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# A stacking ensemble approach for diabetes prediction

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Submitted on: 24-Aug-2024, Accepted on:12-Mar-2025 and published on: 14-Apr-2025 Article ABSTRACT Diabetes Mellitus Preprocess Feature Split data to (DM) is a metabolic PIMA Selection train and test ing disorder which persist for longer duration Dataset in the human body due to fluctuating levels of blood glucose. Continuous monitoring of glucose levels is essential, as Stacked persistent hyperglycaemia can lead to ANN FDT Train Test Ensemble complications such as retinopathy, Data Data nephropathy, and neuropathy. Therefore, Models Trained emerging Machine Learning (ML) and data analytics methods are crucial for the **Best Model** Assess Model identification, and management of DM. Performance Performance Matrices This research aims to develop predictive models that enable early intervention in

diabetes management. A well-known biomedical dataset, PIMA, is used to implement a stacking ensemble method to improve diabetes classification. The stacking ensemble combines multiple diverse base algorithms to harness their collective predictive capabilities. Through comprehensive evaluation, it is found that the stacking ensemble method outperforms individual models and other ensemble techniques across various performance metrics. A metric value greater than 90% is obtained for accuracy, precision and recall. The experimental results highlight the potential of the stacking ensemble method as an effective model for accurate and reliable diabetes classification in biomedical data analysis.

Keywords: Classification, Decision tree, Diabetes, ensemble, feature selection, logistic regression, prediction, precision, and stacking.

# INTRODUCTION

Diabetes is a common chronic disease affecting millions of people in the world. Furthermore, if diabetes is not effectively managed and blood glucose levels are not properly controlled, individuals face an increased threat of developing debilitating complications, such as heart, kidney, eye, nerve, and foot diseases. In this research, predictive models are explored for the prediction of diabetes, taking into account both clinical and genetic factors. The growth of Type 2 Diabetes (T2D) began in the 1970s and 1980s.<sup>1</sup> Table 1 describes the key patterns in prevalence, incidence, complications, care, and socio-demographic factors affecting T2D.

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Period	Summary	
1960s-80s	Minimal T2D	
	Increase in complications	
	Poor care	
1995-2010	Improving care	
	Minimal complications	
	Incidence acceleration	
	Increase in T2D in youth	
2010-2015	Increase in T2D	
	Complications stagnated	
	Young mostly affected	
2015-Forwards	Mortality declined	
	Morbidity diversified	
	Exposure expanded	

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By analyzing the current state of predictive research, the paper will explore the challenges, opportunities, and implications of accurate diabetes prediction. In the past, much literature has focused on predicting diabetes using machine learning models. Many preprocessing approaches, such as random sampling,<sup>2</sup> are deployed for enhancing accuracy of the proposed methods. Two stacking-based approaches for diabetes prediction were developed.<sup>3</sup> The authors used various neural network ensemble techniques resulting in improved accuracy. The proposed method achieved high accuracy, ranging from 92% to 95%. Reza et al. <sup>4</sup> proposed approach outperformed existing kernel functions by delivering improved performance in clinical settings.

Several algorithms, including Decision Trees (DT), AdaBoost, Naive Bayes (NB), and Multilayer Perceptron (MLP), exhibit certain limitations <sup>5</sup>. Decision Trees tend to overfit and are sensitive to minor fluctuations in the training data. AdaBoost is susceptible to outliers and can be computationally intensive. The assumption of feature independence in NB poses challenges when handling rare events. MLP is also prone to overfitting and requires careful hyperparameter tuning. Additionally, DT has limited expressiveness and remains vulnerable to overfitting. Finally, the architecture design and hyperparameter selection of Artificial Neural Networks (ANNs) demand careful consideration. These limitations must be accounted for when selecting appropriate algorithms.

Many base learners were trained and tested by Cheng et al.<sup>6</sup> using the PIMA dataset. The NB model performed well in binary classification when provided with a fine-tuned set of input attributes, whereas RF yielded better results when more attributes were included.

Quality of life has improved with the integration of humancomputer interaction systems<sup>7,8</sup> in healthcare. Therefore, appropriate strategies must be developed to fine-tune hyperparameters and enhance performance metrics. These findings aim to advance diabetes prediction, support healthcare professionals in decision-making, and strengthen preventive strategies for individuals at risk. The significance of the proposed approach lies in building a predictive mechanism using an integrated ML ensemble to identify high-risk diabetic individuals and improve healthcare outcomes. The novelty of the stacking ensemble method in this study stems from its innovative combination of base classifiers.

#### **LITERATURE REVIEW**

Various visualization techniques and models <sup>9</sup> were analyzed for diabetes prediction in women. Among all the models, RF outperformed others across all performance metrics. Hasan et al. <sup>10</sup> investigated the effectiveness of ensembling various ML classifiers for accurate diabetes prediction. Kumari et al. <sup>11</sup> developed a soft voting ensemble for prediction by integrating ML models such as RF, LR, and NB. An empirical evaluation is performedon the base and ensemble learners. All performance metrics were analyzed as part of the evaluation criteria. An accuracy of 79% is achieved.

Shams et al.<sup>12</sup> utilized various types of ML algorithm. Comparative results indicate that the proposed model outperforms existing approaches. Boruta feature selection with ensemble learning is utilized <sup>13</sup>. In this approach, the k-means++ algorithm for unsupervised data clustering is integrated with a stacked ensemble method. The proposed technique achieved 98% accuracy. They also introduced a DL approach for diabetes identification. Yuvaraj and Sri Preethaa<sup>14</sup> presented a study on diabetes prediction using ML algorithms implemented on a Hadoop cluster. Similarly, a DL-based method is used<sup>15</sup> for identifying diabetes. A study<sup>16</sup> focused on classification and diabetes prediction using various ML techniques. Kavakiotis et al.<sup>17</sup> provided a comprehensive overview of ML and data mining techniques applied to diabetes prediction. Ahmed et al.<sup>18</sup> developed a smart web application to present their study on ML for diabetes prediction.

The American Diabetes Association<sup>19,20</sup> provides guidelines for treatment based on the levels of diabetes mellitus in the human body. A comprehensive study is performed to analyze the relationship between fasting blood glucose concentration, diabetes, and heart disease. Chou et al.<sup>21</sup> employed Genetic Algorithms (GA) and a Multi-Objective Evolutionary (MOE) fuzzy classification algorithm for feature extraction and diabetes classification.

A diabetes mellitus classification approach is specifically designed to handle unbalanced samples with missing values <sup>22</sup>. Tasin et al.<sup>23</sup> applied Extreme Gradient Boosting for feature selection. In addition, the LIME and SHAP frameworks were employed to interpret the final results. An accuracy of 0.96 is obtained. A study to identify Type 2 diabetes using phenotypes that include triglycerides and anthropometric measurements is conducted.<sup>24</sup> A machine learning technique is developed <sup>25</sup> for accurate stratification of diabetes risk, addressing the impact of outliers and data scarcity. Basset et al.26 utilized ML techniques to develop a disease prediction model focused on early detection and intervention. Devarajan et al.27 proposed a personalized fogassisted health monitoring system for remote patients with diabetes, leveraging deep learning (DL) architectures. Rundo et al.28 highlighted the importance of human-computer interaction (HCI) in enhancing clinical decision-making and advancing precision medicine. Gangavarapu and Patil<sup>29</sup> proposed a hybrid ensemble approach integrated with GA to reduce the high dimensionality of biomedical datasets.

Chen et al.<sup>30</sup> presented a full migration Biogeography-Based Optimization (BBO) algorithm for multimodal biomedical image registration, enhancing search efficiency and accuracy. Ngan et al. <sup>31</sup> introduced a novel fuzzy-based system for critical decisionmaking. Nazari et al.<sup>32</sup> developed a DSS using a fuzzy inference approach for heart disease prediction. Ngan et al. 33 also applied fuzzy aggregation operators in dental treatment to improve accuracy and consistency. Polat et al.<sup>34</sup> developed a sequential learning model for diabetes identification by combining DA and LS-SVM. Chang and Lilly<sup>35</sup> constructed a fuzzy classifier using evolutionary algorithms to generate fuzzy classification rules. A hybrid system<sup>36</sup> was designed for the treatment of diabetes and heart disease, integrating fuzzy logic (FL) with neural networks (NN). In the domain of medical diagnosis and classification, extensive literature has explored the application of Computational Intelligence (CI) techniques to enhance accuracy. Kamadi et al.<sup>37</sup> applied Principal Component Analysis (PCA) and a modified fuzzy SLIQ Decision Tree for effective diabetes diagnosis and treatment. However, there remains scope for improving the accuracy of diabetes prediction, which is addressed in our proposed work using an integrated model.

## **PROPOSED METHODOLOGY**

A three-phase approach is implemented for the proposed work. Phase 1: Preprocessing and feature selection are performed

Phase 2: The data is split and various base and ensemble models are analyzed during the training and testing phase. The proposed stacking ensemble is built and also compared with FDT. Each of these phases is described in the sections below.

Table 2: Correlation Values and Skewness Type

Feature	Correlation value with outcome column	Skewness
Glucose	0.49	Right
BMI	0.31	Normal
Pregnancies	0.24	Right
Age	0.23	Right
Skin_Density	0.18	Right
Diabetes Likelihood	0.17	Right
BP	0.16	Normal
Insulin	0.14	Right

#### **Data Preparation**

PIMA dataset is devleoped by NIDDK. This dataset contains 769 samples with eight attributes as given in table 1 and a class variable indicating diabetes status. The dataset has been widely used to develop machine learning models for predicting diabetes, considering factors such as insulin levels, age, BP, and BMI. Researchers have made significant progress in understanding the correlations among these attributes and diabetes, enabling early identification and intervention for high-risk individuals. Training, testing and validation is performed on 60%,20% and 20% of the total samples.

Data preprocessing is performed using standard scaler and MinMax techniques. The widely used preprocessing technique, MinMax Scaler, scales the data between 0 and 1. The prediction of a tree-based model may sometimes improve with scaling. Experiments show a significant increase in performance by using standard scalers on non-tree-based approaches.

Significant deviations from most of the dataset points are identified as outliers, which can skew the analysis and negatively impact the performance of predictive models. Outlier removal is implemented based on the correlation values presented in Table 2. This framework enhances the reliability and accuracy of predictions by detecting and eliminating outliers. These outliers can be identified by plotting box plots for all the features. In this dataset, most of the features are normally distributed and right-skewed. A step-by-step strategy, outlined in Table 3, is employed to identify and remove a total of 132 outliers. This approach has been utilized in various research studies.<sup>38</sup> Once detected, these outliers can either be removed or treated separately, ensuring that a

specific and reliable dataset is used for model training. The different outliers are associated with the attributes of the dataset.

Feature	Outliers removed
Pregnancies	768-4=764
Glucose	764-5=759
BP	759-45=714
Skin_Density	714-1=713
Insulin	713-27=686
BMI	686-10=676
Diabetes Likelihood	676-29=647
Age	647-11=636

#### **Feature Engineering**

Feature selection identifies the most important and informative attributes from the complete set of variables. By selecting a relevant subset of attributes and discarding irrelevant or redundant ones, attribute selection enhances the predictive model's performance, reducing overfitting and improving generalization. This process also simplifies computational complexity, making the model more efficient and interpretable. Various techniques, including filter, embedded, and wrapper methods, are employed to determine the optimal feature subset, leading to accurate and robust predictions for diabetes in the PIMA dataset.

#### Correlation

The overfitting problem occurs when highly correlated data are included in the model. If two features are strongly correlated, the feature with the highest correlation should be discarded.



Figure 1: Feature Importance for Class variable Prediction

### **Feature Importance**

Researchers prioritize and focus on the most influential features resulting in effective predictive models constructed for the prediction of diabetes. Bagged decision trees like RF and Extra Trees can be used to calculate the feature importance. ExtraTrees classifier is used for feature selection. The statistics of the eight important attributes in the dataset is shown in Figure 1. These scores indicate the feature importance. From the result, we have narrowed our discussion to four parameters in the end, including glucose, age, BMI, and DiabetesLikelihood because their variable importance is more than 50% using the feature important parameter as depicted in Figure 1. Later, we compared the algorithms using the Minmax Scaled Model with the four priority parameters and obtained the prediction scores for the same.

### **Identification and Evaluation of Base Learners**

Figure 2 shows the proposed architecture. The base learners selected are LR, LDA, KNN, NB, SVM, and CART. All models are trained on dataset D, and the predictions are obtained. The best five base learners are chosen for stacking. Let the predictions of the i-th model be denoted as  $P_i = p_{1i}, p_{2i}, ..., p_{ni}$ , where  $p_{ji}$  represents the predicted probability or class label for the j-th instance. A meta-model is then used to integrate these predictions, refining the initial predictions made by the base learners. Each trained base classifier undergoes cross-validation, if necessary, to fine-tune its hyperparameters. Every classifier is evaluated using various

metrics on a validation set. Meta classifier which is a higher level model is then selected to aggregate the predictions from the base algorithms. In some cases, it may be appropriate to apply another ensemble or deep learning model. The models chosen for metaestimation are Random Forest (RF), AdaBoost (AB), and Extra Trees (XT). The meta-model uses a weighted linear combination to determine the aggregated predictions from the base models.

## **Stacking Integration**

Figure 3 illustrates the stacking ensemble of the proposed system. The outputs of the BL are fed into the ensemble. The final prediction of the stacked model is given by:

$$y_pred = f(w1 * P1 + w2 * P2 + ... + wn * Pn)$$
 (1)

Where  $w_1, w_2, ..., w_n$  are the learned weights for each model's prediction, and **f** represents the activation function of the metamodel. In addition to the stacked ensemble model, the proposed approach was also tested using a deep learning technique, such as Fuzzy Decision Trees (FDT). The notable accuracy of 95.02% achieved through our stacking ensemble highlights its effectiveness in predictive modeling. By leveraging the collaborative efforts of



Figure 2: Proposed Architecture

multiple models, stacking enables the extraction of valuable predictive insights from the data. This demonstrates the potential of stacking ensembles as a powerful technique for enhancing predictive accuracy in our model.

# EXPERIMENTAL ANALYSIS

An experimental analysis is performed to evaluate the base. ensemble and the proposed model. This data distribution was selected carefully to optimize both the model learning and evaluation processes. By providing a substantial training set of 60% from the complete dataset, the model can better discern and internalize the intricate relationships between the features. This ensures that the model captures underlying patterns in the data more accurately, thereby enhancing its predictive capabilities.



Figure 3: The designed Stacking Ensemble

Table 4: Accuracy score of all base, ensemble and proposed classifier

Algorithms	Accuracies found through experimental observation
Logistic Regression	77.43%
Linear Discriminant Analysis	76.74%
KNN	71.88%
CART	70.64%
NB	74.46%
SVM	75.52%
AdaBoost	75.34%
GB Machine	75.34%
RF	74.47%
Extra Tree	73.42%
Stacking Classification (above stated models)	95.02%
Fuzzy Decision Tree (FID3)	84.37%

We carefully evaluated the performance of the stacking ensemble method to enhance diabetes classification using the PIMA dataset. After preprocessing the data, we selected a variety of base classifiers, including DT, RF, SVM, NB, XT, AB, KNN, CART, GBM, and FDT. Cross-validation was used to train and finetune each model. The stacking ensemble combines the predictions of these base classifiers, achieving significantly higher performance than individual models.

We compared the stacking ensemble method with traditional machine learning techniques and found that it outperformed them, demonstrating its suitability for diabetes classification. Furthermore, we tested the ensemble's resilience by applying it to various train-test splits, yielding consistent results that highlighted its reliable generalization ability.

Analysis of feature importance revealed the significant role of biological factors in predicting diabetes. Additionally, the ensemble's affordable processing cost demonstrated its potential for real-world applications. Our research shows that the stacking ensemble method is an effective tool for reliable and accurate diabetes categorization, offering potential benefits for improving healthcare outcomes and enabling early disease detection.

 Table 5: Additional Performance Metrics of Base and Ensemble

 Classifiers

Models	Precision	Recall	F1-Score
LR	72.90%	55.26%	61.89%
LDA	73.19%	54.21%	61.38%
KNN	74%	73%	73%
SVM	77%	71%	73%
CART	76%	74%	75%
ET	69.96%	57.89%	63.08%
RF	71.09%	58.42%	63.67%
AdaBoost	71.09%	60.53%	62.88%

Table 4 presents the accuracy of individual base, ensemble and proposed model. Following this, we applied the stacking ensemble method. Our experimental analysis revealed that the ensemble model is superior. Table 5 shows additional metrics of base and ensemble classifiers. Among all the models tested, the ensemble model demonstrated the best performance, achieving a precision of 91.6%, an accuracy of 95.291%, a recall of 91.3%, and an F1 score of 83.2%. Table 6 demonstrates the metrics of the proposed stacking ensemble model which leads to accurate and reliable

predictions. Additionally, the model yielded an AUC score of 87.17%.To benchmark our proposed ensemble model, we compared it with a fuzzy DT model. The evaluation of the fuzzy DT model showed 85.7% precision, 84.37% recall, 60% recall, a 70.5% F1 score, and an AUC score of 84.85%. These findings emphasize the superior effectiveness of the ensemble approach in achieving robust and reliable predictions. While the fuzzy DT model showed competitive performance, it did not outperform the ensemble model.

## DISCUSSION

The findings from the case study using the well-known PIMA dataset demonstrate the effectiveness of the stacking ensemble method. Our proposed stacking ensemble outperformed individual learners across all performance metrics. By combining various base and ensemble learners, the stacking ensemble method showed superior predictive power. The resilience of the ensemble was assessed through cross-validation, with results consistently indicating reliable performance across different data splits.

The analysis of feature importance revealed that certain biological characteristics, such as age, BMI, and glucose levels, played a significant role in diabetes classification. Furthermore, when compared with traditional machine learning methods, the stacking ensemble method exhibited improved performance, highlighting its potential for real-world healthcare applications.

While the proposed approach demonstrated success, the paper acknowledges some limitations, particularly related to the dataset's size and class imbalance. It suggests that future research could explore the use of balanced datasets to further evaluate and enhance the proposed method. Overall, this case study effectively illustrates the capabilities of the stacking ensemble method and its potential benefits for advancing diabetes categorization research. Table 7 presents a comparative study of existing ensemble approaches versus our proposed work. While most existing ensemble methods showed only marginal improvements in accuracy, our proposed approach achieved the highest accuracy, as the base and metalearners were carefully selected to optimize prediction performance.

Table 6: Performance Metrics of Proposed Ensemble Classifier

Models	Precis	Accuracy	Recall	F1-	AUC
	ion			Score	Score
Stacking Ensemble	91.6%	95.291%	91.3%	83.2%	87.17%
Fuzzy DT Model	85.7%	84.37%	60%	70.5%	84.85%

**Table 7**: Comparative Study of the Ensemble Approaches for Diabetes Prediction

Models	Accuracy
Deep NN stacking ensemble <sup>3</sup>	92%
Voting Ensemble of RF, LR and NB [10]	79%
Semi-Supervised with XGBoost [23]	81%
Proposed Stacking Ensemble	95.291%

## **CONCLUSION**

Diabetes prediction using ML approaches is widely used as there have been better health care with the advancement of technology. A classification framework is built utilizing a stacked ensemble after various levels of evaluating various base and ensemble learners. The proposed method achieved best performance in comparison to individual base classifiers, providing higher accuracy, precision, recall and f1-score in diabetes classification.

#### **CONFLICT OF INTEREST STATEMENT**

Authors declare that there is no associated known academic or financial interests that would have influenced this work.

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### Appendix

Table A1: Nomenclature and Abbreviations

Nomenclature	Abbreviation	
AB	AdaBoost	
BL	Base Learners	
BMI	Body Mass Index	
CART	Classification and Regression Trees	
DL	Deep Learning	
DSS	Decision Support System	
DT	Decision Tree	
DM	Diabetes Mellitus	
DA	Discriminant Analysis	
FDT	Fuzzy Decision Tree	
GA	Genetic Algorithm	
GBM	Gradient Boosting Machine	
GRU	Gated Recurrent Unit	
HGB	Histogram Gradient Boosting	
KNN	K-Nearest Neighbor	
LDA	Linear Discriminant Analysis	
LS-SVM	Least Squares -Support Vector Machine	
LR	Logistic Regression	
ML	Machine Learning	
NB	Naïve Bayes	
NIDDK	National Institute of Diabetes and Digestive and Kidney Diseases	
RF	Random Forest	
RFE	Recursive Feature Elimination	
SLIQ	Supervised Learning in Quest	
XT	Extra Trees	