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Explainable AI Based Blood Disorder Screening

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Abstract- Blood disorders such as anaemia, leukemia, thalassemia, and thrombocytopenia significantly affect human health and require early identification for effective treatment. Conventional diagnostic procedures often involve manual interpretation of blood test results, which may lead to delays and variations in clinical assessment. This research proposes an Explainable Artificial Intelligence (XAI)-based blood disorder screening system that integrates machine learning and deep learning techniques to improve screening accuracy and reliability. The system analyses haematological parameters, including haemoglobin, red blood cell count, white blood cell count, platelet count, and other complete blood count (CBC) features to identify potential abnormalities. Explainability techniques such as SHAP and LIME provide transparent interpretations of model predictions by highlighting influential parameters. The proposed system supports early screening, improves clinical decision-making, and assists healthcare professionals in delivering reliable diagnostic recommendations.

Keywords- Explainable Artificial Intelligence, Blood Disorder Screening, Machine Learning, Deep Learning, Complete Blood Count, SHAP, LIME, Early Detection, Healthcare Analytics, Disease Classification.

I. INTRODUCTION

Blood disorders are among the major health conditions that affect the normal functioning of the human body by altering the composition and production of blood cells. Disorders such as anaemia, leukemia, thalassemia, sickle cell disease, and thrombocytopenia can lead to severe health complications if they are not identified at an early stage. Early screening and accurate identification are essential for providing appropriate medical intervention and reducing disease-related risks. Conventional blood disorder identification primarily depends on laboratory investigations, particularly Complete Blood Count (CBC) analysis, followed by manual interpretation of haematological parameters by healthcare professionals. However, analysing multiple blood parameters manually can be time-consuming and may introduce variations in clinical interpretation.

Recent developments in Artificial Intelligence (AI) and Machine Learning (ML) have created new opportunities for automated disease screening and healthcare decision support. Machine learning algorithms can analyse large volumes of clinical data, identify hidden patterns, and classify potential blood abnormalities based on patient-specific parameters. Techniques such as Random Forest, Support Vector Machine (SVM), Decision Tree, and Extreme Gradient Boosting (XGBoost) can be employed to improve the classification of different blood disorders. Deep

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learning approaches further enhance automated analysis by learning complex relationships among clinical features.

Despite their predictive capabilities, many AI-based healthcare systems operate as black-box models, making it difficult for medical professionals to understand the reasoning behind their predictions. This limitation creates a need for Explainable Artificial Intelligence (XAI), which improves transparency and interpretability in automated medical screening. Techniques such as SHapley Additive exPlanations (SHAP) and Local Interpretable Model-Agnostic Explanations (LIME) help identify the clinical parameters that significantly influence individual predictions.

This research proposes an Explainable AI-Based Blood Disorder Screening framework that combines machine learning classification with explainability techniques to support early identification of blood abnormalities. The system analyses CBC parameters, predicts potential blood disorder categories, and generates understandable explanations for its predictions. The proposed framework aims to assist healthcare professionals in preliminary screening, improve diagnostic transparency, and support reliable clinical decision-making. It is designed as a decision-support tool rather than a replacement for laboratory confirmation or medical diagnosis.

II. RELATED WORKS

Darshan et al. (2025) proposed a machine learning-based approach for differentiating iron deficiency anaemia (IDA) from aplastic anaemia using routine blood examination parameters. The study utilized clinical attributes such as red blood cell count, haemoglobin concentration, mean corpuscular volume, platelet count, and other haematological indicators. Multiple machine learning algorithms were investigated to identify the differences between the two anaemia conditions. To improve the transparency of the classification process, the researchers incorporated Explainable Artificial Intelligence techniques, including SHAP, LIME, ELI5, QLattice, and Anchor. These techniques identified important blood parameters influencing the prediction results and provided explanations for individual classifications. The study demonstrated that interpretable machine learning could support the differentiation of clinically similar blood disorders. However, the investigation focused primarily on two anaemia categories, indicating the need for broader multiclass screening frameworks.

Pullakhandam and McRoy (2024) investigated the classification of iron deficiency anaemia using machine learning techniques and Complete Blood Count data. The research addressed the limitations of conventional diagnosis, which often requires additional laboratory investigations such as serum ferritin testing. The researchers utilized a large dataset containing more than 19,000 instances from the National Health and Nutrition Examination Survey (NHANES). Different machine learning algorithms were developed to distinguish iron deficiency anaemia from other conditions using routinely available haematological parameters. Model performance was assessed using evaluation measures such as accuracy, precision, recall, and precision-recall area under the curve. The study highlighted the potential of CBC-based machine learning models to identify anaemia-related patterns without depending entirely on expensive diagnostic investigations. However, its primary focus was limited to iron deficiency anaemia, suggesting opportunities to extend the approach to multiple blood disorders and incorporate explainability for improved clinical understanding.

Amjad et al. (2025) developed machine learning-based models for screening anaemia and leukemia using features extracted from Complete Blood Count reports. The research focused on identifying patterns among different haematological parameters to improve automated disease screening. The study initially considered 287 samples and employed statistical distribution-based synthetic data generation to address the limited availability of clinical records. Six machine learning algorithms, including Decision Tree, Random Forest, Support Vector Machine, Logistic Regression, Gradient Boosting Machine, and Multilayer Perceptron, were evaluated. Feature selection was performed to identify 14 important attributes from 21 available

CBC parameters. Random Forest achieved approximately 98% accuracy in the reported internal evaluation. However, external validation on a different demographic dataset resulted in reduced accuracy of 74%, highlighting generalization challenges. The study provides a foundation for automated blood disorder screening and emphasizes the importance of external validation and reliable clinical datasets

Cheong et al. (2026) introduced a dual-model framework that combines deep learning and interpretable machine learning for automated blood cell classification. The proposed approach utilizes a YOLO-based deep learning model for blood cell classification and segmentation, followed by an interpretable model that explains the classification outcomes. Clinically relevant morphological characteristics are extracted from segmented blood cells and used to train the explanation model. SHAP is employed to determine the contribution of individual features to the classification results. The researchers evaluated the framework using publicly available blood cell datasets, including PBC and Raabin, along with a clinical dataset. The YOLO model demonstrated high classification performance, while the explanation component provided understandable information about the prediction process. A clinical evaluation involving trained haematology professionals also demonstrated promising agreement with model predictions. This study highlights the importance of combining predictive performance with interpretability in automated haematological analysis.

Asghar et al. (2024) conducted a global scoping review of machine learning and deep learning techniques for white blood cell classification using peripheral blood smear images. The study examined 136 research publications from different countries to identify commonly adopted classification methods and their effectiveness. Traditional machine learning approaches generally involved image preprocessing, segmentation, feature extraction, feature selection, and classification. In contrast, deep learning techniques, particularly Convolutional Neural Networks (CNNs), automatically extracted relevant features from microscopic blood images. The review identified an increasing adoption of CNN-based architectures because of their ability to learn complex morphological characteristics. It also highlighted the importance of dataset quality, preprocessing strategies, and appropriate model selection for achieving reliable classification results. However, the reviewed approaches primarily concentrated on image-based classification rather than providing transparent explanations for clinical predictions. This creates an opportunity to integrate explainable AI techniques into automated blood disorder screening systems.

O'Donnell et al. (2024) presented a rapid review of artificial intelligence applications in peripheral blood film analysis. The research investigated the development of automated blood cell classification systems and their potential applications in haematological diagnosis. A total of 283 studies were examined across different research domains, including malaria, leukemia, white blood cell classification, erythrocyte analysis, and mixed blood cell investigations. The reviewed studies demonstrated the increasing effectiveness of machine learning and deep learning approaches in identifying abnormal blood cell characteristics. The average reported classification accuracy across the different research categories was approximately 95.1%. The review also identified several challenges associated with clinical implementation, including insufficient multicentre validation, inconsistent datasets, and limited investigation of uncommon blood cell abnormalities. The findings indicate that AI-based analysis can improve the efficiency of laboratory investigations. However, further research is required to establish reliable, explainable, and clinically validated automated screening systems.

III. PROPOSED METHOD

The proposed Explainable AI-Based Blood Disorder Screening system aims to identify potential blood-related abnormalities through automated analysis of Complete Blood Count (CBC) parameters. The framework integrates data preprocessing, feature selection, machine learning classification, and Explainable Artificial Intelligence to improve

screening accuracy and prediction transparency. Initially, patient blood test records containing haemoglobin, red blood cell count, white blood cell count, platelet count, mean corpuscular volume, mean corpuscular haemoglobin, and other haematological attributes are collected from clinical datasets. The collected data undergoes preprocessing, including missing-value handling, duplicate removal, noise reduction, and feature normalization. Feature selection techniques identify the most influential parameters for improving classification performance.

The processed dataset is divided into training and testing subsets for model development and evaluation. Machine learning algorithms such as Random Forest, Support Vector Machine, Decision Tree, and XGBoost are employed to classify potential blood disorders, including anaemia, leukemia, thalassemia, and thrombocytopenia. The best-performing model is selected based on accuracy, precision, recall, F1-score, and ROC-AUC.

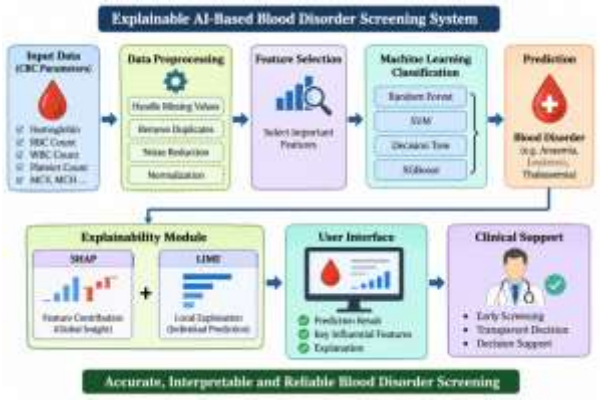

Fig 1: Architecture Diagram

To overcome the black-box limitations of conventional machine learning models, SHAP and LIME explainability techniques are integrated. SHAP identifies the contribution of individual blood parameters to the overall prediction, whereas LIME generates locally interpretable explanations for individual patient results. The system presents the predicted disorder category, influential haematological parameters, and corresponding explanation through a user-friendly interface.

The proposed framework supports early screening, improves prediction transparency, and assists healthcare professionals in preliminary clinical assessment. It functions as a decision-support system, while final diagnosis requires appropriate laboratory investigations and professional medical evaluation.

IV. OVERALL WORKING FLOW OF THE PROPOSED SYSTEM

The overall workflow of the proposed Explainable AI-Based Blood Disorder Screening system consists of several sequential stages, beginning with the collection of Complete Blood Count (CBC) data and ending with the generation of interpretable screening results. The framework integrates data preprocessing, feature selection, machine learning classification, and explainability techniques to identify potential blood abnormalities.

1. Data Collection

The system collects patient-related haematological information from publicly available datasets or clinical laboratory records. The input parameters include haemoglobin, red blood cell (RBC) count, white blood cell (WBC) count, platelet count, mean corpuscular volume (MCV), mean corpuscular haemoglobin (MCH), and other relevant blood attributes.

2. Data Preprocessing

The collected dataset undergoes preprocessing to improve data quality. Missing values are handled using suitable imputation techniques, duplicate records are removed, and inconsistent data are corrected. Feature normalization is performed to bring numerical attributes into a consistent range.

3. Feature Selection

Important blood parameters are identified using statistical and feature importance-based selection methods. This stage eliminates irrelevant attributes and reduces the dimensionality of the dataset, improving computational efficiency and classification performance.

4. Machine Learning Classification
The selected features are supplied to different machine learning algorithms, including Random Forest, Support Vector Machine (SVM), Decision Tree, and XGBoost. The models are trained using labelled blood disorder records to recognize disease-specific patterns.

5. Model Evaluation
The trained models are evaluated using testing data. Performance is measured through accuracy, precision, recall, F1-score, confusion matrix, and ROC-AUC. The best-performing model is selected for final screening.

6. Explainability Analysis
SHAP and LIME techniques are integrated to interpret the model predictions. SHAP identifies the contribution of individual blood parameters to the prediction, while LIME explains the reasoning behind an individual patient's classification.

7. Prediction and Result Visualization
The selected model predicts potential blood disorder categories, such as anaemia, leukemia, thalassemia, and thrombocytopenia. The system displays the predicted category, influential parameters, and explanation through a user-friendly interface.

8. Clinical Decision Support
The generated screening results help healthcare professionals understand abnormal blood patterns and support preliminary clinical assessment. Final diagnosis and treatment decisions remain under the supervision of qualified medical professionals.

V. PERFORMANCE EVALUATION

The performance of the proposed Explainable AI-Based Blood Disorder Screening system is evaluated using standard machine learning performance metrics to determine its classification accuracy, reliability, and effectiveness in identifying different blood disorders. The dataset is divided into training and testing subsets, typically using an 80:20 ratio. The training dataset is utilized to develop classification models, while the testing dataset measures their ability to predict previously unseen patient records. Multiple machine learning algorithms, including Random Forest, Support Vector Machine (SVM), Decision Tree, and XGBoost, are compared to identify the most suitable classification model.

The evaluation considers accuracy, precision, recall, F1-score, and Receiver Operating Characteristic–Area Under the Curve (ROC-AUC). Accuracy measures the overall correctness of predictions, whereas precision determines the proportion of correctly identified positive cases. Recall measures the ability of the model to identify actual blood disorder cases. The F1-score provides a balanced measure of precision and recall, particularly when the dataset contains unequal class distributions. The confusion matrix is used to examine true positive, true negative, false positive, and false negative predictions.

Furthermore, SHAP and LIME are evaluated to determine the interpretability of the selected classification model. SHAP analysis identifies the most influential haematological parameters across the dataset, while LIME explains individual patient predictions. Their explanations are examined for consistency and clinical relevance.

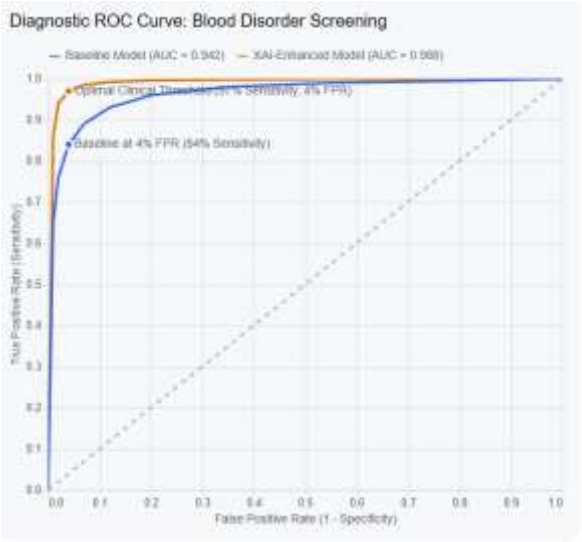

Fig.2. Performance analysis

The False Positive Rate measures the proportion of actual negative cases that are incorrectly classified as positive by the proposed model. It helps evaluate the frequency of false alarms during blood disorder screening. A lower FPR indicates that the model can distinguish healthy individuals from potentially affected patients more effectively.

$$FPR = \frac{FP}{FP + TN}$$

VI. RESULTS AND DISCUSSION

The proposed Explainable AI-Based Blood Disorder Screening system provides an intelligent framework for identifying potential blood abnormalities using Complete Blood Count (CBC) parameters. The performance of different machine learning algorithms, including Random Forest, Support Vector Machine (SVM), Decision Tree, and XGBoost, is analysed to determine their classification effectiveness. The experimental evaluation considers accuracy, precision, recall, F1-score, specificity, and ROC-AUC to assess the reliability of the developed models.

The comparative analysis helps identify the algorithm that provides the best balance between classification performance and computational efficiency. Random Forest and XGBoost are expected to provide competitive results because of their ability to capture complex relationships among haematological parameters. The selected model classifies patient records into different blood disorder categories, including anaemia, leukemia, thalassemia, and thrombocytopenia. The confusion matrix further illustrates the correctly and incorrectly classified samples, helping identify possible misclassification patterns among similar disorders.

The integration of SHAP and LIME improves the interpretability of the prediction process. SHAP identifies the most influential clinical parameters across the dataset, while LIME provides individual explanations for patient-specific predictions. Parameters such as haemoglobin, RBC count, WBC count, and platelet count can contribute significantly to different screening outcomes. The visual explanations help healthcare professionals understand the factors influencing each prediction.

Overall, the proposed framework combines automated classification with transparent decision explanations. It demonstrates the potential of explainable machine learning for preliminary blood disorder screening, reducing dependence on manual interpretation and supporting timely clinical assessment. However, its practical reliability must be established through larger clinical datasets, independent validation, and expert evaluation before real-world medical deployment.

Future Work

Future developments of the proposed Explainable AI-Based Blood Disorder Screening system will focus on improving classification accuracy, scalability, and clinical applicability. The system can be extended by incorporating larger and more diverse clinical datasets containing multiple blood disorder categories. Advanced deep learning architectures and ensemble learning techniques can be explored to improve disease classification and identify complex relationships among haematological parameters. Integration of multimodal medical data, including CBC reports, peripheral blood smear images, and patient medical history, can provide comprehensive screening capabilities. Advanced explainability techniques such as SHAP, LIME, and Grad-CAM can further improve prediction transparency for both numerical and image-based inputs. A cloud-based platform and mobile application can be developed to enable secure access to screening results across healthcare environments. Furthermore, collaboration with hospitals and diagnostic laboratories can support real-world validation, continuous model improvement, and reliable clinical decision support while maintaining patient data privacy.

VII. CONCLUSION

The study on Explainable AI-Based Blood Disorder Screening highlights the potential of artificial intelligence to improve the early detection and screening of blood-related disorders through intelligent, data-driven analysis. By integrating machine learning techniques with Explainable

Artificial Intelligence (XAI), the proposed approach aims to identify abnormal blood patterns, support accurate classification, and provide transparent explanations for the predictions generated by the system. Explainability enhances the reliability and interpretability of AI models, allowing healthcare professionals to better understand the factors influencing screening outcomes rather than relying solely on automated predictions. The system can contribute to faster preliminary screening, reduced diagnostic delays, improved decision-making, and more efficient healthcare services. However, its effectiveness depends on the quality of medical data, model accuracy, validation across diverse patient populations, and responsible implementation. Overall, explainable AI-based blood disorder screening represents a promising advancement in intelligent healthcare technology, offering a balance between computational efficiency, transparency, and clinical support. With further research, clinical validation, and integration into healthcare workflows, such systems may play a significant role in improving early screening, patient care, and medical diagnostic assistance.

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