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Anemia Classification with Clinical Feature Engineering and SHAP Interpretation

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ABSTRACT

Anemia is a global health issue that has a significant impact on quality of life and productivity. Early and accurate detection is essential to prevent more serious complications. This study aims to develop an anemia classification model based on machine learning technology using the XGBoost algorithm, as well as compare its performance with Logistic Regression and Random Forest methods. The dataset used in this study was obtained from the Kaggle platform, consisting of 1,421 samples and six clinical attributes, namely Gender, Hemoglobin (HGB), Mean Corpuscular Hemoglobin (MCH), Mean Corpuscular Hemoglobin Concentration (MCHC), Mean Corpuscular Volume (MCV), Result. During the feature engineering process, the derived feature of the hemoglobin-to-MCV ratio (Hb/MCV) was added, which is medically relevant in distinguishing types of anemia. Evaluation results showed that XGBoost and Random Forest achieved an accuracy rate and F1-Score of 100%, while Logistic Regression achieved a rate of 98.9%. XGBoost was selected as the primary model due to its efficient computational capabilities and support for interpretation using SHAP (SHapley Additive exPlanations). SHAP visualization revealed that the Hb/MCV ratio and hemoglobin were the most influential features in classification. This model has the potential to be used as a decision support system for automated anemia screening and can be further integrated into clinical systems.

I. INTRODUCTION

Anemia is a medical condition characterized by low hemoglobin levels in the blood. Based on 2023 data, it is estimated that 40% of children aged 6 to 59 months and 37% of pregnant women suffer from anemia, which remains a global health problem with high prevalence, especially in developing countries [1]. Conventional methods of diagnosing anemia through laboratory tests, such as Complete Blood Count (CBC) and serum ferritin tests, have several limitations. These procedures require trained personnel, are relatively expensive, and do not provide immediate results. These conditions make this method less than optimal, especially in health facilities with limited resources.

Anemia is generally diagnosed through a complete blood count (CBC), including hemoglobin, MCV, MCH, and MCHC [2]. Several studies have utilized machine learning (ML) to help classify anemia based on complete blood parameters [3], [4]. Methods such as Logistic Regression, Random Forest, and XGBoost have been proven effective in various clinical studies. However, most studies still focus on accuracy without considering medical interpretability [5], [6].

Many previous studies have used label modifications based on MCV values or rule-based techniques to form anemia classifications, rather than using the original labels as in actual diagnoses. In addition, derived features such as the hemoglobin-to-MCV ratio, which has medical relevance, are rarely used to improve predictive ability. Model interpretation that explains the rationale behind classifications is also rarely presented, making it difficult to accept as a clinical decision support system. Anemia was chosen as the focus of this study because of its high prevalence and significant impact on public health. According to the World Health Organization (WHO), approximately 30% of women of reproductive age

worldwide had anemia in 2019, and in 2023 the prevalence remained at around 30.7% [7]. World Health Organization. In Indonesia, anemia remains a serious public health problem: data from the 2018 Basic Health Survey (Riskesdas) show that 48.9% of pregnant women experience anemia. Although CBC diagnostics are widely available, anemia often goes undiagnosed or is detected at a later stage, especially in settings with limited laboratory capacity [8].

The number of studies using interpretation techniques like SHAP to explain feature impact is still limited. Therefore, a new approach is needed that is not only accurate but also understandable to medical professionals. Therefore, this study has three objectives: (1) to compare the performance of different machine learning algorithms, (2) to examine the effect of feature engineering through the addition of the Hb/MCV ratio on model accuracy, and (3) to provide medical interpretability of predictions using SHAP analysis

This study uses the anemia dataset available on Kaggle, which consists of six main attributes, namely Gender, Hemoglobin, MCH, MCHC, MCV, and the Result label. The dataset was derived from real-world clinical laboratory results of Complete Blood Count (CBC) examinations, and not from simulated or artificially generated data. Before use, the data was cleaned and processed using standardization techniques, and a new feature, the Hb/MCV ratio, was added. The data was then trained using three classification models: Logistic Regression, Random Forest, and XGBoost, employing a supervised learning approach. Evaluation results were assessed using the metrics Accuracy, Precision, Recall, and F1-Score. Additionally, the SHAP method was employed to identify which features most significantly influence classification outcomes [6], [9]. To improve clinical relevance and obtain the best model accuracy, this study added the derivative feature of hemoglobin to MCV (Hb/MCV) ratio as an early indicator of microcytic anemia due to iron deficiency [10]. This feature represents the relationship between hemoglobin levels and red blood cell size, which is clinically used in evaluating types of anemia [11]. The addition of this ratio will help the model understand the interaction between two important parameters and has been shown to improve classification performance and facilitate feature interpretation through SHAP.

The accuracy, precision, recall, and F1-score values reached 100% on the test data. The Logistic Regression model produced an accuracy of 98.9%, while Random Forest also showed perfect accuracy like XGBoost. Although Random Forest also showed perfect performance, XGBoost was chosen because it has a regularization mechanism that prevents overfitting and is usually more stable on medical tabular data [12]. The Hb/MCV_ratio feature was found to significantly contribute to the classification process, as shown in the SHAP analysis. The confusion matrix indicates that no classification errors occurred in the 285 test data by XGBoost. This demonstrates that the model is highly effective in distinguishing between normal cases and anemia.

The results obtained show that the use of the Hb/MCV derivative feature provides valuable additional information for the classification process. The SHAP technique successfully identified that the Hemoglobin feature and the Hb to MCV ratio are the main indicators in predicting anemia. This study did not modify the labels but used the original diagnosis data as the basis for validating the results to be closer to real clinical conditions. This combination not only focuses on achieving accuracy but also considers medical and interpretative aspects. Thus, the model built is not only statistically accurate but also aligned with the medical approach commonly applied in clinical practice.

II. METHOD

The research stages were systematically arranged to build a machine learning-based anemia classification model. First, a dataset was collected from open sources, followed by a preprocessing process involving data cleaning and standardization of numerical features using a standard scaler. The next step is to perform feature engineering by adding a derived feature in the form of the ratio of hemoglobin to MCV (Hb/MCV), which is clinically relevant in identifying anemia. The data is then divided into two parts: training data and test data. Both data sets have label standardization to maintain a balanced class proportion. Next, the model is built using three classification algorithms: Logistic Regression, Random Forest, and XGBoost. Classification performance is determined through model evaluation using accuracy and F1-Score metrics. For result interpretation, this study uses the SHAP (SHaple Additive exPlanations) method to understand the contribution of each feature to the model's predictions, ensuring transparent medical review of the results. The complete research is shown in Figure 1.

Figure 1 shows the research methodology flow used in the classification of anemia using the XGBoost model and SHAP-based interpretation. The process begins with the collection of hematology data, followed by a preprocessing stage that includes data scale normalization. Feature engineering is then performed by adding clinically relevant derived attributes of the Hb/MCV ratio. The model is then built using three supervised learning algorithms, namely Logistic Regression, Random Forest, and XGBoost. Evaluation is performed using accuracy and F1-score metrics to determine the performance of each model. The best model, XGBoost, is then interpreted using SHAP to understand the contribution of features to the predictions generated.

A. Dataset

This study uses an anemia dataset sourced from Kaggle [11], which is openly available and derived from complete blood count (CBC) laboratory examinations. The dataset consists of 1,421 samples with six attributes, namely Gender, Hemoglobin, Mean Corpuscular Hemoglobin (MCH), Mean Corpuscular Hemoglobin Concentration (MCHC), Mean Corpuscular Volume (MCV), and Result as the label. The Result variable represents a binary classification with 801 non-anemia cases (label 0, 56.4%) and 620 anemia cases (label 1, 43.6%). In terms of class distribution, this represents

a moderately imbalanced dataset, though still relatively balanced compared to many other clinical datasets.

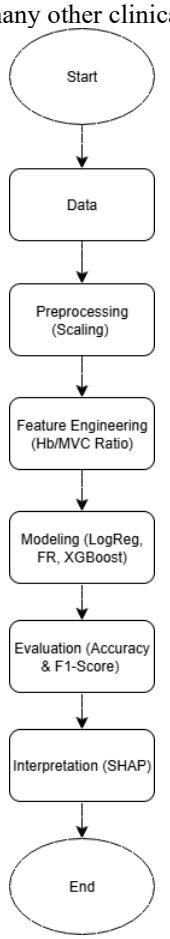

Figure 1. Research Methodology Flowchart for Anemia Classification Using XGBoost with Derived Clinical Features and SHAP Interpretation.

Data quality assessment confirmed that the dataset contained no missing values and all attributes were consistently formatted. Gender, as the only categorical variable, was encoded into numerical form, while hematological attributes such as Hemoglobin, MCH, MCHC, and MCV were retained as continuous numerical variables. To ensure comparability among features and to improve model convergence, feature scaling was applied using the StandardScaler method. Exploratory data analysis (EDA) was also performed to examine the distribution of variables, detect potential outliers using boxplots, and verify the proportion of each class. Since the class imbalance was not severe and preliminary experiments showed high model performance, no balancing techniques such as oversampling or SMOTE were applied in this study.

B. Preprocessing

Data quality checks confirmed that there were no missing values. Outlier detection using boxplots also indicated that no significant noise or anomalies were present, ensuring that preprocessing could focus primarily on scaling and encoding. In the preprocessing stage, an initial assessment was conducted to check for missing values and ensure data consistency. Since the only categorical variable, Gender, consisted of binary values, it was label-encoded to ensure compatibility with machine learning models. Subsequently, feature scaling was performed using StandardScaler to normalize the scale of numerical attributes such as Hemoglobin, MCV, MCH, and MCHC. This transformation was essential to ensure that algorithms relying on distance metrics could learn effectively and without bias caused by differing data scales. Despite a moderate class imbalance, no resampling techniques were applied due to the high model performance achieved in preliminary experiments. This comprehensive preprocessing ensured that the dataset was clean, standardized, and adequately prepared for fair and reliable modeling.

C. Feature Engineering

This study added validated medical knowledge-based derivative features to improve the model's predictive ability and provide added value from a clinical perspective. The added feature is the ratio between hemoglobin (Hb) and MCV (Mean Corpuscular Volume), which is medically relevant in distinguishing types of anemia. The relationship between the Hb-to-MCV ratio has been proven effective in distinguishing iron-deficiency anemia from other conditions such as thalassemia trait [13].

The hemoglobin (HGB) attribute is used in clinical practice to detect anemia based on certain thresholds (e.g., <13.6 g/dL for men and <12 g/dL for women), while MCV serves to distinguish types of anemia based on red blood cell size. The clinical relevance of the Hb/MCV ratio has been reported in hematology research as an early indicator of microcytic anemia, especially iron deficiency anemia [8]. Previous studies have suggested that this ratio can assist in differentiating iron deficiency anemia from thalassemia trait, making it a medically significant feature to be integrated into computational models. To further validate its clinical contribution, descriptive statistics were analyzed, showing that the Hb/MCV ratio differed significantly between the anemia and non-anemia groups.

By including this feature, it is hoped that the model will be able to recognize more complex patterns than when using only the original features from the dataset. After adding the feature, descriptive statistical analysis and feature distribution visualization were performed to ensure that the new feature provided significant information in the classification process.

D. Modeling

At this stage, a classification model was developed to detect anemia based on the processed features. Three supervised learning algorithms were employed: Logistic Regression (LogReg), Random Forest (RF), and Extreme Gradient Boosting (XGBoost). These algorithms were selected because they are effective for tabular clinical datasets with limited features and have been widely applied in medical classification studies. Deep learning methods were not used, as they generally require larger datasets and offer limited interpretability. Logistic Regression served as a simple and

interpretable baseline, Random Forest as a robust ensemble learner capable of handling overfitting and class imbalance, and XGBoost as a powerful gradient boosting approach with high predictive performance, computational efficiency, and built-in regularization.

To maintain comparability, all models were trained using the default parameters of the scikit-learn and XGBoost libraries, without hyperparameter tuning. This decision was made to ensure consistency and focus on evaluating the impact of feature engineering and interpretability rather than parameter optimization. The dataset was divided using a stratified split, with 80% for training and 20% for testing, ensuring balanced proportions of anemia and non-anemia cases. Model performance was then evaluated using accuracy, precision, recall, and F1-score metrics, and the results were used to identify the best-performing model as the basis for subsequent interpretation and clinical analysis.

E. Model Evaluation

The performance of the classification model was evaluated using four main metrics, namely Accuracy, Precision, Recall, and F1-Score. These metrics were chosen because they provide a comprehensive picture of the model's ability to classify data correctly, especially in the case of binary classification. Accuracy measures the proportion of correct predictions against all test data, while precision assesses how many positive predictions are relevant. Recall, or sensitivity, measures how well the model detects all actual positive cases. Meanwhile, F1-Score is the average harmony between precision and recall, which is a balanced performance indicator, especially in conditions of unbalanced class distribution.

The evaluation was conducted on three models: Logistic Regression, Random Forest, and XGBoost. Additionally, a confusion matrix was used to visualize the model's performance in the form of a prediction matrix, showing the number of true positives, false positives, true negatives, and false negatives.

The model evaluation results show that XGBoost achieved perfect accuracy and F1-score (100%) on the test data, with no classification errors. Random Forest also produced identical evaluation scores, but XGBoost was chosen as the main model due to its prediction stability, computational efficiency, and better interpretability through SHAP. Meanwhile, Logistic Regression achieved an accuracy of 98.9% and an F1-score of 98.8%, making it the baseline model. Therefore, XGBoost was designated as the best model for the interpretation stage and integration into the interactive screening system.

To further validate the robustness and generalizability of the models, k-fold cross-validation was applied, with the data partitioned into five folds. This technique ensures that every observation is used for both training and testing, reducing the risk of bias due to a particular train-test split. In addition, a 5-fold cross-validation scheme was applied to ensure that every observation was used for both training and validation. The results showed consistent accuracy and F1-scores across all folds, confirming that the model performance was stable and not due to chance. The results of the cross-validation showed that the XGBoost model consistently achieved an average accuracy and F1-score of 1.00 across all folds. Although the dataset consists of only 1,421 samples, the risk of memorization was mitigated by using stratified train-test splits and k-fold cross-validation. The consistent results across folds suggest that the models generalized well to unseen data. This indicates that the model has excellent stability and predictive power across different subsets of the data, further reinforcing its suitability as the primary model in this study.

F. Model Interpretation

After obtaining the best model in the previous evaluation stage, namely XGBoost, the next stage is to interpret the prediction results using the SHAP (SHapley Additive Explanations) approach. This technique was chosen because it can provide local and global explanations of the contribution of each feature in the model prediction in a systematic and visual manner. This interpretation will ensure that the decisions made are clinically accountable and understandable to healthcare practitioners.

To understand the contribution of each feature to the model's prediction results, interpretability analysis was conducted using SHAP. Figure 2 shows the SHAP summary plot of the XGBoost model, visualizing the influence of features on the probability of anemia classification.

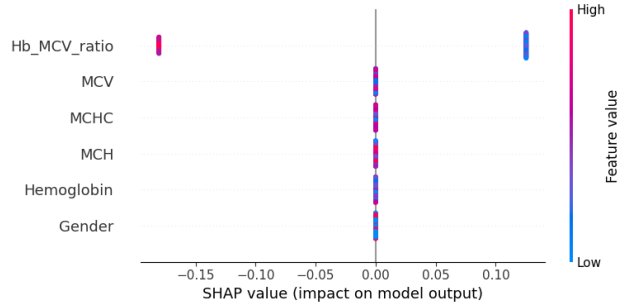

Figure 2. SHAP summary plot of the XGBoost model showing feature importance.

The SHAP summary plot visualization shows that the Hb/MCV ratio feature has the most significant contribution in determining the anemia classification outcome, followed by MCV, MCHC, and MCH. Although hemoglobin is clinically the primary indicator in anemia diagnosis, in this model, the Hb-to-MCV ratio becomes the most dominant determinant. This reinforces the added value of the designed derived features and demonstrates that the model does not rely on a single feature but combines information from multiple hematological attributes. The resulting interpretation also reinforces that the model does not rely on a single feature but considers inter-variable relationshps, making the predictions more contextual and reliable.

Visualization using SHAP explains why an individual is classified as anemic or not. For example, the classification category can be seen from low Hb values or Hb/MCV ratios

below a certain threshold. Accurate and valid visualization will undoubtedly increase user confidence in the prediction system while opening opportunities for collaboration between technology and clinical practice.

III. Results and Discussion

At this stage, an evaluation was conducted on three classification models, namely Logistic Regression, Random Forest, and XGBoost [14-17]. The assessment was carried out using accuracy, precision, recall, and f1-score metrics. Prior to model evaluation, the distribution of hematological features was analyzed using boxplots to detect potential outliers and differences between anemia and non-anemia groups.

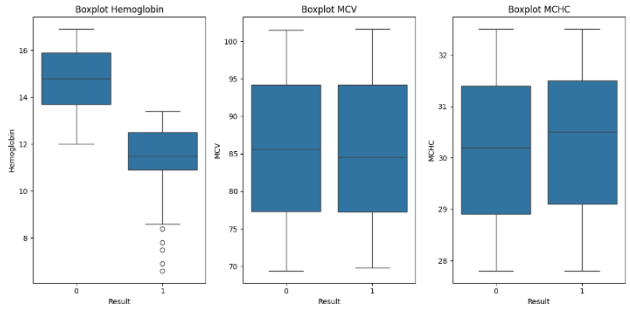

Figure 3. Boxplots of Hemoglobin, MCV, and MCHC for Normal and Anemia groups

Figure 3 shows an exploratory analysis using a box plot that illustrates the distribution of key hematological features (hemoglobin, MCV, and MCHC) between the anemia and non-anemia groups. The graph shows a clear separation in the median values of hemoglobin and MCV, with the anemia group consistently showing lower levels than the non-anemia group. This indicates that these features play a decisive role in distinguishing between the two groups, consistent with the hematological criteria established for the diagnosis of anemia. Meanwhile, MCHC shows a relatively narrower range of separation, suggesting that this feature contributes less dominantly but still adds value when combined with other features in the classification model.

Following this exploratory step, model evaluation was conducted to assess classification performance quantitatively. Table 1 presents the results of comparing the Logistic Regression, Random Forest, and XGBoost models using accuracy, precision, recall, and F1-score as evaluation metrics.

TABLE 1
Comparative Perfomance of Models

Model	Accuracy	Precision	Recall	F1-Score
Logistic Regression	0.989	0.990	0.990	0.988
Random Forest	1.000	1.000	1.000	1.000
XGBoost	1.000	1.000	1.000	1.000

To evaluate the impact of the derived feature, a comparison was conducted between model performances with and without the Hb/MCV ratio. As shown in Table 1, the inclusion of Hb/MCV consistently improved the predictive performance across all models. Notably, XGBoost and Random Forest both achieved perfect accuracy only after the Hb/MCV feature was added, while Logistic Regression showed an improvement from 97.6% to 98.9% accuracy.

The results in Table 1 indicate that XGBoost achieved the best performance, reaching perfect accuracy and F1-score (100%) without any classification errors, making it the primary model for further interpretation and clinical discussion. Random Forest also produced identical performance, while Logistic Regression showed slightly lower results with an accuracy of 98.8%.

Although Logistic Regression also showed good performance, this model recorded several classification errors. This was due to its basic nature, which is only capable of modeling linear relationships between features and targets. In the context of anemia diagnosis, some classification patterns are non-linear and involve interactions between complex clinical features, such as the Hb/MCV ratio and MCH values. In such cases, ensemble algorithms like Random Forest and XGBoost are more effective.

In this scenario, both XGBoost and Random Forest produce identical performance on the test data. However, XGBoost is selected as the best model due to its advantages. XGBoost is known to be more computationally efficient, capable of handling large and complex datasets, and supports advanced interpretability models like SHAP to explain the contribution of each feature in the prediction process. To visualize the distribution of predictions, a confusion matrix was generated for the XGBoost model. The matrix shows that the model perfectly classified all test data without any misclassification, with 124 true positives and 161 true negatives. Similar confusion matrices were also generated for Logistic Regression and Random Forest. While Logistic Regression showed a small number of misclassifications, Random Forest produced an identical result to XGBoost, achieving perfect classification. For brevity, only the confusion matrix of XGBoost is presented in Figure 4.

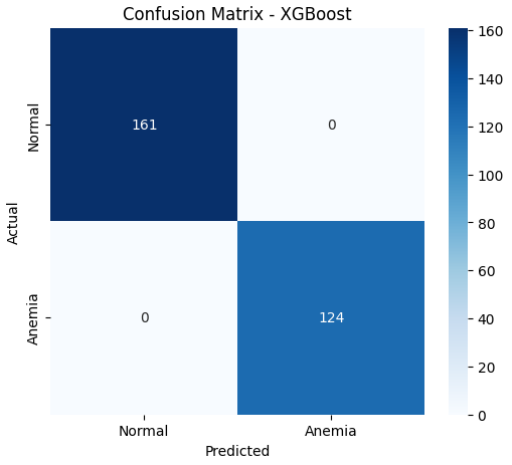

Figure 4. Confusion matrix of the XGBoost model on test data

Figure 4 shows the confusion matrix of the XGBoost model for anemia classification. The matrix shows that the model successfully classified all test data perfectly without any prediction errors, with 124 True Positives (Anemia) and 161 True Negatives (Non-Anemia). No False Positives or False Negatives were found in the evaluation results, indicating that there were no classification errors in this model. This perfect classification result indicates that the test data has a very clear pattern, allowing the model to distinguish between classes perfectly. However, additional validation such as cross-validation and testing on external datasets is necessary to ensure model generalization.

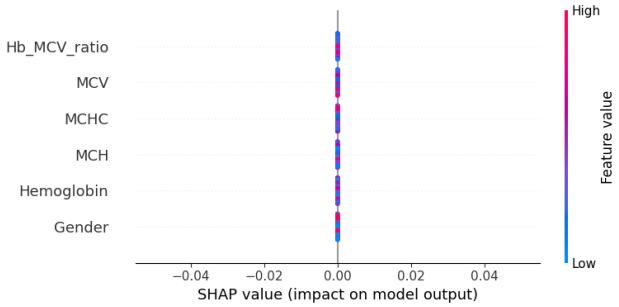

Figure 5. SHAP summary plot of the XGBoost model showing feature importance on test data.

Emphasizing the importance of each component in relation to the classification results, Figure 5 shows the SHAP summary plot. Of all the features analyzed, the Hb/MCV ratio demonstrated the greatest impact, followed closely by Hemoglobin, MCH, and MCHC. This finding highlights the crucial role of both primary hematological markers and derived features in enhancing model accuracy, while also reinforcing their clinical relevance in differentiating anemia from non-anemia cases. The relatively small SHAP values indicate that the model is very confident in its predictions for each sample, so the variation in feature contributions appears narrow. However, the pattern of feature importance remains consistent, with Hb/MCV ratio and hemoglobin being the main contributors. This suggests that the derived feature (Hb/MCV) is crucial for enhancing both the interpretability of the model and its clinical significance. These results are consistent with established practices in hematology, where hemoglobin serves as the main factor for diagnosing anemia, and the Hb/MCV ratio assists in distinguishing between iron deficiency anemia and other forms, such as thalassemia trait. The clarity provided by SHAP indicates that the model did not depend on just one feature, but instead took into account the interactions among features, resulting in predictions that are contextually appropriate and clinically reliable. The SHAP analysis further validates the contribution of the Hb/MCV ratio, confirming that this derived feature, together with hemoglobin, provides a medically consistent interpretation. This suggests that the model is not only statistically reliable but also clinically relevant, bridging the gap between computational methods and practical medical diagnosis.

IV. CONCLUSION

This study developed and evaluated a machine learning-based anemia classification model using hematology parameters from the Kaggle open dataset. Among the three algorithms tested, Logistic Regression, Random Forest, and XGBoost, both XGBoost and Random Forest achieved perfect classification performance with accuracy, precision, recall, and F1 scores of 100%, while Logistic Regression showed slightly lower performance at 98.9%. XGBoost was ultimately selected as the primary model due to its computational efficiency and support for interpretability through SHAP analysis.

The feature engineering process, particularly the introduction of the hemoglobin-to-MCV ratio (Hb/MCV), significantly improved model performance and provided clinical relevance by highlighting the importance of this ratio in distinguishing between types of anemia. SHAP interpretation further confirmed that hemoglobin and the Hb/MCV ratio are dominant predictive features, consistent with established medical knowledge. These findings suggest that XGBoost can serve as a reliable, accurate, and interpretable model for laboratory-based anemia screening, with potential applications as a clinical decision support tool.

In summary, this study not only compared different algorithms but also demonstrated the impact of feature engineering (Hb/MCV) and emphasized SHAP-based interpretability, ensuring that the results are both accurate and clinically meaningful. Despite these promising findings, this study also has limitations. The dataset size was relatively small (1,421 samples) and the evaluation did not include external validation. Future work should test the proposed model on larger and independent clinical datasets, as well as explore other algorithmic approaches and hyperparameter optimization to further strengthen generalizability and clinical applicability.

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