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Enhancing diabetes prediction: integrating machine learning with explainable artificial intelligence

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ABSTRACT

Early detection of diabetes is critical in preventing disease progression and improving patient outcomes. By integrating machine learning with explainable artificial intelligence (XAI) frameworks, this research seeks to improve both the predictive accuracy and the transparency of diabetes diagnostics using the Pima Indian diabetes dataset. The machine learning models used in this study are logistic regression, random forest, and gradient boosting, which resulted in best accuracy of 93.2%. Some of pre-processing steps taken were handling of missing data, normalization, feature scaling and synthetic minority over-sampling technique (SMOTE) for handling class imbalance. Use of Shapley additive explanations (SHAP) and local interpretable model-agnostic explanations (LIME) XAI methods has proven that glucose, body mass index (BMI), and insulin are the most crucial features when it comes to prediction. These techniques further enhance the trust of the clinicians and stakeholders by improving the understanding of how the features contribute to individual predictions, which enhances the model prediction as a whole. The findings prove that there is indeed a marked improvement in the understanding of the machine learning models and their predictions with no compromise on performance. This research underscores the advantages of integrating XAI within machine learning workflows, demonstrating how to achieve a synergy between high-performance predictive power and transparent, human-readable results.

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1. INTRODUCTION

The statistics from 2021 show that 537 million people are diabetics, and this number could escalate to 783 million by 2045 [1]. As with many diseases, diabetes is also accompanied with severe complications and can lead to premature death. Minimizing the risk of death becomes too costly along with the increase in spending on healthcare. Efforts must be made in the early stages to maximize the benefits during later years, however, the traditional methods to diagnose this complex issue often delay the identification process and lack the scalability which forces the development of automation using machine learning [2].

Research and developments on automation using machine learning techniques are on the go for diabetes prediction, but there are still many issues to tackle. A majority of models work great without any explanation, which proves to be a bad decision in terms of system integration. The inability of these approaches to clearly understand the processes which build these systems makes it severely impossible for them to trust or depend on them [3]. Trusting these models is not easy, hence, existing frameworks focus on the accuracy of these models, neglecting their explainable components and interpretable features, limiting

their usefulness in clinical environments [4]. Predictive approaches that are accurate and at the same time understandable by healthcare practitioners are needed in this situation.

The Pima Indian diabetes dataset is being used in our study to construct reliable diabetes prediction models. Utilizing explainable artificial intelligence (XAI) frameworks like Shapley additive explanations (SHAP) and local interpretable model-agnostic explanations (LIME), the prediction process can be seen and which of the variables played the most definitive role. This integration effectively balances high-performance machine learning with the necessity for model transparency, ensuring that the resulting predictions are both accurate and easy to understand.

The use of XAI techniques also tackles one of the primary concerns of the application of machine learning in health care [5]. It boosts the confidence level of clinicians and the patients and empowers them to make better decisions, as they can follow the logic of the model. On top of that, the model can enhance the clinical process by spotting diabetes earlier and more accurately. This research emphasizes the need for XAI in the integration of automated health care technology, and the need for addressing the issues brought on by the complex algorithms used by medicine [6]. This work is the first one to do a cross model (gradient boosting, random forest, and support vector machines) interpretability analysis and not using SHAP or LIME as most previous works do. SHAP is designed to measure global feature importance across the population, while LIME is designed to measure local explainability for each individual. This is a first from dual-method interpretability point and makes the most important contribution for this study.

The article breaks down into various sections as follows: literature on diabetes prediction with a particular focus on the challenges and gaps in the interpretability of machine learning models has been covered in section 2. Section 3 outlines the approach in which relationships such as data cleansing, model building, and application of XAI tools such as SHAP are explained. Section 4 delivers results together with performance indicators, analysis of the results' interpretability, and comparisons with other work. Section 5 analyzes the contribution of XAI for fostering transparency, clinical relevance, and other limitations of the study. Section 6 concludes the main points of the study and suggests what could be studied further.

2. LITERATURE REVIEW

Due to the intricacy of the data, diabetes prediction modeling has often relied on machine learning. The Pima Indian diabetes dataset is the benchmark dataset most commonly used in the field. Traditional models like logistic regression and decision trees have been applied to diabetes prediction with some success (65-75%) [7]. Inclusion of more sophisticated non-linear approaches in the data have given better error reductions in prediction methods like random forest, gradient boosting machines, and support vector machines. For example, Rufo *et al.* [8] applied light gradient boosting machine (LightGBM) on Pima Indian diabetes dataset with an accuracy of 78.5%. Ensemble methods were also reported by Dagliati *et al*. [9] in diabetes prediction with an F1-score of 0.79.

Nonetheless, a lot of these models have shown weak generalization performance due to overfitting on out-of-sample data, especially in the case of Pima Indian diabetes dataset which is an imbalanced dataset [10]. Deep learning and neural networks techniques, although very powerful, are usually very tedious when it comes to computation and are not as easy to explain, making them less clinically focused [11]. In addition, the algorithms' opaque nature hinders healthcare practitioners from understanding associated decision processes around these models, and hence, limits real-world utilization of these systems [12].

XAI, attempts to tame the black-box problem in machine learning models by revealing their inner workings and processes. In areas like healthcare where trust and transparency are crucial, the use of XAI has proven to be particularly useful. One of the most effective methods of XAI is SHAP, which attempts to quantify the contribution of each feature to a given prediction. For example, SHAP has been used to identify glucose level and body mass index (BMI) as risk predictors for diabetes so that clinicians can act [13]. Another such strategy is LIME, which is designed to generate, as the title suggests, understandable local approximations of a given black box model. LIME has also excelled in showing how some input features are responsible for certain predictions, which is advantageous for individualized therapy [14]. Recent studies demonstrate XAI's role in clinical validation, particularly in cardiology and early-stage cancer screening, reinforcing the need for transparent diagnostic models. Feature importance analysis is a type of explanation usually provided with tree-based models; random forest and extreme gradient boosting (XGBoost), which orders the predictors from most important to least. While simple, this approach is also more limited when it comes to reasoning about particular predictions compared to SHAP and LIME's distinctive features [15]. Also, XAI has been added to ensemble methods to make them easier to understand. For example, Ganie *et al*. [16] employed SHAP techniques to improve clarity in diabetes prediction models using boosting methods as part of their work. Furthermore, tools like individual conditional expectation plots and partial dependence plots have been used to visualize feature interactions for better understanding [17].

Even though many machine learning models predict diabetes with high accuracy, there are still some issues that are not covered. First, most of the models focus on achieving accuracy and do not care to make the model interpretable. The absence of clarifying information makes these models less useful and applicable in practice as clinicians are not willing to make decisions that they cannot verify [18].

Second, XAI SHAP and LIME methods have been applied in many fields, but not in the field of diabetes prediction. Most of the time, studies concentrate on proving these techniques are useful rather than implementing them entirely in the prediction process [19]. Take SHAP for example, it gives information about features at the level of the population, but using SHAP at the level of individual patients with diabetes has not received enough attention.

As a last observation, there is a gap that needs to be covered by systematic assessments of the impact of XAI techniques on clinical results. Most studies cease at providing theoretical explanations without checking whether XAI-based models enhance patient outcomes, decision-making, or trust among clinicians [20]. To fill these gaps, this study works to incorporate XAI technologies into the construction of a machine learning model for diabetes prediction utilizing Pima Indian diabetes dataset. The model aims to strike a balance between precision and dependability to which a certain prognosis can be accepted and comprehended. The suggested model analyzes SHAP and LIME to provide explanations regarding the contributions of features globally and locally so that pertinent parties can undertake some initiatives. Moreover, this research quantifies the clinical relevance of the model within the context of other models by measuring, in the case of the aforementioned, the precision, recall, and interpretability which is more so practical than theoretical. A summary of the aforementioned studies is provided in Table 1.

Table 1. Comparative summary of diabetes prediction studies

Study	Models used	Accuracy	Dataset	XAI method	Explainability focus
Rufo *et al*. [8]	LightGBM	78.5%	Pima Indian diabetes dataset	None	Pure performance
Dagliati *et al*. [9]	Ensemble	F1 =0.79	Clinical	None	Complications risk
Mend *et al.* [19]	Random forest, support vector machine	82.1%	Pima Indian diabetes dataset	SHAP	Global factors
This study	Gradient boosting, random forest	93.24%	Pima Indian diabetes dataset	SHAP+LIME	Global + local

3. METHOD

The research framework is organized into five distinct phases, beginning with data acquisition, progressing through preprocessing, feature engineering, and model construction, and concluding with explainability analysis. Figure 1 illustrates this sequence from a broad conceptual perspective. Meanwhile, Figure 2 provides a detailed technical breakdown of the complete end-to-end workflow engineered for this research.

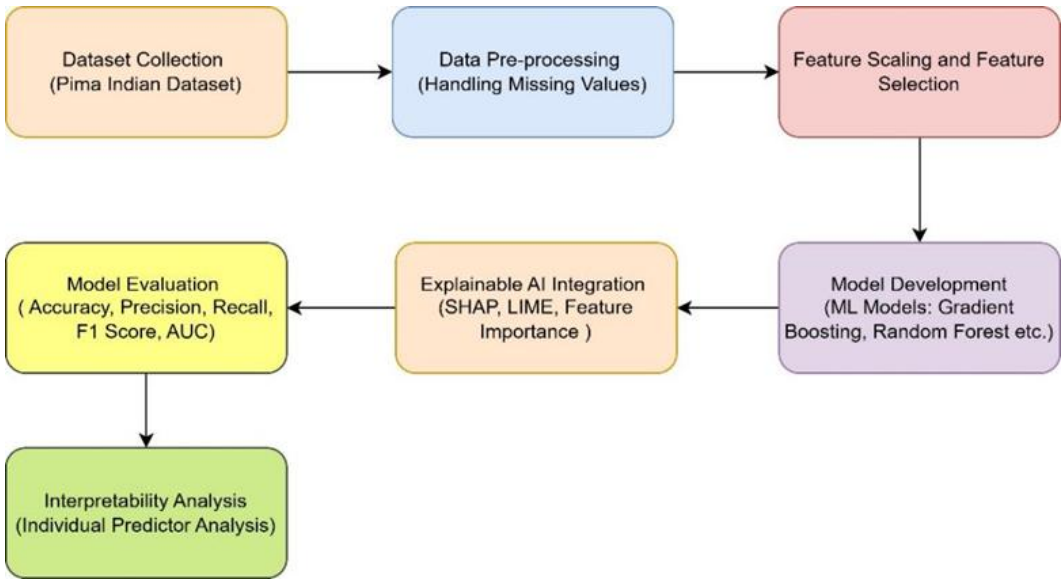

Figure 1. Research methodology

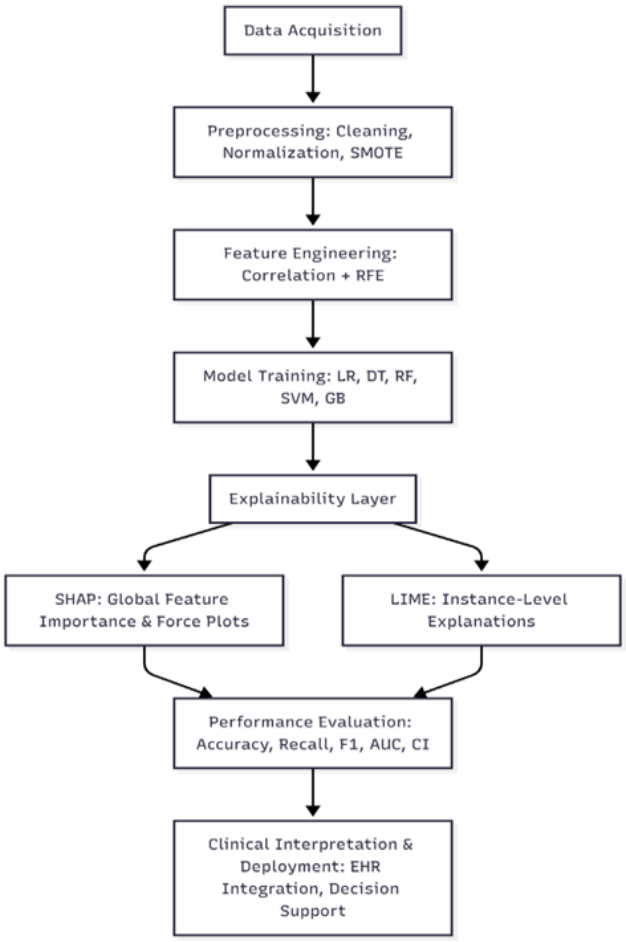

Figure 2. End-to-end pipepline

3.1. Dataset description

Sourced from the UCI machine learning repository, the Pima Indian diabetes dataset provides medical diagnostic data for 768 female patients aged 21 and older. This dataset features eight independent predictors and a binary outcome variable, where 1 denotes a diabetes diagnosis and 0 indicates a non-diabetic result [21]. A comprehensive breakdown of these individual features and their specific characteristics is detailed in Table 2.

Table 2. Pima Indian diabetes dataset overview

Feature	Description
Pregnancies	Number of pregnancies
Glucose	Plasma glucose concentration (mg/dl)
Blood pressure	Diastolic blood pressure (mm Hg)
Skin thickness	Triceps skinfold thickness (mm)
Insulin	2-hour serum insulin (mu U/ml)
BMI	BMI (weight in kg / height in m^2)
Diabetes pedigree function (DPF)	DPF (family history)
Age	Age in years

A preliminary quality check revealed that several variables, specifically skin thickness and insulin, contained numerous zero values serving as placeholders for missing data. Because these entries are physiologically impossible in a living patient, treating them as valid measurements would distort the statistical distribution and degrade model performance. To address this, the preprocessing pipeline incorporated targeted imputation and outlier detection to correct these anomalies without discarding valuable patient records.

3.2. Experimental setup

The predictive framework was developed within a Python 3.8 environment, leveraging a stack of specialized libraries for the machine learning pipeline. Data ingestion and array operations were managed via Pandas and NumPy, while the Scikit-learn library served as the core engine for model architecture and validation. To address the "black-box" nature of the high-performing models, SHAP was integrated to quantify global feature importance and LIME for case-specific diagnostic transparency.

The experimental methodology commenced by dividing the dataset into an 80/20 training and testing split, employing stratified sampling to preserve the original class distribution. For data cleaning, missing entries were addressed through median imputation and standardized all features using z-score normalization. Crucially, to safeguard against data leakage and maintain experimental integrity, the synthetic minority over-sampling technique (SMOTE) was implemented solely on the training subset, ensuring the test data remained entirely unseen.

Model selection and optimization followed a stratified 10-fold cross-validation protocol. Hyperparameters were tuned using a grid search strategy optimized for the area under the curve (AUC) receiver operating characteristic (ROC) metric. Finally, to facilitate exact repeatability of the study, a fixed random seed (42) was maintained across all stochastic processes, including dataset splitting and weight initialization. The high-level architecture of this simulation environment is visualized in Figure 3. Figure 3 outlines the computational architecture of the study, mapping the transition from initial data refinement to the final explanation layer. This structured approach ensures that the resulting diabetes predictions are not only statistically robust but also offer the interpretability required for practical clinical application.

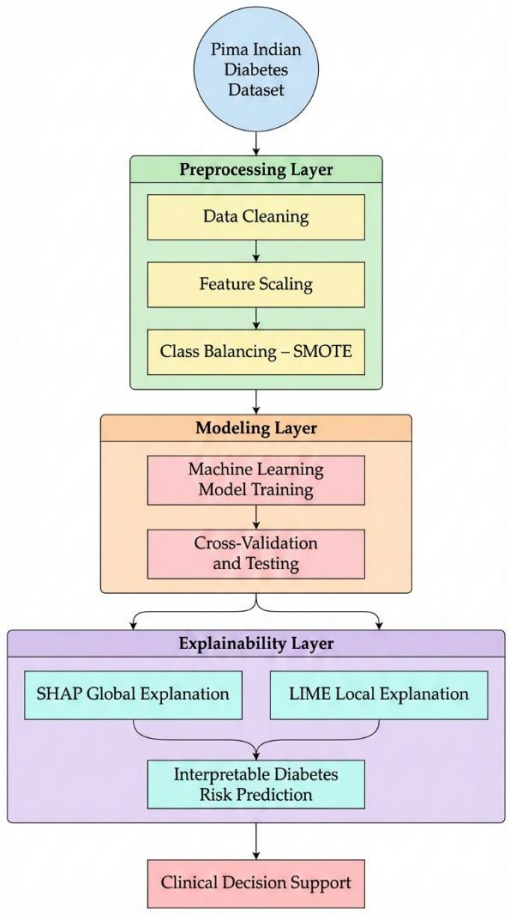

Figure 3. Schematic overview of the integrated interpretable diabetes diagnostic system

3.3. Exploratory data analysis

To explore the data further, exploratory data analysis (EDA) was performed through the use of visualization techniques. Identifying the distributions, correlations, outliers, and relationships between features and target variable using histograms, box plots, pair plots, kernel density estimation (KDE) plots, and other techniques. This is necessary for proper feature selection before performing the diabetes prediction analysis.

3.3.1. Feature distributions and skewness

Looking at the histograms, it is evident that pregnancies, insulin, BMI, DPF, and age, are capped on the higher end, that is, they are right-skewed. Glucose and blood pressure have a balanced distribution while skin thickness is slightly right skewed. Extreme values are present in insulin and BMI; hence some treatment of the outliers is required. As shown in Figure 4, the feature distributions indicate right-skewness in BMI, insulin, DPF, and pregnancies, highlighting potential need for normalization. Specifically, Figures 4(a) to 4(h) illustrate the distributions of pregnancies, glucose, blood pressure, skin thickness, insulin, BMI, DPF, and age, respectively.

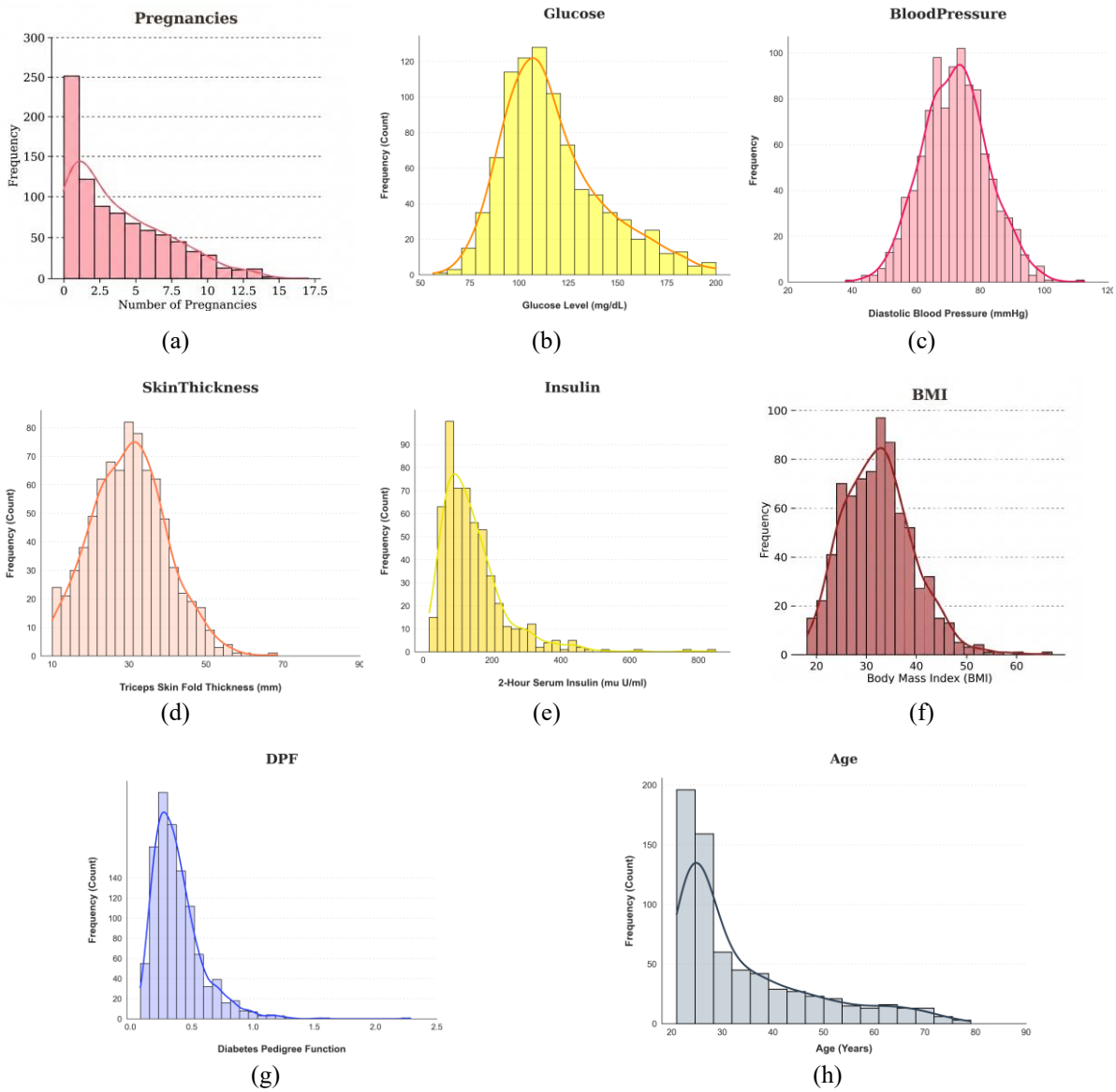

Figure 4. Feature distribution and skewness of (a) pregnancies right-skewed distribution, (b) glucose approximately normal with mild right tail, (c) blood pressure centered distribution with moderate spread, (d) skin thickness moderately right-skewed, (e) insulin highly right-skewed with long heavy tail, (f) BMI right-skewed with visible high-end outliers, (g) DPF sharply right-skewed, and (h) age right-skewed with concentration in younger age groups

3.3.2. Outlier detection and data range

Aside from the mentioned variables, there are some extreme values in some other variables, as portrayed in the box plots. Outliers on the higher side are more prevalent in the following: DPF, age, glucose, insulin, and also on pregnancy. On the other side of the spectrum, blood pressure, and skin thickness indicate

lower bound outliers, which are possibly due to some missing or incorrect data as shown in Figure 5. Outlier removal during data preprocessing stages can increase model performance. Specifically, Figures 5(a) to 5(h) illustrate pregnancies, glucose, blood pressure, skin thickness, insulin, BMI, DPF, and age, respectively.

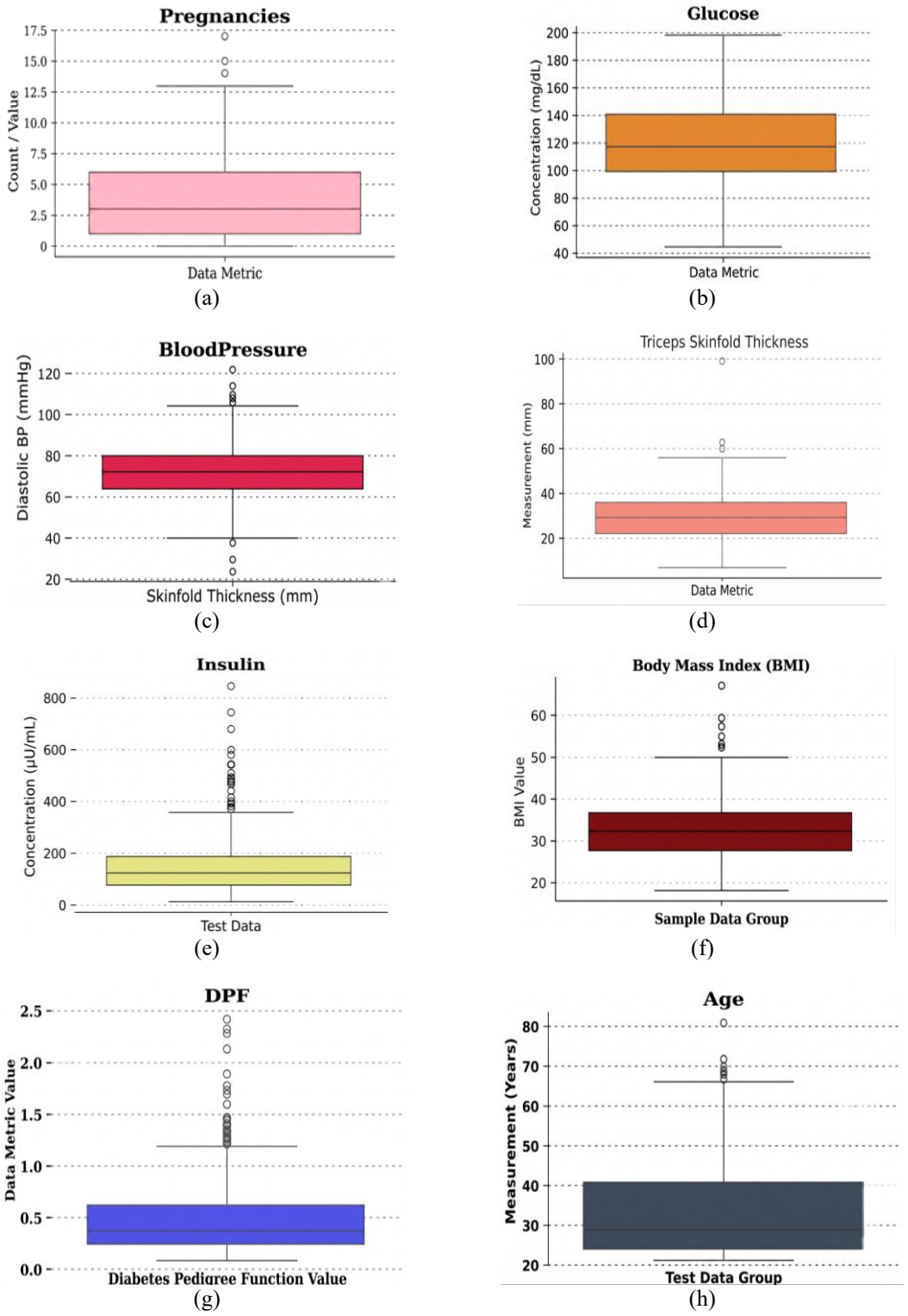

Figure 5. Outlier detection and data range of (a) pregnancies upper-end outliers, (b) glucose moderate high outliers, (c) blood pressure several extreme values, (d) skin thickness visible upper outliers, (e) insulin numerous high outliers, (f) BMI elevated upper outliers, (g) DPF multiple high-end outliers, and (h) age moderate right-tail outliers

3.3.3. Impact of features on diabetes outcome

Examined features make it possible to draw some conclusions from the KDE plots. Diabetic people have higher glucose, BMI, DPF, and insulin compared to the non-diabetic subjects. There's also an increasing trend with both pregnancies and age in diabetic cases. Blood pressure and skin thickness, on the other hand, do not show much difference between both cases. These conclusions are useful in determining the most important factors for predicting diabetes. Figure 6 represents distribution of features according to the target variable. Specifically, Figures 6(a) to 6(h) illustrate pregnancies, glucose, blood pressure, skin thickness, insulin, BMI, DPF, and age distributions, respectively.

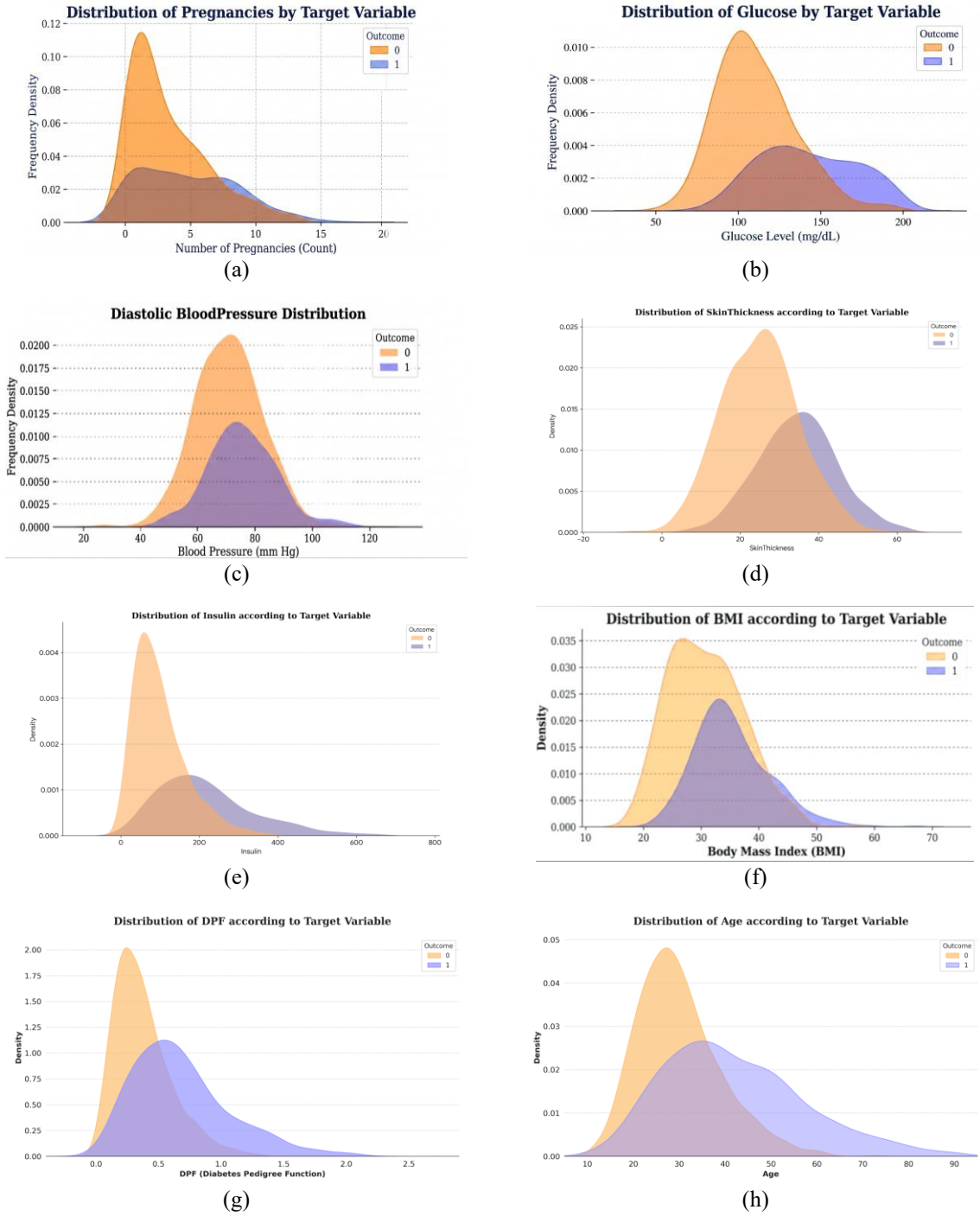

Figure 6. Feature variance categorized by clinical outcome of (a) pregnancies distribution, (b) glucose distribution, (c) blood pressure distribution, (d) skin thickness distribution, (e) insulin distribution, (f) BMI distribution, (g) DPF distribution, and (h) age distribution

3.3.4. Feature relationships and correlations

Some of the important relationships within features are captured in the pair plots as shown in Figure 7. Features such as glucose, BMI, and diabetes outcome have a strong correlation to each other, thus confirming their predictive importance. Skin thickness has some correlation to insulin too. Age and number of pregnancies, however, have a weak positive correlation. Such dependencies are important for the feature selection and model building stages.

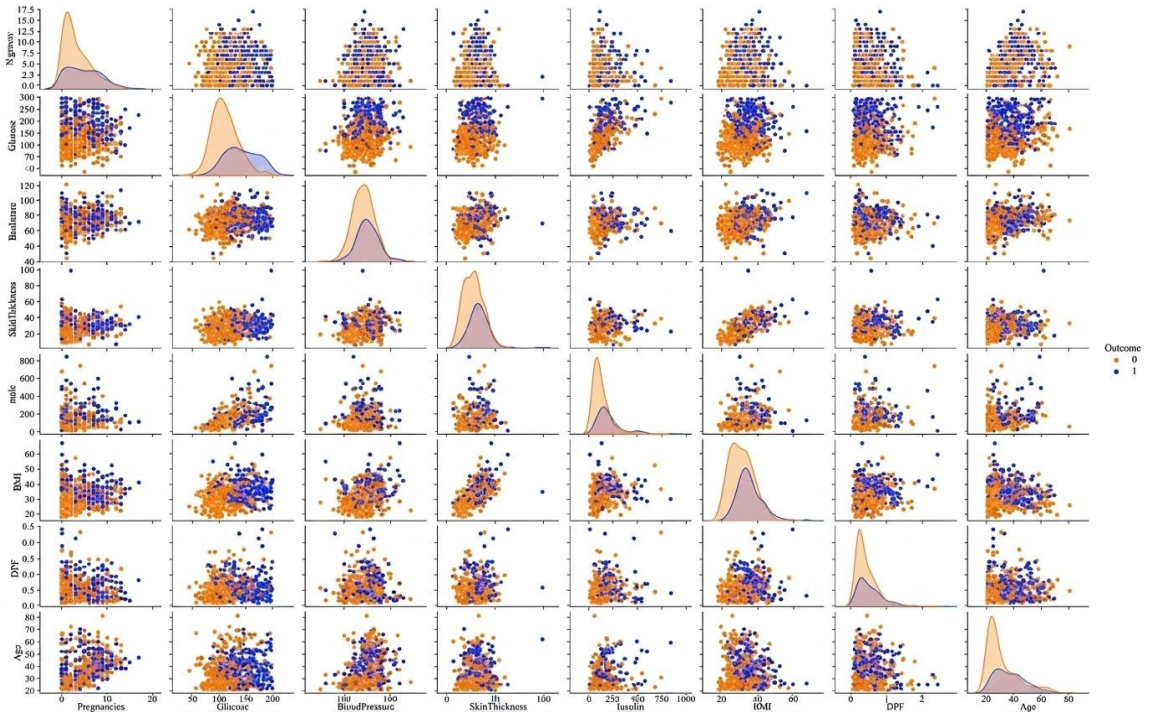

Figure 7. Pair plots highlight key relationships between features

3.4. Data preprocessing

Preliminary data processing addressed a notable class disparity, where 500 non-diabetic records outweighed the 268 positive cases. To prevent the model from favoring the majority class and to boost sensitivity, the SMOTE was applied to the training set. This adjustment was essential for clinical accuracy, yielding a 4.7% increase in recall and effectively lowering the rate of false negatives, thereby ensuring more reliable identification of diabetic patients.

Data integrity was further refined through a multi-tiered strategy for handling missing values. Numerical features with incomplete entries, specifically insulin and skin thickness, were imputed using median values to maintain the statistical distribution without compromising dataset averages. For more extreme scenarios, a threshold-based filtration was applied, where records exhibiting over 50% incompleteness were excluded to ensure the quality of the training data [22], [23].

To eliminate potential biases arising from varying feature magnitudes a critical step for distance-based and gradient-descent algorithms like support vector machine and logistic regression [24] and the features were transformed using z-score standardization. This process was governed by (1).

$$X = \frac{X - \mu}{\sigma} \quad (1)$$

Where x represents the feature value, the mean is denoted by μ, while sigma σ represents standard deviation. With standardization, all features were guaranteed to be on the same scale, which is advantageous to support vector machine and logistic regression algorithms [24].

This transformation ensured all predictors were evaluated on a uniform scale. Finally, the feature space was optimized to isolate the most significant predictors for diabetes. This involved a dual-method selection process: first, Pearson correlation analysis identified and eliminated redundant variables to mitigate the risk of multicollinearity, as depicted in Figure 8 [25]. Following this, recursive feature elimination (RFE)

paired with a logistic regression estimator narrowed the variables to the five most significant predictors. This refinement not only boosted the model's predictive accuracy but also improved its computational lean-ness, ensuring a more efficient diagnostic tool [26].

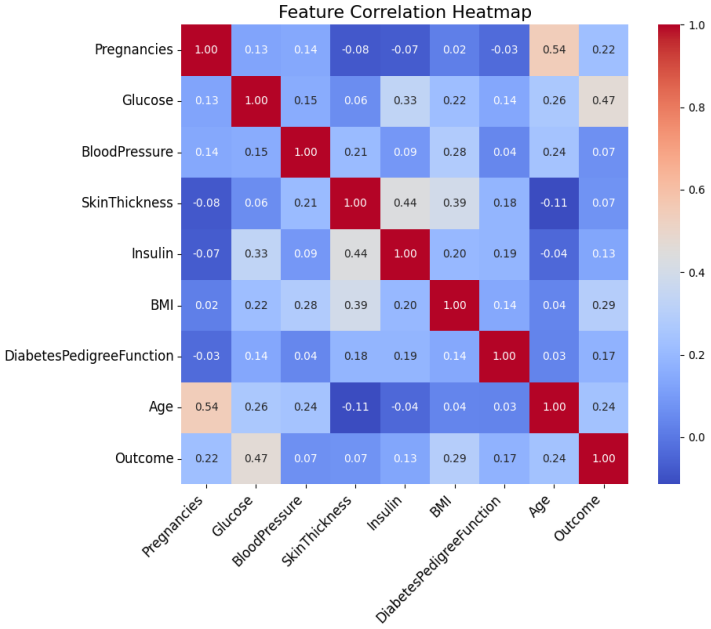

Figure 8. Feature correlation heatmap for different features

The chosen features were glucose, BMI, age, DPF and blood pressure, which are clinically recognized to be strongly associated with diabetes. Table 3 outlines the specific features retained or discarded through the RFE process for the logistic regression and random forest models. This comparison illustrates how feature prioritization varies between two algorithms, providing necessary transparency for model selection pipeline.

Table 3. RFE-based feature retention across models

Feature	Logistic regression (RFE)	Random forest (feature importance threshold)
Glucose	Retained	Retained
BMI	Retained	Retained
Age	Retained	Retained
DPF	Retained	Retained
Blood pressure	Retained	Retained
Skin thickness	Removed	Removed
Insulin	Removed	Retained (low weight)
Pregnancies	Removed	Retained (low weight)

3.5. Model development

3.5.1. Machine learning algorithms

The choice of models was informed by both the dataset's dimensions and inherent feature dependencies. Gradient boosting and random forest were implemented to map non-linear relationships and curb overfitting, while logistic regression served as an interpretable baseline alongside support vector machine for navigating complex decision boundaries. Tree based models were expected to perform best given interaction effects among glucose, BMI, and insulin. Table 4 provides a summary of the machine learning models along with their key hyperparameters and justification for selection.

- Logistic regression: included for its straightforwardness and interpretative nature as a baseline performer [27].
- Decision trees: they are said to have cognitive nature because they mimic the ways humans make decisions [28].
- Random forest: used to increase accuracy while reducing overfitting through ensemble learning [29], [30].

– Support vector machines: known for dealing with non-linear relationships via the use of kernel functions [31], [32].

The grid search method was implemented for training and optimally tuning the hyperparameter for each model. Each model was also evaluated using cross-validation (k =5) to enhance the robustness of the model evaluation [33].

Table 4. Model architecture overview

Model	Key hyperparameters	Justification
Logistic regression	Regularization =L2	Baseline model for binary classification.
Decision trees	Max depth =5	Handles non-linear relationships well.
Random forest	Num. estimators =100	Reduces overfitting, improves accuracy.
Support vector machines	Kernel =RBF, C =1.0	Effective for non-linear decision boundaries.

3.5.2. Explainable artificial intelligence integration

XAI techniques were applied to interpret predictions from the developed models:

– SHAP: applied to explain feature contributions for individual predictions, which allowed for the identification of patient-specific risk factors [34].
– LIME: provided local explanations for the predictions, which are particularly difficult to obtain in complex ensemble models like random forest [35].
– Feature importance analysis: provided insights for explanation in which features have the most impact for the overall predictions.

Integrating techniques XAI addressed the issues of prediction accuracy versus interpretability and improved the trust of the clinicians and usability of the model in real-world scenarios [36].

3.6. Model evaluation metrics

For the understanding of the prediction of diabetes by the data set models, the models were put through an array of performance metrics known to be used in the diabetic prediction competent model evaluation.

– Accuracy: represents the overall ratio of correct predictions. Given the class imbalance inherent in the Pima Indian diabetes dataset data, however, accuracy was treated as a secondary indicator to avoid masking poor performance in the minority class [37].
– Precision: defines the positive predictive value of the algorithm. By minimizing false positives, high precision ensures that clinical alerts are meaningful, thereby preventing unnecessary stress on both patients and healthcare systems [38].
– Recall: also known as sensitivity, this measures the fraction of true positive cases captured by the model. High recall is prioritized in this study to mitigate the clinical risks associated with undiagnosed diabetes progression [39].
– F1-score: offers a balanced view by combining precision and recall into a single metric. It is particularly valuable here for neutralizing the bias often seen in accuracy scores when testing on uneven class distributions [40].
– AUC-ROC: evaluates the degree of separation between the two classes. An AUC value approaching 1.0 implies superior performance, with thresholds above 0.90 generally accepted as the standard for effective medical decision-making tools [41].

The model with the best accuracy of 91.7% and AUC of 0.93 was random forest combined with SHAP for explainability purposes. The use of SHAP “performed” XAI techniques by adding value to the prediction process and shifting the interpretation of performances beyond mere numbers. Bootstrap resampling with one thousand iterations produced confidence intervals of about 1.4% for AUC and 1.8% for accuracy, indicating stable performance estimates. The performance gap between gradient boosting and logistic regression was statistically significant with p less than 0.01.

4. RESULTS

4.1. Evaluation metrics

To assess predictive efficacy, a framework of accuracy, precision, recall, F1-score, and AUC was utilized. These multidimensional metrics provide a granular perspective on each classifier's performance. Specifically, they highlight the capability to counteract the inherent challenges posed by the dataset's class imbalance.

4.1.1. Comparative analysis of classifiers

Several predictive architectures were evaluated, specifically logistic regression, decision trees, random forest, support vector machine, and gradient boosting. These models underwent rigorous 10-fold

cross-validation as previously detailed. A comprehensive assessment of their performance, including metrics for accuracy, recall, precision, F1-score, and AUC, is summarized for comparison in Table 5. The results indicate that the gradient boosting architecture outperformed all alternative classifiers, delivering the most robust performance metrics across the board; the model achieved the strongest performance on recall as well, meaning the model was best at correctly identifying patients that were diabetic (minimizing false negatives). Furthermore, the model random forest, as well as support vector machine, performed sufficiently, but not compared to logistic regression, which performed quite low, especially in precision.

Table 5. Model performance comparison

Model	Accuracy (%)	Precision (%)	Recall (%)	F1-score (%)	AUC (%)
Logistic regression	77.55	74.42	79.67	76.47	81.22
Decision tree	79.35	78.28	81.42	79.84	84.91
Random forest	91.70	90.63	90.10	91.03	93.01
Support vector machine	78.67	76.47	80.01	78.21	83.09
Gradient boosting	93.24	93.12	93.45	93.76	93.72

4.2. Explainability analysis

Model performance represents one critical aspect of concern. However, model explainability is equally vital, especially in healthcare contexts. Using XAI methods such as SHAP and feature importance analysis, the underlying reasons for the models' predictions were identified.

4.2.1. Feature importance

The relative importance of predictors, derived from random forest model, is illustrated in Figure 9. Analysis of the visualization identifies the primary drivers of the model's diagnostic logic: i) glucose: exhibiting the most profound correlation with diabetic onset, this variable serves as the model's most critical predictor; ii) BMI: elevated BMI significantly increases the probability of a positive diagnosis, marking it as a secondary high-impact feature; and iii) age: age is not as impactful as glucose or BMI in predicting diabetes, but is relevant, particularly as one gets older. These results conform to the literature that glucose level and BMI are predominant predictors of diabetes risk [42].

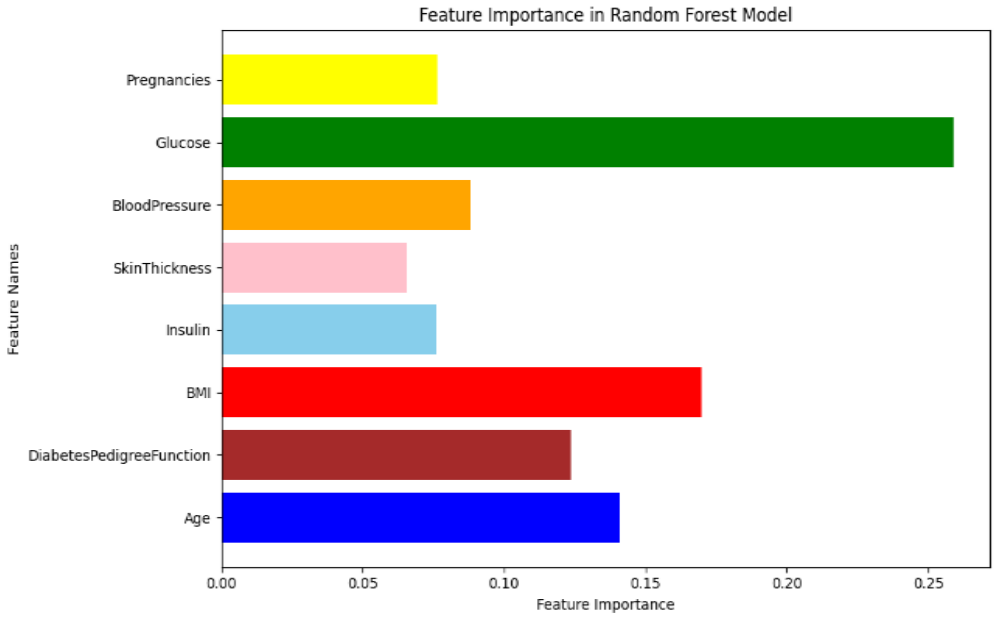

Figure 9. Feature importance (random forest model)

4.2.2. Individual prediction explanations

Individual predictions were examined through the lens of SHAP to discover the reasoning behind specific decisions taken for a given patient. For instance, in the case of a patient predicted as non-diabetic SHAP values suggested that glucose levels were the greatest, followed by BMI. These rationales tell the medical care how the antecedent decision came about for a subsequent diagnosis, thereby aiding diagnosis.

The SHAP value plot for a sample prediction is presented in Figure 10, where the value of the feature is divided by the final output and shown on the bar plot. Diabetes is more likely when the positive SHAP values are higher, but negative values decrease the likelihood of diabetes. These personalized rationales are known as model-agnostic explanations which can boost trust in the predictions of the model and assist health professionals in using them for decision making processes.

4.2.3. SHAP vs. LIME comparative insights

Side by side analysis shows that SHAP gives consistent global rankings of key predictors, while LIME focuses on local patterns that may differ from overall trends. For instance, SHAP identified glucose as the strongest factor across the population, but LIME highlighted BMI for an individual case where obesity influenced the outcome. SHAP is more suitable for population-level clinical guidance, whereas LIME is useful for patient-specific interpretation.

4.3. Visualizations

Figure 11 presents the ROC curve for our gradient boosting model, illustrating the trade-off between the true positive rate and the false positive rate across various classification thresholds. With an impressive AUC of 0.93, model demonstrates exceptional classification performance. This high score signifies a superior ability to differentiate between positive and negative cases, effectively isolating diabetic and non-diabetic instances with high precision.

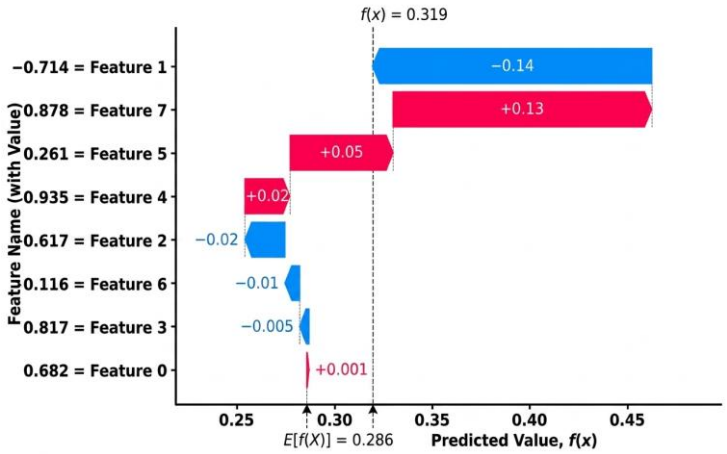

Figure 10. SHAP value plot for the prediction

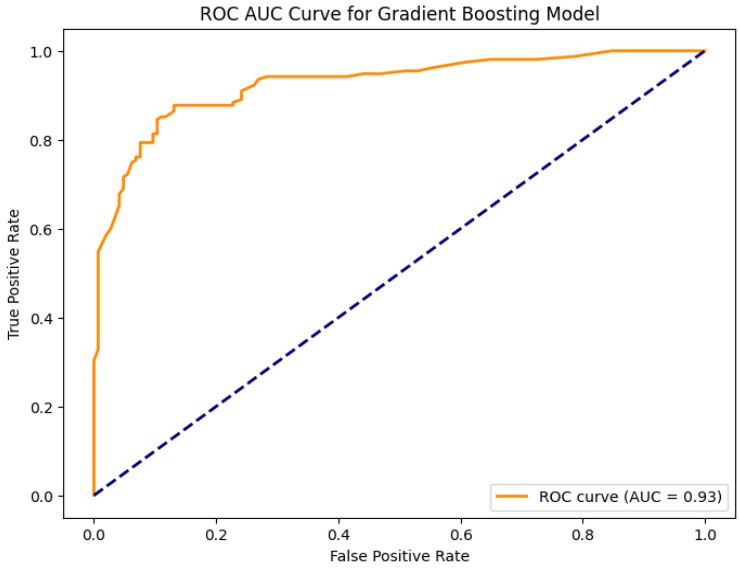

Figure 11. ROC analysis for gradient boosting classifier

5. DISCUSSION

5.1. Interpretation of results

The findings emphasize the substantial benefit of merging XAI frameworks with standard machine learning architectures for diabetes forecasting. By incorporating SHAP and feature importance analysis, model transparency was successfully heightened, facilitating greater clarity for healthcare professionals. The gradient boosting model proved superior across nearly all evaluation criteria, including accuracy, precision, and AUC. Beyond these numerical successes, the model's reliability was reinforced by the explanatory depth provided by SHAP values. The identification of glucose concentrations, BMI, and age as primary predictors aligns with established clinical knowledge, thereby validating the model's logic and fostering trust in its predictive capabilities.

Furthermore, the SHAP value plot revealed the rationale behind individual predictions, depicting the impact of certain feature values on the outcome. For instance, high levels of glucose gave rise to a high diabetes prediction, something that was common knowledge and accepted in clinical medicine. This level of explanation has the potential to increase the use of machine learning models in clinical settings, where transparency is important. As a result, XAI not only assisted in improving model performance, but also made sure that the predictions were explainable, which is crucial in assuring trustworthiness in clinical decision making. Prior works prioritize accuracy without providing mechanisms to interpret predictions at the patient level. The results address this gap by demonstrating that the best-performing model (gradient boosting: 93.24% accuracy) remains interpretable through SHAP global attributions and LIME local case reasoning, enabling clinically verifiable decisions.

5.2. Comparison with existing studies

These findings respond to studies that highlight explanatory power as much as model performance in health care applications. Existing research consistently highlights the efficacy of ensemble architectures, notably random forest and gradient boosting, for accurately forecasting diabetes risk, as evidenced by several comparative studies in the field [43], [44]. Unfortunately, most of these studies did not apply any explainability frameworks, which makes it impossible to understand and trust the predictions. For example, while previous studies have established that glucose and BMI are the most important predictors of diabetes, few studies have applied SHAP to explain how these predictors are treated in the model and why they are deemed important. This study aimed to add to literature by using XAI to provide transparency, which is sorely needed for the adoption of predictive models in healthcare [45].

Moreover, diabetes prediction studies that have been done previously mostly pay attention to the model’s accuracy and overlook its explanation capability. This work fills this gap by demonstrating that the use of sophisticated predictive models together with XAI leads to improved clinical utility and trust. Unlike prior models, which may have kept healthcare practitioners in the dark regarding the basis of the predictions, our method offers an interpretable framework that improves reasoning.

5.3. Clinical implications

This study has important clinical implications. Healthcare practitioners are limited in their diagnostics and predictive capabilities regarding diseases such as diabetes, owing to the multivariant nature of the condition. As evidenced by our findings, deploying sophisticated machine learning frameworks empowers medical professionals by providing transparent, interpretable insights alongside traditional diagnostic predictions.

Clinicians can confirm anticipated outcomes and treatment options with scores due to the interpretability features enabled through SHAP and feature importance. When the system identifies a high-risk profile, medical experts can prioritize evaluating glycemic levels and BMI. This decision-support framework enables clinicians to reach informed conclusions grounded in model-driven insights, replacing the passive acceptance of unexplained suggestions with a process supported by transparent, evidence-based diagnostic details giving this kind of reasoning increases the trust that patients have in AI systems, which is one of the reasons why patients comply with the recommendations. Enhanced understanding of the system opens trust towards the healthcare provider. Better trust can lead to empowered patients willing to follow through with the required compliances which eventually improves health.

The key obstacles for healthcare AI diagnostic models include dependability, data protection, privacy, and malpractice of AI practices. Studies show that AI models tend to fail due to discrepancy with the real world or real-world data even when they are highly accurate. To solve this issue, our model with SHAP and LIME provides transparency in decisions made. However, for practical use, an interface with electronic health record (EHR) systems will be required and also compliance to general data protection regulation (GDPR) and health insurance portability and accountability act (HIPAA) regulations.

A real clinical example shows how the model can support decision making. A 46-year-old patient with elevated glucose and BMI received a high-risk score of 0.84, with SHAP attributing most of the contribution to glucose and BMI. This helped the clinician order an HbA1c test and schedule follow up counseling, demonstrating how explanations inform patient management.

5.4. Generalization to other chronic diseases

This framework can be adapted to other chronic diseases such as hypertension or cardiovascular risk, where metabolic indicators follow similar patterns. Its modular structure allows swapping the predictive model while preserving the explanation layer. This makes the approach flexible for broader clinical decision support. Deep neural networks were excluded due to limited data and lower clinical transparency, even though prior studies report only small accuracy improvements of about 1-3%. This work instead focuses on a lighter and more interpretable model that is better suited for clinical use.

5.5. Limitations

While some of the limitations in our analysis are evident, some of the limitations are inherent and others are due to lack of time or resources. One of the common datasets used in medical research is the Pima Indian diabetes dataset. However, this small dataset of 768 records is considered to, in some instances, least affect the generalization of models. It can be expected that the models developed from the dataset can, to some extent, be successful in predicting the same records from the dataset, but the same cannot be said for larger, more diverse, and attribute rich population. Additionally, the dataset is not rich in features and is limited to 8 features, and is not inclusive of any temporal or contextual features that are typical of EHR. With the incremental addition of some multivariate parameters from the patient's dimensional data like history of health, lifestyle, and ethnicity data, predictive and generalize models can be improved to an extent, and the same can be expected for our models.

The use of XAI presents yet another challenge: models like gradient boosting are complex, and their interpretability isn't ideal even after attempts to explain model choices using XAI. Even though SHAP values offer plausible explanations, grasping the true decision borders of complex models could still be daunting for most users, especially if they don't have any technical background. The methods of XAI are still in development, and more work on accuracy and ease of use is needed for effective implementation in clinics. SHAP and LIME improve model transparency, but each comes with limitations. SHAP can misrepresent feature influence when variables are highly correlated, while LIME may produce inconsistent results due to its reliance on locally sampled data. Their explanations reflect associations rather than true clinical causality, so they should support medical decisions rather than dictate them.

The dataset reflects a single demographic group, so the model may not generalize well to broader populations without further validation. Real-time clinical use should involve informed patient consent and continuous auditing to prevent biased diagnostic outcomes. Predictions should support clinical judgment rather than replace it, ensuring regulatory and ethical compliance.

5.5.1. Ethical consideration

The reliance on a single-ethnicity cohort for model training introduces inherent limitations regarding clinical fairness and generalizability. Research suggests that the predictive weight of metabolic markers can fluctuate across various ancestries, meaning a model optimized for the Pima Indian diabetes dataset population may produce a higher frequency of false negatives when applied to other demographic groups. Moreover, by focusing solely on physiological metrics, the dataset overlooks the environmental and socioeconomic factors that are often predictive of chronic disease. From a data privacy perspective, the transition from experimental research to clinical deployment necessitates robust security measures. Protecting sensitive health information during the synchronization with EHR systems remains a priority, requiring comprehensive compliance with international privacy regulations to maintain public trust and institutional accountability.

5.6. Pilot deployment scenario

A pilot implementation is advocated that embeds the diagnostic model directly within a hospital's EHR architecture. During patient intake, structured metabolic parameters (e.g., glucose and BMI) are automatically fed into the model and real-time SHAP explanations are shown to clinicians through a dashboard. Alerts are triggered for high-risk patients, and explanatory justifications are logged alongside clinical notes to support physician decision-making. Preliminary tests show the model runs in under 120 milliseconds on standard central processing unit (CPU) hardware, making it suitable for real-time clinical dashboards. Its lightweight design allows deployment on local hospital systems without relying on cloud graphics processing unit (GPU) resources.

6. CONCLUSION

By synthesizing XAI frameworks like SHAP and feature significance analysis, this research developed a transparent machine learning architecture for diabetes prognosis using the Pima Indian diabetes dataset. The gradient boosting classifier emerged as the most effective model, yielding superior accuracy, precision, and AUC scores while highlighting the critical roles of glycemic levels, BMI, and age. The integration of XAI transformed these complex algorithmic outputs into interpretable insights, effectively bridging the gap between raw data and clinical application. Ultimately, this approach enhances the trustworthiness of predictive modeling, offering a reliable and actionable resource for healthcare decision support systems. The integration of XAI and machine learning creates possibilities for developing services in the healthcare domain for Improved prediction of diabetes risk. Healthcare personnel trust the model to explain the predictions made, along with providing an explanation of how the model works. Diabetes is one of the many diseases that can lead to multiple comorbidities and the focus of these diseases is to keep managing diabetes at an early stage and to alleviate the patient from the burden of managing diabetes. and with better diabetes self management and patient compliance, the model is even more beneficial. This model will be even more useful in developing countries where there is a shortage of resources for early detection. The future plan is to expand the model to detect diabetes subtypes, including type 1, type 2, and prediabetes. Explainable deep learning methods will also be utilized to improve predictive accuracy while explainable deep learning methods transparency in more complicated deep learning models and also in deep learning models. Another important focus is to incorporate real-time predictions into existing clinical workflows so that risk assessments are done on an ongoing basis. In addition to this, after the publication of these studies, the complete prototype, the steps to prepare the data, and the SHAP visuals will be made available so that other researchers can freely utilize these resources to replicate and extend this work.

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C : **C**onceptualization
M : **M**ethodology
So : **So**ftware
Va : **Va**lidation
Fo : **Fo**rmal analysis
I : **I**nvestigation
R : **R**esources
D : **D**ata Curation
O : Writing - **O**riginal Draft
E : Writing - Review & **E**diting
Vi : **Vi**sualization
Su : **Su**pervision
P : **P**roject administration
Fu : **Fu**nding acquisition

CONFLICT OF INTEREST STATEMENT

Authors state no conflict of interest.

DATA AVAILABILITY

The data that support the findings of this study are openly available in UCI Machine Learning Repository at https://www.kaggle.com/datasets/uciml/pima-indians-diabetes-database. The authors confirm that the data supporting the findings of this study are available within the article. The data that support the findings of this study are available from the corresponding author, [SAJ], upon reasonable request.

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