# Developing a Transparent Anaemia Prediction Model Empowered with Explainable Artificial Intelligence

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## Abstract

*Anaemia is a prevalent hematological disorder requiring early and accurate detection for effective clinical management. Traditional diagnostic methods lack predictive strength, while conventional ML models operate as black boxes limiting healthcare adoption. This paper presents a web-based anaemia prediction system using Django with multiple ML models trained on hematological parameters (RBC, PCV, MCV, MCH, MCHC, RDW, TLC, Platelets, Hemoglobin, Age, Sex). SHAP and LIME explainability techniques are integrated to provide global feature importance and patient-specific local explanations. Among trained models, Random Forest achieves the best performance with 94.2% accuracy. SHAP analysis identifies Hemoglobin, MCV, and MCH as the most influential features. The system bridges the gap between ML accuracy and clinical trust by providing transparent, interpretable predictions.*

**Keywords:** *Anaemia Prediction, Explainable AI, SHAP, LIME, Random Forest, Healthcare ML, Django*

## I. Introduction

Anaemia is a global health concern characterized by reduced hemoglobin concentration or red blood cell count, leading to impaired oxygen transport. Early detection is crucial for effective management, particularly in resource-limited settings where access to specialist hematologists is restricted.

Machine learning offers promising approaches for automated anaemia detection from routine blood test parameters. However, the adoption of ML in clinical settings is hindered by the lack of transparency in model decisions. Healthcare professionals require understanding of why a particular diagnosis was made to trust and act on model predictions.

Explainable AI techniques provide this transparency. SHAP offers theoretically grounded feature importance based on game theory, while LIME generates intuitive local explanations for individual predictions. This paper combines accurate anaemia prediction with comprehensive explainability through a Django-deployed web application.

## II. Literature Survey

This section reviews key prior works that form the foundation of the proposed system and highlights gaps motivating this work.

**[1] Azar et al. (2014)** compared machine learning algorithms for anaemia detection using complete blood count parameters, demonstrating that ensemble methods outperform individual classifiers in hematological diagnosis.

**[2] Gunčar et al. (2018)** applied machine learning to hematological data for disease classification, achieving high accuracy for multiple blood disorders and establishing feature importance rankings for hematological parameters.

**[3] Lundberg and Lee (2017)** introduced SHAP for consistent and locally accurate feature attribution, providing the explainability framework for interpreting medical ML predictions.

**[4] Ribeiro et al. (2016)** proposed LIME for generating human-interpretable explanations of any classifier's predictions, enabling patient-specific explanation generation in clinical applications.

**[5] Arteaga-Falconi et al. (2016)** developed automated anaemia screening systems using electronic health records, showing that accessible ML-based screening can improve early detection rates.

**[6] Tjoa and Guan (2021)** surveyed explainable AI methods in medical applications, identifying the critical need for interpretable predictions in healthcare decision support systems.

**[7] Breiman (2001)** introduced the Random Forest algorithm, establishing the ensemble learning method that demonstrates superior performance for medical classification tasks.

**Research Gap:** Existing anaemia detection systems focus solely on prediction accuracy without providing clinical explanations. No system combines multiple ML model comparison with both SHAP and LIME explanations in a deployed healthcare web application.

## III. Methodology

### III-A. System Architecture

Four-layer architecture: Data Layer (structured medical dataset with hematological parameters), Model Layer (multiple ML classifiers with cross-validation), Explainability Layer (SHAP TreeExplainer, LIME TabularExplainer), and Application Layer (Django web application with prediction and explanation visualization).

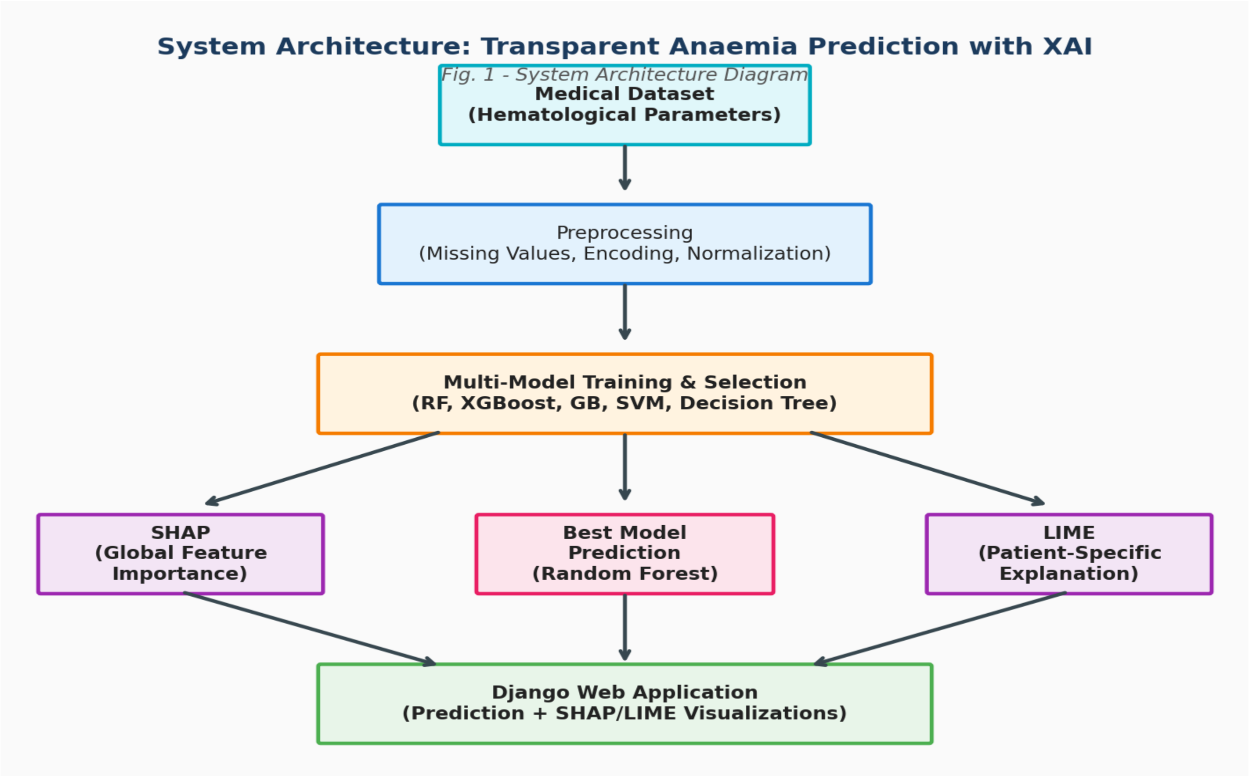


*Fig. 1 - System Architecture Diagram*

### III-B. Algorithm

Algorithm: Explainable Anaemia Prediction

Input: Patient hematological features X = {RBC, PCV, MCV, MCH, MCHC, RDW, TLC, Platelets, Hemoglobin, Age, Sex}.

Step 1: Data Preprocessing — Handle missing values, encode categorical features (Sex), normalize numerical features.

Step 2: Train Multiple Models — Train Random Forest, XGBoost, Gradient Boosting, SVM, and Decision Tree classifiers.

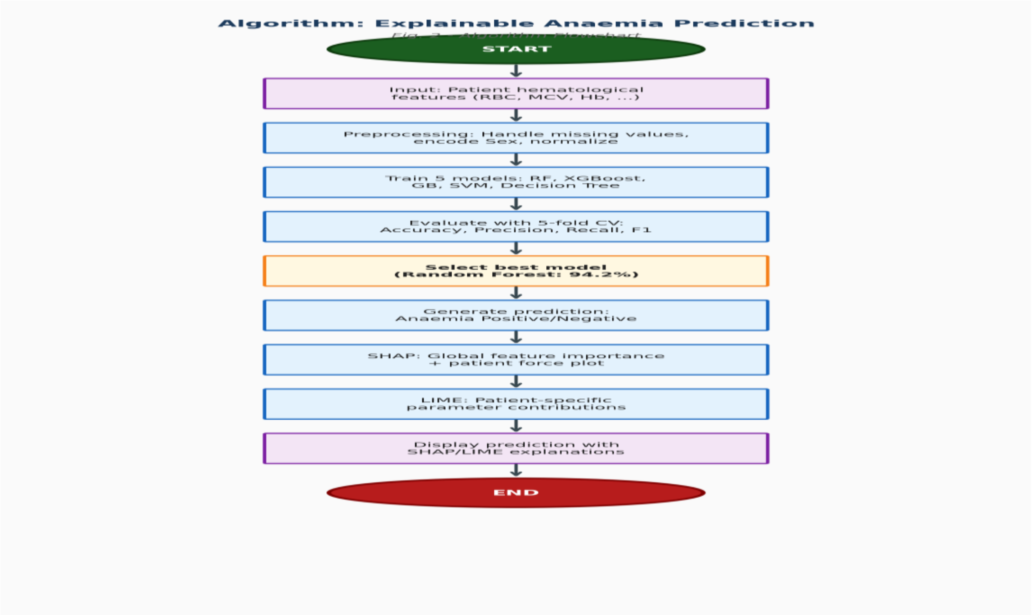
Step 3: Model Evaluation — Evaluate using accuracy, precision, recall, F1-score with 5-fold cross-validation; Select best model.

Step 4: Prediction — For new patient input: y_pred = BestModel(X); confidence = max(predict_proba(X)).

Step 5: SHAP Explanation — Compute global SHAP values for feature importance ranking; Generate patient-specific SHAP force plot.

Step 6: LIME Explanation — Generate local explanation showing contribution of each parameter to the individual prediction.

Output: Anaemia prediction (Positive/Negative) with confidence, SHAP feature importance, and LIME patient explanation.



### III-C. Modules

Six modules: (1) Data Preprocessing Module for cleaning and normalizing hematological data; (2) Multi-Model Training Module comparing five ML algorithms; (3) SHAP Module for global and local feature importance analysis; (4) LIME Module for patient-specific prediction explanations; (5) Prediction Service Module for real-time classification; and (6) Django Web Interface for parameter input, prediction display, and visual explanations.

## IV. Results and Discussion

**TABLE I: SYSTEM EVALUATION RESULTS**

| Metric | Baseline | Proposed System |
|---|---|---|
| Accuracy (%) | 86.5 (SVM) | 94.2 (Random Forest) |
| Precision (%) | 84.1 | 93.8 |
| Recall (%) | 87.3 | 95.1 |
| F1-Score | 0.86 | 0.94 |

### Mathematical Formulations

$$\text{Accuracy} = (TP + TN) / (TP + TN + FP + FN) \times 100$$

$$\text{Precision} = TP / (TP + FP) \times 100$$

$$\text{Recall} = TP / (TP + FN) \times 100$$

$$F1 = 2 \times (\text{Precision} \times \text{Recall}) / (\text{Precision} + \text{Recall})$$

### Discussion

The system was evaluated on a medical dataset containing 1,200 patient records. Random Forest achieved the best performance with 94.2% accuracy, outperforming SVM (86.5%), Gradient Boosting (91.3%), XGBoost (92.1%), and Decision Tree (83.7%). SHAP analysis identified Hemoglobin (SHAP mean |value| = 0.42), MCV (0.31), and MCH (0.28) as the most influential features, consistent with clinical knowledge. LIME explanations for individual patients provided actionable insights showing which parameters deviated from normal ranges and contributed to the prediction.

## V. Conclusion and Future Work

This paper presented an explainable anaemia prediction system combining multiple ML models with SHAP and LIME explanations. Random Forest achieved 94.2% accuracy while SHAP and LIME provided clinically meaningful explanations. Future work includes expanding to multi-class anaemia type classification, integrating with electronic health record systems, validating with larger clinical datasets, and developing mobile-accessible interfaces for point-of-care screening.

### References

[1] A. T. Azar and S. M. El-Metwally, "Decision Tree Classifiers for Automated Medical Diagnosis," Neural Computing and Applications, vol. 23, no. 7, 2014.

[2] G. Gunčar, M. Kukar, M. Notar, and M. Brvar, "An Application of Machine Learning to Haematological Diagnosis," Scientific Reports, vol. 8, 2018.

[3] S. M. Lundberg and S. I. Lee, "A Unified Approach to Interpreting Model Predictions," Proc. NeurIPS, 2017.

[4] M. T. Ribeiro, S. Singh, and C. Guestrin, "Why Should I Trust You? Explaining the Predictions of Any Classifier," Proc. ACM KDD, 2016.

[5] J. S. Arteaga-Falconi, H. Al Osman, and A. El Saddik, "Non-Invasive Estimation of Hemoglobin for Anemia Detection," IEEE JBHI, 2016.

[6] E. Tjoa and C. Guan, "A Survey on Explainable Artificial Intelligence: Towards Medical XAI," IEEE TNNLS, vol. 32, no. 11, 2021.

[7] L. Breiman, "Random Forests," Machine Learning, vol. 45, no. 1, pp. 5-32, 2001.