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Publication Date

2023

DOI

10.1109/access.2023.3321509

IEEE Access
Multidisciplinary ⋮ Rapid Review ⋮ Open Access Journal

Received 18 September 2023, accepted 28 September 2023, date of publication 2 October 2023, date of current version 9 October 2023.

Digital Object Identifier 10.1109/ACCESS.2023.3321509

RESEARCH ARTICLE

Assessment of Hematological Predictors via Explainable Artificial Intelligence in the Prediction of Acute Myocardial Infarction

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ABSTRACT Acute myocardial infarction (AMI) is the main cause of death in developed and developing countries. AMI is a serious medical problem that necessitates hospitalization and sometimes results in death. Patients hospitalized in the emergency department (ED) should therefore receive an immediate diagnosis and treatment. Many studies have been conducted on the prognosis of AMI with hemogram parameters. However, no study has investigated potential hemogram parameters for the diagnosis of AMI using an interpretable artificial intelligence-based clinical approach. The purpose of this research is to implement the principles of explainable artificial intelligence (XAI) in the analysis of hematological predictors for AMI. In this retrospective analysis, 477 (48.6%) patients with AMI and 504 (51.4%) healthy individuals were enrolled and assessed in predicting AMI. Of the patients with AMI, 182 (38%) had an ST-segment elevation MI (STEMI), and 295 (62%) had a non-ST-segment elevation MI (NSTEMI). Demographic and hematological information of the patients was analyzed to determine AMI. The XAI approach combined with machine learning approaches (Extreme Gradient Boosting, XGB; Adaptive Boosting, AB; Light Gradient Boosting Machine, LGBM) was applied for the estimation of AMI and distinguishing subgroups of AMI (STEMI and NSTEMI). The SHAP approach was used to explain the predictions intuitively. After selecting the 10 most important hematological parameters for AMI, the LGBM model achieved 83% and 74% accuracy for prediction of AMI, and distinguishing subgroups of AMI (STEMI and NSTEMI), respectively. SHAP results showed that neutrophil (NEU), white blood cell (WBC), platelet width of distribution (PDW), and basophil (BA) were the most important for AMI prediction. Mean corpuscular volume (MCV), BA, monocytes (MO), and lymphocytes (LY) were the most important hematological parameters that distinguish STEMI from NSTEMI. The proposed model serves as a valuable tool for physicians, facilitating the diagnosis, treatment, and follow-up of patients with AMI and distinguishing subgroups of AMI (STEMI and NSTEMI). Analyzing readily accessible hemogram parameters empowers medical professionals to make informed decisions and provide enhanced care to a wide range of individuals.

INDEX TERMS Acute myocardial infarction, NSTEMI, clinical classification, explainable artificial intelligence, SHAP, hematological parameters.

I. INTRODUCTION

Acute myocardial infarction (AMI) is the main cause of death in developed and developing countries. The annual prevalence of the disease exceeds three million people worldwide [1], [2], [3].

In AMI, oxygen deficiency due to partial or complete cessation of coronary blood flow causes irreversible damage to the myocardium. Providing coronary reperfusion as soon as possible minimizes the complications that may occur. The

The associate editor coordinating the review of this manuscript and approving it for publication was Junhua Li.

earlier coronary reperfusion is achieved, the better the prognosis, especially in the first six hours [4].

Previous studies have also shown that red cell distribution width (RDW) predicts mortality and morbidity in AMI (STEMI and NSTEMI), chronic coronary syndromes, and heart failure [5], [6], [7]. In addition, it has been shown in other studies that the indices produced from hematological parameters such as neutrophil-lymphocyte ratio (NLR), platelet-lymphocyte ratio (PLR), and mean platelet volume-lymphocyte ratio (MPVLR) can predict poor prognosis and no-reflow in patients with STEMI who have no-reflow after interventional treatment [8], [9], [10], [11], [12]. Many studies have been conducted on the prognosis of AMI with hemogram parameters. However, no study has investigated potential hemogram parameters for the diagnosis of AMI using an interpretable artificial intelligence-based clinical approach.

Artificial intelligence (AI) is a core part of versatile clinical decision-aid systems. It also enables methods to make computationally close human decisions [13]. The methods here are obtained automatically by machine learning based on clearly analyzed medical knowledge [14]. Explainable AI (XAI) can help patients stay at the center of treatment and help them make autonomous and sound decisions about their health in coordination with doctors [15]. While the quality of current AMI prognostic methods varies widely, models for predicting labor loss and death after AMI are limited by sample size, clinical and risk factor breadth, and often clinical method. An accurate prognosis based on estimated life expectancy and clinical history can improve discharge planning after AMI and help physicians individualize aggressive treatment or palliative care. Building on the valuable information emphasized in various medical studies, the current research aims to assess hematological markers to predict AMI based on the implications of XAI.

The potential contributions of this study can be listed down:

- The XAI approach combined with machine learning approaches (Extreme Gradient Boosting, XGB; Adaptive Boosting, AB; Light Gradient Boosting Machine, LGBM) is applied for the estimation of AMI and distinguishing subgroups of AMI (STEMI and NSTEMI).
- After selecting the 10 most important hematological parameters for AMI, the LGBM model achieves 83% and 74% accuracy for prediction of AMI, and distinguishing subgroups of AMI (STEMI and NSTEMI), respectively.
- SHAP results show that neutrophil (NEU), white blood cell (WBC), platelet width of distribution (PDW), and basophil (BA) are the most important for AMI prediction.
- The proposed model serves as a valuable tool for physicians, facilitating the diagnosis, treatment, and follow-up of patients with AMI and distinguishing subgroups of AMI (STEMI and NSTEMI).

II. MATERIAL AND METHODS

The current study was planned as an observational study. Patients admitted to our hospital due to AMI between January 2020 and May 2023 were retrospectively included in the present study. Our current study included 981 individuals (477 in the patients with AMI group and 504 in the healthy control group, individuals without AMI who applied to the cardiology department). We divided AMI into two main categories: STEMI and NSTEMI. The research was approved by our university ethics committee (Date: 21.06.2023; Protocol number: 2023/12/19).

In this study, the patients with the following AMI criteria according to 2017 the European Society of Cardiology (ESC) Guidelines for the management of AMI in patients presenting with STEMI (https://doi.org/10.1093/eurheartj/ehx393) and 2020 ESC Guidelines for the management of ACS in patients presenting without persistent ST-segment elevation (NSTEMI) (https://doi.org/10.1093/eurheartj/ehaa575) are included [16], [17], [18], [19].

a) Age $>$ 18 years and 80 years.

The exclusion criteria from the study are given below:

a) Age $<$ 18 years and $>$80 years,
b) Patients use drugs known to affect the complete blood count,
c) Patients with a hemoglobin value of less than 10 g/dl,
d) Patients with active bleeding,
e) Patients with acute or chronic infections.
f) Patients with severe renal impairment [estimated glomerular filtration rate (eGFR) 15 ml/min/m2],
g) A history of cancer was detected within the previous year,
h) Patients with severe liver impairment,
i) Patients with chronic obstructive pulmonary disease,
j) Patients with chronic inflammatory diseases.

Age, gender, underlying diseases, left ventricular ejection fraction (LVEF) percentage, and clinical/echocardiographic characteristics were obtained from the medical records of the patients and the control group at the first admission to the hospital. At the same time, the hematological and biochemical laboratory results from the venous blood taken at the first application to the emergency department gathered from the groups were; urea (mg/dL), creatinine, c-reactive protein (CRP), aspartate transaminase (AST), alkaline phosphatase (ALT), troponin (Tn), hemoglobin (HGB) values, hematocrit (HCT) values, mean corpuscular volume (MCV) values, mean corpuscular hemoglobin (MCH) values, mean corpuscular hemoglobin concentration (MCHC) value, red-cell distribution width-standard deviation (RDW-SD) values, RDW-coefficient of variation (RDW-CV) values, mean platelet volume (MPV) values, platelet width of distribution (PDW) values, procalcitonin (PCT) values, platelet (PLT) counts and white blood cell (WBC), neutrophil (NEU), lymphocyte (LY), NLR, basophil (BA), monocytes (MO)

and eosinophil (EO) counts. The dataset is presented in the Supplementary files.

A. PROPOSED METHODOLOGY

Our proposed research study is based on an experimental setup consisting of several components. We utilized the Python 3.10 Programming Language to conduct the research experiments. All experiments were evaluated using the open-source platform Google Colab. The environment used for these experiments includes 13 GB of RAM and 90 GB of disk space.

We have comprehensively analyzed our proposed research methodology, as shown in Figure 1. The materials and methods used for detecting heart disease in AMI patients are presented. The step-wise exploration of the proposed methodology is as follows:

Step 1: For conducting our research experiments, we used a benchmark dataset. The dataset is composed of hematological blood parameters from 981 patients, including both individuals with AMI disease and healthy subjects. Our proposed methodology utilizes the related dataset at each step to infer results.

Step 2: As the original dataset contains a high number of feature dimensions for building AI methods, we implemented AI feature selection to the dataset and selected the top 10 features based on their high-importance values in this analysis.

Step 3: Then, the newly selected feature dataset is utilized for training and testing in the artificial intelligence methods. We have used a 5-fold cross-validation mechanism to evaluate the performance results.

Step 4: For performance evaluations, we applied three advanced AI methods: Extreme Gradient Boosting, Adaptive Boosting, and Light Gradient Boosting Machine. We compared the performance scores of each method using cross-validation analysis.

Step 5: Through performance evaluation, the proposed approach outperforms other methods reviewed. The model is then used both to distinguish healthy control from patients with AMI and to differentiate STEMI patients from NSTEMI patients.

Step 6: The proposed approach for decision-making in heart disease detection is then analyzed through XAI analysis. We have utilized the SHapley Additive exPlanations (SHAP) approach to analyze the results.

B. FEATURE SELECTION

In this research study, we applied a feature selection mechanism based on an artificial intelligence-driven random forest method for the detection of AMI using hematological blood parameters. Feature selection is a crucial step in building robust and interpretable predictive models. In our approach, we leverage the power of the random forest, a popular ensemble learning algorithm, to efficiently assess the importance of each hematological blood parameter in predicting the presence of AMI. The random forest method employs a multitude of decision trees and aggregates their predictions to improve accuracy and reduce overfitting [20]. By employing this AI-driven approach, we aim to identify the most relevant and informative blood parameters, leading to a concise and efficient diagnostic model for early detection and better management of AMI. Our AI-based feature selection process ensures that the selected parameters are more interpretable, enabling clinicians and researchers to gain valuable insights into the underlying disease pathology and potential risk factors.

C. VALIDATION METHOD

To assess the performance of different AI techniques for AMI detection based on blood parameters, we applied the k-fold cross-validation method in this research study. We split the selected features of the dataset into five subsets of equal size and ran five iterations of training and validation. In each iteration, one subset was used as the validation set and the other four subsets were used as the training set. We ensured that every data point was involved in both training and validation, minimizing the possibility of overfitting and providing a more reliable evaluation of the AI techniques [21].

D. CLASSIFICATION METHODS

Extreme Gradient Boosting (XGB): The XGB classifier has emerged as a powerful and widely adopted machine learning technique for various applications, including medical diagnosis. In the context of detecting AMI, XGB holds great promise due to its ability to handle complex and high-dimensional datasets. By employing XGB, this study seeks to create a robust and efficient predictive model that can effectively utilize the multitude of hematological parameters to discern patterns and signatures specific to AMI. The strengths of the XGB algorithm lie in its capacity to handle nonlinear relationships, and feature interactions, and its resistance to overfitting, thereby enhancing its suitability for capturing intricate patterns in the data [22], [23]. The mathematical equation for the XGB classifier can be represented as follows: Let X be the input feature matrix with 'n' samples and 'm' features: X = [x_1, x_2, . . . , x_n] where each x_i is a vector of length 'm'. Let y be the corresponding target labels: y = [y_1, y_2, . . . , y_n], where y_i is the label (1 for positive cases and 0 for negative cases) for the corresponding sample x_i. Given a new input sample x_i, the final prediction for the probability of the positive class (AMI disease) can be calculated as:

$$P(y_i = 1|x_i) = \frac{1}{(1 + \exp(-F(x_i)))} \quad (1)$$

where F(xi) is the sum of predictions from each base learner for the input sample xi.

Adaptive Boosting (AB): The AB classifier is an effective machine-learning technique used for detecting AMI by leveraging hematological blood parameters. The AB classifier utilizes a combination of weak learners, typically decision trees, and assigns weights to them based on their performance in classifying the data. By iterative training and reweighting

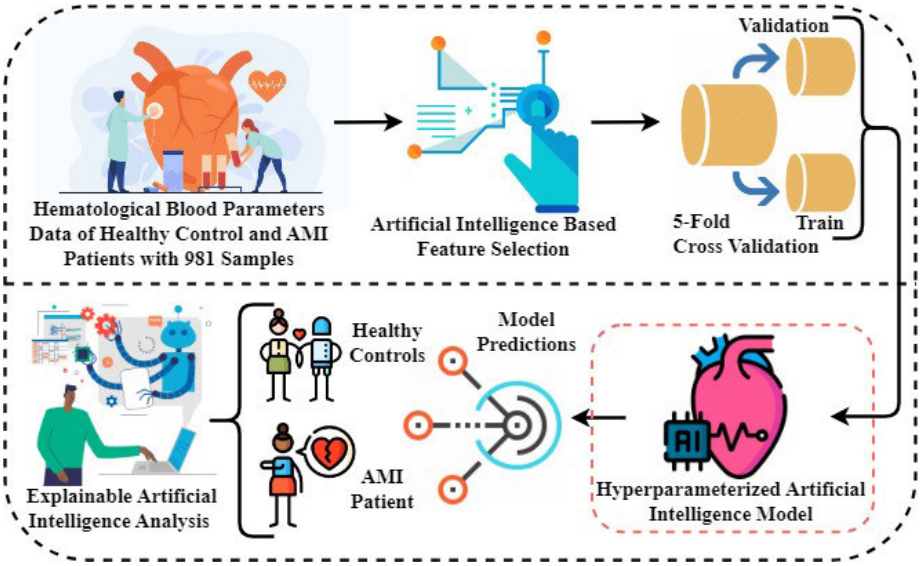

FIGURE 1. The architecture analysis of our proposed study methodology for AMI detection; AMI: acute myocardial infarction.

the weak learners, AB creates a robust and accurate ensemble model that effectively captures complex relationships within the hematological parameters and their association with myocardial infectious heart disease. We can represent the AdaBoost algorithm mathematically [22]. Suppose we have a dataset consisting of 'N' samples, where each sample is denoted as xi, and the corresponding target labels as yi, where yi is either 0 (negative class - healthy) or 1 (positive class - AMI). After T iterations, the final classification is obtained by combining the predictions of all weak learners using their corresponding weights:

$$H(x) = \text{sign}(\sum_t (\text{alpha\_t} * h_{t(x)})) \quad (2)$$

where H(x) is the final AB classifier, and 'sign' is the sign function that returns $+1$ if the sum is positive or 0, and -1 otherwise.

Light Gradient Boosting Machine (LGBM): The LGBM classifier is a powerful and efficient machine-learning algorithm that has shown promising results in various applications, including medical diagnosis. By harnessing the strengths of LGBM, such as its ability to handle large-scale datasets and capture nonlinear relationships, we aim to develop a robust and accurate classifier for the early detection of AMI. The LGBM classifier aims to find an ensemble of weak learners (usually decision trees) that can make accurate predictions. The final prediction for a patient can be computed as the weighted sum of the predictions made by individual weak learners [24], [25]. The mathematical equation for the LGBM classifier can be represented as:

$$F(x) = w_0 \sum (w_i * f(x_i)) \quad (3)$$

where: X is the feature matrix of size $(n \times m)$, where each row represents a patient's hematological blood parameter values. F(x) is the final prediction for a patient's myocardial infectious heart disease status.

w0 is the bias term or the intercept of the model.

$\sum (w_i * f(x_i))$ is the summation of all weak learners (trees).

wi is the weight associated with the ith weak learner.

f(xi) is the prediction of the ith weak learner for the input xi (hematological blood parameters for the patient).

In this study, we used accuracy (A), precision (P), recall (R), F1, and Area under the Curve (AUC) as evaluation metrics for the applied artificial intelligence methods.

Hyper-Parameters Settings: The hyperparameters settings of the applied artificial intelligence method with selected values are analyzed in this section. The best-fit hyperparameters are determined, as shown in Table 1. This analysis demonstrates that our applied artificial intelligence approaches achieved a high-performance score for AMI patient detection using these selected hyperparameters in this study.

E. BIOSTATISTICAL ANALYSIS

The conformity of the variables to the normal distribution was examined by visual (histogram and probability graphs) and analytical (Shapiro-Wilk Test) methods. The assumption of homogeneity of variances was examined with the Levene test. Descriptive statistics are expressed as a median, interquartile range for non-normally distributed variables, and mean $\pm$ standard deviation for normally distributed variables. The Mann-Whitney U test was used to compare the two groups in terms of variables that did not meet the parametric test assumptions. One-way ANOVA and Kruskal Wallis H test were used where appropriate for the comparison of more than two groups. Frequency (n) and percentage (%) values were calculated for the qualitative variables, and the relationships between the two qualitative variables were examined using the Chi-square test. A p-value of ≤ 0.05 was considered

TABLE 1. Hyper-parameters settings result from the analysis.

Method	*Hyper-parameters Values*
XGB	learning_rate=0.1, n_estimators=300, max_depth=300, nthread=-1, scale_pos_weight=1, base_score=0.5, colsample_bylevel=1, colsample_bytree=1
AB	n_estimators=300, random_state=0, learning_rate=1.0, algorithm='SAMME.R',
LGBM	n_estimators=300, boosting_type='gbdt', num_leaves=31, learning_rate=0.1, subsample_for_bin=200000, min_child_weight=0.001, min_child_samples=20, subsample=1.0, subsample_freq=0, colsample_bytree=1.0, importance_type='split'

XGB: Extreme Gradient Boosting; AB: Adaptive Boosting; LGBM: Light Gradient Boosting Machine

TABLE 2. Descriptive statistics regarding demographical factors concerning the groups.

Variable		Group			*p*-value
		STEMI	NSTEMI	CONTROL	
Gender *	F	54 (29.67%)	106 (35.93%)	253 (50.20%)	0.013#
	M	128 (70.33%)	189 (64.07%)	251 (49.80%)	
Age**		59.59±10.72	60.675±10.08	58.17±11.22	<0.001 &

*: Data presented as frequency (%); **: Data presented as mean±standard deviation; #: Chi-square test; &: One-way ANOVA; F: Female; M: Male; STEMI: ST-elevation myocardial infarction; NSTEMI: Non-STEMI

statistically significant in all results. Statistical analyzes were performed using the SPSS 28.0 (IBM Corp., Armonk, NY, United States) package program.

III. RESULTS

A total of 981 patients were included in the study; 477 (48.6%) patients with AMI and 504 (51.4%) healthy controls. Of the patients with AMI, 182 (38%) had a STEMI, and 295 (62%) had a NSTEMI. Table 2 presents the descriptive statistics of the patients' sociodemographic data concerning the groups.

According to Table 3, WBC, BA, MO, NEU, NLR, MCV, RDW-CV, MCHC, and PDW results were significantly higher in AMI patients compared to healthy controls ($p \leq 0.05$). EO, PLT/LY ratio, MPV/LY ratio, LY/MO ratio, MPV, and PCT results were significantly lower in the AMI group ($p \leq 0.05$). RBC, HGB, LY, PLT, HCT, RDW-SD, and MCH results were unchanged in AMI and controls ($p > 0.05$).

Table 4 offers descriptive statistics on hematological variables regarding STEMI, NSTEMI, and healthy control. WBC, HGB, LY, MO, NEU, PLT, HCT, MCV, MCH, MCHC, PDW, and PCT results were significantly higher in the STEMI group as compared to the NSTEMI group ($p \leq 0.05$). However, BA, EO, LY/MO ratio, MPV, RDW-CV, and NLR did not change in the STEMI and NSTEMI groups.

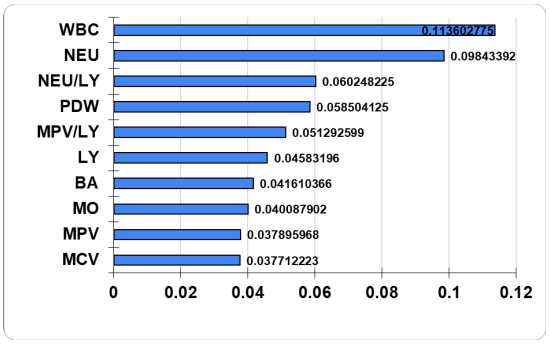

FIGURE 2. The top 10 selected features importance analysis by random forest approach; white blood cell (WBC), neutrophil (NEU), neutrophil/lymphocytes (NEU/LY), distribution (PDW), mean platelet volume/lymphocytes (MPV/LY), lymphocytes (LY), basophil (BA), monocytes (MO), mean platelet volume (MPV), and mean corpuscular volume (MCV).

A. FEATURE SELECTION RESULTS

One of the primary aims of the study was to identify the most important hematological blood parameters to differentiate AMI patients. After random forest-based feature selection, 10 biomarker blood parameters with distinctive features for AMI could be determined. Figure 2 presents the importance graph of these biomarkers for AMI detection.

B. PERFORMANCE RESULTS ANALYSIS

The performance analysis of the AI methods using various performance metrics is presented in this section. Table 5 contains the results of the applied methods for both outputs. For each output, we employ a 5-fold cross-validation approach to evaluate the results. The analysis is conducted using all dataset features and the top 10 selected features.

With all dataset features used for AMI output, the AB method achieved low-performance scores. On the other hand, the XGB and LGBM methods achieved acceptable scores. Specifically, the LGBM model achieved 84% accuracy when all features were used as input. When analyzing the results for STEMI output, the AB method once again exhibited low scores in comparison. However, the LGBM approach demonstrated a high AUC score of 88% in this analysis.

Then, the results with the top 10 selected features are determined. For the AMI output, the AB classifier gained low-performance scores. However, the proposed LGBM method achieved a high AUC score of 92% for detecting AMI patients in this analysis. For the STEMI output, the AB method yielded poor performance scores. Conversely, the proposed LGBM method achieved a high accuracy score of 74% compared to other models in this analysis.

The SHAP chart-based analysis of the proposed LGBM for AMI and STEMI output with selected features is illustrated in Figures 3 and 4, respectively. This analysis reveals the

TABLE 3. Descriptive statistics on hematological variables between AMI and healthy control.

Variable*	Group		*p*-value#
	CONTROL	AMI	
WBC (109/L)	7.5(2.282)	10.38(4.5)	<0.001
RBC (1012/L)	4.7(0.685)	4.79(0.82)	0.384
HGB (g/dL)	13.7 (2.125)	13.9(2.5)	0.107
BA (109/L)	0.04(0.04)	0.06(0.08)	<0.001
EO (109/L)	0.13(0.13)	0.1(0.15)	0.004
LY (109/L)	2.28(0.883)	2.36(1.76)	0.077
MO (109/L)	0.56(0.215)	0.7(0.39)	<0.001
NEU (109/L)	4.3(1.745)	6.45(3.93)	<0.001
NLR	1.808(0.912)	2.697(2.723)	<0.001
PLR	111.462(52.1)	102.632(67.846)	0.002
MPVLR	4.32(1.832)	3.866(3.273)	<0.001
LMR	4.13(1.735)	3.526(2.466)	<0.001
MPV (fL)	10.1(1.3)	9.4(1.69)	<0.001
PLT (109/L)	256.5(84.5)	253(92)	0.499
HCT (%)	41(5.625)	41.2(6.41)	0.265
MCV (fL)	87.2(5.325)	86.3(6.6)	0.003
RDW-SD	41(4.425)	41.2(4.7)	0.117
RDW-CV	13.2(1.3)	13.6(1.3)	<0.001
MCH (pg)	29.1(2.4)	29.3(2.8)	0.095
MCHC (g/dL)	33.2(1.9)	33.9(1.6)	<0.001
PDW (fL)	12(3.625)	15.9(5.29)	<0.001
PCT (%)	0.255(0.07)	0.23(0.09)	<0.001

*: Variables are summarized as 'median (interquartile range)'; #: Mann Whitney U test; AMI: Acute Myocardial Infarction; WBC: leukocyte; RBC: erythrocyte; HGB: hemoglobin; BA: basophil; EO: eosinophil; LY: lymphocyte; MO: monocyte; NEU: neutrophil; NLR: neutrophil/lymphocyte ratio; PLR: platelet/lymphocyte ratio; MPVLR: mean platelet volüme/lymphocyte ratio; LMR: lymphocyte/monocyte ratio; MPV: mean platelet volume; PLT: platelet; HCT: hematocrit; RDW-SD: red cell distribution width-standard deviation; RDW-CV: Red cell distribution width-coefficient of variation; MCH: mean erythrocyte hemoglobin; MCHC: mean corpuscular hemoglobin concentration; PDW: platelet distribution width; PCT: procalcitonin test.

most important features responsible for the prediction of AMI patients by the LGBM approach. The results for the AMI output show that the features NEU, WBC, PDW and BA are most important for the diagnosis of the AMI patient. Similarly, the results for the STEMI output indicate that the features MCV, BA, MO, and LY are most important for the diagnosis of the patient. LY most important for the diagnosis of the patient.

IV. DISCUSSION

In clinical practice, medical devices have traditionally relied on medical images and sensor data to study patient health. However, with the increasing volume of data, there is a growing need for more advanced technologies in the medical industry. These innovations aim to improve patient care quality and efficiency. An intelligent system that can detect early disease symptoms and offer timely treatment is essential to enhance healthcare outcomes and optimize patient management. The current study investigated comprehensive data analysis and the chosen LGBM model combined with XAI to investigate potential hematological predictors of AMI. In this study, the SHAP chart-based analysis of the proposed LGBM for the AMI group with selected features of the hematological predictors showed us the most important features responsible for the prediction of AMI patients by the LGBM approach. The results for the AMI group show that the features NEU, WBC, PDW, and BA are most important for the diagnosis of the patient with AMI. In addition, in AI subgroup analysis; the most important hematological predictors distinguishing subgroups of AMI (STEMI and NSTEMI) were MCV, BA, MO, and LY.

The LGBM model proposed in this study showed a very successful performance in AMI prediction. With the LGBM prediction model, 84% accuracy and 92% AUC value were obtained in AMI prediction. The estimation of the LGBM model is intuitively explained based on the SHAP chart to identify important hematological parameters. The proposed LGBM model gave us clinicians much more specific hematological parameters than the descriptive statistical method in predicting AMI. AI may help clinicians focus on the more important risk factors in predicting AMI. In the next stage, clinical studies on the disease may also help us to do more specific research.

A study conducted in the literature utilized chest X-ray images to segregate COVID-19-positive cases from healthy individuals. Two feature-extraction techniques, linear discriminant analysis (LDA) as a linear method, and principal component analysis (PCA) as a non-linear feature-extraction

TABLE 4. Descriptive statistics on hematological variables regarding STEMI, NSTEMI, and healthy control.

Variable*	Group**			*p*-value#
	STEMI	NSTEMI	CONTROL	
WBC (109/L)	12a (3.69)	9.17b (3.6)	7.5c (2.282)	<0.001
RBC (1012/L)	4.82 (0.758)	4.76 (0.825)	4.7 (0.685)	0.225
HGB (g/dL)	14.5a (2.375)	13.6b (2.6)	13.7b (2.125)	<0.001
BA (109/L)	0.07a (0.07)	0.06a (0.08)	0.04b (0.04)	<0.001
EO (109/L)	0.12ab (0.218)	0.1a (0.13)	0.13b (0.13)	0.015
LY (109/L)	2.735a (2.223)	2.13b (1.335)	2.28b (0.883)	<0.001
MO (109/L)	0.775a (0.432)	0.62b (0.395)	0.56c (0.215)	<0.001
NEU (109/L)	7.735a (4.028)	5.7b (3.23)	4.3c (1.745)	<0.001
NLR	2.811a (3.438)	2.65a (2.374)	1.808b (0.912)	<0.001
PLR	91.299a (66.943)	107.692b (73.154)	111.462b (52.1)	<0.001
MPVLR	3.245a (2.947)	4.235b (3.104)	4.32b (1.832)	<0.001
LMR	3.734a (2.606)	3.444a (2.316)	4.13b (1.735)	<0.001
MPV (fL)	9.4a (2)	9.5a (1.59)	10.1b (1.3)	<0.001
PLT (109/L)	272a (93.75)	245b (81)	256.5c (84.5)	<0.001
HCT (%)	42.2a (6.4)	40.79b (6.65)	41a (5.625)	<0.001
MCV (fL)	87.8a (6.8)	85.5b (6.3)	87.2a (5.325)	<0.001
RDW-SD	41.3 (5)	41.1 (4.8)	41 (4.425)	0.253
RDW-CV	13.5a (1.275)	13.7a (1.4)	13.2b (1.3)	<0.001
MCH (pg)	29.8a (2.8)	28.9b (2.8)	29.1b (2.4)	<0.001
MCHC (g/dL)	34a (1.377)	33.7b (1.81)	33.2c (1.9)	<0.001
PDW (fL)	16.3a (4.165)	14.5b (5.59)	12c (3.625)	<0.001
PCT (%)	0.25a (0.1)	0.23b (0.08)	0.255a (0.07)	<0.001

*: Variables are summarized as 'median (interquartile range)';

**: There is a statistically significant difference in the group categories that do not contain the same letter; #: Kruskal Wallis H test; WBC: leukocyte; RBC: erythrocyte; HGB: hemoglobin; BA: basophil; EO: eosinophil; LY: lymphocyte; MO: monocyte; NEU: neutrophil; NLR: neutrophil/lymphocyte ratio; PLR: platelet/lymphocyte ratio; MPVLR: mean platelet volume/lymphocyte ratio; LMR: lymphocyte/monocyte ratio; MPV: mean platelet volume; PLT: platelet; HCT: hematocrit; RDW-SD: red cell distribution width-standard deviation; RDW-CV: Red cell distribution width-coefficient of variation; MCH: mean erythrocyte hemoglobin; MCHC: mean corpuscular hemoglobin concentration; PDW: platelet distribution width; PCT: procalcitonin test; STEMI: ST-elevation myocardial infarction; NSTEMI: Non-STEMI

TABLE 5. Performance analysis of the applied methods with different approaches.

	Output: "AMI"					Output: "STEMI"				
	Performance results with all input features									
Method	A (%)	P (%)	R (%)	F1(%)	AUC (%)	A (%)	P (%)	R (%)	F1 (%)	AUC (%)
	Results with a 5-fold cross-validation					Results with a 5-fold cross-validation				
XGB	82	85	80	81	91	71	71	70	71	87
AB	80	79	79	81	88	63	65	65	61	76
LGBM	84	84	80	81	91	71	71	71	71	88
	Performance results with top 10 selected features									
	Results with a 5-fold cross-validation					Results with a 5-fold cross-validation				
XGB	83	82	79	83	91	73	71	71	73	87
AB	79	80	77	79	87	66	63	64	65	77
LGBM	83	85	80	82	92	74	72	71	71	86

AMI: Acute Myocardial Infarction; STEMI: ST-elevation myocardial infarction; XGB: Extreme Gradient Boosting; AB: Adaptive Boosting; LGBM: Light Gradient Boosting Machine; AUC: Area under the ROC Curve

method, were applied to extract highly discriminant feature sets. Finally, these feature sets were used to train various classification models [26]. Similarly, in another study, a smart auxiliary framework was utilized for the identification of COVID-19-affected patients using X-ray images. Three different transfer-learning networks were employed to extract pertinent features from the images; these networks encompassed AlexNet, ResNet101, and SqueezeNet. The pertinent features generated were subsequently refined through the application of feature-selection methods, including iterative

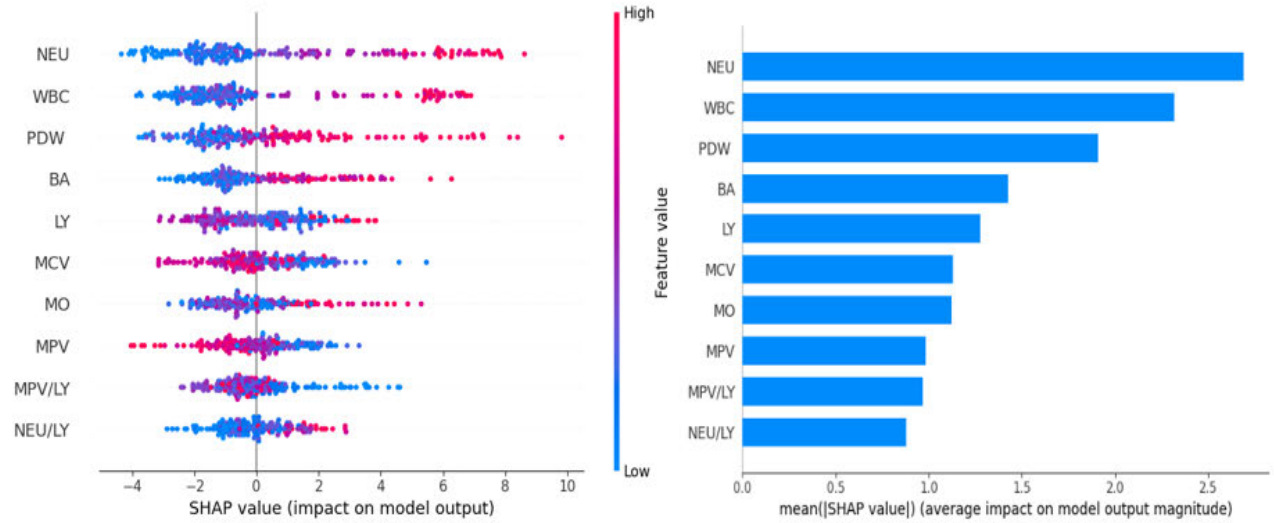

FIGURE 3. SHAP analysis of LGBM for AMI output; white blood cell (WBC), neutrophil (NEU), neutrophil/lymphocytes (NEU/LY), distribution (PDW), mean platelet volume/lymphocytes (MPV/LY), lymphocytes (LY), basophil (BA), monocytes (MO), mean platelet volume (MPV), and mean corpuscular volume (MCV).

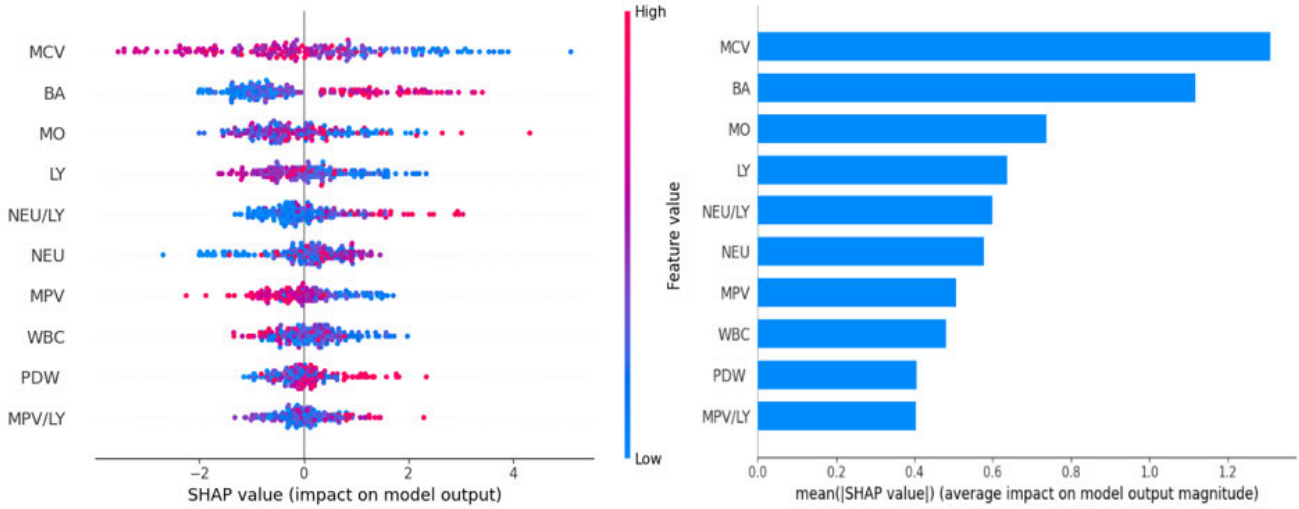

FIGURE 4. SHAP analysis of LGBM for STEMI output; white blood cell (WBC), neutrophil (NEU), neutrophil/lymphocytes (NEU/LY), distribution (PDW), mean platelet volume/lymphocytes (MPV/LY), lymphocytes (LY), basophil (BA), monocytes (MO), mean platelet volume (MPV), and mean corpuscular volume (MCV).

neighborhood component analysis (iNCA), iterative chi-square (iChi2), and iterative maximum relevance–minimal redundancy (iMRMR). Finally, classification was conducted using convolutional neural networks (CNN), linear discriminant analysis (LDA), and support vector machine (SVM) classifiers [27]. In another study, Hemoglobin, Serum Creatinine, LDL (Low-density lipoprotein) cholesterol, HDL (High-density lipoprotein) cholesterol, Triglycerides, ALT, AST, high-sensitive cardiac troponin I (hs-cTnI), and C-reactive protein (CRP) results of 59 patients with heart failure (HF) and 108 patients with chronic-ischemic heart disease (CHD) were evaluated. A predictive model based on logistic regression was created in the study, which aimed to identify important independent markers of the outcome of HF versus CHD. The authors obtained 80.5% AUC with the model (Hb + Serum Creatinine + AST + hs-cTnI + CRP) created to differentiate between HF and CHD [28]. The current and the mentioned studies exemplify the effectiveness of machine learning and advanced data analysis techniques in medical research, emphasizing AMI prediction, and showcasing COVID-19 diagnosis and differentiation between heart conditions. These results underscore the potential of data-driven approaches to enhance medical decision-making and improve patient care. The mentioned papers shows that

different methods can be used to diagnose COVID-19 and predict AMI using different types of data, such as images and blood tests. Also, feature-extraction and feature-selection techniques are important steps to improve the performance of classification models, and machine learning models can provide interpretable results that can assist clinical decision-making and research.

A series of pathophysiological events occur in AMI that produce an intense inflammatory response mediated by myocardial ischemia. Neutrophils, white blood cells first detected at the infarct site due to oxidative stress. This is followed by white blood cells monocytes and lymphocytes, which then phagocytize the necrotic remnants by releasing proteo-enzymes and cytokines [29]. In addition, activated platelets interact with neutrophils, monocytes, and lymphocytes, both acutely accelerating coronary artery occlusion and enhancing the inflammatory response [30]. Previous studies have shown that the stronger this inflammatory response, the more severe the vascular thrombogenic state and the increased development of coronary no-reflow in invasive percutaneous coronary procedures, resulting in a worse prognosis in AMI [31], [32], [33], [34]. In another study, it was found that MPVLR, neutrophil count, NLR, PLR, and LMR showed moderate diagnostic performance in predicting no-reflow after primary percutaneous coronary intervention in patients with STEMI [35]. Similarly, in another study, it was found that neutrophilia and lymphocytosis were the most leukocyte abnormalities in patients with HF. It was also found to be significantly associated with neutrophilia, especially in female patients with HF [36]. In our current study, the AI LGMB models employed in our present investigation have demonstrated that NEU is the most hematological parameter for predicting AMI. In addition, AI subgroup analysis; MO, and LY were the most important hematological parameters that distinguish STEMI from NSTEMI. The reason why the WBC and NEU numbers were higher in the STEMI group compared to both the NSTEMI and healthy groups may be due to the more severe inflammatory response of myocardial ischemia due to the complete occlusion of the coronary artery in STEMI patients. As a result, this can lead to a poor AMI prognosis.

PDW, a laboratory test, is a hematological parameter that measures the degree of variability in platelet size distribution [37]. In previous studies, it was found that PDW value increased in individuals diagnosed with malignancy, cardiovascular disease, diabetes mellitus, and respiratory tract disease [38], [39], [40], [41], [42], [43], [44], [45]. There are also studies showing that there is a positive correlation between high platelet distribution width and high mortality and morbidity rates in individuals with ischemic heart disease, pulmonary thromboembolism, and advanced cancer [46], [47], [48], [49]. However, a specific etiological cause of high PDW in these diseases is not known. There is a lack of studies examining the relationship between high PDW levels and their predictive and prognostic value in AMI. In this study, the PDW value was found to be a predictor in patients with AMI as compared to the healthy control group. In addition, AI LGBM models used in this study showed that PDW is one of the important hematological parameters in predicting AMI. The reason for high PDW levels in AMI patients may be the increased production of immature platelets in the bone marrow of some chemokines and cytokines that occur in the inflammatory state due to oxidative stress. More comprehensive studies are needed on this subject.

Basophils, a type of white blood cell, are defense cells. Their role in disease and health status was not clear until the last 20 years, but research in recent years has begun to partially understand the role of basophils in physiological and pathological processes. Basophils have a short lifespan of 2-3 days and can be mobilized quickly in inflammatory situations [50], [51]. They can produce several defined effector molecules such as proteolytic enzymes, bioactive lipids (prostaglandins and leukotrienes), and histamine, TNF-α, IL-6, IL-4, and IL-13 cytokines. Basophils are cells that provide protective immunity, mostly in allergic conditions and against parasites [52], [53]. Furthermore, recent research suggests that basophils interact highly with other cells and may perform extraordinary functions that are not performed by other hematopoietic cells, particularly immune imprinting, host response to bacteria, autoimmune disease, and allograft fibrosis [54], [55], [56], [57], [58]. However, its effects on cardiovascular diseases are not known clearly and there are not enough studies on the subject. In this study, according to the descriptive statistics results, basophil count was found to be significantly higher in patients with AMI than in the healthy control group ($p < 0.05$). In addition, artificial intelligence LGBM models used in this study showed that basophil is one of the important hematological parameters in predicting AMI. Similarly, in AI subgroup analysis, BA was one of the important hematological parameters that distinguish STEMI from NSTEMI.

The MCV, obtained by multiplying the hematocrit percentage by 10 and dividing the result by the erythrocyte number, is a hematological parameter that shows the mean size and volume of erythrocytes. This parameter helps clinicians identify erythrocyte-related abnormalities and the type of anemia [59], [60]. In the previous study, it was found that MCV, MCH, and PDW levels predicted oxidative stress in patients with STEMI [61]. In one study, patients with peripheral artery disease with low MCV levels were found to have significantly higher percutaneous intervention-related major cardiovascular events (MACE) [62]. In another study, low MCV value was found to be associated with mortality in hemodialysis patients [63]. In contrast, another study found that MCV was not associated with MACE in diabetic patients with STEMI, no STEMI, or unstable angina. However, high MCV was found to be associated with high MACE in the non-diabetic group [64]. In a previous study, it was associated with higher mortality and worse prognosis in patients with acute coronary syndrome with high MCV without anemia [65]. The

reason for reporting different results in terms of mortality in different patient groups with high or low MCV values may be related to the co-morbidities of the patients or the prevalence of the disease. In the current study, MCV value was a significant factor in AMI. According to AI subgroup analysis, MCV was the most important hematological parameter that distinguished STEMI from NSTEMI.

In a paper, a progressive distributed and parallel similarity retrieval method (DPRS) was proposed for large-sized computed tomography image sequences (CTIS) in resource-constrained mobile telemedicine networks (MTN). The DPRS method was based on four supporting techniques: (1) PCTI-based similarity measurement, (2) lightweight privacy protection strategy, (3) SSL-based data distribution scheme, and (4) UDI framework. Experimental evaluation showed that the DPRS method is more progressive and efficient than existing methods. Similar to the related study [66], in the current research, machine learning methods were integrated with explainable artificial intelligence techniques, and the outcome variable was estimated with high predictive values. In parallel with our study, a diverse range of investigations in the literature has demonstrated the remarkable effectiveness of machine learning and advanced data analysis techniques in medical research. These studies span various domains, including AMI prediction, COVID-19 diagnosis, and differentiation between heart conditions, underscoring the versatility and potential of data-driven approaches to enhance medical decision-making and ultimately improve patient care.

V. CONCLUSION

In this study, we found that combining LGBM with XAI helped identify specific hematological parameters for predicting AMI. Elevated NEU, WBC, BA counts, and high PDW values were identified as primary predictors. The CBC test, a widely available and cost-effective diagnostic tool, can be used to assess these parameters in individuals showing signs of AMI. Moreover, we suggest employing XAI in cardiology research to uncover more accurate risk factors for better risk assessment.

SUPPLEMENTARY FILES

The raw data file is provided in the supplementary file.

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