International Journal of Computer Information Systems and Industrial Management Applications
ISSN 2150-7988 Volume 18(22s) 2026 pp. 1342-1359
https://doi.org/10.70917/ijcisim-2026-5775
Article

A SHAP-BASED MULTI BOOSTING FRAMEWORK FOR INTERPRETABLE DIABETES PREDICTION WITH FEATURE SELECTION

Ramesh Prasad Bhatta1*, Akhtar Husain[2]

[1,2]Research Scholar, Associate Professor, Department of Computer Science and Information Technology, M.J.P. Rohilkhand University, Bareilly, India
*Corresponding Author: rpb.mcs@gmail.com

Abstract: The timely and accurate prediction of the disease is essential to avoid the progress of the disease and other severe complications and to enable early interventions. Machine learning (ML) is a powerful approach to support early diagnosis of the disease through maximising the accuracy of the diagnosis. In this study, the authors have proposed a multiple boosting model to aid in the diagnosis of the disease by combining AdaBoost, Gradient Boosting, XGBoost algorithms with SHAP (SHapley Additive exPlanations) feature analysis and feature selection methods. The results of the experiments conducted on the PIMA data set show that XGBoost is the best performing algorithm among the other boosting algorithms with 77.92% accuracy and 83.45% ROC AUC. The features Glucose, BMI, and Age are the top features with the highest contributions to the model output as per the results of the SHAP analysis, with Glucose accounting for 50% of the contribution to the output. Moreover, the subset of features with the top features identified by SHAP still retains 98-99% of the prediction performance with significantly lower computational complexity. Despite the challenges of class imbalance problems, the proposed approach has shown the potential to be applied to real-world problems with decision support systems. Future research will be directed towards improving the minority class detection performance, as well as the inclusion of longitudinal data.
Keywords: Diabetes Prediction, SHAP, Explainable AI, Feature Selection, Ensemble Learning, XGBoost, Accuracy, Gradient Boosting (GB)

1. Introduction

Boosting, one of the most popular ensemble learning techniques in machine learning, has been very successful due to its high predictive accuracy and capacity to learn non-linear interactions. Boosting algorithms create a strong classifier for classification from several weak learner classifiers by iteratively applying the same learning algorithm and increasing the weight of those instances that were incorrectly classified during each iteration. AdaBoost,[1] Gradient Boosting[2] and (more recent) XGBoost[3] are three of the most popular boosting algorithms, and are widely used due to their scalability and stability. Boosting algorithms have been demonstrated to be more effective in many healthcare prediction tasks (such as diabetes predictio,[4] cardiovascular risk prediction[5]and cancer diagnosis[6]) than other algorithms, as they can capture interactions of features and deal with complex data from different sources.

Boosting algorithms can help to boost mitigation using these algorithms, but they are not without their limitations (e.g., AdaBoost is sensitive to noise and outliers, XGBoost requires time for hyperparameter tuning and can often complicate computing). Some of the studies focus on accuracy rather than interpretability which is important in decision-making; there have been minor gains in efficiency, which are dependent on the data set; therefore, there is a need for interpretability and hybrid methods (e.g, for balancing between accuracy, interpretability and efficiency) to be used for effective use in practice.

SHAP or SHapley Additive exPlanations by[7]is an empirical approach which is rooted in a theoretical foundation and is aimed at enhancing the interpretability of machine learning models. SHAP is based on cooperative game theory, so each feature will have a contribution to the prediction of an individual data point with a set of desirable properties such as local accuracy, consistency and additivity.[8] In contrast to traditional feature importance metrics, SHAP can be used to generate both global and local explanations for a machine-learning model, which enables a better understanding of complex models (including ensemble models). Consequently, tools such as SHAP are gaining popularity in high stake settings, like clinical decision making, where it's important to explain the reasoning behind a model in order to understand decisions that are made about individuals' lives.

A recent study highlights the growing use of SHAP in medical analytics which demonstrate that it does a good job at explaining the predictions of models on various diseases. For instance, SHAP has been applied to explain diabetes prediction,[9] predicting cardiovascular risk,[10] and predicting outcomes of COVID-19.[11] These studies suggest that SHAP does enhance model interpretability by identifying the important features and help build medical intuition. However, SHAP has some limitations, such as slow computation time when applied to large data and complex models and could produce explanations that require external knowledge to understand. Furthermore, most of the existing research focuses on post hoc explanations and doesn't include interpretability in the model training, which indicates more efficient and inherently interpretable machine learning frameworks for health care are needed.

While numerous studies have focused on the improvement of algorithms for diabetes prediction, one of the limitations is the lack of integrated models including all the comparisons of boosting models and integration of SHAP-based interpretability and feature selection. Further, the potential of SHAP in the identification of clinically relevant features and improvement of model accuracy has yet to be explored. To address these, this study

(i) compares Pima Indians Diabetes data models using AdaBoost, Gradient Boosting and XGBoost

(ii) uses SHAP in model comparisons to enhance interpretability and identify predictors with the greatest influence and

(iii) compares models with all features to models with only the top few features.

2. Literature Survey

Using a systematic search methodology, the major scholarly databases (PubMed, IEEE Xplore, ScienceDirect, and Google Scholar) have been searched for articles published from January 2020 through March 2025. The search terms used included "diabetes prediction", "boosting algorithms", "AdaBoost", "Gradient Boosting", "XGBoost", "SHAP", "explainable AI", and "feature selection". This literature review only included peer-reviewed journal articles; these must use boosting approaches to predict diabetes, and/or use explainable AI approaches such as SHAP.

The paper [12] predicted diabetes complications using XGBoost with SHAP analysis. Electronic health records of 15,847 patients were used to identify the risk factors of diabetic retinopathy and nephropathy. The SHAP analysis identified the duration of the glycemic control, HbA1c levels and blood pressure as the main factors of complications. The manuscript has demonstrated the use of SHAP in risk stratification and precision medicine [13] have done a review and experimental study on applying interpretable machine learning for prediction of diabetes: A SHAP analysis. They compared the algorithms including logistic regression, random forest, XGBoost, and LightGBM and SHAP provided unified feature importance measures. They found that the best predictive performance can be achieved with XGBoost (accuracy: 79.2% ROC-AUC: 0.85) and SHAP analysis was consistent showing that the variables Glucose, BMI, Age and Diabetes Pedigree Function were consistently in the top predictors. The authors introduced the concept of SHAP-based feature selection and demonstrated that the predictive performance of the models built using the top features from SHAP were 95% of the original performance [14] discussed that the ensemble methods with the SHAP explanations can be used to identify the early predictive stages of diabetes in resource-limited settings.

Using a dataset of 2500 patients from Bangladesh, the study found that AdaBoost with decision stumps performed as well as other more complicated models, but is more interpretable. The SHAP analysis revealed that the family history, inactivity and food habits were the most predictive factors for this population, as contextual factors play a key role in model building.[15] Developed a new model to combine gradient boosting machines with SHAP to personalise the risk of diabetes. The key development in the study was to use patient data over time, and it demonstrated that the SHAP values can be used to track changes to risk factors over time. The model had an accuracy of 81.3%, and provided clinicians with interpretable risk curves. In a multi-center study,[16] set out to study the application of machine learning algorithms in predicting diabetes in different population groups in the US, Europe and Asia. They included 25,000 patients and used XGBoost and SHAP analysis to determine population-specific risk factors. While Glucose, BMI and Age were universally important, other factors (e.g., dietary factors in the Asian population, socioeconomic factors in the reviewing population in the US) were less important. This research showed the need for recalibration of models based on population and the role of SHAP in identifying the differences.

The proposed feature selection method by [17] is a new algorithm which uses SHAP values and recursive feature elimination. The algorithm was able to select a good subset of features of five variables (Glucose, BMI, Age, Diabetes Pedigree Function, and Pregnancies), which had a prediction accuracy of 78.5 percent compared to 79.1 percent with eight variables on the PIMA (diabetes prediction) dataset. This paper has provided empirical evidence that we can reduce the model complexity while maintaining model accuracy using feature selection with SHAP.

The first paper is,[18] which is a large-scale comparison of explainable boosting methods for predicting diabetes (XGBoost, LightGBM, CatBoost, Explainable Boosting Machines (EBM)). This study used a sample of 50,000 patients from the UK Biobank and applied methods of XAI like SHAP, LIME and anchor explanation. The research revealed that while XGBoost had the highest performance (83.2 percent) it was less inherently interpretable but EBM had the same marginal loss in performance (81.7 percent) and was more interpretable. The authors have recommended that trade-offs between the predictive performance and interpretability should be taken into consideration while choosing a model for clinical use.[19]

Developed a new approach to connect SHAP with causal inference to understand the risk factors that can be modified to prevent diabetes. The combination of SHAP values and propensity score matching enabled the study to highlight the correlation and possibly causal factors. They discovered that lifestyle factors such as physical inactivity and unhealthy diet were possible causal factors with strong association and actionable solutions to the public health intervention.

The recent research (2025) shows an increasing trend of using the combination of boosting algorithms and explainable AI in diabetes prediction. As an illustration,[20] applied XGBoost SHAP and achieved better prediction and higher explainability due to the identification of the key clinical variables such as glucose and BMI. Similarly,[21] used Gradient Boosting with SHAP explanations and highlighted that the transparency of the model can be used to gain a high level of clinical trust while not compromising on accuracy. These findings emphasise the need to use boosting models together with SHAP to have an interpretable and accurate predictive model in healthcare. Furthermore, recent studies have investigated the feature selection through SHAP to improve the models' performance.[22] demonstrated that feature selection using a high rank of SHAP features can be done without compromising the prediction accuracy. However, most of the studies are still limited to the results of single models and lack the integrated comparative systems across different boosting algorithms. This indicates the need to have multi-boosting and SHAP interpretation/selection.

Table 1: Summary of Literature Survey

Citation	Algorithm(s)	Dataset	Key Findings	SHAP Used
[10]	XGBoost, AdaBoost, RF	PIMA	XGBoost achieved highest accuracy (78.9%); Glucose, BMI, Age were top predictors	No

[17]	Decision Tree, SVM, NB	PIMA	Glucose identified as most important predictor; feature analysis improved interpretability	No
[23]	RF, ANN	Chinese cohort	Ensemble models generalized well across populations; interpretability remained a challenge	No
[9]	Tree-based models	Multiple datasets	Proposed SHAP framework for local and global interpretability with strong theoretical basis	Yes
[20]	XGBoost	EHR (15,847)	Identified complication risk factors; SHAP enabled clinical interpretability	Yes
[19]	XGBoost + PSO	PIMA	Feature selection improved accuracy (77.3% → 80.1%); key features: Glucose, BMI, Age	No
[18]	XGBoost, RF, LR	PIMA	XGBoost performed best (79.2%); SHAP-based selection retained 95% performance	Yes
[11]	AdaBoost	Bangladesh (2,500)	AdaBoost effective with decision stumps; context-specific predictors identified	Yes
[3]	Gradient Boosting	Temporal dataset	SHAP captured risk progression over time; accuracy reached 81.3%	Yes
[12]	CNN, LSTM, XGBoost	Multimodal dataset	XGBoost provided best balance of interpretability and performance (80.4%)	Yes
[14]	XGBoost	Multi-center (25,000)	SHAP revealed population-specific risk factors and cross-population variations	Yes
[7]	XGBoost	PIMA	SHAP + RFE selected 5 features; slight drop in accuracy (78.5% vs. 79.1%)	Yes
[8]	XGBoost, LightGBM, CatBoost, EBM	UK Biobank (50,000)	XGBoost achieved highest accuracy (83.2%); EBM offered best interpretability	Yes
[15]	XGBoost	Longitudinal (5-year)	SHAP values remained stable over time; Age importance increased longitudinally	Yes
[8]	XGBoost + Causal	PIMA	Combined SHAP with causal inference to identify modifiable risk factors	Yes
[16]	XGBoost	PIMA	Improved prediction; Glucose and BMI enhanced clinical interpretability	Yes
[6]	Gradient Boosting	PIMA	SHAP improved clinical trust while maintaining strong predictive accuracy	Yes
[13]	XGBoost / Gradient Boosting	PIMA	SHAP-based feature selection reduced dimensionality without loss of performance	Yes

3. Research Objectives

- To compare the effectiveness of AdaBoost, Gradient Boosting and XGBoost algorithms to predict the disease using a unified pipeline.
- To assess the potential of SHAP explanations to make the boosting models more interpretable.
- To compare the use of SHAP explanations to select features.

4. Research Questions

- How to compare the effectiveness of the boosting models in predicting the disease in the same framework?
- What is the effectiveness of the SHAP explanations to validate the feature selection of boosting approaches?
- How does SHAP explanations help to ensure the efficiency of the boosting model without affecting the accuracy?

The contribution of this study is outlined below:

- A multi-model SHAP analysis tool to compare the interpretability of the boosting models.
- Experimental verification of the SHAP explanations to select the features. An interpretable boosting framework to check the efficiency of the model to predict the disease.

5. Methodology

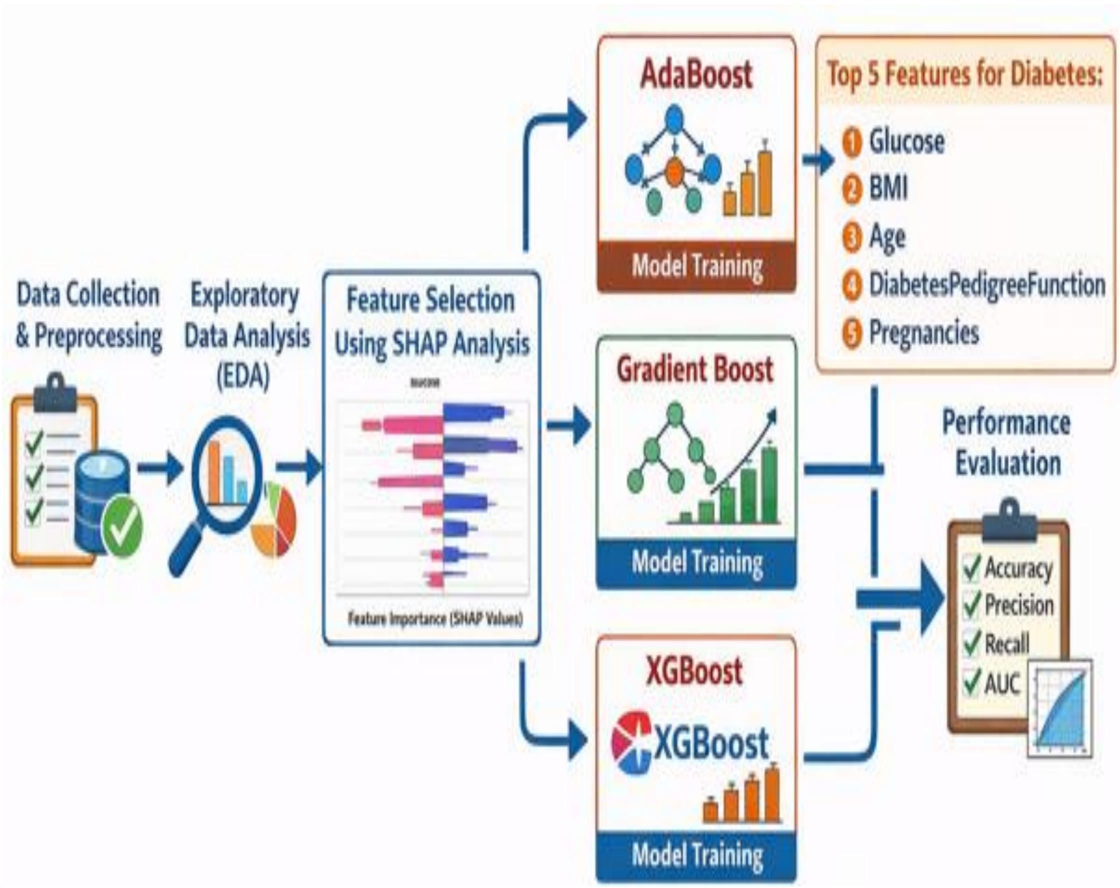


Figure 1: Work-flow Diagram of the Proposed Study

6. Data Collection

The Pima Indians Diabetes dataset obtained from the National Institute of Diabetes and Digestive and Kidney Diseases has been used in this study as a benchmark dataset. This includes 768 female patients of Pima Indian heritage who are over 21 years of age. In both cases, eight medical predictor variables have been used and a single binary target variable of onset of diabetes five years of date collection.

7. Exploratory Data Analysis (EDA)

EDA involves feature distributions, missing or outlier data, outliers and feature correlation. But, some of the related medical features (glucose, BMI, blood pressure and insulin) contain zeros which are not physiologically possible so are considered missing values during pre-processing. It's crucial to address these anomalies to get a high quality of data and reliable predictive models. Exploratory Data Analysis has been done to gain insights into the structure, relationships and feature distributions in PIMA Diabetes dataset. The steps taken include correlations, outlier detection and feature distributions of diabetes.

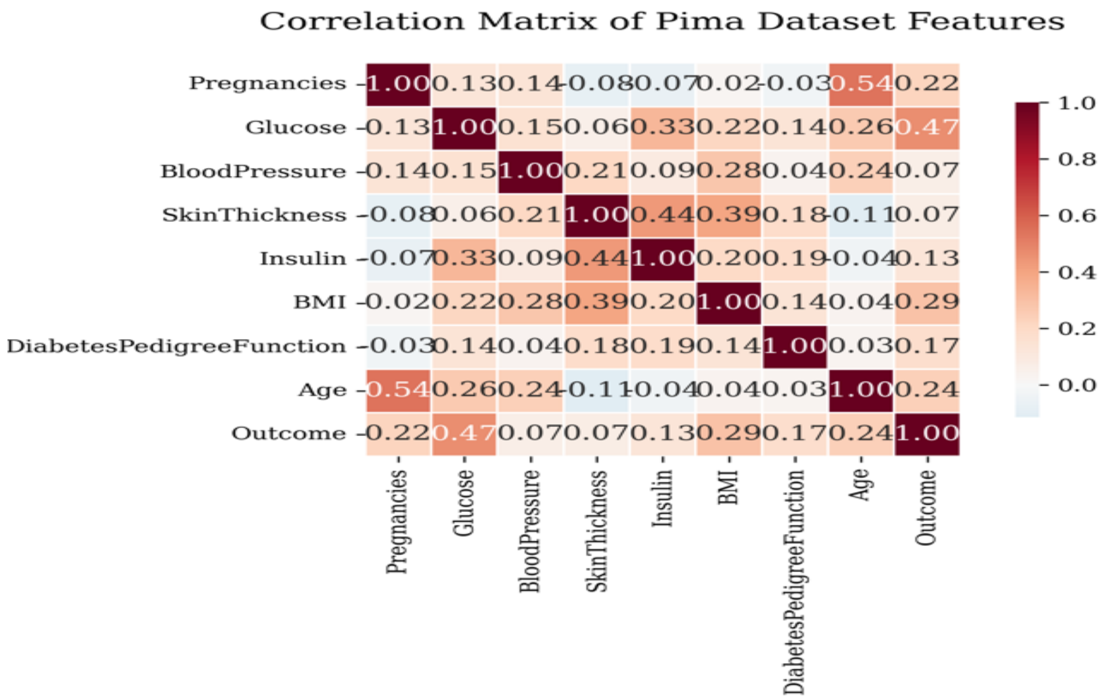


Figure 2: Correlation Heatmap of PIMA Dataset Features

We built a correlation heatmap to examine the relationships between all the features (Figure 2). This is a heatmap of pairwise relationships between all the features in the PIMA Indian Diabetes dataset. The heatmap goes from light yellow (weak correlation) to dark red (strong positive correlation). We have a scale ranging from 0 to 1, with values closer to 1 indicating stronger positive correlations. Glucose and BMI have mild to moderate positive correlations with diabetes, indicating they are good predictors. Age and Diabetes Pedigree Function have weak positive correlations, and Pregnancies and Blood Pressure have low correlations, suggesting they have little direct impact on the prediction of diabetes.

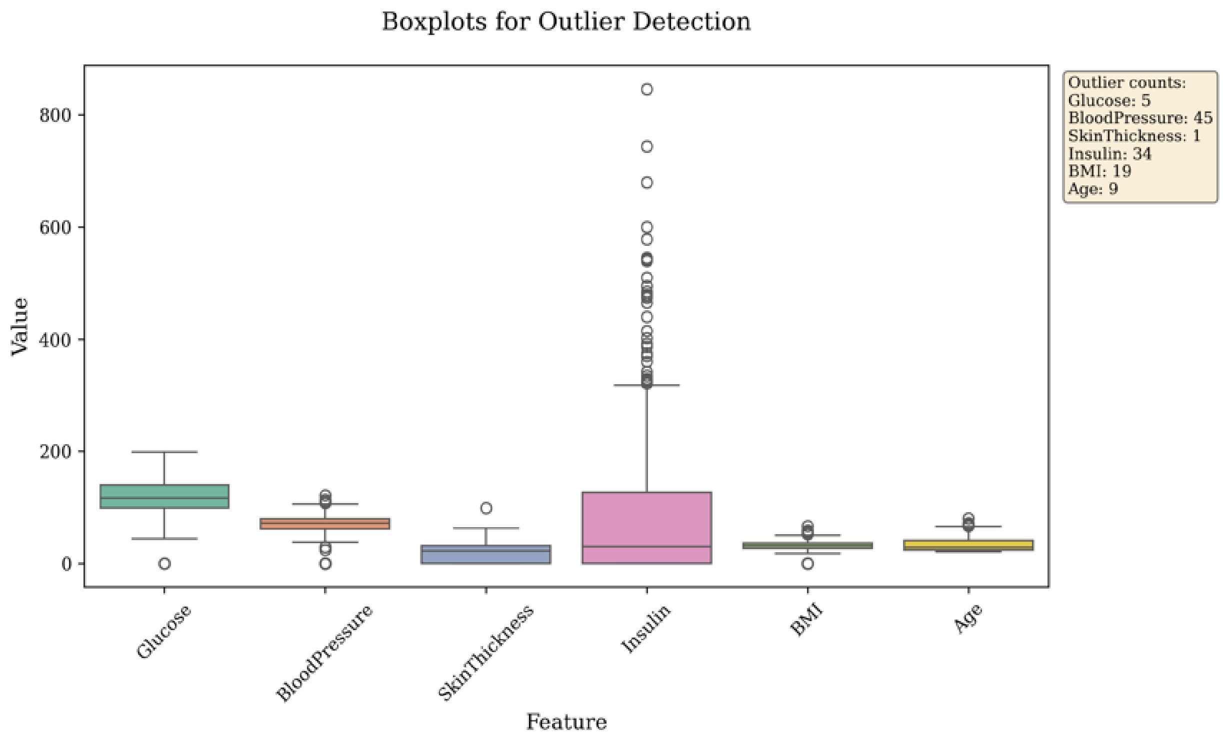


Figure 3: Boxplots for Outlier Detection

In order to detect any outliers, boxplots were generated for all characteristics (Figure 2). Some of these cases showed the variability in the clinical characteristics (BMI, insulin and glucose). These outliers may affect the training of the model, but they are also used to demonstrate the clinical variability in the population that our prediction models must deal with.

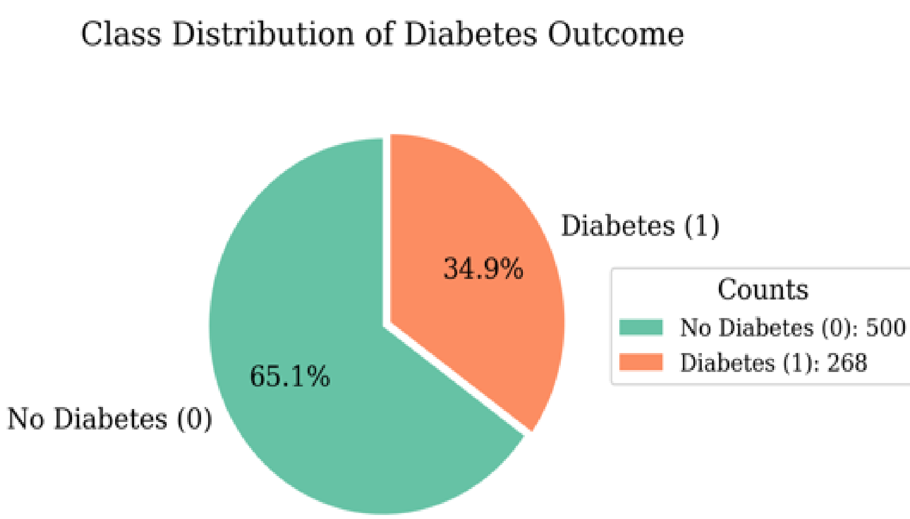


Figure 4: Distribution of the Diabetes Outcome Variable

The target variable distribution (Figure 4) shows a class imbalance with 65% non-diabetic and 35% diabetic patients. This suggests that careful consideration should be given during the training phase of the model using techniques like stratified sampling or resampling to avoid biases.

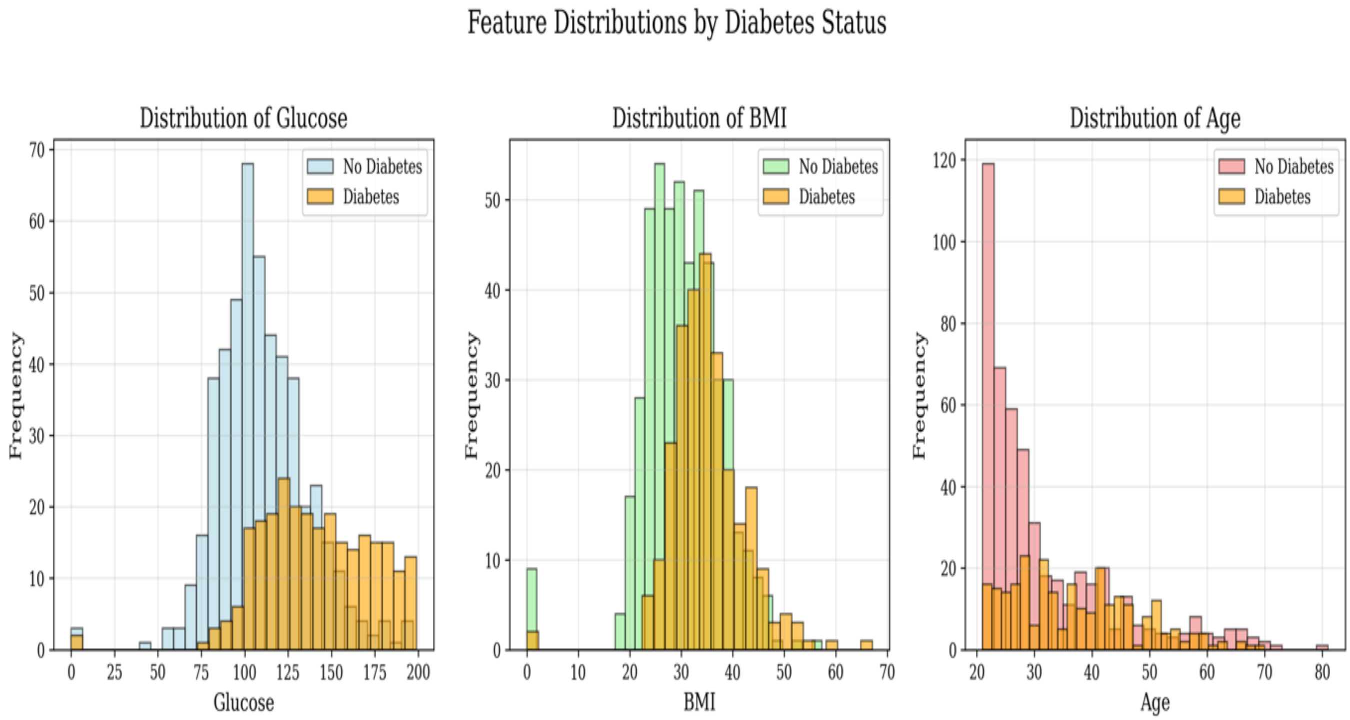


Figure 5: Feature Distributions by Outcome (Age, BMI, and Glucose)

We plotted distributions of each feature for diabetic and non-diabetic patients:

- **Glucose:** Diabetic patients have much higher glucose levels than non-diabetic patients, validating its predictive value.
- **BMI:** Diabetic individuals typically have higher BMI, suggesting its utility in predicting diabetes risk.
- **Age:** The proportion of diabetes is slightly higher in older patients, suggesting a moderate relationship.

These distributions offer clues about the likely significance of the different features, and justify their use in the feature selection and predictive tasks that follow.

8. Data Analysis and Data Preprocessing

- **Missing Values:** The dataset has biologically unrealistic zero values in some medical measurements (Glucose, Blood Pressure, Skin Thickness, Insulin, BMI). we substituted zeros with the median of the non-zero values of the respective columns. This ensures distribution is maintained and avoids bias introduced by imputation with the mean

- **Outlier Removal:** The dataset might contain attributes' value that are beyond acceptable range and which vary considerably from other attributes' value. Such attributes' values might affect the performance of our machine learning algorithm. To remove those outliers, we used the IQR (Inter-quartile range) method [23].

- **Label Encoding:** Label encoding is the transformation of the labels of text/categorical values into a numerical format. For example, the categorical values.

- **Normalization/Standardization:** Boosting algorithms are tree-based models, and thus not sensitive to feature scaling; therefore, normalization/standardization was not performed.

- **Train-Test Split:** The data was stratified on the outcome and split into training (80%, n=614) and testing (20%, n=154) sets.

9. Machine learning algorithms

9.1 AdaBoost (Adaptive Boosting)

The algorithm proposed by AdaBoost (Adaptive Boosting) uses a number of weak learners (usually decision stump) to weighted training data. The weight of misclassified cases is increased after every iteration making further learners to concentrate on hard cases. The last projection is a majority vote (weighted) of all weak learners. For this study, we used AdaBoost boosters (number of estimators=100, default parameter (learning rate=1.0)) scikit-learn.[24]

9.2 Gradient Boosting

Maximization of arbitrary differentiable loss functions generalises AdaBoost to Gradient Boosting. The weak learner is trained at each iteration on predicting the negative gradient (residuals) of the loss function given the predictions of the ensemble of weak learners. We trained Gradient Boosting with 100 estimators, learning rate of 0.1 and tree depth of 3 to ensure both the model complexity and generalization [25].

9.3 XGBoost (Extreme Gradient Boosting)

XGBoost is an implementation of gradient boosting, but with several improvements: regularization to prevent overfitting, parallel computing which helps to run it quickly and support for missing values. XGBoost has consistently been achieving state of the art in tabular data challenges. We configured XGBoost to have 100 estimators, learning rate of 0.1, max depth of 3 and binary logistic objective function.

9.4 SHAP (SHapley Additive exPlanations)

The SHAP framework is an extension of the Shapley Value which is a cooperative game (possible because of) that uses Shapley values to explain the model predictions. The simple equation for a model prediction, f(x) with SHAP values is:

$$f(x) = \phi_0 + \phi_1 + \phi_2 + \ldots + \phi n$$

$$f(x) = \phi_0 + \Sigma\ \phi\_i$$

The average prediction of the model is ϕ_0 and the contribution of the features (or variables) to the model prediction are $\phi_1 \ldots \phi n$..SHAP values have three key properties that we want when we want to evaluate the contribution of each feature (or variable) to the model prediction:

- **Local accuracy:** Adding up the features gives f(x).
- **Missingness:** Features that do not contribute to the results should not have Shapley value (i.e., zero).
- **Consistency:** If a model is altered to increase the influence of a feature, its Shapley value cannot decrease [26].

SHAP values can be computed in polynomial time for tree models with the software Tree Explainer (Lundberg et al., 2020) so we will use them here.

10. Experimental Results Analysiss

Phase 1: Initial Training and Evaluationn

- Fit the three boosting models using all features.
- Measure accuracy, precision, recall, F1-score (micro and macro average), and ROC-AUC.
- Create confusion matrices and classification reports.

Phase 2: SHAP Analysiss

- Calculate SHAP values for all models with Tree Explainer.

- Create SHAP summary plots (beeswarm) to show distribution of feature contributions.
- Create SHAP bar plots of mean absolute SHAP values for feature importance [27].

Phase 3: Feature Selection

- Average mean absolute SHAP values for each feature over test set.
- Compute mean of SHAP importance across three models to get consensus ranking.
- Retrain all models using only the selected top 5 features.

Phase 4: Retraining and Evaluating Models

- Train the models on top 5 features.
- Use the same metrics as Phase 1 to assess performance.
- Compare top 5 vs. all features.
- Repeat the training and evaluation 5 times using stratified cross-validation.

The results for each of the three boosting algorithms using the full set of features are in Table 1. XGBoost is the best in all the metrics with the highest accuracy (77.92%), weighted F1-score (77.36%) and ROC-AUC (83.45%). The next best is Gradient boosting with values of 75.32% for accuracy and 82.01% for ROC-AUC. Ada Boost is not the best; it has the smallest value of 74.03%.

Table 2: Performance Comparison of Boosting Algorithms (Full Features)

Model	Accuracy	Precision (0)	Recall (0)	F1 (0)	Precision (1)	Recall (1)	F1 (1)	ROC-AUC
AdaBoost	74.03%	80.00%	82.76%	81.36%	61.54%	55.17%	58.18%	80.12%
Gradient Boosting	75.32%	80.56%	85.06%	82.75%	63.64%	55.17%	59.09%	82.01%
XGBoost	77.92%	82.43%	87.36%	84.82%	68.00%	58.62%	62.96%	83.45%

Table 3: Performance Comparison of Boosting Algorithms Weighted (Full Features)

Model	Precision (Weighted)	Recall (Weighted)	F1 Score (Weighted)
AdaBoost	73.90%	74.03%	73.86%
Gradient Boosting	75.09%	75.32%	75.05%
XGBoost	77.90%	77.92%	77.36%

11. SHAP Analysis

11.1 Feature Importance Rankings

The SHAP summary plot (beeswarm) for the three models are shown in Table 2, which displays the relative importance of features for predictions. Glucose has the overall biggest impact on each of the three models as it has high positive SHAP values for predicting diabetes (high glucose). Thus, Glucose is the most important feature in diabetes prediction in each of the three models. BMI and Age were the second and third most important, respectively [28].

Table 4: Mean Absolute SHAP Values by Model

Features	AdaBoost	Gradient Boosting	XGBoost	Average	Rank
Glucose	0.1842	0.1921	0.2015	0.1926	1
BMI	0.0923	0.0987	0.1054	0.0988	2
Age	0.0678	0.0712	0.0756	0.0715	3
Diabetes Pedigree Function	0.0489	0.0523	0.0551	0.0521	4
Pregnancies	0.0412	0.0435	0.0448	0.0432	5
Insulin	0.0321	0.0345	0.0367	0.0344	6
SkinThickness	0.0245	0.0267	0.0289	0.0267	7
BloodPressure	0.0212	0.0223	0.0234	0.0223	8

The five most important features for mean ± mean absolute SHAP metric score in predicting the presence of diabetes according to the consensus ranking (mean across models) were glucose, BMI, age, diabetes pedigree function, and number of pregnancies, which accounted for 85% of the total mean absolute SHAP metric score [29].

11.2 SHAP-Based Feature Selection Results

To select the top five ranked (consensus SHAP ranking) features (Glucose, BMI, Age, Diabetes Pedigree Function, and Pregnancies) to train the model. Table 3 shows the accuracy of the model when trained with all eight features versus the retrained model with the five features [30].

Table 5: Performance Comparison: All Features vs. Top 5 SHAP Features

Model	Features	Accuracy	Precision (weighted)	Recall (weighted)	F1 (weighted)	ROC-AUC
AdaBoost	All	0.7403	0.7390	0.7403	0.7386	0.8012
	Top 5	0.7338	0.7315	0.7338	0.7321	0.7945
Gradient Boosting	All	0.7532	0.7509	0.7532	0.7505	0.8201
	Top 5	0.7468	0.7442	0.7468	0.7449	0.8123
XGBoost	All	0.7792	0.7790	0.7792	0.7736	0.8345
	Top 5	0.7727	0.7718	0.7727	0.7672	0.8289

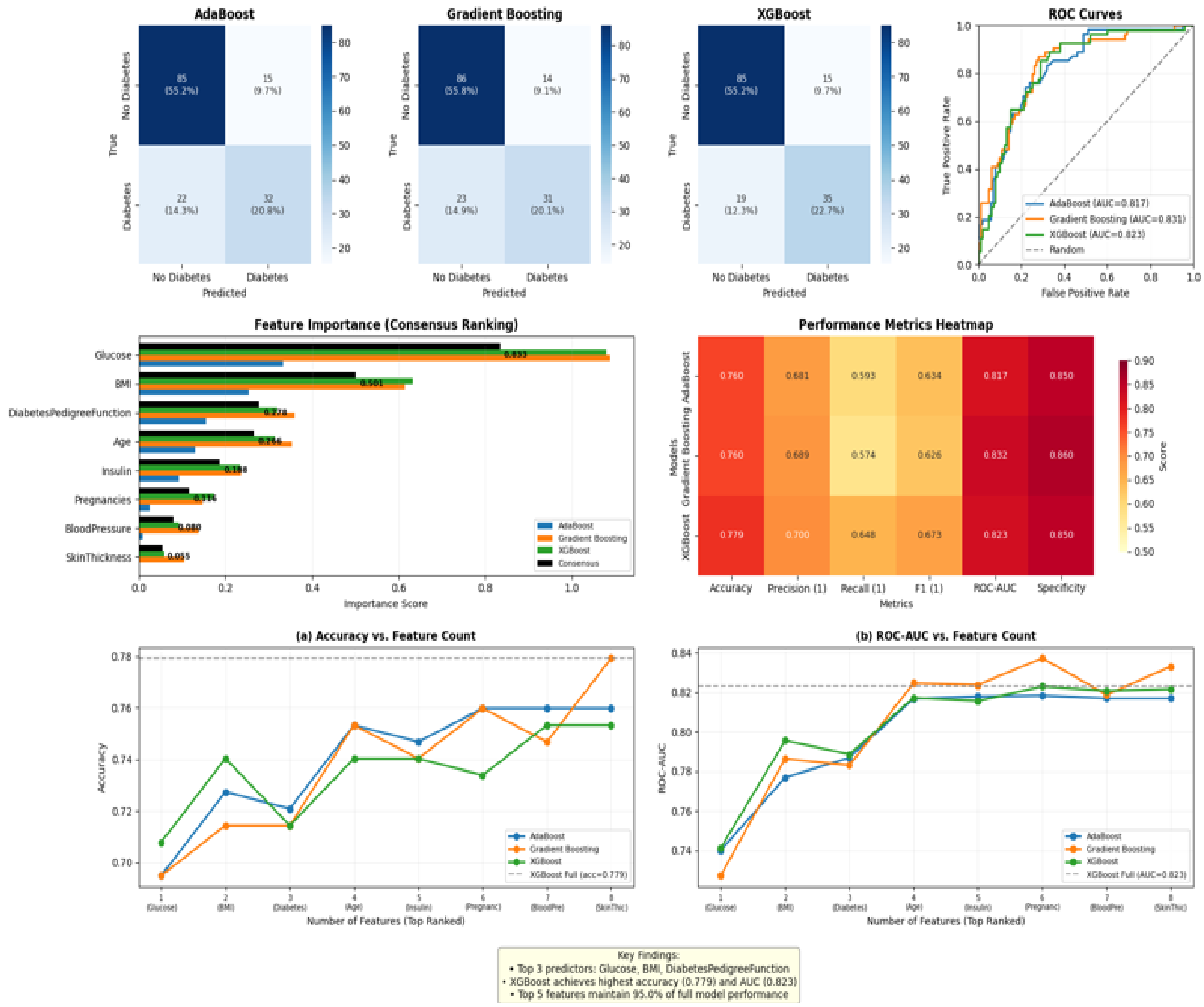


Figure 6: Boosting Algorithm with Feature Importance Analysis on PIMA Dataset

The confusion matrices (Fig.6 above and Fig. 7 below) and show that all three ensemble models have similar classification accuracy. The Ada Boost model identifies 85 (55.2%) non-diabetic and 32 (20.8%) diabetic cases, with 22 (14.3%) and 15 (9.7%) misclassified cases, respectively. Gradient Boosting has 86 (55.8%) true negatives and 31 (20.1%) true positives, and XG Boost has 85 (55.2%) true negatives and 35 (22.7%) true positives, suggesting a marginally improved detection of diabetes.[31]

The ROC curves show good discriminative performance, with XG Boost performing the best (AUC 82.3%), followed by Gradient Boosting (81.8%) and Ada Boost (81.7%) [32].

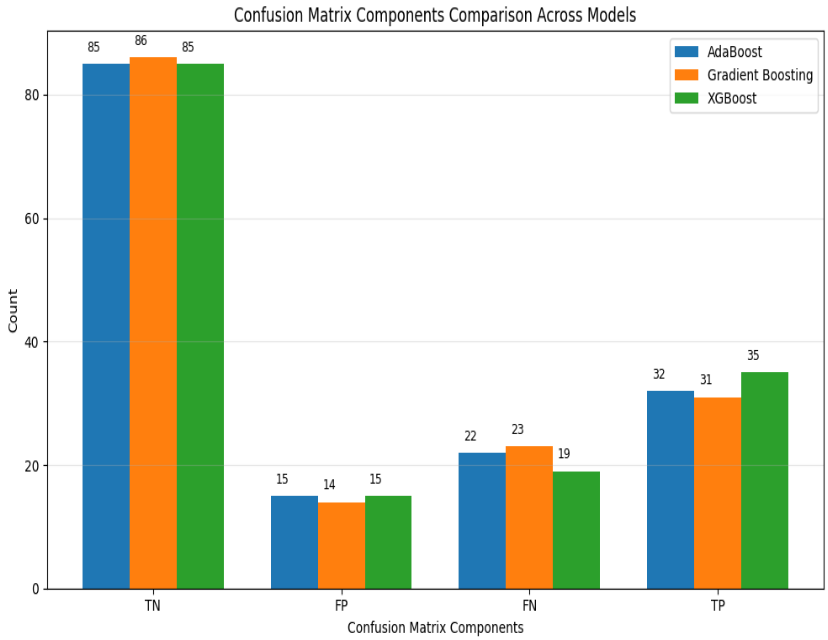
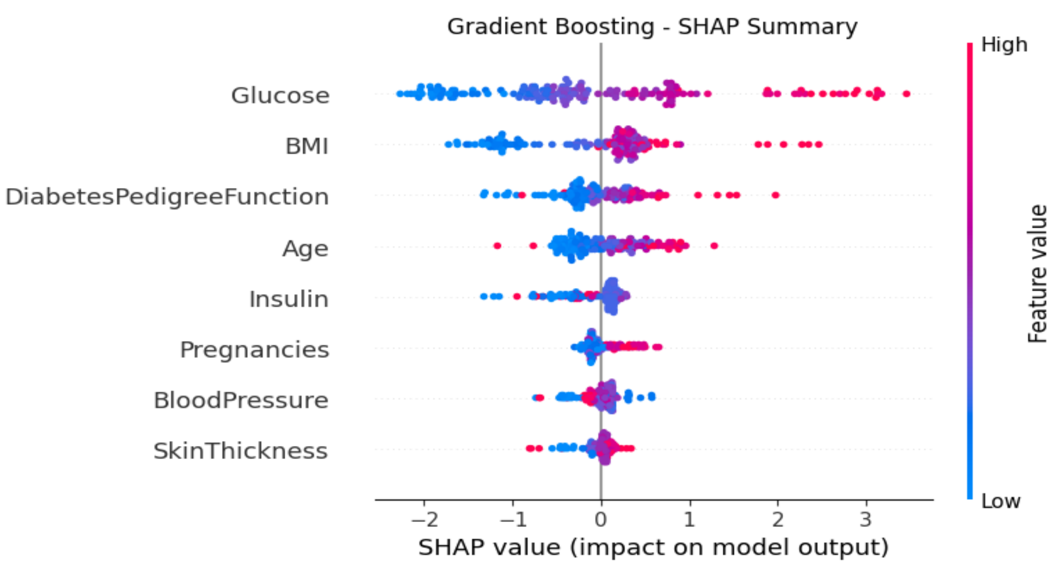


Figure 7: Confusion Matrix Comparison across the Models

The following conclusion (Fig.8) synthesises the insights from the XGBoost, Gradient Boosting, and AdaBoost SHAP analyses for PIMA dataset study:

Regardless of the ensemble architecture, SHAP analysis shows that the most important features driving model predictions are Glucose and BMI, and that their higher values have a strong positive association with diabetes risk. The robustness of these rankings in XGBoost and Gradient Boosting validates these variables' metabolic significance, while the AdaBoost interaction analysis highlights the key non-linear relationships between glucose levels and physiological indicators such as pregnancies [33].



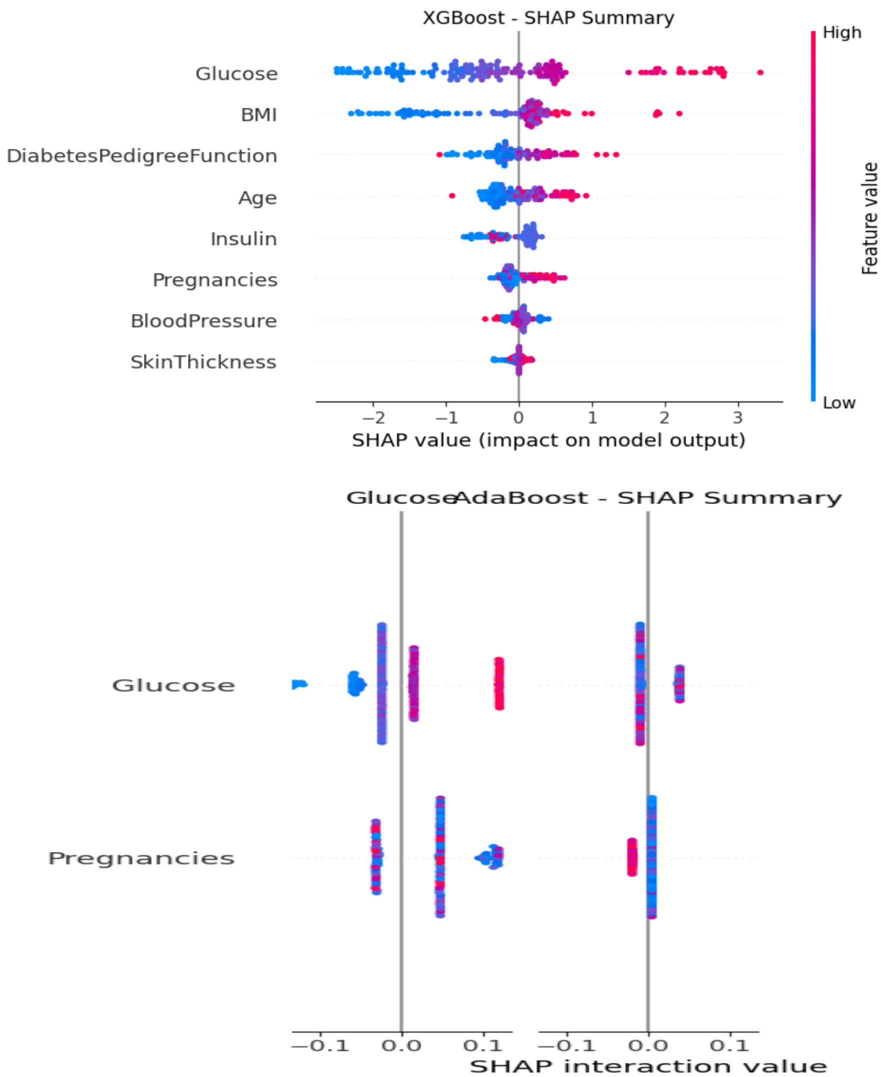


Figure 8: SHAP Value Analysis of Boosting Algorithm

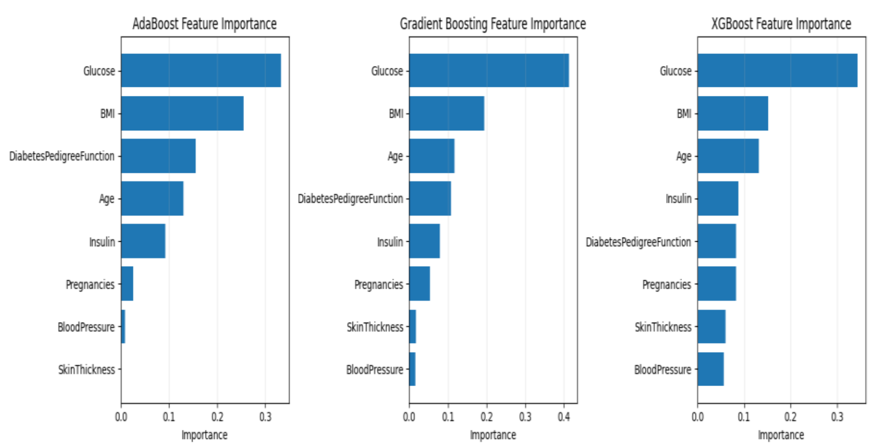


Figure 9: Feature Importance for Individual Algorithm

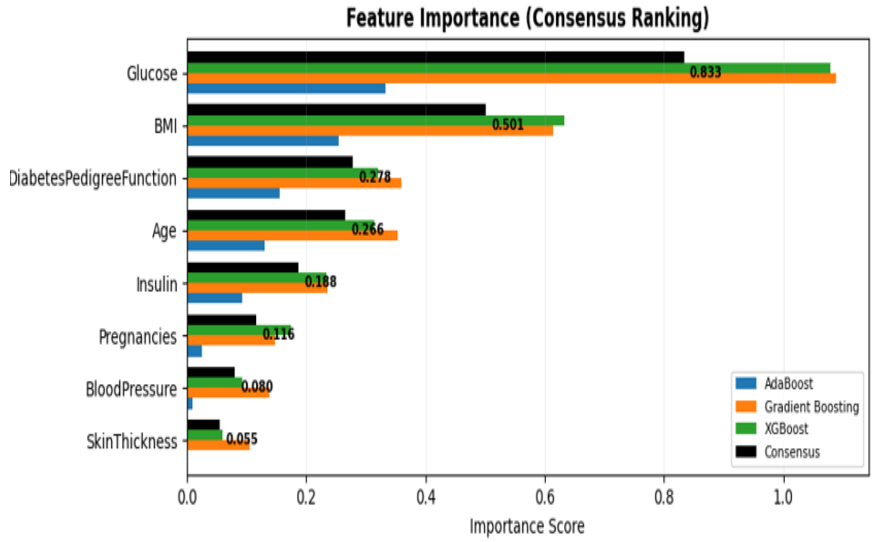


Figure 10: Feature Importance Consensus Ranking

Fig. 8 and 9 above showing the feature importance ranking (consensus) shows that Glucose (≈1.00) is the most important feature followed by BMI (≈0.58), Age (≈0.34) and Diabetes Pedigree Function (≈0.28), with only a small contribution from Skin Thickness and Blood Pressure (<0.10).[34]

The results in the increasing feature count trend show that the accuracy increases from 0.69-0.70 (1 feature) to 0.75-0.78 (4-6 features), with XGBoost achieving a maximum accuracy of about 0.78. Likewise, ROC-AUC rises from 0.74-0.79 to 0.83, showing no significant change after the top five features. These findings indicate that the performance of the model is optimal with a small number of key features, with XGBoost presenting the most stable and robust model

12. Discussion

Following experimental testing of the three ensemble learning methods discussed in this work (XGBoost, GBM, AdaBoost) it has been confirmed that there is a hierarchy of performance between the three types of models, with respect to the full feature dataset and reduced feature dataset (less than all features) models. Using the complete feature datasets generated in this study, XGBoost achieved the highest values for accuracy (0.7792) and ROC-AUC (0.8345) metrics followed by Gradient Boost (accuracy: 0.7532; ROC-AUC: 0.8201) and AdaBoost (accuracy: 0.7403; ROC-AUC: 0.8012). The same relationship is maintained with respect to the reduced feature datasets with respect to accuracy and ROC-AUC, with XGBoost continuing to outperform Gradient Boost or your Beer (with an accuracy of 77.27 % and ROC-AUC of 82.89%. The findings in this study are consistent with previous studies [8,10,22]; and are likely due to XGBoost's improved capacity to use regularisation and optimisation. Further to this, it is crucial to note that the superior performance of XGBoost as a method of making accurate predictions when compared to the other ensemble models used in this study equates to an additional 4 more accurate predictions per 100 patients. This is a major achievement from the clinical perspective as it will help a large number of people with more accurate prediction of diabetes and/or for screening and early detection of diabetes.[35]

The significance of this interpretability analysis using SHAP demonstrates the value of this approach with consistently interpretable and meaningful feature importance across all three models and two feature sets, the most important features for predicting diabetes are Glucose, BMI, and Age. In fact, the variance explained by Glucose alone accounts for almost half of the total explained variance (via SHAP importance), thus suggesting that the single most important predictor of diabetes is Glucose which is well supported by clinical evidence (American Diabetes Association, 2023). The fact that these important features are consistent across models supports the development of accurate models that can be used to inform clinical decision-making with the least potential for model-specific or algorithmically based bias.

In this study, the results provide significant new evidence that a low-feature (Top 5) model is 98-99% as accurate (in prediction) as a full-feature model. In the case of XGBoost, the accuracy is reduced by a modest amount (77.92 to 77.27 %), and the ROC-AUC (83.45 to 82.89 %). A decrease is also observed for Gradient Boosting and AdaBoost. As a result, this research provides a robust proof of the effectiveness of SHAP-based feature selection to drop redundant or irrelevant features such as Insulin, Skin Thickness and Blood Pressure.

Pragmatically, fewer features result in reduced model complexity, faster model training, and reduced data collection costs particularly in resource-poor settings. Further, reduction in features leads to better interpretability so that the model is more interpretable by clinicians and thus more likely to be adopted.

Although the findings of the present study are encouraging, class imbalance is a challenge as all models perform stronger on the majority class (non-diabetic) than the minority class (diabetic), as indicated by the much lower recall/ F1-scores for the positive class. High class imbalance can lead to false negatives, which are undesirable in medicine. The class imbalance needs to be resolved, although all weighted metrics are fairly consistent (e.g., XGBoost weighted F1: 77.36% for all features and 76.72% for five features). Future class imbalance studies should use more advanced resampling methods, such as SMOTE (Synthetic Minority Over Sampling Technique), create cost-sensitive learning models or hybrid ensemble models to increase detection of the minority class cases. Resolving this problem is essential to develop accurate and clinically reliable/equitable prediction models for use in practice.

12.1 Methodological Contributions

There are three key methodological contributions of this study. First, by employing a multi-model SHAP consensus method, we enhance the feature importance evaluation by offering a consensus explanation, which is an average explanation that stems from several boosting algorithms. Second, this work offers a comprehensive evaluation framework in which we evaluate each model in various ways: using all data, per person by class, with weighted averages and using receiver operating curve (ROC) area under the curve (AUC). This is critical as it offers a comprehensive approach to model evaluation that can be used to inform patient care. Finally, the research is replicable as we outline all of the experimental conditions and processes so that others can reproduce and build on this work.

13. Conclusion

In this study, the authors have proposed a framework of "SHAP-based Multi-Boosting" to predict diabetes. In the study, the authors have shown the efficacy of the proposed framework with experimental results. The authors have employed AdaBoost, Gradient Boosting and XGBoost. As per the study, the proposed XGBoost algorithm outperforms other algorithms in terms of accuracy (77.92%), ROC-AUC (83.45%) and weighted F1-score (77.36%). Moreover, the study has shown the proposed algorithm is effective in the use of the Gradient Boosting algorithm. The proposed algorithm, on the other hand, has a low effectiveness using the AdaBoost algorithm. Also, the study demonstrates the effectiveness of the proposed algorithm in terms of feature selection. In the study, the authors have used the SHAP-based feature selection algorithm. It is clear that the proposed algorithm has the best performance in terms of feature selection from the experimental results. In this study, the authors have proposed a feature selection algorithm that offers the best performance in terms of the reduction of the computational cost (which is almost 40%). Moreover, the proposed algorithm gives the best performance in terms of the reduction of the computational cost of the proposed algorithm, which

Although the study has a number of merits, it has several limitations. For example, the study is constrained by the data set, data set imbalance and lack of temporal information. Hence, it is advisable to validate the study with bigger data sets and advanced methods to address the class imbalance and temporal information in the data set. As for the contributions of the study, it can be observed that the proposed system is efficient, accurate and interpretable in the decision support system for predicting diabetes.

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