing values. The smoking history variable includes a category indicating whether information about the patient's smoking history is available [9]. Initially, we examined the categorical variables present in the dataset, as illustrated in Figure 4.

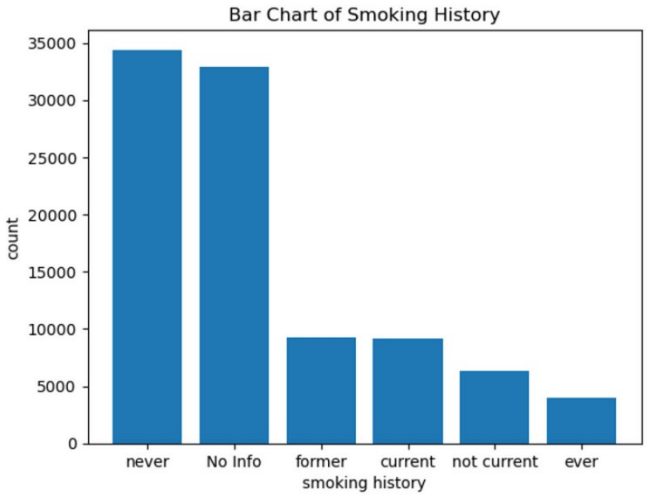

Figure 4: Analysis of Smoking History with Cases

There are many individuals for whom we lack information about smoking habits, so we have decided to retain that category in the variable. While we could consider consolidating other less frequent categories, we will keep this variable unchanged for now. We also conducted a chi-squared test to assess the correlation between this variable and the output, which indicated a significant relationship [10].

Additionally, there is another category that appears to be an error in data collection. Due to the lack of correlation between gender and other variables, we cannot manually correct these values. Since there are only 18 such entries, we will assign them to the most frequent category, which is Female. A chi-squared test confirmed that there is indeed a correlation between the output and these variables. After reviewing the categorical data, we will move on to analysing the numerical data [11]. Given that we have both binary and continuous numerical values, we performed two separate analyses, as shown in Figure 5.

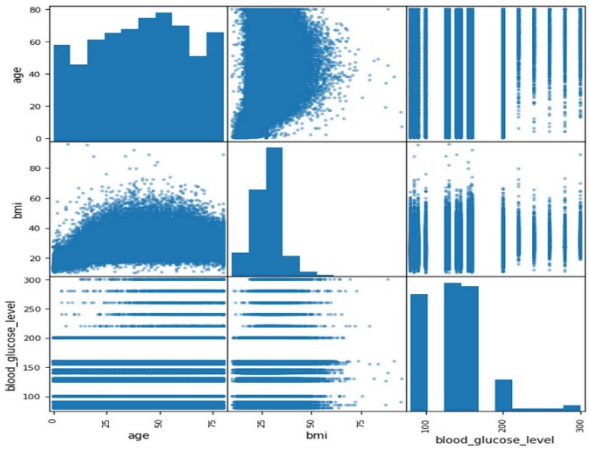

Figure 5: Distribution Analysis of the Dataset

2.2.2. Data Preprocessing

2.2.2.1. Data Cleaning

The BMI variable contains numerous outliers, which we will leave as is for now since a multivariable outlier analysis will be conducted later. Other variables mostly show normal distributions, with a few outliers that are not concerning. We can now proceed to analyse the binary variables.

Initially, there is a significant class imbalance in the dataset, with only 5% of individuals having diabetes, making accuracy an inadequate metric for evaluation [12]. There is also a correlation between the output and the input binary variables, as indicated by the Pearson correlation coefficient, highlighting their substantial impact on the outcome. The next step involves converting categorical variables into numerical data.

3.2.2.2. Data Transformation and Splitting

For feature encoding in this study, we applied One-Hot Encoding to enhance the performance and generalization of the machine learning models. The dataset was split into training, validation, and test sets, with 70% designated for training, 15% for validation tuning, and 15% for final evaluation.

As gender is a binary categorical variable, we utilized binary encoding, assigning a value of 1 for Female and 0 for Male. Regarding the smoking history variable, we used One Hot Encoder, creating five new columns corresponding to each unique value. The final preprocessing step involved normalizing the data using Min Max Scaler, especially given the numerous columns created by One Hot Encoder [13]. With the preprocessing complete, we can now shift our focus to anomaly detection, followed by the separation of the training, validation, and test sets for further modelling.

3.3. Models

3.3.1. XGBoost

XGBoost is a flexible and efficient library designed for distributed gradient-based decision boosting. Developed by Dr. Tianqi Chen at the University of Washington, it is founded on the gradient boosting decision tree (GBDT) algorithm. In GBDT, a tree is trained using the training dataset along with the actual values of the samples, with the predictions subtracted from these true values to obtain residuals. A new tree is then trained on these residuals instead of the original values [14]. This iterative process continues, with each subsequent tree learning to predict the residuals of the ensemble created by previous trees. The number of trees can be specified manually, and training can be monitored and halted based on various performance metrics, such as validation set error.

When making predictions on new samples, each tree in XGBoost contributes an initial value that is combined to generate the final prediction, resulting in better performance compared to the standard GBDT algorithm [15]. In contrast to GBDT, which depends solely on first-order derivatives, XGBoost employs a second-order Taylor expansion of the loss function, allowing for a more effective and reliable solution. By incorporating a

regularization term, XGBoost reduces the model's variance, leading to a simpler model that helps prevent overfitting.

3.3.2. Other Models

In this study, we compared seven different models for data analysis: Logistic Regression (LR), Random Forest (RF), Decision Trees (DT), Gradient Boosting Decision Trees (GBDT), AdaBoost, and Neural Networks (NN).

3.4. Experimental Setup

The dataset was divided into a training set and a test set. We utilized 3,000 cases in the training phase to train and validate the XGBoost models, while 27,000 patients were used for performance evaluation in the test phase.

The hyperparameters set for the experiment included 50 epochs and a batch size of 100. Increasing the batch size reduces the number of iterations (updates) per epoch, which can lead to underfitting, necessitating an increase in epochs. For each set, we employed Grid Search for hyperparameter optimization and cross-validation for model assessment [16]. Four grid search objects—grid Tree, grid KNN, grid Logistic, and grid Boost—were established for tuning the decision tree classifier, K-nearest neighbour classifier, logistic regression model, and gradient boosting classifier, respectively. Each object defined a unique parameter grid and cross-validation fold. In DT, three parameters—

- 'Min_samples_leaf,'
- 'Max_depth,'
- 'Min_samples_split'

were tuned with a cross-validation fold of 3. The KNN model had a fold of 5 with 'estimators' specified, while Logistic Regression also used a fold of 5 with 'Param grid.' The Boost model had a fold of 3 with 'learning rate' and 'estimators' defined.

3.5 Assessment Metrics

We utilized accuracy, precision, recall, AUC, and F1 score as assessment metrics in this study. In the formulas used, the first letter indicates the correctness of the prediction (T for true and F for false), while the second letter denotes the category of the prediction (P for positive and N for negative) [17]. The number of positive samples is denoted as M, and the number of negative samples as N, with the index i belonging to the set of positive sample counts.

Table 2. Model Performance Outcomes.

	LR	DT	RF	GBDT	AdaBoost	XGBoost	NN
Accuracy	0.90	0.96	0.97	0.97	0.95	0.98	0.93
AUC	0.97	0.87	0.98	0.98	0.99	0.99	0.98
Precision1	0.45	0.69	0.79	0.75	0.60	0.95	0.53
Recall1	0.90	0.76	0.77	0.82	0.88	0.75	0.90
F1|1	0.58	0.72	0.59	0.77	0.72	0.85	0.68
Precision0	0.99	0.97	0.99	0.99	0.98	0.98	0.98
Recall0	0.90	0.98	0.99	0.98	0.96	0.99	0.93
F1|0	0.95	0.98	0.98	0.98	0.97	0.99	0.96

$$Precise = P = \frac{TP}{Predicted\ Positive} = \frac{TP}{TP+FP} \quad (1)$$

$$Recall = R = \frac{TP}{Actual\ Positive} = \frac{TP}{TP} + FN \quad (2)$$

$$F = \frac{2}{\frac{1}{R}+\frac{1}{P}} = 2 * P * \frac{R}{P+R} = \frac{2TP}{2TP+FP+FN} \quad (3)$$

$$Accuracy = A == TP + \frac{TN}{TP+FP+TN+FN} \quad (4)$$

$$AUC = \sum rank_i - \frac{\frac{M(1+M)}{2}}{M*N} \quad (5)$$

where,

$P = Precision.$

$R = Recall.$

$TP = True\ Positive.$

$FP = False\ Positive.$

$FN = False\ Negative.$

$TN = True\ Negative.$

$AUC = Area\ Under\ Curve.$

$i = Set\ of\ Positive\ Sample\ Numbers.$

$M = Number\ of\ positive\ Samples.$

$N = Number\ of\ Negative\ Samples.$

IV. RESULTS AND DISCUSSION

4.1. Results

In this study, we selected a diabetes dataset containing 8 feature variables and 30,000 samples to investigate diabetes diagnosis. We developed an Extreme Gradient Boosting (XGBoost)-based model for data training, incorporating deep neural networks (NN) and visualizing the training process [18]. The final model achieved an accuracy of 98.01%, precision of 95.05%, and recall of 99.02%. This research successfully diagnosed diabetes mellitus using a deep neural network approach, yielding significant findings that facilitate diabetes diagnosis, effectively reducing medical costs and enhancing diagnostic efficiency.

The performance metrics for XGBoost were as follows: an accuracy of 0.98, a recall of 0.99, a precision of 0.95, an F1 score of 0.82, and an F0 score of 0.99. These outcomes suggest that XGBoost exhibits a high degree of accuracy, with some precision rates and overall accuracy significantly surpassing those of other models [19-23]. Our findings suggest that XGBoost provides superior prediction accuracy compared to alternative models, including Logistic Regression (LR), Decision Trees (DT), Random Forests (RF), Gradient Boosting Decision Trees (GBDT), and AdaBoost, when applied to unsupervised learning with multiple data sources, as summarized in Table 2.

DISCUSSION

In this experiment, the various model metrics indicate that XGBoost outperformed Gradient Boosting Decision Trees (GBDT) and other models in terms of accuracy, recall, and especially precision [24]. The metrics reported for accuracy, AUC, precision, recall, and F1 score were 0.98, 0.99, 0.95, 0.75, and 0.85, respectively. Comparing GBDT and XGBoost reveals several factors such as sampling methods, tree depth, choice of base learner,

parallel processing capabilities, and approaches to handling missing data and anomalies that influence performance.

XGBoost shares similarities with Random Forests (RF) by utilizing column sampling to enhance computational efficiency and reduce overfitting, while GBDT employs all available features. Additionally, XGBoost can utilize either CART regression trees or linear classifiers as its base learner, in contrast to GBDT, which is restricted to CART regression trees [25-27]. By parallelizing feature selection, XGBoost accelerates the search for optimal split points through pre-sorted features. It also applies L1 and L2 regularization to leaf nodes, which helps mitigate overfitting, and employs second-order Taylor expansion for improved loss curve fitting compared to GBDT's reliance on first-order gradients. The incorporation of shrinkage helps scale leaf node weights, facilitating learning in subsequent stages; practitioners often adjust the eta parameter to lower values with increased iterations for enhanced learning as illustrated in Figure 6 and Figure 7.

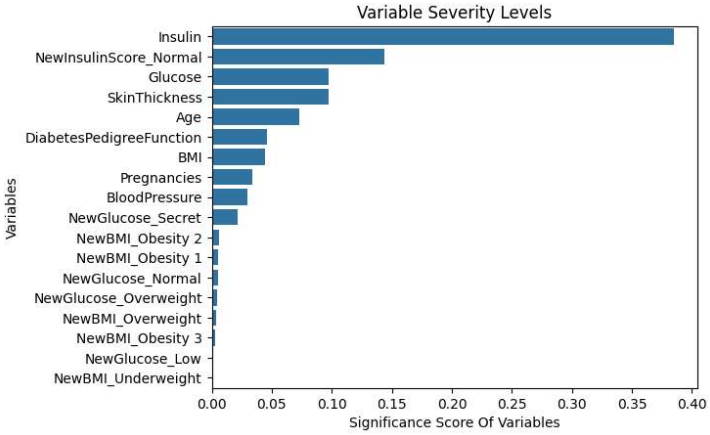

Figure 6: Variable Severity Levels Analysis.

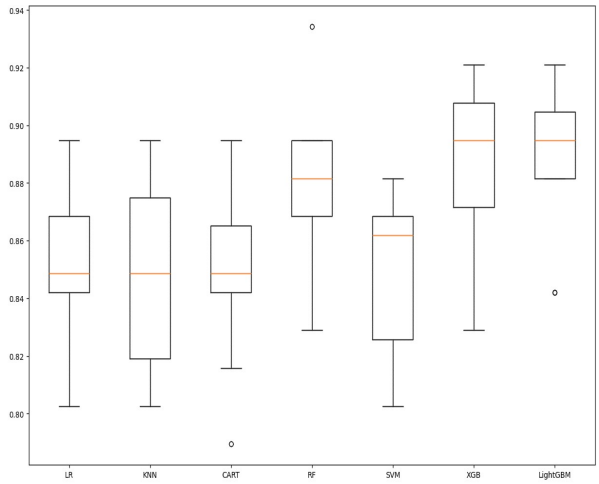

Figure 7: Algorithm Performance Analysis.

Logistic Regression (LR) is effective for discrete features, as discretized features are more robust against anomalies. It is categorized as a generalized linear model with limited expressive power; after discretization into N categories, each variable receives a distinct weight, introducing nonlinearity and enhancing model expressiveness [28]. Crossover of features can transform M + N variables into M * N variables, further increasing nonlinearity and improving model capability.

Random Forest improves upon decision tree algorithms by generating a forest of classification trees. It repeatedly samples k observations from the original training set N with replacement to form new training sets, then builds k trees based on these sets. Each tree plays a role in the overall classification decision, with the final outcome being determined through a voting process. This approach helps minimize overfitting, as each tree is trained on a different subset of the data [29-31]. The randomness introduced through both row sampling (with replacement) and column sampling (selecting m features from M) prevents overfitting, eliminating the necessity

for pruning. Each decision tree is constructed until leaf nodes are either pure or unable to split further, resulting in a robust ensemble that enhances classification accuracy while reducing bias.

Decision trees create partitions in samples based on a hierarchical evaluation of attributes. While they can fit well to the training set, an overfitted model has limited utility for testing samples, necessitating branch pruning to mitigate overfitting risks. A validation set is employed to assess the tree's performance, informing which branches should be pruned. GBDT offers more nonlinear transformations and strong expressive capabilities, eliminating the need for complex feature engineering. However, it also presents drawbacks; its sequential execution is not conducive to parallel processing, leading to high computational demands, and it struggles with high-dimensional sparse features. Traditional GBDT relies solely on first-order derivative information during optimization [32]. AdaBoost's adaptability is showcased through reweighting misclassified samples from the preceding classifier, which are then used to train subsequent classifiers. A new weak classifier is introduced in each iteration until an acceptable error rate is reached or a predetermined iteration limit is met.

In this study, the training process for a Neural Network (NN) is iterative, where initial weights are randomly assigned. Each iteration sees input samples processed through neurons, weighted by existing connections, and passed through an activation function, progressing layer by layer until the final output is produced. This output is compared to the target, and the cost is calculated, prompting adjustments to weights throughout the network to minimize cost. This iterative process continues until convergence.

The dataset's limited size, featuring only 8 variables, constrains the effectiveness of neural networks, heightening the risk of overfitting and limiting the potential for high-dimensional feature interactions. The time investment required for model structuring and training parameter selection is also considerable given the small dataset [33]. Conversely, tree-based models are well-suited for smaller datasets, focusing on manual identification of significant features. While boosting algorithms excel with tabular data, deep learning techniques perform better with larger, non-tabular datasets [34]. Deep learning is adept at automatically generating hidden features for complex data, but it is generally less efficient than gradient boosting trees. Although deep learning can surpass gradient boosting in tabular contexts, it requires substantial time for network tuning. In instances where tabular data lacks discernible patterns, neural networks may necessitate inefficient fully connected architectures, making traditional machine learning models and specialized networks like Deep FM (Deep Factorization Machine) more pragmatic choices [35].

This study acknowledges certain limitations that should be addressed in future research to enhance model performance and predictive accuracy. The primary limitation is the insufficient sample size, which impacts the efficacy of current machine learning models. The dataset of 30,000 instances with 8 feature variables is relatively small and affects the accuracy of the findings. Additionally, due to limited data sources and patient privacy considerations, existing publicly available datasets often lack comprehensive updates and adequate sample sizes [36]. Future studies should seek to expand data resources by exploring alternative datasets, including variables related to family history of diabetes or lifestyle factors as illustrated in Figure 8.

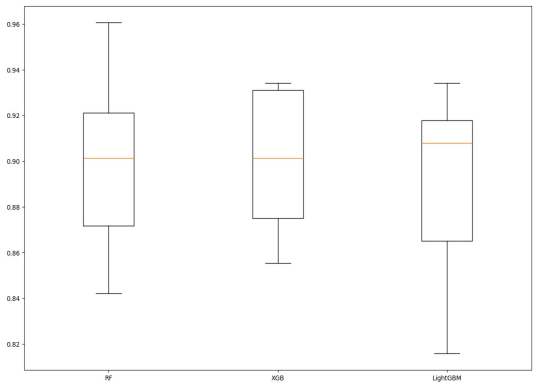

Figure 8: Contrasting Algorithms

IV. CONCLUSION

Diabetes remains a critical health concern, and this study highlights the significance of using XGBoost for diabetes prediction. By performing data preprocessing and visualization on the dataset utilized in this

experiment, and optimizing hyperparameters using Grid Search, we compared the performance of XGBoost with six other models. XGBoost consistently outperformed other models, attaining an accuracy of 98%, a precision of 95%, and a recall of 99%. This research underscores the clinical utility of XGBoost for effectively diagnosing diabetes mellitus, providing valuable support for healthcare professionals in patient assessments.

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