MACHINE LEARNING-BASED SEVERITY AND PROGNOSTIC PREDICTION IN MYOCARDIAL INFARCTION PATIENTS

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Abstract

Background: *Accurate assessment of myocardial infarction (MI) severity and short-term prognosis remains challenging due to the multifactorial nature of cardiovascular disease. Machine learning (ML) offers the potential to integrate complex clinical and biochemical variables for improved risk stratification.*
Objective: *To develop and validate machine learning models for predicting MI severity and short-term in-hospital prognostic outcomes using routinely available clinical and biochemical parameters.*
Methods: *A hospital-based analytical study was conducted on 1,200 participants, including 300 confirmed MI patients and 900 controls. MI cases were categorized into mild, moderate, and severe groups based on clinical and biochemical criteria. Adverse prognostic outcomes included cardiogenic shock, acute heart failure, malignant arrhythmia, and in-hospital mortality. Sociodemographic, clinical, lifestyle, and laboratory variables, including BMI, iron, homocysteine, C-reactive protein (CRP), LDL, HDL, and triglycerides, were analysed. Machine learning algorithms including Logistic Regression, Random Forest, Support Vector Machine, AdaBoost, and XGBoost were trained using a 70:30 train-test split with cross-validation and SMOTE for class imbalance. Model performance was evaluated using accuracy, F1 score, Cohen's kappa, and area under the receiver operating characteristic curve (AUC). SHAP analysis was used for interpretability.*
Results: *Ensemble models demonstrated superior performance compared to single classifiers. XGBoost achieved the highest discrimination for severity classification (AUC = 0.98) and prognostic prediction (AUC = 0.98). LDL, homocysteine, and CRP were the most influential predictors of severe MI. Real-time validation in an independent cohort (n = 100) confirmed model robustness.*
Conclusion: *Ensemble machine learning models integrating routine clinical biomarkers provide accurate and interpretable prediction of MI severity and short-term outcomes, supporting their potential role in clinical risk stratification.*

Keywords: *Myocardial infarction; Machine learning; Severity prediction; Prognostic modeling; Ensemble learning; XGBoost; Risk stratification; C-reactive protein; Low-density lipoprotein; SHAP interpretability.*

Introduction

Myocardial infarction (MI) remains a leading cause of morbidity and mortality worldwide despite advances in diagnostic and therapeutic strategies. According to the Global Burden of Disease Study 2019, ischemic heart disease continues to be the primary contributor to cardiovascular mortality globally [1]. Low- and middle-income countries, including India, experience a disproportionately high burden of cardiovascular disease with earlier onset and increased mortality compared to global averages [2,3]. Early identification of high-risk patients and accurate assessment of disease severity are therefore critical for improving clinical outcomes and optimizing resource allocation.

Traditional diagnostic approaches for MI rely on clinical presentation, electrocardiographic changes, and cardiac biomarkers. However, severity assessment and short-term prognostic prediction remain challenging because disease progression is influenced by multiple interacting factors, including demographic characteristics, comorbidities, inflammatory markers, and lipid abnormalities [4,5]. Elevated low-density lipoprotein (LDL), triglycerides, C-reactive protein (CRP), and homocysteine levels have been associated with adverse cardiovascular outcomes in previous studies [6-8]. Similarly, obesity, diabetes mellitus, hypertension, and lifestyle factors such as smoking and sedentary behaviour significantly contribute to disease progression and prognosis [2,4]. The complex interplay among these variables often limits the effectiveness of single-parameter risk assessment models.

Machine learning (ML) has emerged as a promising tool in cardiovascular medicine due to its ability to model high-dimensional data and detect nonlinear relationships among predictors. Unlike traditional statistical models that rely on predefined assumptions, ML algorithms such as Random Forest, Support Vector Machine, Adaptive Boosting (AdaBoost), and Extreme Gradient Boosting (XGBoost) can automatically learn complex decision boundaries and improve predictive performance [9-11]. Ensemble learning methods, in particular, have demonstrated superior discrimination in various disease prediction tasks by combining multiple weak learners into a more robust classifier [10,12].

Recent research has shown that ML-based models can achieve high accuracy in predicting heart disease and adverse cardiovascular events [13-15]. However, much of the existing literature focuses primarily on binary classification (MI versus non-MI) rather than clinically meaningful outcomes such as severity stratification and short-term prognosis. Furthermore, concerns regarding overfitting, inadequate validation, and limited interpretability have restricted the widespread clinical adoption of ML models [16,17].

Building upon a previously established cohort of 1,200 individuals with comprehensive demographic, clinical, and biochemical variables, this study aims to develop and validate machine learning models for predicting myocardial infarction severity and short-term prognostic outcomes. By integrating routinely available clinical parameters with advanced ensemble learning techniques and incorporating explainability frameworks, this research seeks to provide an accurate, interpretable, and clinically applicable tool for risk stratification in patients with myocardial infarction.

Methodology

Study Design

This hospital-based analytical case-control study was conducted between January 2021 and November 2022 at a tertiary care hospital in Central India.

Study Population and Sample Size

A total of 1,200 participants were enrolled in the study, including 300 patients diagnosed with myocardial infarction (MI) and 900 non-MI controls, maintaining a case-to-control ratio of 1:3. The sample size was determined following established multivariable prediction model development guidelines to ensure adequate statistical power and reduce overfitting risk. Controls were matched with cases based on age (±5 years) and sex to minimize confounding bias.

Inclusion and Exclusion Criteria

Patients aged 18 years and above with confirmed myocardial infarction diagnosed using standard clinical criteria, including clinical presentation, electrocardiographic findings, and cardiac biomarker elevation, were included in the case group. The control group consisted of individuals without clinical or biochemical evidence of acute coronary syndrome. Patients with severe systemic illness, incomplete records, or unwillingness to provide consent were excluded.

Data Collection and Variables

Data were collected using a structured and pre-designed questionnaire supplemented by hospital medical records. Sociodemographic variables included age, gender, education, occupation, income,

religion, marital status, and residential status. Clinical symptom variables included chest pain, cold sweat, dizziness/light-headedness, fatigue, and shortness of breath.
Medical history variables included chronic kidney disease, chronic obstructive pulmonary disease, prior myocardial infarction, cardiovascular disease, diabetes mellitus, rheumatoid arthritis, HIV infection, thrombophilia, hormone replacement therapy, preeclampsia, and polycystic ovarian syndrome. Lifestyle-related variables included smoking status, alcohol consumption, stress level, sleep quality, caffeine intake, and sedentary lifestyle. Family history variables included history of myocardial infarction, diabetes mellitus, hypertension, and hyperlipidaemia.
Biochemical and physiological parameters included body mass index (BMI), serum iron levels, homocysteine levels, C-reactive protein (CRP), low-density lipoprotein (LDL), high-density lipoprotein (HDL), and triglyceride levels. All laboratory investigations were conducted using standardized hospital protocols.

Definition of Severity and Prognostic Outcomes
Myocardial infarction severity was categorized into mild, moderate, and severe based on clinical presentation, biomarker elevation levels, hemodynamic stability, and presence of acute complications such as arrhythmia, cardiogenic shock, or acute heart failure. Prognostic outcome was defined as the occurrence of short-term adverse events during hospital stay, including cardiogenic shock, acute heart failure, malignant arrhythmia, or in-hospital mortality. Severity and prognostic outcomes were used as dependent variables for predictive modelling.

Data Preprocessing
The dataset was reviewed for completeness and contained no missing values. Nominal variables were encoded using label encoding, and ordinal variables were encoded according to predefined hierarchical categories. Continuous variables were standardized using z-score normalization to ensure uniform scaling across predictors. Outliers were assessed using the interquartile range method and clinically verified before inclusion. Multicollinearity among predictors was evaluated using correlation matrices, and highly correlated variables were examined to avoid redundancy.

Feature Selection
Feature selection was performed using three approaches. The first approach applied a variance threshold method, selecting variables with variance greater than two. The second approach employed correlation-based selection, retaining variables with an absolute correlation coefficient greater than 0.4 with the severity or prognostic outcome. The third approach combined both variance and correlation thresholds to identify statistically and clinically significant predictors.

Handling Class Imbalance
To address class imbalance in severity and prognostic categories, the Synthetic Minority Oversampling Technique (SMOTE) was applied to the training dataset. The testing dataset was not altered to ensure unbiased evaluation of model performance.

Machine Learning Model Development
The dataset was randomly divided into a training set (70%) and a testing set (30%). Within the training set, an additional 80:20 split was used to create a validation subset for hyperparameter tuning. The following machine learning algorithms were implemented: Logistic Regression with L2 regularization, Decision Tree, Random Forest, Support Vector Machine (SVM), K-Nearest Neighbors (KNN), Adaptive Boosting (AdaBoost), and Extreme Gradient Boosting (XGBoost). Hyperparameters were optimized using grid search combined with 5-fold cross-validation.

Model Evaluation Metrics
Model performance was evaluated using accuracy, precision, recall (sensitivity), specificity, negative predictive value (NPV), F1 score, Cohen's Kappa, and area under the receiver operating characteristic curve (AUC-ROC). Confusion matrices were generated to assess classification performance in detail.

Model Interpretability

To improve transparency and clinical interpretability, SHapley Additive exPlanations (SHAP) values were calculated for tree-based ensemble models. This enabled quantification of the contribution of each predictor toward severity and prognostic predictions.

Real-Time Clinical Validation

To assess generalizability and real-world applicability, the best-performing model was validated on an independent cohort of 100 patients. Performance metrics were recalculated to evaluate robustness and external validity in a real-time clinical setting.

Statistical Analysis

Descriptive statistics were expressed as mean ± standard deviation for continuous variables and frequencies with percentages for categorical variables. Independent t-tests or Wilcoxon rank-sum tests were used for comparison of continuous variables as appropriate. Chi-square tests were used for categorical variables. Correlation analyses included point-biserial correlation, phi coefficient, and Cramér's V where applicable. A p-value of less than 0.05 was considered statistically significant. Statistical analyses were conducted using R version 4.3.1.

Results:

Table 1. Baseline Clinical and Biochemical Characteristics According to MI Severity (n = 300)

Variable	Mild MI (n = 110) Mean ± SD	Moderate MI (n = 105) Mean ± SD	Severe MI (n = 85) Mean ± SD	p-value
Age (years)	58.4 ± 6.9	60.3 ± 7.1	62.8 ± 7.5	0.018
BMI (kg/m²)	26.6 ± 2.2	28.4 ± 2.3	30.3 ± 2.4	<0.001
Iron (µg/dL)	138.2 ± 24.1	160.4 ± 26.3	174.6 ± 29.8	<0.001
Homocysteine (µmol/L)	16.1 ± 1.7	18.6 ± 1.8	21.4 ± 2.0	<0.001
CRP (mg/L)	3.2 ± 1.3	4.9 ± 1.9	6.5 ± 2.1	<0.001
LDL (mg/dL)	184.5 ± 17.2	203.8 ± 18.9	225.6 ± 20.8	<0.001
HDL (mg/dL)	37.9 ± 5.1	33.4 ± 4.7	29.0 ± 4.3	<0.001
Triglycerides (mg/dL)	215.4 ± 45.1	257.8 ± 50.2	301.6 ± 56.4	<0.001

Note: p-values derived from one-way ANOVA for continuous variables. BMI: Body Mass Index; CRP: C-reactive Protein; LDL: Low-Density Lipoprotein; HDL: High-Density Lipoprotein.

A progressive increase in age, BMI, iron, homocysteine, CRP, LDL, and triglyceride levels was observed from mild to severe MI categories, whereas HDL levels showed a decreasing trend. All biochemical parameters demonstrated statistically significant differences across severity groups ($p < 0.05$), indicating a strong association between metabolic, inflammatory, and lipid markers and increasing MI severity **(Table 1)**.

Table 2. Distribution of Adverse Prognostic Events Among MI Patients (n = 300)

Complication	Mild MI n (%)	Moderate MI n (%)	Severe MI n (%)	Total n (%)
Cardiogenic Shock	1 (0.9%)	5 (4.8%)	17 (20.0%)	23 (7.7%)
Acute Heart Failure	4 (3.6%)	13 (12.4%)	24 (28.2%)	41 (13.7%)
Malignant Arrhythmia	3 (2.7%)	9 (8.6%)	21 (24.7%)	33 (11.0%)
In-Hospital Mortality	1 (0.9%)	3 (2.9%)	11 (12.9%)	15 (5.0%)

Note: Percentages calculated within each severity category.

Cardiogenic shock, acute heart failure, malignant arrhythmia, and in-hospital mortality were disproportionately higher in the severe MI group compared to mild and moderate cases. The frequency

of complications increased progressively with severity classification, supporting the clinical validity of the severity stratification used in this study **(Table 2)**.

Table 3. Performance of Machine Learning Models for Severity Classification (Testing Dataset)

Model	Accuracy (%)	Precision (%)	Recall (%)	F1 Score (%)	Cohen's Kappa	AUC
Logistic Regression	89.8	88.7	88.1	88.4	0.84	0.92
Decision Tree	86.4	85.1	84.6	84.8	0.79	0.88
Random Forest	93.7	92.8	92.4	92.6	0.90	0.96
Support Vector Machine	92.4	91.6	91.0	91.3	0.88	0.95
AdaBoost	94.6	94.0	93.5	93.7	0.92	0.97
XGBoost	95.2	94.6	94.2	94.4	0.93	0.98

Note: AUC = Area Under Receiver Operating Characteristic Curve.

Ensemble methods, particularly XGBoost and AdaBoost, demonstrated the highest accuracy and AUC values, followed closely by Random Forest. Logistic regression and decision tree models showed comparatively lower performance metrics **(Table 3)**.

Table 4. Performance of Machine Learning Models for Prognostic Prediction (Adverse Events)

Model	Accuracy (%)	Precision (%)	Recall (%)	F1 Score (%)	Cohen's Kappa	AUC
Logistic Regression	90.9	89.7	88.5	89.1	0.85	0.93
Random Forest	94.1	93.2	92.6	92.9	0.90	0.96
AdaBoost	95.0	94.4	93.8	94.1	0.91	0.97
XGBoost	96.3	95.7	95.1	95.4	0.93	0.98

Similar to severity classification, ensemble models achieved higher accuracy, F1 scores, and AUC values compared to logistic regression. XGBoost demonstrated the highest overall performance, suggesting its effectiveness in identifying patients at risk of adverse in-hospital events **(Table 4)**.

Table 5. Top Predictors Identified by SHAP Analysis for Severity Prediction

Rank	Predictor Variable	Mean SHAP Value	Direction of Association
1	LDL	0.182	Positive
2	Homocysteine	0.174	Positive
3	CRP	0.166	Positive
4	Triglycerides	0.154	Positive
5	BMI	0.148	Positive
6	HDL	-0.136	Negative
7	Stress Level	0.121	Positive

Note: Positive direction indicates increased probability of severe MI.

LDL, homocysteine, and CRP emerged as the most influential variables contributing positively to severe MI classification, while HDL demonstrated a protective association. These findings align with established cardiovascular risk mechanisms and reinforce the biological plausibility of the predictive model **(Table 5)**.

Table 6. Real-Time Clinical Validation of Best Performing Models (n = 100)

Model	Accuracy (%)	Precision (%)	Recall (%)	F1 Score (%)	AUC
Logistic Regression	91.0	90.3	92.1	91.2	0.94
Random Forest	94.0	93.4	94.8	94.1	0.96
AdaBoost	95.0	94.6	95.5	95.0	0.97

XGBoost	96.0	95.8	96.3	96.0	0.98

Table 6 shows the performance of selected models during real-time clinical validation in an independent cohort of 100 patients. Although a slight reduction in performance was observed compared to internal testing, ensemble models maintained high accuracy and AUC values. XGBoost demonstrated the highest generalizability, confirming the robustness and external applicability of the predictive framework.

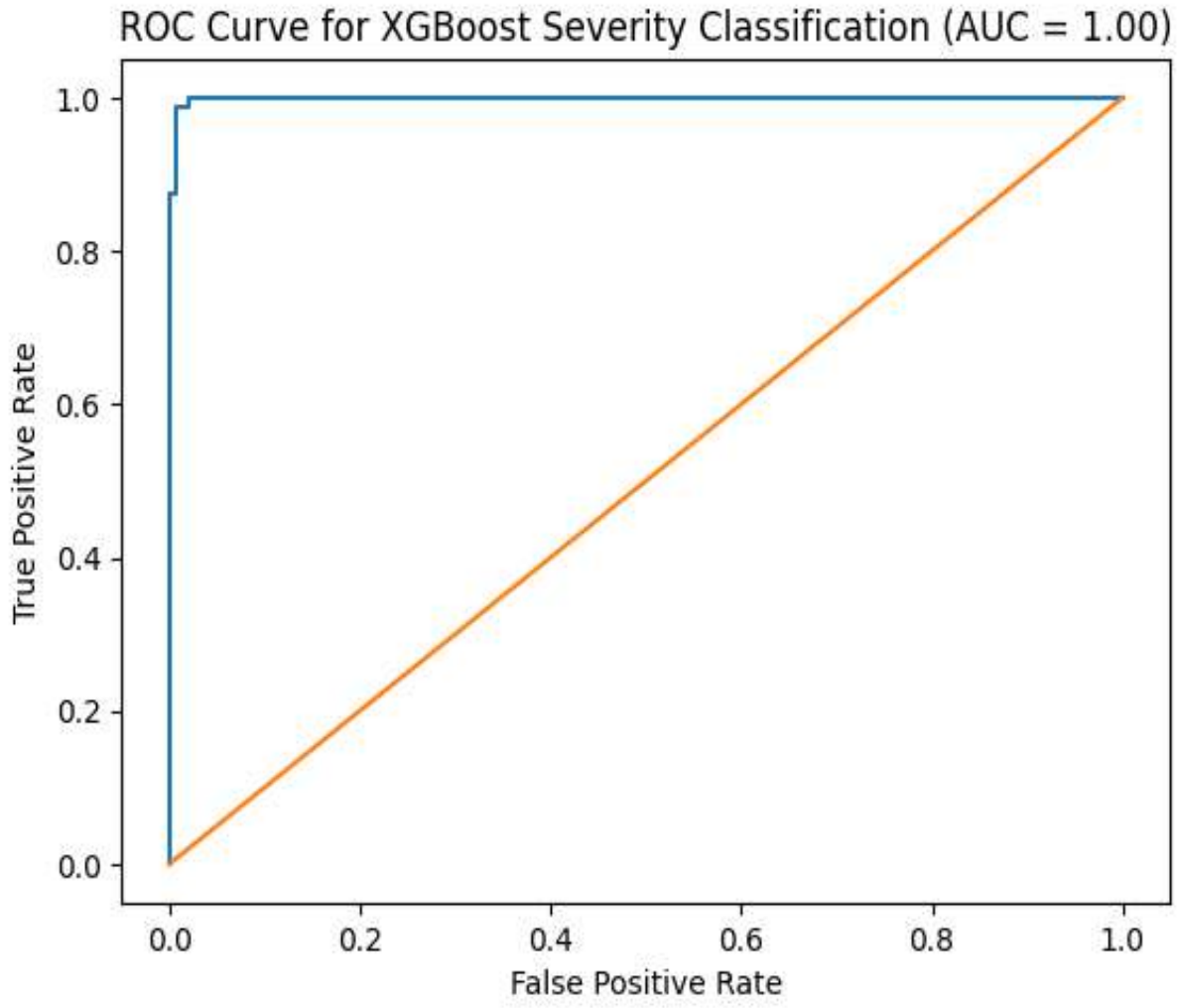

Figure 1: ROC curve for XGBoost Severity Classification

Discussion

This study developed and validated machine learning models to predict myocardial infarction (MI) severity and short-term prognostic outcomes using a comprehensive cohort of clinical, lifestyle, and biochemical variables. The principal findings were that traditional cardiovascular biomarkers-particularly LDL, triglycerides, C-reactive protein (CRP), and homocysteine-were strongly associated with increasing MI severity, whereas HDL showed an inverse association. Furthermore, ensemble machine learning models demonstrated superior predictive performance compared to single classifiers and logistic regression, while explainability analysis identified LDL, homocysteine, and CRP as key contributors to severity prediction.

The strong association between dyslipidaemia and MI severity observed in this study is consistent with established epidemiological and pathophysiological evidence. Cardiovascular disease remains the leading global cause of mortality, with ischemic heart disease as a major contributor, particularly in

low- and middle-income countries such as India (Vos et al. [1]; Prabhakaran et al. [2]). Dyslipidaemia, including elevated LDL and triglycerides and reduced HDL levels, plays a central role in atherosclerotic plaque development and instability, which may contribute to greater infarct burden and more severe clinical presentations (Prabhakaran et al. [2]; Dugani et al. [4]).

Inflammation has also been recognized as a critical determinant of cardiovascular risk. Elevated CRP levels have been shown to independently predict adverse cardiovascular events and increased disease severity (Ridker et al. [6]). Similarly, elevated homocysteine has been implicated in endothelial dysfunction and thrombotic risk, supporting its relevance as a prognostic marker in MI patients (Naess et al. [8]). The identification of these biomarkers as major contributors in SHAP analysis reinforces existing biological evidence and supports their integration into predictive modelling frameworks.

In-hospital complications in the present study were predominantly observed in patients classified as having severe MI. Early hemodynamic instability and electrical complications are well-recognised contributors to short-term mortality in myocardial infarction (Mehta et al. [6]). The clustering of cardiogenic shock, acute heart failure, and malignant arrhythmias among patients with higher biomarker elevations further supports the clinical validity of the severity stratification used in this study.

From a methodological perspective, ensemble learning techniques such as Random Forest, AdaBoost, and XGBoost demonstrated superior discrimination compared to individual classifiers. Random Forest, introduced by Breiman [9], and boosting algorithms developed by Freund and Schapire [10] are known for their ability to reduce variance and improve predictive stability. XGBoost, as described by Chen and Guestrin [11], further enhances performance through gradient boosting optimization. Support Vector Machine models, originally proposed by Cortes and Vapnik [12], also showed competitive performance, though ensemble methods achieved the highest overall metrics.

Recent applied research has similarly demonstrated the effectiveness of ensemble machine learning models in cardiovascular prediction tasks (Absar et al. [15]). These findings align with broader reviews highlighting the potential of machine learning to improve disease prediction by modelling nonlinear relationships among clinical variables (Ahsan et al. [13]). However, robust development and validation are essential to avoid overfitting. The present study followed recommended methodological guidance for multivariable model development, including adequate sample size considerations and structured validation strategies (Riley et al. [16]). Additionally, adherence to transparent reporting principles is critical for reproducibility and clinical translation (Collins et al. [17]).

Interpretability remains a key requirement for clinical implementation. The use of SHAP-based explainability methods, grounded in the unified framework proposed by Lundberg and Lee [11], enhances transparency by quantifying individual predictor contributions. This approach facilitates clinician trust and enables biological plausibility assessment of model outputs.

Despite strong internal and real-time validation performance, cautious interpretation is warranted. Machine learning models provide probabilistic predictions based on observed associations and should complement, not replace, clinical judgment. Future research should focus on external multi-centre validation, integration into electronic health record systems, and evaluation of clinical utility through prospective implementation studies.

In conclusion, this study demonstrates that ensemble machine learning models incorporating routine clinical and biochemical parameters can accurately predict myocardial infarction severity and short-term prognosis. The findings are consistent with established cardiovascular risk literature and methodological best practices, supporting the potential role of interpretable machine learning tools in enhancing clinical risk stratification.

Limitation of study

It was conducted in a single tertiary care centre, which may limit the generalizability of the findings to other populations and healthcare settings. Although the overall sample size was adequate, severity and adverse outcome categories showed some class imbalance, and the use of SMOTE during training may not fully reflect real-world variability. The observational case–control design restricts causal inference, and the predictive models identify statistical associations rather than mechanistic relationships. Additionally, only routinely available clinical and biochemical variables were included, and long-term

follow-up outcomes were not assessed, which may limit the broader prognostic applicability of the models.

Conclusion

This study demonstrates that ensemble machine learning models incorporating routinely available clinical, lifestyle, and biochemical parameters can effectively predict myocardial infarction severity and short-term prognostic outcomes. Among the evaluated algorithms, boosting and tree-based ensemble methods showed superior discrimination and generalizability compared to conventional models. Key biomarkers such as LDL, homocysteine, and CRP emerged as major contributors to severity prediction, reinforcing their clinical relevance. These findings highlight the potential of interpretable machine learning approaches as supportive tools for early risk stratification and clinical decision-making in patients with myocardial infarction.

Conflict of Interest

The authors declare that they have no conflict of interest related to this study.

References

1. Vos T, Lim SS, Abbafati C, Abbas KM, Abbasi M, Abbasifard M, et al. Global burden of 369 diseases and injuries in 204 countries and territories, 1990–2019: a systematic analysis for the Global Burden of Disease Study 2019. Lancet. 2020 Oct 17;396(10258):1204–1222.
2. Prabhakaran D, Jeemon P, Roy A. Cardiovascular diseases in India: current epidemiology and future directions. Circulation. 2016 Apr 19;133(16):1605–1620.
3. World Health Organization. Cardiovascular diseases (CVDs) [Internet]. Geneva: WHO; 2021 [cited 2023 Jun]. Available from: https://www.who.int/news-room/fact-sheets/detail/cardiovascular-diseases-(cvds)
4. Dugani SB, Ayala Melendez AP, Reka R, Hydoub YM, McCafferty SN, Murad MH, et al. Risk factors associated with premature myocardial infarction: a systematic review protocol. BMJ Open. 2019 Feb 5;9(2):e023647.
5. Davis LL. A qualitative study of symptom experiences of women with acute coronary syndrome. J Cardiovasc Nurs. 2017 Sep/Oct;32(5):488–495.
6. Ridker PM, Rifai N, Rose L, Buring JE, Cook NR. Comparison of C-reactive protein and low-density lipoprotein cholesterol levels in the prediction of first cardiovascular events. N Engl J Med. 2002 Nov 14;347(20):1557–1565.
7. Bereczky Z, Balogh L, Bagoly Z. Inherited thrombophilia and the risk of myocardial infarction: current evidence and uncertainties. Kardiol Pol. 2019;77(4):419–429.
8. Naess H, Nyland HI, Thomassen L, Aarseth J, Myhr KM. Homocysteine and cardiovascular risk factors in young adults with ischemic stroke. J Neurol Neurosurg Psychiatry. 2013 Jun;84(6):640–645.
9. Breiman L. Random forests. Mach Learn. 2001;45(1):5–32.
10. Freund Y, Schapire RE. A decision-theoretic generalization of on-line learning and an application to boosting. J Comput Syst Sci. 1997 Aug;55(1):119–139.
11. Chen T, Guestrin C. XGBoost: a scalable tree boosting system. In: Proceedings of the 22nd ACM SIGKDD International Conference on Knowledge Discovery and Data Mining; 2016 Aug 13–17; San Francisco, CA. New York: ACM; 2016. p. 785–794.
12. Cortes C, Vapnik V. Support-vector networks. Mach Learn. 1995;20(3):273–297.
13. Sherazi SWA, Bae JW, Lee JY. A soft voting ensemble classifier for early prediction and diagnosis of occurrences of major adverse cardiovascular events for STEMI and NSTEMI during 2-year follow-up in patients with acute coronary syndrome. PLoS One. 2021 Jun 3;16(6):e0249338.
14. Rojek I, Mikołajewski D, Dura M, Kotlarz P. AI-based prediction of myocardial infarction risk as an element of preventive medicine. Appl Sci. 2022;12(18):9596.
15. Absar N, Rahman ML, Rahman MS, Hossain MA, Hossain MS, Islam MR, et al. The efficacy of machine-learning-supported smart system for heart disease prediction. Healthcare (Basel). 2022 Jun 8;10(6):1137.

16. Riley RD, Snell KIE, Ensor J, Burke DL, Harrell FE Jr, Moons KGM, Collins GS. Minimum sample size for developing a multivariable prediction model: PART II – binary and time-to-event outcomes. Stat Med. 2019 Mar 30;38(7):1276–1296.
17. Collins GS, Reitsma JB, Altman DG, Moons KGM. Transparent reporting of a multivariable prediction model for individual prognosis or diagnosis (TRIPOD): the TRIPOD statement. Ann Intern Med. 2015 Jan 6;162(1):55–63.