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XAI-Powered Comparative Diabetes Prediction with XGBoost, SVM and Artificial Neural Networks

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Abstract – In this study, diabetes prediction was conducted using XGBoost, Support Vector Machines (SVM), and a Multilayer Artificial Neural Network (ANN). Attributes that cannot be biologically '0' (e.g. glucose, BMI) were first marked as NaN. After filling the missing values with the median, the data were transformed with StandardScaler. To address class imbalance, the Synthetic Minority Over-sampling Technique (SMOTE) was applied, and feature selection was performed using the VarianceThreshold method. Hyperparameter optimization for all models was conducted using the RandomizedSearchCV approach.Model performance was evaluated based on ROC-AUC (Receiver Operating Characteristic – Area Under Curve), accuracy, and F1 score. The best results were achieved by the ANN model (ROC-AUC: 0.829, accuracy: 0.76, F1 score: 0.678), followed by XGBoost (ROC-AUC: 0.820, accuracy: 0.734, F1 score: 0.667), and SVM (ROC-AUC: 0.809, accuracy: 0.734, F1 score: 0.661).As part of the Explainable Artificial Intelligence (XAI) framework, global SHAP (SHapley Additive exPlanations) analysis was applied to the XGBoost model, while local explanations were generated using LIME (Local Interpretable Model-Agnostic Explanations) for the SVM and ANN models. SHAP analysis identified glucose, body mass index (BMI), and age as the most influential features. LIME provided case-specific interpretations by highlighting the contribution of individual features for each patient. These approaches contributed to enhanced transparency in clinical decision-making processes.

Keywords – XAI, *Diabetes, XGBoost, SVM, ANN, Artificial Intelligence, SHAP, LIME.*

I. Introduction

The World Health Organization (WHO) reports that diabetes is a long-term condition affecting hundreds of millions globally. Timely identification and management especially for Type 2 diabetes are therefore critical for population health.[9]. Early diagnosis of chronic diseases such as diabetes is critical to reduce clinical burden and improve quality of life. [20] Traditional diagnostic methods are often time-consuming and lack clinical decision support. Therefore, modern data science approaches and machine learning (ML) algorithms are increasingly used in the early prediction of chronic diseases such as diabetes [10]. Many studies have shown the applicability of these algorithms on reference datasets such as the Pima Indians dataset [3][4]. Especially powerful classifiers such as Artificial Neural Networks (ANN), Support Vector Machines (SVM) and XGBoost provide successful results thanks to their ability to learn complex data patterns [6][7]. However, the lack of explainability of these models constitutes an important limiting factor, especially in healthcare applications [11]. Interpretability and transparency are at least as important as accuracy for machine learning-based models to become widespread in the medical field. [13]
Developments in the field of Explainable Artificial Intelligence (XAI) have made it possible to understand the decision mechanisms of models. XAI approaches such as SHAP (SHapley Additive Explanations) [1] and LIME (Local Interpretable Model-Agnostic Explanations) [2] produce both global and local explanations about the features on which the model makes predictions. [14] In this way, it is possible to develop more reliable and explainable artificial intelligence systems for clinicians. [12]. In this study, diabetes prediction was performed with ANN, SVM and XGBoost models using the Pima Indians data set; processes such as missing data removal, scaling, class balancing with SMOTE and feature selection were applied in the data preprocessing steps. Balancing techniques such as SMOTE increase the performance of machine learning models to reduce class imbalance in data sets. [18] Models were optimized with the RandomizedSearchCV method, and then model explanations were presented with SHAP and LIME methods. The results obtained demonstrate both classification performance and explainability. In this respect, the study contributes to explainable modeling approaches in the field of health informatics.

II. Materials and Method

A. Data Preprocessing

Data preprocessing techniques and feature engineering are critical steps that directly affect the performance of models used in diabetes prediction.[15] In this study, the Pima Indians diabetes dataset was used. In the dataset, the inputs showing 0 values such as glucose, blood pressure, BMI, etc. were marked as NaN and filled with the median, since they were biologically invalid. Then, the features were scaled with StandardScaler to have a mean of 0 and a variance of 1. VarianceThreshold (threshold 1e-4) was applied to remove features with low variance (e.g. fixed columns that did not affect the prediction were eliminated). Since the class distribution in the dataset was unbalanced, the minority class was multiplied using the SMOTE method. A balanced training set was obtained by creating new examples with SMOTE.

B. Setup and Optimization of Models

Three models are derived: XGBoost: The gradient boosting tree classifier proposed by Chen and Guestrin [8] is used. Binary logistic objective and AUC metric optimization are targeted. Artificial Neural Network (ANN): Models with single hidden layer or multi-layer MLPClassifier with relu activation function were created. Instead of grid, parameters such as number of layers, number of neurons, learning rate were adjusted with RandomizedSearchCV. Support Vector Machine (SVM):An SVC model that can provide probability estimation was used. RBF and polynomial kernels were used to scan C and gamma parameters with RandomizedSearchCV. In each model, the training set was partitioned with k-fold CV with re-stratification (5 folds, 2 repetitions) and optimization was performed. The models obtained with the best hyperparameters were evaluated on the test data after the training was completed.

C. Justification of Model Hyperparameter Choices

The hyperparameters of three different machine learning models (XGBoost, ANN, SVM) used in this study were determined based on the value ranges suggested in the literature and application experiences. The hyperparameter optimization process provides a large but meaningful search space for each model RandomizedSearchCV**.** This approach enables more efficient scanning of the parameter space with a limited number of trials and reduces the computational cost [5].

XGBoost model: The parameters used for are the basic hyperparameters that are frequently optimized, especially in medical classification problems. Parameters such as n_estimators, max_depth, learning_rate, subsample, colsample_bytree, gamma, and lambda are critical for the model to avoid over-learning and increase its generalization ability [6]. In particular, keeping the learning_rate low and adding random components such as subsample and colsample_bytree make the model robust against high variance.

Artificial Neural Network (ANN): In the model, hyperparameters such as hidden_layer_sizes, alpha (L2 regularization coefficient) and learning_rate_init are optimized. It has been reported in the literature that ANN models generally show high performance with single or two hidden layers on small-medium sized medical datasets [7]. Using adaptive learning rate allows the learning rate to be dynamically adjusted according to the validation loss during the training process, and the risk of overfitting is reduced with the early stopping strategy.

SVM: The C, gamma and kernel parameters have been optimized for the model. The C parameter controls the tolerance of the model at the decision boundary, while gamma determines the curvature of the model, especially in RBF and polynomial kernels. Using the loguniform distribution, these parameters have been scanned on a large scale. It is stated in the literature that SVM shows strong performance on small data sets and that careful tuning of these parameters directly affects the model success [8].

These parameter configurations also contributed to the consistent results of explainability analyses such as SHAP and LIME. Because overly complex or overly simple models can cause misleading effects in these explanation methods. With the applied parametric adjustments, both the high classification performance and the interpretability level of the models were balanced.

D. Explainable AI Analytics

XAI analyses were applied for the best models obtained. Global importances were calculated using TreeSHAP for XGBoost. After training, the test data was entered into SHAP values and the contribution of each feature to the prediction was visualized as a summary graph (SHAP summary). SHAP values are very useful in interpreting the effect of clinical variables such as glucose and BMI on the model output. [16] XAI enables the explanation of not only the model outputs but also the rationales in the decision-making process of the model. [17] The SHAP summary graph obtained from the XGBoost model is shown in Figure 1. LIME local explanations were used for SVM and ANN models. The explanation window (LimeTabularExplainer) was run on randomly selected examples from the training data, and it was shown which features of each example made the result positive or negative. With this approach, a bar graph explanation with a maximum of 10 features was produced for each test example. These graphs show the contributions in green (positive effect) and red (negative effect) colors. Figure 2 shows the LIME explanation graph obtained for a test example of the SVM model.

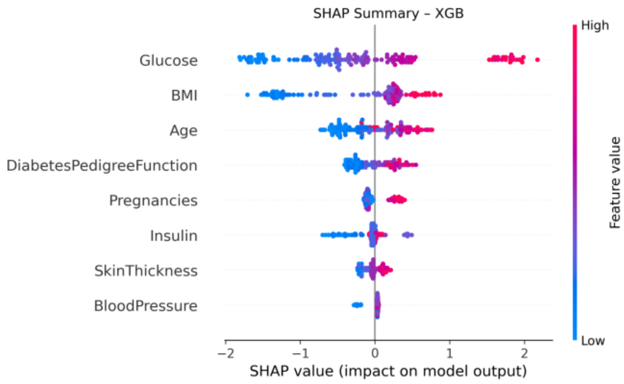

Figure 1. SHAP Summary Chart of The XGBoost Model.

As seen in Figure 1, The SHAP Summary Chart of The XGBoost Model. This graph shows the effects of the features used in the model on the prediction with SHAP (SHapley Additive exPlanations) values. The features in the model are listed on the Y-axis, and the SHAP values calculated for each observation are on the X-axis. Each point represents an observation, and the color coding indicates the magnitude of the feature value in that observation (blue: low value, red: high value).Glucose and BMI stand out as the features that affect the model output the most. High glucose (red dots) and high BMI values increase the SHAP values positively and increase the probability of an individual having diabetes. On the other hand, low glucose and low BMI values (blue dots) negatively affect the model prediction. Variables such as age, DiabetesPedigreeFunction and Pregnancies are also seen to be effective at certain levels. The wide distribution of SHAP values, especially for the glucose variable, shows that this variable has a strong and variable effect on the prediction.

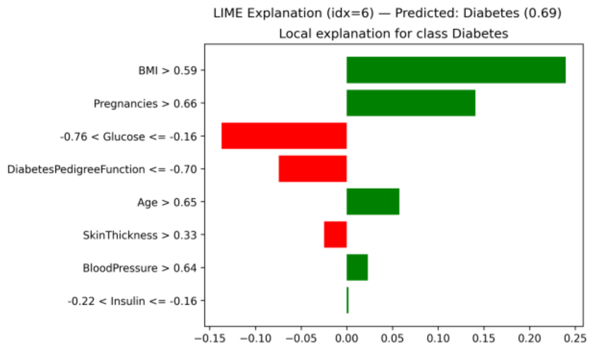

Figure 2. LIME Local Explanation for 0.69 Diabetes

As seen in Figure 2, the LIME Local Explanation for 0.69 Diabetes for a test case of the SVM model.The green bars show the positive effect of the features, increasing the probability of diabetes, and the red bars show the negative effect, decreasing it. In this example, high BMI and number of previous pregnancies have a positive effect, while low glucose values negatively affect the prediction.

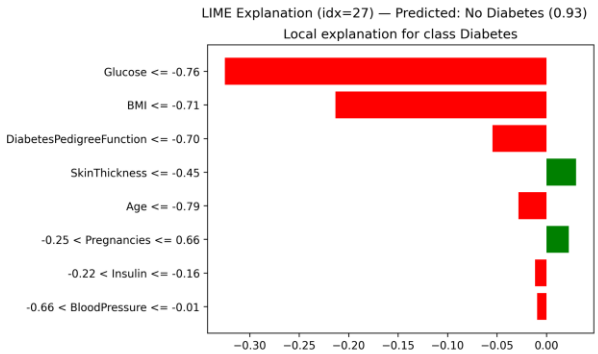

Figure 3. LIME Local Explanation for 0.93 No Diabetes

As seen in Figure 3, the LIME Local Explanation for 0.93 No Diabetes, in this patient, who the model predicted to be nondiabetic, low levels of glucose and BMI appeared to be negative factors that significantly decreased the probability of diabetes. Other low-level traits, such as DiabetesPedigreeFunction and SkinThickness, also decreased the risk of diabetes. However, moderate BloodPressure values slightly increased the risk.

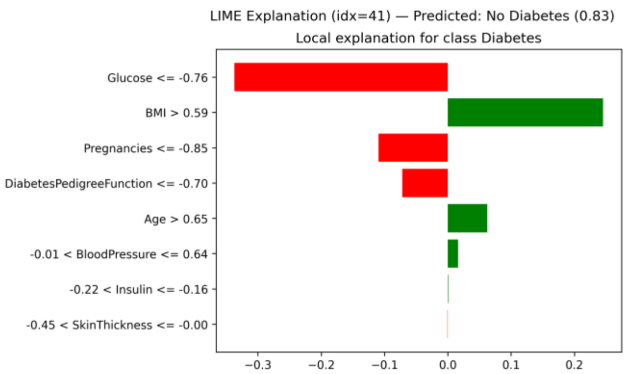

Figure 4. LIME Local Explanation for 0.83 No Diabetes

As seen in Figure 4, the LIME Local Explanation for 0.83 No Diabetes indicates an 83% probability of not having diabetes for this patient. Low glucose levels and low number of previous pregnancies decreased the risk of diabetes. On the other hand, high BMI values seem to be a significant positive factor increasing the probability of diabetes in the patient.

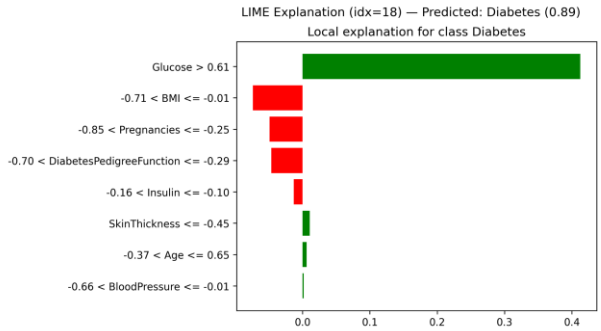

Figure 5. LIME Local Explanation for 0.89 Diabetes

As seen in Figure 5, the LIME Local Explanation for 0.89 Diabetes, the most critical factor in the diagnosis of diabetes in this patient is the high glucose level. The low intermediate levels of BMI and the low number of pregnancies slightly reduced the probability of diabetes in the patient. In general, the effect of the high glucose level in this patient clearly suppressed all negative factors.

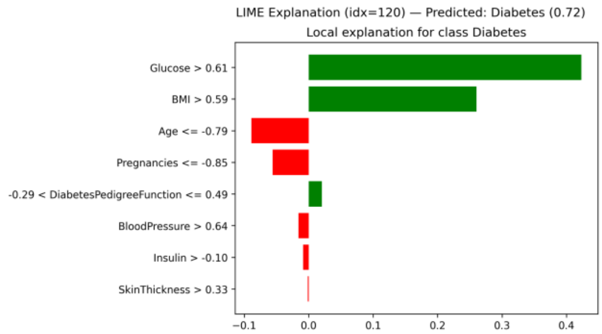

Figure 6. LIME Local Explanation for 0.72 Diabetes

As seen in Figure 6, the LIME Local Explanation for 0.72 Diabetes, this patient was predicted to have diabetes with a probability of 72% by the ANN model. The factors that most strongly support the prediction are high glucose and high BMI. Young age and low number of pregnancies are negative factors that reduce the probability of the patient having diabetes. However, the positive contributions of high glucose and BMI values overcame the effect of the negative factors and led to the prediction of the patient having diabetes.

Table 1. Models Comparison

Model	ROC-AUC	Accuracy	F1
ANN	0.829	0.760	0.678
XGBoost	0.820	0.734	0.667
SVM	0.809	0.734	0.661

The test data results of the models are summarized in Table 1. According to the results, ANN gave the highest ROC-AUC value. In terms of accuracy, ANN and XGBoost showed similar performance with SVM. The results obtained are consistent with similar findings in other studies[3][4] Table 1. Performance metrics of the models (test data). In the SHAP analysis (Figure 1. SHAP Summary Chart of The XGBoost Model), glucose, BMI and age features stood out as having the highest mean absolute SHAP value. It is seen that high values of these features increase the risk of diabetes. LIME outputs (Figure 2) showed the contribution of different features for each patient in detail. For example, in the case in Figure 2, high BMI and number of pregnancies increase the probability of diabetes, while low glucose decreases this probability. These comments made it clinically understandable how the model responds to which criteria

The success of our models is consistent with the studies in the literature [3][4]. Mohan and Jain [3] also reported that SVM gave similar AUC (~0.80) on Pima data. Revathi et al. [4] achieved high accuracy in comparing ANN and SVM. In our study, ANN gave slightly higher ROC-AUC, but the overall performance of different models was similar. Importantly, SHAP and LIME results ensured that the models were not black boxes. As Lundberg and Lee [1] stated, understanding the mechanism behind model prediction is as critical a goal as the prediction itself. Ribeiro et al. [2] also showed that local explanations increase the reliability of individual decisions. The obtained explanations clearly showed clinicians which patient characteristics influenced the model decision. For example, glucose and BMI are known to be strongly associated with diabetes in the medical literature; SHAP analysis ranked them first in accordance with this literature. XAI results offer important gains for clinical decision support systems. Patient-specific LIME explanations allow the physician to ask "why was this patient predicted to have diabetes?" While answering the question, global SHAP graphics answered the question "Which factors are more decisive in general?" Thus, confidence and transparency increased. In a real application, doctors can identify risky individuals more quickly and request additional tests based on these explanations. As a result of the study, understandable outputs were obtained despite the complexity of the models, and the model insights were made clinically meaningful.

III. Results

In this study, XGBoost, SVM and ANN classifiers were successfully trained on the Pima Indians Diabetes dataset and achieved a ROC-AUC of roughly 0.80 accuracy of roughly 0.75. The models were produced through a pipeline that included median imputation for implausible zero values, feature scaling, SMOTE-based class rebalancing and hyper-parameter tuning via RandomizedSearchCV. SHAP and LIME analyses enhanced the interpretability of the predictions and consistently highlighted glucose and BMI as the most influential risk factors, thereby increasing confidence in the system's potential as a clinical decision-support tool.

IV. DISCUSSION

Several limitations, should be noted. Because development and validation relied on a single, demographically narrow cohort, the results may not extrapolate to broader, multi-ethnic clinical populations. In addition, the combination of median imputation and synthetic oversampling may have shifted feature distributions and introduced patterns that are absent in real-world data. Finally, although SHAP and LIME explanations were produced, their practical usefulness has yet to be confirmed by practising clinicians. Addressing these constraints through larger, multi-centre datasets and prospective clinician-in-the-loop evaluations will be essential for translating the proposed approach into routine clinical care.Future investigations should move beyond the current retrospective analysis and involve *multicentre, prospective clinical trials*. Deploying the explainable decision-support model in routine care will allow its diagnostic accuracy, usability and effect on patient outcomes to be tested across diverse patient groups and clinical workflows.

V. CONCLUSION

This study showed that ANN, XGBoost, and SVM predict diabetes on the Pima Indians dataset with roughly 0.80 ROC-AUC and 0.75 accuracy. SHAP and LIME analyses confirmed glucose and BMI as the key risk factors driving predictions. The pipeline thus delivers an accurate, explainable decision-support tool, but it still needs validation in real clinical settings and more diverse patient populations.

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