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Posted Date: 6 May 2025

doi: [10.20944/preprints202505.0135.v1](https://doi.org/10.20944/preprints202505.0135.v1)

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Article

Machine Learning and Deep Learning Approaches for Predicting Diabetes Progression: A Comparative Analysis

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Abstract: The global burden of diabetes mellitus (DM) continues to escalate, posing significant challenges to healthcare systems worldwide. This study compares machine learning (ML) and deep learning (DL) methods and their ensembles for predicting the health outcomes of diabetic patients. This work aims to find the best solutions that strike a compromise between computational economy and good prediction accuracy. The study systematically assessed a range of predictive models, including sophisticated DL techniques and conventional ML algorithms, based on computational efficiency and performance indicators. The study assessed prediction accuracy, processing speed, scalability and resource consumption, and interpretability using publicly accessible diabetes datasets. It methodically evaluates the selected models using key performance indicators (KPIs), training times, and memory usage. DT achieved the highest F1-score of 0.98, indicating excellent overall performance in balancing precision and recall. However, the RF model demonstrated higher accuracy on the hospital dataset. The results highlight how lightweight, interpretable ML models work in resource-constrained environments and for real-time health analytics. The study also compares its results with existing prediction models, confirming the benefits of selected ML approaches in enhancing diabetes-related medical outcomes. This study is substantial for practical implementation, providing a reliable and efficient framework for automated diabetes prediction to support proactive disease management techniques and tailored treatment.

Keywords: deep learning; diabetes mellitus; diabetes prediction; healthcare management outcomes; machine learning; performance indicators

1. Introduction

The hallmark of diabetes mellitus (DM), a chronic metabolic disease, is persistent hyperglycemia brought on by either decreased insulin action, insulin secretion, or both. Diabetes mellitus has become a pandemic in prevalence, impacting millions of people globally and dramatically raising morbidity, death, and medical costs of patients. For DM to be effectively managed, major complications like retinopathy, neuropathy, and cardiovascular diseases need to be avoided, and healthcare costs be significantly reduced. Accurate prediction and early diagnosis of diabetes and its related health outcomes are crucial [1,2]. Machine learning (ML) and deep learning (DL) techniques are now essential for delivering predictive insights, facilitating individualized patient care, and supporting clinical decision-making processes with high precision due to improvements in processing power and data availability [3–5]. Obesity, changes in lifestyle, and genetic susceptibility have all been implicated in the sharp rise in diabetes incidence. Diabetes can cause serious consequences, such as renal failure, neuropathy, and cardiovascular disorders if it is not treated or is not adequately controlled [6,7].

International Diabetes Foundation (IDF) has reported the rapid rise of people with diabetes aged 18 to 79 years from 4.7% to 8.5% within three decades from 1980 to 2015. The prevalence in 2019 increased to an estimated percentage of 9.3% (463 million) and is projected to rise to 10.2% (578

million) by 2030 and 10.9% (700 million) by 2045 respectively [2,8]. This indicates a serious problem for both developed and developing countries. China, India, and the United States of America are the most impacted nations, although this rise is unevenly spread, with estimates of 143% in Africa (undiagnosed cases) and 15% in Europe [8].

Early identification and precise diabetes prediction are essential for prompt management and better patient outcomes, given the disease's increasing cost on healthcare systems [9–11]. Wearable technology combined with powerful ML and DL algorithms has enabled real-time glucose monitoring and insulin adjustment, significantly enhancing patients' liberation and lifestyle [12]. Recent research has proven that ML and DL techniques have evolved in this area. These case studies demonstrate industry advancements while laying the groundwork for future advancements [13]. DL-based prediction models have also revealed remarkable accuracy in detecting early signs and progressions of DM-related issues, such as retinopathy, neuropathy, and nephropathy.

On the other hand, healthcare systems are designed to improve sickness detection and diagnosis while simultaneously providing patients with the essentials for optimum health [13,14]. Concerns over the quality of care offered by the healthcare system and the availability of treatment resources are common among patients [15]. Most people who would immediately benefit from better healthcare systems are those who have serious illnesses, including diabetes, hypertension, and irregular blood sugar levels [16]. A healthy society must prioritize health and healthcare. Hence, it is imperative to use state-of-the-art techniques to track the development of diabetes. Encouraging a healthy population and reducing the risk of illnesses like diabetes in future generations enables the development of novel techniques or hybrids that may be used in healthcare systems to improve the quality of life [17–20].

With their automated, data-driven insights that can improve clinical decision-making, ML and DL models have become potent medical diagnosis and prediction technologies [21,22]. While DL models like convolutional neural networks (CNNs) and recurrent neural networks (RNNs) offer sophisticated feature extraction capabilities, a variety of ML models, such as decision trees (DT), random forest (RF), logistic regression (LR), and support vector machines (SVM), have been extensively utilized for diabetes prediction. Research is ongoing to determine how well these models perform in comparison regarding accuracy, dependability, and computing economy.

This study focuses on two main research topics. The first centres around the differences in accuracy and reliability of ML and DL models in predicting diabetic patient outcomes across various healthcare settings. The second one compares ML, DL, and ensemble models regarding processing time and computational efficiency when applied to selected datasets for diabetes mellitus personalized medicine. This demonstrate the effectiveness of various ML, DL, and ensemble models in diagnosing diabetes, tracking its progression, and evaluating performance indicators by analyzing multiple datasets and comparing different predictive models.

The rest of the paper is organized into sections as follows: Section 2 presents the review of previous related literature addressing diabetes prediction, Section 3 provides an overview of the methodology, datasets used, including data preprocessing performance metrics and the models employed in this study; Section 4 presents the results of each model, highlighting their respective metrics and time efficiency; Section 5 presents a detail discussion of the results and the comparative analysis; Section 6 provides the conclusion to the study and future direction. The paper also presents a report on the datasets used.

2. Related Works

2.1. Synopsis of Diabetes Mellitus

The term "diabetes" describes a group of metabolic disorders characterized by high blood sugar levels caused by inadequate insulin synthesis, use, or both [23]. Chronic hyperglycemia is linked to long-term damage and dysfunction of organs such as the heart, blood vessels, kidneys, eyes, and nerves [23,24]. Individuals with diabetes have varying effects based on their age, income, race, and

ethnicity. Environmental and genetic factors are catalysts for diabetes, resulting in insulin resistance and beta-cell death [25–27].

To prevent comorbidities such as cardiovascular disease, neuropathy, and retinopathy, diabetes care entails initial identification and aggressive control. Diabetes is a complicated condition with a tendency to develop silently due to lifestyle, environmental, and hereditary factors [9]. Early indicators of prediabetic diseases are often misrepresented by traditional diagnostic and treatment techniques, which can increase healthcare expenses and delayed interventions. Thus, new methods for anticipating and controlling diabetes are crucial for reducing its impact on people and enhancing positive world health outcomes [24,28]. Type 1 diabetes mellitus (T1DM), type 2 diabetes mellitus (T2DM), and gestational diabetes mellitus (GDM) are the three general forms of diabetes mellitus [29]. The hallmark of T1DM, also known as insulin-dependent diabetes, is the autoimmune destruction of the pancreatic beta-cells, which leads to insufficient insulin production. T1DM affects 5–10% of people with diabetes. Ketoacidosis, or high blood acid due to ketones, is often the initial sign of T1DM, which can develop slowly in adults or swiftly in children. It is one of the irreversible types. T1DM is becoming more common worldwide at a rate of 3% every year, affecting both sexes equally and leading to a sharp decline in life expectancy [29,30].

Non-insulin-dependent diabetes is another name for type 2 diabetes (T2DM). It is characterized by beta-cell malfunction and insulin resistance [29,30]. T2DM accounts for 90 to 95 percent of all diabetes cases. The body creates more insulin to compensate for the deficiency; nevertheless, beta-cell activity progressively decreases, leading to insulin insufficiency [31]. T2DM is associated with aging, obesity, sedentary lifestyles, high blood pressure, impaired lipid metabolism, and genetic factors. Ethnicity, which is more prevalent in some racial groups, is another aspect [31–33].

Pregnancy-related hyperglycemia is a common side effect of gestational diabetes mellitus (GDM) [30,34]. Despite impacting the mother and the foetus, it is frequently controllable with medicine, food, and exercise. GDM risk factors include obesity, advanced maternal age, and a history of glucose intolerance. Women with GDM have a greater lifetime risk of developing T2DM diabetes. Although there are differences in international diagnostic methods for GDM, early detection is crucial for therapy and issue prevention [35,36].

2.2. Existing Comparative Analysis of ML, DL, and Ensemble Models for DM Prediction

By extracting information from publicly available datasets and comparing various ML, DL and ensemble techniques for improved health outcomes based on accuracy, F1-score and computation time, a few researchers have made substantial contributions to the study of DM prognosis, progression, and therapy. On this wise, the scope of this study is primarily to perform a comparative analysis of several ML, DL, and ensemble models to predict the diabetic health outcomes of patients using different datasets. The comparative process would focus on the differences in accuracy, F1-score, and reliability between ML and DL models in predicting diabetic patient outcomes across various healthcare settings, as well as comparing these models and their ensembles regarding processing time and computational efficiency.

Firstly, Mahajan et al. [37] uses 16 datasets from the UCI Machine Learning Repository and Kaggle to provide a thorough comparative analysis of 15 ensemble ML approaches for illness prediction. Heart disease, liver problems, diabetes, renal disease, and skin cancer are the five main chronic illnesses that are the subject of this study. The authors evaluated the performance of various bagging, boosting, and stacking ensemble variations using various measures, including accuracy, precision, recall, F1 score, AUC, and AUPRC.

To guarantee strong model performance, datasets are subjected to thorough preparation as part of the technique, which includes data cleaning, normalization, and hyperparameter tuning. According to experimental data, stacking techniques consistently performed better than alternative ensemble approaches, especially multi-level and classical stacking. Regarding accuracy and AUC, stacking variants performed the best across all datasets with the highest frequency, whereas Logit Boost performed the worst. The results show that ensemble learning (stacking) can greatly improve

prediction accuracy in illness detection by utilising the advantages of several classifiers. Researchers and practitioners may use this work's valuable insights to help choose the best ensemble methodologies for creating accurate and dependable illness prediction systems, eventually enhancing patient outcomes in healthcare settings.

To predict early-stage diabetes, Flores et al. [38] compares various ML approaches, highlighting the need for early detection for efficient disease treatment. To decrease dimensionality and eliminate less important qualities, the study initially uses a relief-based feature selection approach on a dataset of clinical and demographic characteristics gathered from diabetes patients in Bangladesh. Improving the prediction models' accuracy and efficiency requires this preprocessing step. The study looks at three main classifiers: Support Vector Machines (SVM), Random Forest (RF), and Neural Networks (NN). The models are assessed using a 10-fold cross-validation method to ensure reliable performance evaluation on unseen data. Performance indicators, including recall, specificity, accuracy, and precision were computed for every classifier. According to their results, the RF model performs better than the other models, attaining a 98.5% accuracy rate and greater precision, recall, and specificity. On the other hand, the prediction performance of NN and SVM models is slightly worse. The authors demonstrate how ensemble learning techniques, particularly RF, may manage complex feature interactions and non-linear connections in medical data. It also emphasizes how crucial thorough validation procedures and efficient feature selection are to creating trustworthy diagnostic tools. To improve early-stage diabetes prediction further, the authors suggest more study using hybrid models and larger datasets.

Using the PIMA Indian Diabetes Dataset (PIDD), Gupta et al. [39] compares the effectiveness of DL and quantum ML (QML) for diabetes prediction. The study offers two prognostic models to help doctors deal with the growing worldwide burden of diabetes. Several data preparations were performed to improve model performance, such as normalization, missing value imputation, and outlier rejection. The QML model uses a variational quantum circuit with adjustable hyperparameters, whilst the DL model is built as a multilayer perceptron with four hidden layers and optimized via root mean square propagation (RMSprop). By obtaining a precision of 0.90, accuracy of 0.95, and an F1 score of 0.93, as opposed to lower values for the QML model, the DL model surpasses the QML model, according to a thorough evaluation utilizing metrics including precision, accuracy, recall, F1 score, and diagnostic odds ratio. The results indicate that the DL approach presently provides better performance for diabetes prediction, even with the promising elements of quantum approaches.

Using the PIMA Indian Diabetes dataset, eight ML classifiers were compared for early diabetes prediction. To assess how well they predict diabetes, Aggarwal et al. [40] used Logistic Regression, Decision Tree, AdaBoost, Gradient Boosting, K-Nearest Neighbours (KNN), RF, SVM, and Naive Bayes (NB). Their study uses assessment criteria, including accuracy, confusion matrix, and F1 score, to describe the technique and performance of each classifier. Notably, the outcomes show that the NB model attains the maximum accuracy out of the methods evaluated. A thorough history of diabetes is also given in the article, along with an explanation of its many forms and related consequences and the need for early detection. To enable better clinical decision-making and patient care, the study compares these various ML techniques to determine the best effective algorithm for diabetes prediction. The results offer insightful information on medical diagnostics and ML applications in the healthcare industry.

Comparing DL and ML techniques for early-stage diabetes prediction, a benchmark UCI diabetes dataset with 16 features from 520 patients, implanting 416 training and 104 testing sets, respectively, were used by Refat et al. [41]. Performance criteria, including accuracy, recall, F1-score, ROC-AUC, and execution time were used to assess a variety of classifiers, including Extreme Gradient Boosting (XGBoost), Decision Tree (DT), RF, SVM, Multi-layer Perceptron (MLP), and Logistic Regression (LR). According to experimental data, the authors concluded that the XGBoost classifier performs better than other models, with a testing accuracy of 99.0% and training accuracy of 99.99%. The significance of preprocessing procedures and feature selection for enhancing diagnostic

accuracy are emphasized in this study. Despite encouraging results, the study admits limitations because of the small dataset size and recommends that future research concentrate on obtaining larger datasets and investigating new predicting markers for improved early diabetes identification.

Swathy & Saruladha [42] delivered a thorough comparison of several categorization and prediction methods for cardiovascular diseases (CVD), one of the comorbidities of DM, using various ML and DL approaches. The authors highlight the importance of early identification to enhance clinical outcomes, acknowledging CVD as a primary cause of death. The study divides methods into three main categories: DL models for CVD prediction, conventional ML models, and data mining and classification strategies. Along with sophisticated DL frameworks like convolutional neural networks (CNN) and recurrent neural networks (RNN), it examines a few ML techniques, including DR, NB, SVM, RF and neural networks (NN). Performance criteria such as accuracy, precision, recall, F1-score, ROC-AUC, and execution time are used to evaluate various approaches. The datasets and tools used (e.g., WEKA, TANGARA, MATLAB) are also considered. According to their results, a hybrid strategy that combines many methods might improve prediction accuracy and help doctors make decisions. The study highlights the promise for individualized healthcare solutions through enhanced model integration and real-time data analysis while discussing its limits and future research approaches.

The crucial problems of diabetes prediction utilizing ML and DL approaches are addressed in the studies of Fregoso-Aparicio et al. [43] and Butt et al. [5]. Fregoso-Aparicio et al. in their study compared 18 distinct model types in a comprehensive analysis of 90 papers on T2DM diabetes prediction. Their analysis shows that while deep neural networks (DNN) can handle large and dirty datasets, they were suboptimal in several cases. In contrast, like RF, tree-based algorithms typically perform better, with high accuracy and near-perfect AUC scores. According to the review, data balance and rigorous feature engineering are crucial for model efficiency and interpretability, which also emphasized problems with study heterogeneity and opaque feature selection. In a related study, Butt et al. integrated an Internet of Things-based monitoring system for real-time blood glucose tracking with a useful ML-based framework for diabetes categorization and prediction. Their work employed long short-term memory (LSTM), moving averages, and LR for predictive analysis and evaluated classifiers such as RF, LR, and MLP for diabetes classification using the benchmark PIMA Indian Diabetes dataset. The results of their experimental assessment demonstrated the applicability of the suggested technique in healthcare applications, with the MLP classifier and LSTM predictor achieving accuracies of 86.08% and 87.26%, respectively [5].

Uddin et al. [44] compares several supervised ML methods for disease prediction. Their study finds important trends in algorithm performance, utilization, and illness prediction accuracy by examining 48 research publications. SVM was the most used algorithm among the methods studied, appearing in 29 papers. Other algorithms included RF, Artificial Neural Networks (ANN), DT, K-Nearest Neighbours (KNN), LR, and NB. Nonetheless, RF continuously showed better accuracy, coming in first in 53% of experiments that used it and second in 41% of those that used SVM. The authors emphasize how data type, dataset size, and validation techniques frequently influence algorithm selection. Their study highlights how RF's ensemble nature makes it resilient, although SVM did well on various datasets. According to their results, future medical informatics research should use RF and SVM for reliable illness prediction, considering algorithm-specific benefits to enhance clinical judgment and patient outcomes.

Advanced ML techniques for estimating the risk of cardiovascular disease (CVD), a chronic consequence of T2DM) were compared by Zarkogianni et al. [9]. Their study looks at Self-Organizing Maps (SOMs) and Hybrid Wavelet Neural Networks (HWNNs), using ensemble approaches to tackle the problem of imbalanced datasets. Using clinical data from 560 T2DM patients over a five-year follow-up, the authors assessed their models, considering various risk variables, including age, BMI, cholesterol, glycosylated hemoglobin, smoking status, hypertension, and medication use. With an Area Under the Curve (AUC) of 71.48%, ensemble approaches considerably improved predicted accuracy when compared to conventional statistical techniques like Binomial Linear Regression

(BLR). The hybrid ensemble, which combined HWNN and SOM outputs using intricate voting procedures, performed better than the others, highlighting the advantages of intricate, data-driven models over traditional regression techniques. The suggested ML architecture enhances risk prediction for diabetes-related cardiovascular problems, providing doctors with a valuable decision-support tool despite the study's acknowledgement of limitations pertaining to dataset size and complexity.

In addition, several other studies conducted analysis on diabetes prediction. Studies such as Naz and Ahuja [45], Hasan et al. [46], Ayon and Islam [4], Sahoo et al. [47], Lai et al. [48] and Dagliati et al. [25], all outlined the importance of ML and DL models in predicting DM. These evaluated papers investigate ML and cutting-edge DL methods to improve early diagnosis and diabetes prediction accuracies.

Using classifiers like RF, AdaBoost, NB, XGBoost, and MLP, Hasan et al. [46] created an ensemble framework. By addressing important issues, including missing data and controlling outliers, the authors achieved a 95% AUC with better sensitivity and specificity than conventional techniques. The effectiveness of integrating many ML approaches for reliable diabetes predictions was demonstrated by the ensemble approach's considerable outperformance over individual models. Ayon and Islam [4], on the other hand used the PIMA dataset to present a DNN-based diabetes prediction algorithm. Their DL model outperformed more conventional ML techniques, including LR, KN, and SVM, exhibiting remarkable accuracy (98.35%) and great sensitivity. This demonstrates how DL models can manage intricate, nonlinear relationships in clinical data, improving the prediction accuracy of diabetes diagnosis.

Using the same PIMA dataset, Naz and Ahuja [45] similarly used DL and other ML methods, such as ANN, DT, and NB, reporting accuracy rates as high as 98.07%. Their findings support the promise of deep learning for early diabetes diagnosis and better prognostic tools by confirming its capacity to extract predictive patterns from medical datasets.

Lai et al. [48] used LR and gradient boosting machines (GBM) to propose predictive models that were specially created for the Canadian population. Their GBM model outperformed other approaches like RF and DT with an AROC of 84.7% using demographic and clinical factors, including fasting glucose, BMI, HDL, and triglycerides. This shows that GBM may provide good predictive performance with standard clinical laboratory data, making it easier for early diabetes identification in clinical settings.

Further study that showed how the ML technique, namely LR, may be used to predict diabetic sequelae such as retinopathy, neuropathy, and nephropathy was conducted by Dagliati et al. [25]. Their data mining pipeline successfully managed missing data and class imbalance using electronic health records, resulting in up to 83.8% prediction accuracies. Their work demonstrates how ML models can be used to produce better management for diabetic complications by identifying high-risk individuals early and enhancing clinical decision-making.

Additionally, Sahoo et al. [47] carried out a comparison analysis using a Convolutional Neural Network (CNN) and several ML techniques for health-related decision-making. Their results demonstrated DL's strength in handling complicated and high-dimensional healthcare datasets, confirming the superiority of DL-based CNN methods over conventional ML techniques regarding prediction accuracy.

All these research shows that conventional ML techniques, deep learning frameworks and sophisticated ensemble methods show increased prediction accuracy in diabetes diagnosis and progression. As crucial elements of successful diabetes prediction models, they stress the significance of appropriate data preparation, including managing missing values and class imbalance. Using these innovative techniques to use ordinary clinical data, medical practitioners may efficiently apply automated, accurate, and timely diabetes prediction, improving patient outcomes through proactive disease management.

Therefore, this study will be conducting a comparative analysis of various ML and DL models and many ensembles to determine the differences in accuracy and reliability between ML and DL

models in predicting diabetic patient outcomes across various healthcare settings. This study will compare ML, DL, and ensemble models in terms of their processing time and computational efficiency when applied to selected datasets for diabetes mellitus personalized medicine. This study employs five different datasets and will implement outlier removal, missing values, and comparative analysis using each model's accuracy and the F1 score and their ensembles as a baseline. As such, this gives our study a robust approach to comparing the processing time and computational efficiency of such selected models regarding diabetes prediction in the existing literature.

As such, the following ML and DL models would be considered as their ensembles. They are LR, NB, DT, RF, SVM, KNN, XGBoost, Adaptive Boosting (AdaBoost), CNN, DNN, Recursive Neural Network (RNN), LSTM, Autoencoders and Fated Recurrent Unit (GRU) – a variant of RNN. Performance metrics such as accuracy, precision, recall,

F1-score, Area Under the Receiver Operating Characteristic Curve (AU-ROC), and confusion matrix will be applied. In contrast, the computation time of the model's performance would be computed.

3. Materials and Methods

An extensive summary of the techniques and algorithms used in this study is presented in this section. Its primary goals are to define the methods used and provide a succinct description of how they operate. It is separated into different sections: (i.) sampling techniques for dataset imbalance, (ii.) ML and DL employed where each model provides an overview of the basic ideas behind the techniques, guaranteeing that their function in the research is understood, (iii.) Performance metrics used, (iv.) Datasets, and finally (v.) Preprocessing.

3.1. Sampling Techniques for Datasets Imbalance

3.1.1. Oversampling Techniques

1. Synthetic Minority Oversampling Techniques (SMOTE): By creating artificial samples for the minority class, SMOTE is a synthetic minority oversampling technique that balances class distribution [49,50]. Rather than simply duplicating existing minority class samples, SMOTE interpolates between them to create new instances, selecting k nearest neighbours for each minority class observation and creating synthetic points along the line segments connecting them, with a random interpolation factor between 0 and 1 to ensure diversity [51]. SMOTE is represented as:

$$S = \{x_i \mid x_i \in \mathbb{R}^n, i = 1, 2, \dots, N\} \quad (1)$$

where x_i = i^{th} minority instances, n = No. of features (dimensions) and N = number of minority class instances.

The k nearest neighbours of x_i based on a distance metric (usually Euclidean distance) denoting the set of these neighbours as:

$$NN(x_i) = \{x_j \mid x_j \in S, j \neq i\} \quad (2)$$

where x_j = k -nearest neighbours of x_i . Finally, it creates a new synthetic sample x_{new} by randomly choosing a neighbour $x_j \in NN(x_i)$ and then generate the x_{new} through interpolation between x_i and x_j

$$x_{new} = x_i + \alpha \cdot (x_j - x_i) \quad (3)$$

where α is the random scalar randomly drawn from the uniform distribution between 0 and 1 i.e. $U(0,1)$. These steps continue until the desired amount of synthetic minority samples has been created.

2. SMOTE and Edited Nearest Neighbours (SMOTE-ENN): To improve the data quality, this method combines SMOTE with Edited Nearest Neighbours (ENN). To balance the dataset, SMOTE first creates artificial minority samples. Then, the noisy cases, synthetic and original,

where most of their nearest neighbours are in the opposite class, are eliminated using ENN [50,52]. By removing incorrectly categorized or unclear samples, this two-step procedure guarantees more precise decision limits and improves generalization in classification tasks.

3. Random Oversampling: To rectify class imbalance, minority class samples are replicated at random until the required balance is reached. This approach, in contrast to SMOTE, replicates current observations without producing artificial data. Although efficient and straightforward, it risks the danger of overfitting if the same data are used too frequently. Subsets of minority cases can be resampled using replacement to lower this risk and guarantee variety in the enhanced dataset [53].
4. Adaptive Synthetic Sampling (ADASYN): As an adaptive extension of SMOTE, ADASYN focuses on complex minority class samples. Minority occurrences that are close to the decision border or encircled by majority class samples are given greater weights by ADASYN [54]. For these "hard-to-learn" situations, more synthetic data is produced, directing the classifier's focus to unclear areas [51,54]. By decreasing bias and fine-tuning the decision boundary in unbalanced datasets, this adaptability increases model resilience. Mathematically, it is represented in this regard:

$$\text{Minority Dataset} = S_{min} = \{x_i \mid x_i \in \mathbb{R}^n, i = 1, 2, \dots, N_{min}\} \quad (4)$$

and

$$\text{Majority Dataset} = S_{maj} = \{y_i \mid y_i \in \mathbb{R}^n, j = 1, 2, \dots, N_{maj}\} \quad (5)$$

K nearest neighbours computation for majority class for each minority samples x_i is given as:

$$\hat{r}_i = \frac{\text{Number of Majority class Neighbours of } x_i}{K}, \quad i = 1, 2, \dots, N_{min} \quad (6)$$

where if $\hat{r} \approx 0$, x_i is easy to classify but if $\hat{r} \approx 1$, x_i is difficult to classify and hence requires more synthetic samples. Normalized density distribution for each minority sample (difficult scores)

$$\hat{r}_i = \frac{r_i}{\sum_{j=1}^{N_{min}} r_j}, \quad i = 1, 2, \dots, N_{min} \quad (7)$$

where the distribution \hat{r}_i represents the importance of each minority sample in oversampling. The method then computes how many synthetics to generate from each minority sample as:

$$g_i = \hat{r}_i \times G, \quad i = 1, 2, \dots, N_{min} \quad (8)$$

where g_i can be rounded to the nearest integer. Therefore, for each minority sample x_i , it then generates g_i synthetic samples by randomly selecting a minority-class neighbour x_{zi} from the K -nearest neighbours of x_i belonging to minority class and then generate the synthetic samples x_{new}

$$x_{new} = x_i + \alpha \cdot (x_{zi} - x_i), \quad \alpha \sim U(0,1) \quad (9)$$

This process continues g_i times for each minority sample x_i

2.1.1. Undersampling Techniques

1. Random Undersampling: Most class samples are randomly discarded to balance the dataset. Despite being computationally efficient, this approach may increase model variance by eliminating useful cases [55,56].
2. Clustering Centroids: Swapping out clusters for corresponding centroids lowers the number of majority class samples. Groups of majority occurrences are compressed into a single representative point using K-means clustering [55].
3. Random Undersampling with Tomek Links: Firstly, random undersampling is used to lower the size of the majority class. Next, it eliminates Tomek Links, which are pairings of instances of the

opposite class nearest to each other. It then lowers noise and clarifies the decision boundary by eliminating the majority of samples from these pairings. This hybrid strategy compromises increased classifier performance and efficiency [55].

4. NearMiss-3: This method chooses samples from the majority class according to how far away they are from minority cases. It finds each minority observation's M nearest neighbours in its first phase. Next, it eliminates duplicate or overlapping locations by keeping most samples with the most significant average distance to these neighbours. This method improves class separability by prioritising the majority instances farthest from the minority class [55,57].
5. One-Sided Selection (OSS): This method prunes superfluous majority samples by combining Condensed Nearest Neighbour (CNN) and Tomek Links elimination. First, questionable situations are removed from Tomek Links. CNN then keeps a small subset of majority instances that faithfully capture the initial distribution. By ensuring a small but representative majority class, this two-step procedure improves the accuracy and efficiency of the model [55].
6. Neighbourhood Cleaning: This method improves undersampling by eliminating the noisy majority of samples. It detects and removes misclassified majority cases using a k-NN classifier. While maintaining essential data structures, this focused cleaning lessens class overlap. For best effects, it is frequently used with other undersampling techniques [55].

3.2. Machine Learning and Deep Learning Techniques employed

3.2.1. Machine Learning Models

ML approaches are a subfield of artificial intelligence (AI) that enables computers to recognize patterns in data, learn from them, and respond to them with little to no human intervention. These techniques, which have distinct applications in various organizations, can be divided into three main categories: supervised learning (classification and regression models dealing with labelled datasets), unsupervised learning (clustering and dimensionality reduction processes dealing with unlabelled datasets), and reinforcement learning.

1. Logistic Regression (LR): LR is an ML and statistics algorithm for binary classification tasks. The sigmoid (logistic) function, which converts real-valued inputs to a range between 0 and 1, describes the connection between input data and the likelihood of a class label. Using methods such as Gradient Descent, the log-likelihood function is optimized to train the model. It assumes that the log odds of the dependent and independent variables have a linear relationship [58,59].
2. Naïve Bayes (NB): Based on the Bayes theorem, the Naïve Bayes algorithm is a probabilistic classification algorithm that assumes all features are conditionally independent, given the class label. Despite this high independence assumption, It works effectively in various real-world applications, including spam filtering and text categorization. It uses observed data and past knowledge to determine a class's posterior probability [59–61].
3. Decision Trees (DT): This supervised learning system iteratively divides data into subsets according to feature requirements to generate predictions. It is composed of leaves (final predictions), branches (outcomes), and nodes (decision points). Mean Squared Error (MSE) for regression and Gini Index or Entropy (Information Gain) for classification serve as the foundation for the splitting criterion. To minimize impurity until a stopping condition is satisfied, the tree develops by choosing the best feature at each stage [61].
4. Random Forest (RF): This ensemble learning system builds many DTs during training and aggregates their results to provide more accurate predictions. To minimize overfitting and

enhance generalization, each tree is trained on a randomly sampled fraction of the data (bagging) and employs a randomly chosen subset of features at each split. Either majority voting (classification) or average (regression) over all trees determines the final prediction. RF delivers feature relevance ratings, is noise-resistant, and can handle numerical and categorical data [10,16,59,62].

5. Support Vector Machine (SVM): This supervised learning technique determines the best hyperplane to divide data points by maximising the gap between classes. The most important data points defining the decision boundary are support vectors, which are what it depends on. SVM uses kernel functions (such as linear, polynomial, and Radial Basis Functions – RBF) to translate data that is not linearly separable into a higher-dimensional space where separation is possible. It works well with high-dimensional [10,16,59,63].
6. K-Nearest Neighbours (KNN): Data points are categorized using this instance-based, non-parametric learning approach according to the majority class of their k -closest neighbours. The Euclidean, Manhattan, or Minkowski distances are commonly used to quantify the separation between two points. Because KNN does not require explicit training, it is computationally cheap while training but costly when inferring because it needs to store and search the full dataset. The amount of k impacts model performance; small values may result in overfitting, while high values may result in underfitting [16,64–66].
7. Extreme Gradient Boosting (XGBoost): XGBoost is a sophisticated gradient boosting method that has been fine-tuned for accuracy and efficiency. It approximates the loss function using a second-order Taylor expansion to provide more accurate updates during training. Through cache-aware access patterns, histogram-based split discovery, and parallelized execution, the approach enhances computing performance. L1 (alpha) and L2 (lambda) penalties are two regularization strategies that assist in reducing overfitting and managing model complexity. To improve generalization, XGBoost further uses column subsampling and shrinkage (learning rate tuning) [10,16,62,63].
8. Adaptive Boosting (AdaBoost): An ensemble learning method builds a robust classifier by combining several weak learners, usually decision stumps. Iteratively, it forces weaker learners to concentrate on more challenging examples by giving misclassified samples larger weights. All weak classifiers cast a weighted majority vote to determine the final prediction. AdaBoost dynamically modifies sample importance to enhance model performance and minimizes an exponential loss function [16,59].

3.2.2. Deep Learning Models

Multiple hidden layers in DL models, which are sophisticated artificial neural networks (ANN), allow them to extract intricate and nonlinear patterns from big datasets. Because they can automatically extract hierarchical feature representations without requiring much manual engineering, they perform very well in fields including image recognition, natural language processing (NLP), speech recognition, and healthcare diagnostics. Substantial data and processing power are needed for these models to function at their best.

1. Convolutional Neural Networks (CNN): CNNs are DL models that manage grid-like data, including time series and pictures. It comprises fully connected layers that carry out classification or regression, pooling layers that lower dimensionality while preserving important information, and convolutional layers that use filters to identify spatial characteristics. CNNs extract features well because they use weight sharing and

local connection. Activation functions like Rectified Linear Unit (ReLU) introduce non-linearity, which improves learning. Achieving the best performance requires careful architectural design consideration, including the number of layers, filter sizes, and pooling algorithms [16,67,68].

2. Deep Neural Networks (DNN): There are hidden layers between the input and output layers of this kind of ANN. The DNN model can learn intricate patterns because each layer comprises linked neurons with nonlinear activation functions. Backpropagation and optimization algorithms such as Adam or Stochastic Gradient Descent (SGD) are used for training. DNNs are very good at tasks like image recognition, NLP, and time-series forecasting because of their superiority in feature extraction and representation learning. Overfitting may be avoided, and generalization can be enhanced via regularization techniques like batch normalization and dropout [5,14,69]
3. Recurrent Neural Networks (RNN): RNN is a kind of NN that uses hidden states to retain a memory of prior inputs to interpret sequential data. RNNs can capture temporal dependencies because, in contrast to feedforward networks, they exchange parameters across time steps. They are often employed in applications like NLP, time-series forecasting, and speech recognition. However, learning long-term dependencies is challenging for ordinary RNNs due to issues like disappearing and exploding gradients [16].
4. Long Short-Term Memory (LSTM): Long-term relationships in sequential data can be captured efficiently by this sophisticated RNN. The vanishing gradient issue is solved by adding the forget gate, input gate, and output gate, which control the information flow. Because of these gates, LSTMs may selectively keep or reject data, which makes them ideal for applications like time-series forecasting, language modelling, and speech recognition. Long-range dependencies may be learned by LSTMs without a substantial loss of information, in contrast to conventional RNNs. Gate activations and sequence durations must be tuned appropriately for best results [14,16,68].
5. Gated Recurrent Unit (GRU): It is a sophisticated RNN that deals with the vanishing gradient issue and processes sequential input. Introducing gating techniques that control information flow enables the network to save essential historical data and eliminate extraneous details. GRUs are computationally easier and perform similarly to LSTMs since they feature update and reset gates. GRUs are frequently employed in machine translation, time-series forecasting, and speech recognition applications. They are effective at identifying long-term relationships in sequences because they can adaptively regulate memory retention [16].

3.2.3. Ensemble Models

These ML and DL models integrate predictions from individual models to increase overall generalization, accuracy, and resilience. These techniques lessen variance, bias, and sensitivity to noisy data by using the diversity among individual classifiers or regressors. Boosting, stacking, and bagging are examples of common ensemble approaches. Stacking uses an extra meta-model to combine predictions from other models. By utilizing complementary capabilities, ensemble techniques sometimes outperform single models despite the possibility of higher implementation complexity and processing resources [70,71].

3.3. Performance Metrics Tools

3.3.1. Hyperparameter Tuning

Through methodical adjustment of configuration parameters that govern the learning process, hyperparameter tuning is crucial for optimizing model performance. While more sophisticated approaches like Bayesian optimization provide more effective substitutes, conventional methods like grid search and random search are frequently computationally costly. To intelligently explore the hyperparameter space, this study uses Optuna, a sophisticated optimization system that uses Tree-structured Parzen Estimators (TPE). Optuna is especially well-suited for intricate ML and DL models because of its adaptive sampling and early pruning features, drastically lowering computing expenses while guaranteeing ideal parameter selection. Faster convergence to high-performing configurations, smooth interaction with different ML frameworks, and improved reproducibility through thorough logging and visualization are benefits of utilising Optuna. Optuna is more efficient than traditional methods since it dynamically prioritizes promising trials and discards underperforming ones. This makes it the perfect option for creating reliable models with enhanced generalization powers, especially when computing resources are limited. The framework has shown to be a helpful tool for contemporary ML pipelines due to its efficacy in various applications.

3.3.2. Evaluation Metrics

To guarantee a thorough model evaluation, we examined six important classification metrics:

1. Accuracy: calculates the ratio of true predictions (both positive and negative) to all forecasts produced to get the total percentage of accurate predictions. Although accuracy seems straightforward, it might be deceptive for unbalanced datasets since it does not differentiate between different kinds of mistakes.

$$Accuracy = \frac{TP+TN}{TP+TN+FP+FN} \quad (10)$$

where TP = True Positive, TN = True Negative, FP = False Positive, and FN = False Negative.

2. Precision: determines how reliable positive predictions are by calculating the percentage of TP among all positive forecasts. This measure is crucial when FP might result in significant expenses, such as unneeded medical procedures or fraudulent notifications.

$$Precision = \frac{TP}{TP+FP} \quad (11)$$

3. Recall (Sensitivity): calculates the percentage of TP that are successfully detected, which indicates how well the model detects positive cases. In applications like illness screening or security threat identification, where it is risky to overlook positive instances, high recall is crucial.

$$Recall = \frac{TP}{TP+FN} \quad (12)$$

4. F1-Score: It combines accuracy and recall using their harmonic mean to assess model performance fairly. This is our primary assessment statistic since it evenly weights FP and FN , effectively managing class imbalance.

$$F_1 = \frac{Precision \times Recall}{Precision + Recall} \quad (13)$$

5. AUC-ROC: The model's capacity to differentiate between classes across all potential classification thresholds is assessed using the Area Under the Receiver Operating Characteristic curve. A perfect classifier obtains an AUC of 1, whereas 0.5 is obtained by random guessing.

$$AUC = \int_0^1 ROC(\tau) d\tau \quad (14)$$

where τ represents the decision threshold

6. Inference Time: This logs the time needed to produce predictions to assess the model's computational efficiency. Although it has no bearing on the statistical performance of the model, this parameter is essential for real-time applications and deployment in contexts with limited resources.

Because the F1 score offers the fairest assessment for medical diagnostics by equally considering false positives and false negatives, the results are sorted by F1 score in the tables in Section 4.

3.4. Datasets

This study examines five diabetes-related datasets from the UCI Machine Learning Repository, CDC and Kaggle. Appendix A contains information on all five datasets, including their source, number of characteristics, total instances, and positive and negative instances. To guarantee the quality and integrity of the data, preprocessing and data cleaning were done before analysis. A crucial stage in this process was normalization, which maintained all the data on the same scale and increased the precision of the findings. Recursive Feature Elimination (RFE) was used for feature selection to remove the least important feature from the dataset. To improve performance, hyperparameter tuning (using Optuna) was done for each classifier throughout the model's construction.

3.4.1. Dataset 1

This is the PIMA Indian Diabetes dataset called Dataset 1. It has 768 samples and nine features, including clinical measures and patient characteristics. The dataset features are Pregnancy, Blood Pressure, Insulin, Skin Thickness, BMI, Diabetes Pedigree-Function, Age, and Outcome. The dataset contains no duplicate entries or missing values (NaNs); all characteristics are numerical. However, several features, especially those related to blood pressure, skin thickness, insulin, glucose, and BMI, contain sundry zero values, which is biologically impossible. Section 3.3 will discuss these discrepancies and their ramifications [72–76].

3.4.2. Dataset 2

This is also PIMA Indian Diabetes dataset, henceforth referred to as Dataset 2. It also has numerical characteristics about clinical measures and patient demographics and is structured similarly to Dataset 1. However, it is much larger with 2000 samples rather than 768 but 9 features.

3.4.3. Dataset 3

This is an annual Behavioral Risk Factor Surveillance System (BRFSS) dataset captured by the Center for Disease Control (CDC). This dataset is for the year 2015. Henceforth, the dataset would be known as Dataset 3. The target variable has three classes (0, 1, 2). 0 is for no diabetes or only during pregnancy, 1 is for prediabetes, and 2 is for diabetes. There is a class imbalance in the dataset, but it has 21 features and 253,680 samples [77]

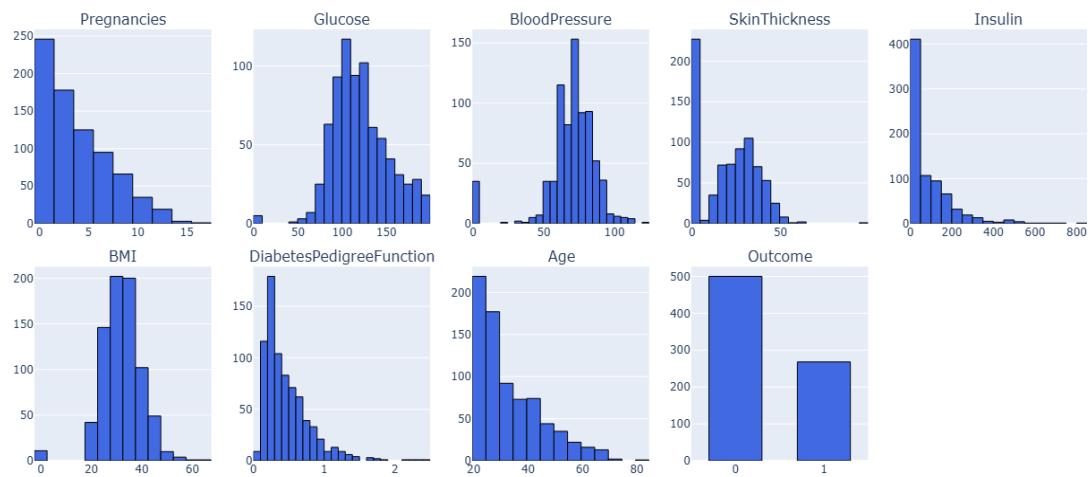


Figure 1. Feature Distribution for Dataset 1 and Dataset 2 (PIMA dataset).

3.4.4. Dataset 4

This variant of Dataset 3 consists of 253,680 samples and 21 features of the BRFSS dataset captured by CDC for 2015. Here, the target consists of two classes (0, 1). 0 is for no diabetes, and 1 is for prediabetes or diabetes. It also contains class imbalance and would be known as Dataset 4 in this study.

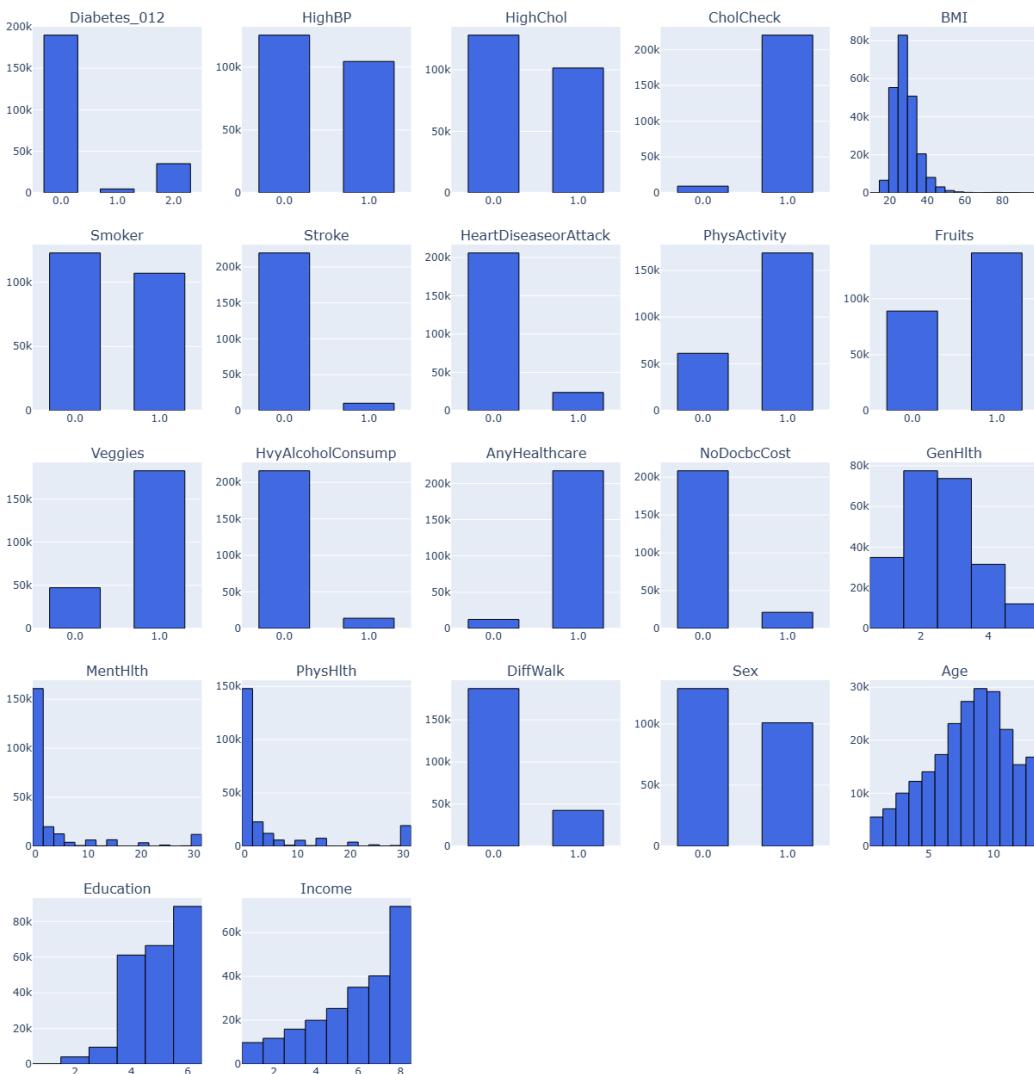
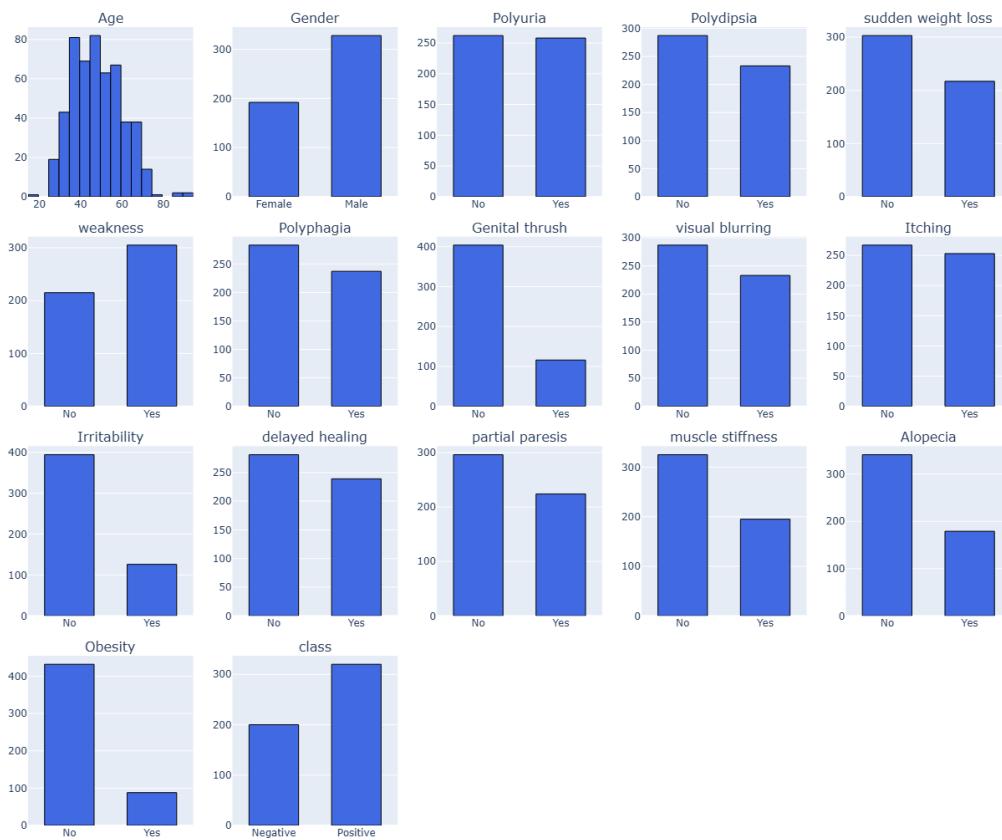


Figure 2. Feature Distribution for Dataset 3 and Dataset 4 (BRFSS_2015 dataset).

3.4.5. Dataset 5

The early-stage diabetes risk prediction of patients from Sylhet Diabetes Hospital, Bangladesh, were captured in this dataset. Direct surveys from the patients were used in the study [78]. This dataset report includes 520 people with diabetes-related symptoms and information on people who may have diabetes-related symptoms. The dataset has 520 cases and 17 features, including the target class. A certified physician from Sylhet Diabetes Hospital verified the dataset, collected in 2020. The dataset, which includes several categorical (Yes/No) variables associated with diabetes diagnosis, is displayed in Appendix A. The "Class" property indicates the patient's diabetes status as either positive (1) or negative (2). The values of 1 (yes) or 2 (no) for each feature indicate whether the associated symptom or condition is present. However, there are four categories for the "Age" attribute: 1 for those aged 20–35, 2 for those aged 36–45, 3 for those aged 46–55, 4 for those aged 56–65 and 5 for those aged above 65. These characteristics and values serve as the foundation for developing a classification algorithm that uses patient data to forecast the diagnosis of diabetes [79,80].

**Figure 3.** Feature Distribution for Dataset 5 (BRFSS_2015 dataset).

3.5. Preprocessing

Improving model accuracy and dependability through preprocessing datasets is essential in getting raw data ready for ML. Cleaning to deal with outliers and missing values, data transformation through standardization or normalization, and categorical feature conversion using one-hot encoding is usually part of it. Different dimensionality reduction techniques aid in the management of big feature collections. Sampling techniques such as SMOTE can be used to rectify class imbalance. Hence, to properly assess this study model performance, the five datasets are divided into ratio 80:20 subsets for the training and testing/validation process. In addition to lowering computing complexity

and improving the prediction ability of ML models, proper preprocessing guarantees the dataset's quality.

Performing the exploratory data analysis (EDA) of each dataset, it was observed that zero values exist in columns where they are not physiologically conceivable, which is a significant problem in both Datasets 1 and 2. Missing data may be entered as zeros instead of NaN, resulting in inaccurate numbers. Table 1 shows zero values concerning affected features under Datasets 1 and 2.

Table 1. Number of data labelled as zero values.

Feature	Dataset 1	Dataset 2
Pregnancies	111	301
Glucose	5	13
BloodPressure	35	90
SkinThickness	227	573
Insulin	374	956
BMI	11	28
DiabetesPedigreeFunction	0	0
Age	0	0

Two imputation techniques are employed to deal with the problem of zero values in columns such as BMI, Insulin, Glucose, Blood Pressure, and Skin Thickness) is biologically impossible:

1. Median Imputation: In each column, the median of non-zero values for zeros is substituted.
2. Minimum Imputation: Instead of actual measurement, the zeros may mean data was not collected.

This might indicate that the physiological levels of the patients with missing results were normal.

Consequently, we used each column's smallest non-zero value to impute missing data.

Remarkably, models trained using minimum imputation on the datasets consistently performed better than those trained with median imputation. This validates our prediction that missing data were likely connected with patients having normal measures rather than abnormal or severe results. Given that various imputation techniques can substantially influence model performance, this conclusion implies that comprehending the nature of missing data is essential in medical datasets.

The imbalance in the target variable, where one class was noticeably underrepresented, provided another difficulty for us while analyzing all datasets. From the outcome class in Table 2, Dataset 1 has 400 entries of 0(No) values and 214 entries of 1(Yes) values, while dataset 2 shows 1053 entries for a 0(No) values and 547 entries for a 1(Yes) value. The study concentrated on oversampling approaches to balance the dataset because undersampling was impractical given the already small quantity of data points. The study experimented with various oversampling techniques, such as ADASYN, SMOTE-ENN, random oversampling, and SMOTE. In overall, ADASYN produced the most significant outcomes out of all of these. ADASYN, like SMOTE, generates synthetic samples near the decision border, to improve minority class categorization. Thus, selecting the appropriate data balancing strategy is important as it impacts model performance.

Table 2. Imbalance values in the Outcome (Target) variable.

Outcome (Target class)	Dataset 1	Dataset 2	Dataset 3	Dataset 4	Dataset 5
0	400	1053	213703	218334	200
1	214	547	4631	35346	320
2	-	-	35346	-	-

Datasets 3 and 4 had considerable data points and were unbalanced, but Datasets 1 and 2 had fewer data points, as shown in Table 2. We thus used undersampling to the datasets to lessen this problem. Instead of random undersampling, we employed clustering-based undersampling on datasets 3 and 4, which maintains the underlying data distribution. Clustering-based undersampling

chooses representative samples from each cluster, guaranteeing that important patterns and class features are preserved, in contrast to conventional techniques that randomly exclude data points. It keeps crucial information from being lost despite its high computational cost.

Simple binary encoding was used to transform (encode) categorical characteristics into numerical representations to guarantee consistency across all datasets. To normalize the data and guarantee that each feature had a similar range, feature scaling was also used. This step is essential for optimising ML models because it keeps characteristics with bigger magnitudes from overpowering those with smaller values.

Because of the considerable class imbalance, where the dominant class significantly outnumbered the minority class, the experimental assessment showed that modelling Datasets 3 and 4 presented significant obstacles. As demonstrated by the models' total incapacity to detect any occurrences of the minority class, this extreme imbalance ratio made it difficult to create useful prediction models. Despite the thorough use of a variety of sampling strategies, including undersampling techniques like cluster centroids, Tomek links, and random undersampling for the majority class and oversampling techniques like SMOTE, ADASYN, and random oversampling for the minority class, the failure persisted. This is essentially based on the size of the datasets and the corresponding features.

4. Results Analysis

The results demonstrate the outcomes of a comprehensive investigation by using comparison tables, confusion matrices, density graphs and informative bar charts across all models used. Python programming language platform was used to implement all these processes. The model training procedure was systematically conducted for each model, following an encoded sequence of features. The datasets were split into training and testing groups. The training process was managed using the X_{train} and y_{train} values. The performance of the models was recorded by generating the predictions on the test datasets (X_{test}). In contrast, the efficiency of the models was accessed by evaluating their performance through metrics such as accuracy, precision, recall, F1-score, AUC-ROC, among others.

Confusion matrix and AUC-ROC visualization were also used in this study to gain detailed information on the performance of each model. This allowed for TP, TN, FP, and FN identification, while heatmaps visualization was presented to enhance the perception of performance complexities in these matrices. Graphs were used to visualize the outputs and comparisons, while the tables illustrate the values assigned to each model's performance.

4.1. Result Analysis on Dataset 1

After performing a series of analysis on Dataset 1 (PIMA – 768/9) shown in Table 3 and Figure 4, Figure 5 demonstrate the analysis results, its corresponding confusion matrix, Precision/Recall and the AUC-ROC representation. The XGBoost model performed the best on this dataset, achieving an F1 score of 0.72.

Table 3. Model Performance Comparison for Dataset 1 using F1-score as reference.

Model	Accuracy	Precision	Recall	F1 Score	AUC-ROC	Time Taken (s)
XGBoost	0.7727	0.6301	0.8519	0.7244	0.8356	0.0122
XGBoost-CNN	0.7727	0.6338	0.8333	0.7200	0.8224	4.3404
AdaBoost	0.7727	0.6338	0.8333	0.7200	0.8411	0.0091
DNN	0.7727	0.6377	0.8148	0.7154	0.8219	0.0144
RF-GRU	0.7597	0.6164	0.8333	0.7087	0.8120	9.1299
Random Forest	0.7597	0.6232	0.7963	0.6992	0.8196	0.0095
Decision Tree	0.7597	0.6308	0.7593	0.6891	0.7984	0.0167
SVM	0.7532	0.6176	0.7778	0.6885	0.8213	0.0145

KNN	0.7403	0.5946	0.8148	0.6875	0.8077	0.0147
RF-CNN	0.7597	0.6349	0.7407	0.6838	0.8120	0.0134
Logistic Regression	0.7468	0.6087	0.7778	0.6829	0.8189	0.0138
LR-MLP	0.7403	0.6029	0.7593	0.6721	0.8200	2.4844
SVM-RNN	0.7468	0.6119	0.7593	0.6777	0.8225	6.7487
XGBoost-LSTM	0.7403	0.6000	0.7778	0.6774	0.8219	11.4212
DT-CNN	0.6818	0.5275	0.8889	0.6621	0.7946	5.4317
AdaBoost-DBN	0.7013	0.5526	0.7778	0.6462	0.8004	18.8776
CNN	0.7143	0.5694	0.7593	0.6508	0.8219	0.0165
KNN-Autoencoders	0.6883	0.5417	0.7222	0.6190	0.7711	9.5224
Naive Bayes	0.6948	0.5522	0.6852	0.6116	0.7676	0.0908
RNN	0.6948	0.5522	0.6852	0.6116	0.7806	0.0110
GRU	0.6623	0.5156	0.6111	0.5593	0.7000	0.0106
LSTM	0.6688	0.5246	0.5926	0.5565	0.7013	0.0171

* All values are rounded to four decimal places.

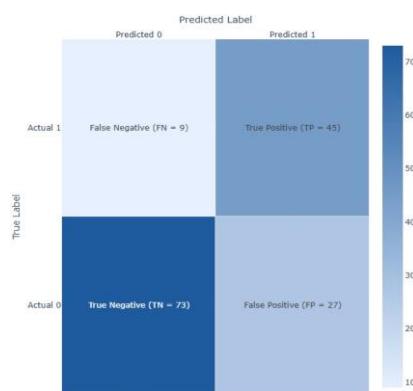


Figure 4. Confusion matrix for XGBoost model.

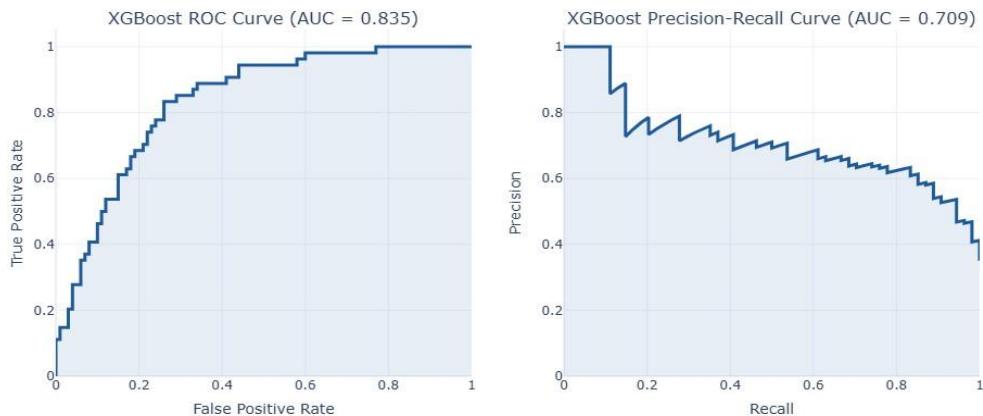


Figure 5. AUC Curves for XGBoost model. **Table 3.** Model.

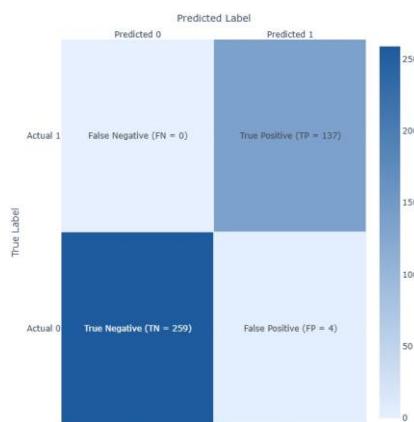
4.2. Result Analysis on Dataset 2

Performance analysis on Dataset 2 (PIMA – 2000/9) shown in Table 4 and Figures 6 and 7 demonstrate the analysis results, its corresponding confusion matrix, Precision/Recall and the AUC-ROC representation. The Decision Tree model performed the best on this dataset, achieving an F1 score of 0.98.

Table 4. Model Performance Comparison for Dataset 2 sing F1-score as reference.

Model	Accuracy	Precision	Recall	F1 Score	AUC-ROC	Time Taken (s)
Decision Tree	0.9900	0.9716	1.0000	0.9856	0.9924	0.0276
Random Forest	0.9850	0.9781	0.9781	0.9781	0.9972	0.0104
KNN	0.9850	0.9781	0.9781	0.9781	0.9942	0.0097
AdaBoost	0.9850	0.9781	0.9781	0.9781	0.9993	0.0091
RF-CNN	0.9850	0.9781	0.9781	0.9781	0.9972	0.0158
XGBoost-LSTM	0.9850	0.9781	0.9781	0.9781	0.9893	14.9132
RF-GRU	0.9850	0.9781	0.9781	0.9781	0.9958	9.6351
XGBoost-CNN	0.9850	0.9781	0.9781	0.9781	0.9888	6.3965
DT-CNN	0.9750	0.9504	0.9781	0.9640	0.9757	7.1950
SVM-RNN	0.9575	0.9167	0.9635	0.9395	0.9767	8.6150
SVM	0.9550	0.9103	0.9635	0.9362	0.9693	0.0136
XGBoost	0.9475	0.8867	0.9708	0.9268	0.9867	0.0107
KNN-Autoencoders	0.9125	0.8036	0.9854	0.8852	0.9871	21.7245
AdaBoost-DBN	0.8350	0.7052	0.8905	0.7871	0.9349	22.0284
DNN	0.8250	0.6872	0.8978	0.7785	0.9140	0.0123
LR-MLP	0.7975	0.6628	0.8321	0.7379	0.8891	11.9994
CNN	0.7800	0.6369	0.8321	0.7215	0.8590	0.0108
RNN	0.7600	0.6051	0.8613	0.7108	0.8549	0.0104
Logistic Regression	0.7600	0.6145	0.8029	0.6962	0.8524	0.0263
GRU	0.7400	0.5846	0.8321	0.6867	0.8467	0.0186
Naive Bayes	0.7525	0.6159	0.7372	0.6711	0.8322	0.0269
LSTM	0.7000	0.5464	0.7299	0.6250	0.7963	0.0240

* All values are rounded to four decimal places.

**Figure 6.** Confusion matrix for Decision Tree model.

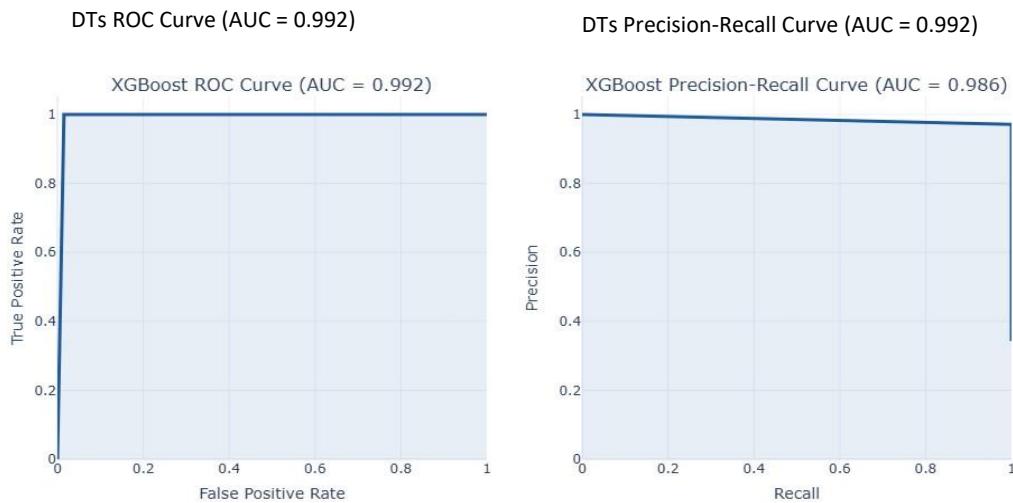


Figure 7. AUC and Precision-Recall Curves for Decision Tree model.

4.3. Result Analysis on Dataset 3

Performance analysis on Dataset 3 (BRFSS – 253,680 samples/21 features with three classes outcomes) are shown in Table 5, Figure 8, and Figure 9 demonstrate the results of the analysis, its corresponding confusion matrix, Precision/Recall and the AUC-ROC representation. The AdaBoost model performed better than other models on this dataset, achieving an F1 score of 0.43.

Table 5. Model Performance Comparison for Dataset 3 using F1-score as reference.

Model	Accuracy	Precision	Recall	F1 Score	AUC-ROC	Time Taken (s)
AdaBoost	0.6973	0.4317	0.5122	0.4314	0.7103	19.4743
XGBoost-CNN	0.7018	0.4304	0.5088	0.4271	0.7167	55.5742
XGBoost	0.7044	0.4293	0.5068	0.4265	0.7137	6.0555
RF-CNN	0.6693	0.4314	0.5112	0.4249	0.7107	37.4420
Random Forest	0.6799	0.4274	0.5045	0.4244	0.6997	14.5153
XGBoost-LSTM	0.6936	0.4273	0.5049	0.4240	0.7094	198.5152
RF-GRU	0.6599	0.4328	0.5115	0.4230	0.7085	141.7040
DT-CNN	0.6890	0.4227	0.4783	0.4218	0.6566	43.6537
Logistic Regression	0.6259	0.4498	0.5154	0.4192	0.7077	3.2978
GRU	0.6678	0.4327	0.4752	0.4161	0.6729	210.8736
DNN	0.6428	0.4281	0.5109	0.4134	0.7052	51.4291
LR-MLP	0.5936	0.4561	0.5197	0.4117	0.7117	0.8947
Decision Tree	0.6329	0.4247	0.5028	0.4079	0.6878	0.2390
Naive Bayes	0.6245	0.4364	0.4892	0.4083	0.6803	0.1709
CNN	0.5787	0.4358	0.5180	0.3988	0.7037	69.0522
SVM	0.5775	0.4418	0.5012	0.3978	0.7005	453.5940
KNN-Autoencoders	0.5590	0.4116	0.4473	0.3650	0.6232	19.3189
KNN (Normal)	0.5327	0.4125	0.4476	0.3589	0.6251	25.1546
AdaBoost-DBN	0.5393	0.4414	0.4854	0.3806	0.6775	364.6265
RNN	0.5858	0.4197	0.4958	0.3878	0.6863	119.7845
LSTM	0.6769	0.4097	0.4746	0.4030	0.6728	278.3175

* All values are rounded to four decimal places.



Figure 8. Confusion matrix for the Logistic Regression model.

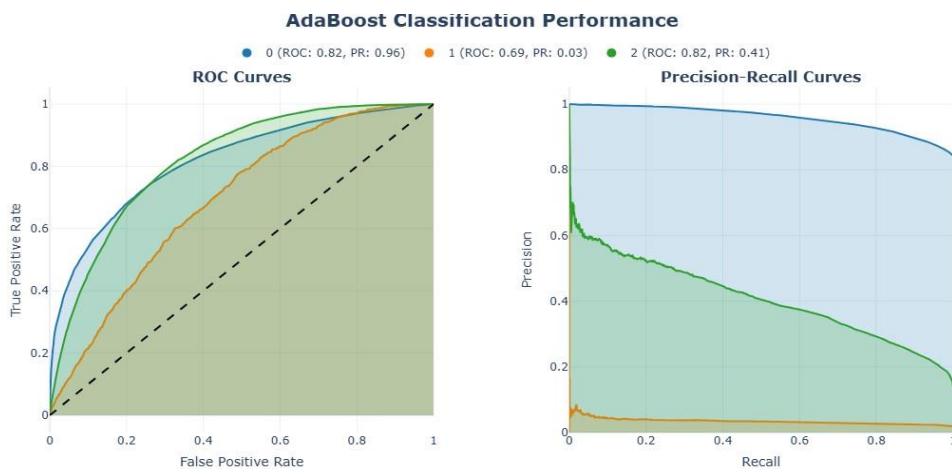


Figure 9. AUC and Precision-Recall Curves of Logistic Regression Model.

4.4. Result Analysis on Dataset 4

Performance analysis on Dataset 4 (BRFSS – 253,680 samples/21 features with two classes outcomes) shown in Table 6, Figure 10 and Figure 11 demonstrate the results of the analysis, its corresponding confusion matrix, Precision/Recall and the AUC-ROC representation. The logistic regression model performed better than other models on this dataset, achieving an F1 score of 0.44.

Table 6. Model Performance Comparison for Dataset 4 using F1-score as reference.

Model	Accuracy	Precision	Recall	F1 Score	AUC-ROC	Time Taken (s)
Logistic Regression	0.7249	0.3067	0.7731	0.4392	0.8197	0.2650
LR-MLP	0.7144	0.3017	0.7990	0.4381	0.8235	50.7898
AdaBoost	0.7251	0.3062	0.7690	0.4380	0.8187	2.0871
XGBoost	0.7132	0.3005	0.7971	0.4365	0.8209	0.9791
XGBoost-CNN	0.7079	0.2969	0.8010	0.4332	0.8212	58.5367
GRU	0.7111	0.2985	0.7947	0.4340	0.8187	217.5773
CNN	0.7044	0.2959	0.8131	0.4339	0.8238	53.9654
XGBoost-LSTM	0.7072	0.2960	0.7990	0.4320	0.8204	208.5252
SVM-RNN	0.7021	0.2943	0.8138	0.4322	0.8112	1804.6831
RNN	0.7047	0.2947	0.8037	0.4313	0.8184	113.6648
DNN	0.6872	0.2864	0.8345	0.4264	0.8229	53.0682
RF-GRU	0.7036	0.2919	0.7906	0.4263	0.8101	252.4819
LSTM	0.7043	0.2925	0.7911	0.4271	0.8149	203.2224

Random Forest	0.7025	0.2899	0.7833	0.4232	0.8070	9.8154
RF-CNN	0.7034	0.2911	0.7864	0.4249	0.8095	76.8140
AdaBoost-DBN	0.6859	0.2855	0.8345	0.4254	0.8221	58.1984
SVM	0.7002	0.2917	0.8068	0.4285	0.8162	1541.3782
KNN-Autoencoders	0.6753	0.2624	0.7349	0.3868	0.7566	85.9556
KNN	0.6751	0.2620	0.7333	0.3861	0.7563	38.4936
Decision Tree	0.6599	0.2391	0.6599	0.3510	0.6606	0.3532
DT-CNN	0.6649	0.2417	0.6571	0.3534	0.6618	62.1882
Naive Bayes	0.7235	0.2941	0.7029	0.4147	0.7799	0.0977

* All values are rounded to four decimal places.



Figure 10. Confusion matrix for the Logistic Regression model.

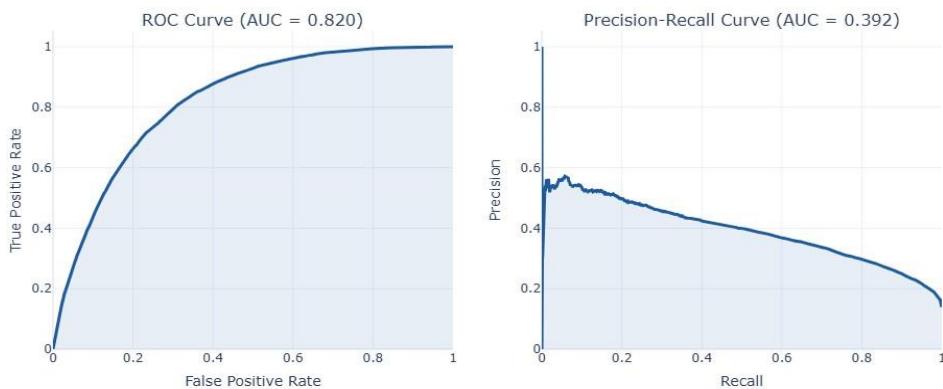


Figure 10. AUC Curves of Logistic Regression Model.

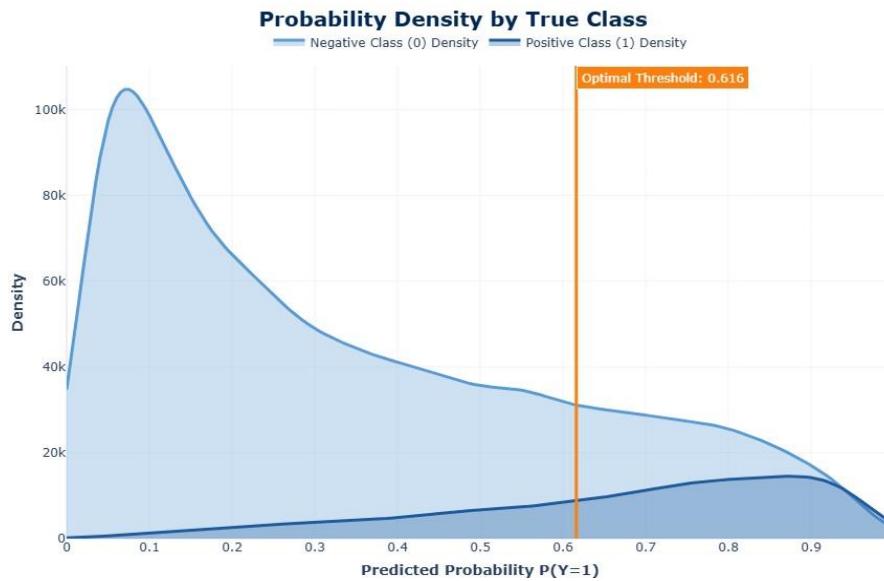


Figure 11. Threshold-dependent metrics for LR. The vertical line denotes the chosen threshold.

4.5. Result Analysis on Dataset 5

Performance analysis on Dataset 5 (early-stage diabetes risk prediction of patients of 520 samples and 17 features from Sylhet Diabetes Hospital, Bangladesh, shown in Table 7, Figure 12, and Figure 13 demonstrate the results of the analysis, its corresponding confusion matrix, Precision/Recall and the AUC-ROC representation. The Random Forest Tree, DT, and AdaBoost models performed the best on this dataset, achieving an F1 score of 0.9921 and a reasonable accuracy of 0.9904. RF is picked as the best of their best computation time in predicting diabetes in 0.0074s.

Table 7. Model Performance Comparison for Dataset 5 using F1-score as reference.

Model	Accuracy	Precision	Recall	F1 Score	AUC-ROC	Time
						(s)
Random Forest	0.9904	1.0000	0.9844	0.9921	1.0000	0.0074
Decision Tree	0.9904	1.0000	0.9844	0.9921	0.9922	0.0299
AdaBoost	0.9904	1.0000	0.9844	0.9921	0.9992	0.0389
SVM	0.9808	0.9844	0.9844	0.9844	0.9977	0.0181
SVM-RNN	0.9808	0.9844	0.9844	0.9844	0.9984	6.6874
RF-GRU	0.9808	1.0000	0.9688	0.9841	1.0000	8.2692
RF-CNN	0.9808	1.0000	0.9688	0.9841	0.9992	0.0132
XGBoost-LSTM	0.9808	1.0000	0.9688	0.9841	1.0000	11.2858
XGBoost-CNN	0.9808	1.0000	0.9688	0.9841	0.9977	4.1041
CNN	0.9712	0.9841	0.9688	0.9764	0.9977	0.0132
DT-CNN	0.9712	0.9841	0.9688	0.9764	0.9826	5.6472
LR-MLP	0.9712	0.9841	0.9688	0.9764	0.9992	9.9053
XGBoost	0.9615	0.9688	0.9688	0.9688	0.9926	0.0244
KNN-Autoencoders	0.9615	1.0000	0.9375	0.9677	0.9828	8.6576
DNN	0.9615	0.9839	0.9531	0.9683	0.9988	0.0146

RNN	0.9615	0.9839	0.9531	0.9683	0.9918	0.0112
Logistic Regression	0.9519	1.0000	0.9219	0.9594	0.9914	0.0515
KNN	0.9519	0.9836	0.9375	0.9600	0.9633	0.0190
Naive Bayes	0.9423	0.9677	0.9375	0.9524	0.9863	0.0146
AdaBoost-DBN	0.9231	0.9828	0.8906	0.9344	0.9863	9.2428
LSTM	0.8654	0.9464	0.8281	0.8833	0.9512	0.0118
GRU	0.8365	0.9273	0.7969	0.8571	0.9305	0.0124

* All values are rounded to four decimal places.

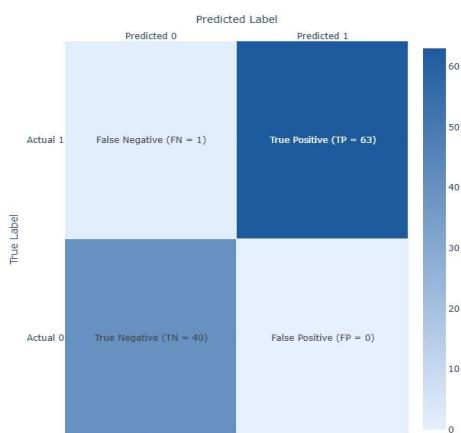


Figure 12. Confusion matrix for Random Forest model.

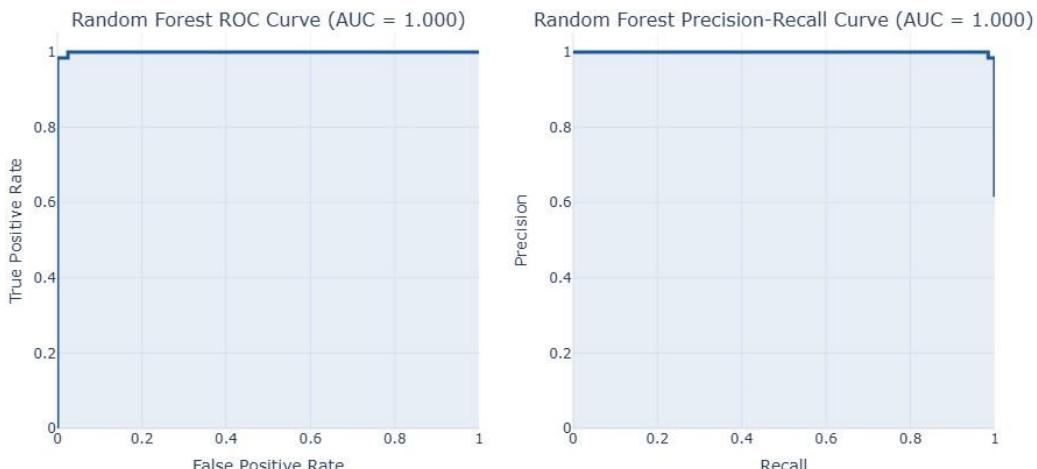


Figure 13. AUC Curves for Random Forest model.

5. Discussion

Regarding both computational efficiency and predictive effectiveness, the experimental findings from all five datasets consistently show that classical machine learning models outperform deep learning techniques. These results address our study issues about processing time and model correctness based on the size of the datasets and the importance of the features concerning the datasets.

According to the analysis, tree-based models continuously strike the optimum balance between speed and accuracy. On Dataset 1, XGBoost performs best with an F1-score of 0.7244 and completes predictions in 0.0122 seconds, about 350 times quicker than similar hybrid models such as XGBoost-LSTM (11.4212s). Decision Trees demonstrate perfect recall (1.0000) on Dataset 2, while Random

Forest achieves immaculate precision (1.0000) on Dataset 5, all while keeping prediction durations under a second. This trend is consistent across datasets.

Compared to their computing cost, deep learning models routinely perform poorly, which is evident based on the size of all the datasets that might not be adequate for DL models. Some neural network variations in need orders of magnitude demand more processing time, even when they attain competitive accuracy (within 2-3% of the top ML models). AdaBoost, for example, performs correspondingly results to XGBoost- CNN (F1 0.4314 vs 0.4271) on Dataset 3, but completes predictions three times quicker (19.4743s vs. 55.5742s). A distinct hierarchy in model efficiency is evident from the time measurements.

Across all datasets, traditional machine learning techniques (Decision Trees, Random Forest, XGBoost) consistently provide the quickest prediction speeds, usually less than a second. On Dataset 4, Logistic Regression is especially effective, obtaining a decent result (F1 0.4392) in just 0.2 seconds. On the other hand, DL models and hybrid techniques show noticeably higher processing times; for Dataset 4 predictions, some RNN variations take more than 1800 seconds to make their predictions. Nevertheless, Xie et al. [77] in their study proved that NN produces a better accuracy of 0.8240 but a lower recall of 0.3781. This is evident because the dataset size is inadequate for DL models.

According to the comparative analysis of Dataset 5, the results show ML models performing well across all metrics compared to DL models as reported by Xie et al. [78] even though both studies showed that RF outperformed other classical ML models. However, the analysis shows a value of 0.9740 across all metrics, while our study performed better using the same ML model with a value of 0.9921.

5.1. Comparative Analysis of Results with Already Developed Diabetes Prediction Models

The results analysed above compare the methods of ML and DL and their ensembles for predicting the health outcomes of diabetic patients. The generated outcomes must be compared with other models and existing developed predictive models based on the datasets used in this study (i.e. Datasets 1 – 5). It was observed that ML models demonstrated excellent accuracy and computation time with sufficient results, although this cannot be denied concerning the size of the datasets. However, the ML models presented good accuracy, speed, F1-score, AUC-ROC, and a reasonable computation time frame compared to DLs and ensembles, as well as some existing predictive models based on the same samples and features. Table 8 presents a comparative analysis of the results of the models for datasets and existing predictive models.

Table 10. Comparative analysis of models used and existing diabetes prediction models using F1-score [39].

Datasets	Authors	Outliers	Missing Values	Model	Precision	Accuracy	Recall	F ₁ score
Dataset 1	[46]	IQR	Attribute Mean	AB + XB	--	--	0.7900	--
Dataset 2	[48]	-	-	GBM	-	-	0.8700	--
	[81]	--	--	DA	--	0.7400	0.7200	--
	[82]	-	-	ANN	-	0.7600	0.5300	-
	[83]	ESD	k-NN	HM-BagMoov	-	0.8600	0.8500	0.7900
	[39]	IQR	Class wise median	QML	0.7400	0.8600	0.8500	0.7900
	[84]	-	NB	RF	0.8100	0.8700	0.8500	0.8300
	[85]	-	-	k-NN	0.8700	0.8800	0.9000	0.8800
	[59]	Group Median	Median	RF	-	0.9300	0.7970	-
	[86]	--	--	RF	0.9400	0.9400	0.8800	0.9100

[39]	IQR	Class wise median	DL	0.9000	0.9500	0.9500	0.9300	
Our Study	IQR	ADASYN	RF	0.9781	0.9850	0.9781	0.9781	
Our Study	IQR	ADASYN	k-NN	0.9781	0.9850	0.9781	0.9781	
Our Study	IQR	ADASYN	DT	0.9716	0.9900	1.0000	0.9856	
Dataset 3	[77]	--	Excluded	NN	--	0.8240	0.3781	--
Dataset 4	Our Study	IQR	Clustering	AdaBoost	0.4317	0.6973	0.5122	0.4314
	Our Study	IQR	Clustering	LR	0.3067	0.7249	0.7731	0.4392
Dataset 5	[78]	--	Ignoring Tuple	RF	0.9740	0.9740	0.9740	0.9740
	Our Study	IQR	--	RF	1.0000	0.9904	0.9844	0.9921
	Our Study	IQR	--	DT	1.0000	0.9904	0.9844	0.9921
	Our Study	IQR	--	AdaBoost	1.0000	0.9904	0.9844	0.9921

* *IQR* – Interquartile Range, *GBM* – gradient boosting machine, *DA* – discriminant analysis, *ESD* – extreme studentized deviate, *QML* – Quantum ML, *HM-BagMoov* – hierarchical multi-level classifiers bagging with multi-objective optimized voting.

6. Conclusions

In this study, we used five publicly accessible datasets to compare different machine learning, deep learning, and ensemble algorithms and their modifications in the context of predicting the health outcomes of diabetic patients. The outcome of the analysis was also compared with existing predictive models. The results showed that ML models were consistently superior to alternative DL and ensemble techniques, demonstrating their efficacy in correctly predicting DM illnesses across various datasets considering accuracy, reliability, processing time and computational efficiency. ML models demonstrated their promise as a robust and dependable approach by achieving notable accuracy, recall, and F1-score with strong AUC-ROC scores on almost all five datasets. However, given the scale of the datasets, these performances of DL and ensemble models might not be disregarded. Nevertheless, RF, DT, AdaBoost, LR, k-NN, and XGBoost performed well, while other classifiers in ML, DL, and ensemble performed to their capacity, depending on size. However, ensemble models, including XGBoost-CNN, RF-CNN, RF-GRU, and XGBoost-LSTM, also showed exceptional performance across all five datasets.

People of all ages are becoming more susceptible to diabetes. The current study showed that early diabetes identification might be crucial for treatment and enhanced health outcomes for individuals with the disease. Obesity may be prevented by taking easy awareness-raising steps like eating a low-sugar diet, exercising frequently, and leading a healthy lifestyle. Its relevance in healthcare is apparent since models and its ensembles show increasing promise in predicting diabetes and eventually lowering treatment costs and increasing computing efficiency. Finding the optimal model for predicting datasets created for diabetes progression and risk prediction is the primary contribution of this work.

We discovered that the ML models had the best accuracy and better computing cost. Lastly, using the same dataset, a comparison of the models with current predictive models showed how important it is to improve the health outcomes for diabetes patients. The ML models in this study performed better than the existing predictive models in terms of accuracy, F1-score, and recall. Nonetheless, this study may be updated often with a more complete dataset and additional examples, and it can include other commonly used methods for prediction.

There are not many restrictions on our study, though we could not prove causation since some datasets were cross-sectional, particularly the health risk indicators (Datasets 3 and 4) and Dataset 5

(BRFSS_2015) data, and the biological entries were inaccurate. Another drawback of the Dataset 5 data was that it was self-reported and hence susceptible to memory biases, which may impact how well our prediction models performed. Nonetheless, our prediction algorithms could be more effective in forecasting the health outcomes of diabetes patients now that clinical data and biomarkers are available.

Author Contributions: Conceptualization, methodology, software, validation, formal analysis, investigation, resources, data curation, writing—original draft preparation, O.B.A.; writing—review and editing, visualization, supervision, project administration, S.S., C.R.; funding acquisition, S.S., O.B.A.

Funding: This research was funded by the Australian Research Training Program (RTP) Postgraduate Research Scholarship Award, and “The APC was funded by a waiver on my Principal Supervisor”. The Australian Government awarded the scholarship.

Data Availability Statement: All datasets used in this research are publicly available in Kaggle, CDC, and UCI Machine Learning Repository.

Acknowledgments: This work is part of the doctorate research under the Research Training Program (RTP) scholarship opportunity. The authors thank the anonymous reviewers for their valuable suggestions and comments on this paper.

Conflicts of Interest: The authors declare no conflicts of interest.

Abbreviations

DM	Diabetes Mellitus
ML	Machine Learning
DL	Deep Learning
AU-ROC	Area under the ROC
KPI	Key Performance Indicators
IDF	International Diabetes Federation
T1DM	Type 1 DM
T2DM	Type 2 DM
GDM	Gestational DM
RF	Random Forest
LR	Logistic Regression
XGBoost	Extreme Gradient Boosting
NB	Naive Bayes
SVM	Support Vector Machine
NN	Neural Networks
RNN	Recurrent NN
CNN	Convolutional NN
DNN	Deep NN
QML	Quantum ML
KNN	k-Nearest Neighbour
CVD	Cardiovascular diseases
DT	Decision Tree
LSTM	Long Short-Term Memory
AdaBoost	Adaptive Boosting
GRU	Gated Recurrent Unit
ANN	Artificial Neural Networks

Appendix A

Table A1. Datasets Information.

Datasets	Dataset 1	Dataset 2	Dataset 3	Dataset 4	Dataset 5
Statistics	Description				
Source	UCL Machine Learning Repository, Kaggle and CDC websites				
Samples	768	2000	253,680	253,680	520
Features	9	9	21	21	17
Positive instances	268	684	35346	35346	320
Negative instances	500	1316	218334	35346	200

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