

**EXPLAINABLE ARTIFICIAL INTELLIGENCE MODEL FOR EARLY PREDICTION OF  
HEART ATTACK USING LIME ON CLINICAL DATA**

Ipek Balikci Cicek\* and Zeynep Kucukakcali

Department of Biostatistics and Medical Informatics, Inonu University Faculty of Medicine, 44280, Malatya, Turkey.

\*Corresponding Author: Ipek Balikci Cicek

Department of Biostatistics and Medical Informatics, Inonu University Faculty of Medicine, 44280, Malatya, Turkey.

Article Received on 18/08/2023

Article Revised on 08/09/2023

Article Accepted on 28/09/2023

**ABSTRACT**

**Object:** Cardiovascular Diseases (CVD) have become one of the leading causes of mortality on a global scale, claiming almost 17.9 million lives each year. According to studies, it is responsible for around 35% of all fatalities worldwide. Heart attack (HA) diagnosis and prognosis are critical medical duty to ensure accurate categorization, which allows cardiologists to deliver appropriate therapy to patients. Machine learning (ML) applications in the medical field have grown in popularity because they can spot patterns in data. Using ML to classify the occurrence of HA can assist decrease misdiagnosis. This study aims to create a model that can accurately forecast HA in order to reduce the number of people who die from them. **Method:** An open-access data was employed within the scope of the study to investigate the risk factors related with HA. The dataset used contains the values of 1319 patients and 8 input variables. The extreme gradient boosting (XGBoost) model was chosen to predict and classify patients, and an explainable approach based on the Local Interpretable Model-Agnostic Explanations (LIME) method was used to generate individual explanations for the model's decisions. The 10-fold cross validation approach was employed in the modeling, and the dataset was divided as 80%: 20% as training and test datasets. For model assessment, the measures of accuracy (ACC), balanced accuracy (b-ACC), sensitivity (SE), specificity (SP), positive predictive value (ppv), negative predictive value (npv), and F1-score were utilized. **Results:** When the HA positive and HA negative groups were examined, statistically significant differences were found in age, CK-MB and troponin variables. As a result of modeling with the XGBoost method, 98.5%, 98.6%, 99.3%, 97.9%, 96.8%, 99.6%, and 98.1% was obtained from ACC, b-ACC, SE, SP, ppv, npv and F1-score performance metrics, respectively. When the variable importance values obtained as a result of the model are examined, it is seen that the variables that best explain the HA and are most associated with the HA are troponin and CK-MB, respectively. When we examine at the individual-based LIME findings of the patients in the test data set, troponin  $\geq 0.01$ , kcm  $> 5.79$ ,  $117.00 < \text{glucose}$ ,  $58.00 < \text{age}$ ,  $72.00 \leq \text{pressurelow}$ ,  $\text{pressurehigh} > 144.00$  values enhance the likelihood of being HA positive. **Conclusion:** ML combined with LIME might provide a clear explanation of personalised risk prediction and provide clinicians with an intuitive knowledge of the effect of important model variables.

**KEYWORDS:** Heart attack, classification, machine learning, risk factor, Local Interpretable Model-Agnostic Explanations.

**INTRODUCTION**

Acute myocardial infarction (AMI or MI), also known as HA, is a blockage in one of the vessels reaching the heart and the resulting damage to the heart tissue. According to World Health Organization (WHO) statistics, CVD, which ranks first among the causes of death in the world, accounts for 30% of all deaths, while this rate is around 47% in Turkey<sup>[1]</sup> Almost half of the adult population in Turkey is at risk of CVD. According to WHO, 85 percent of deaths from CVD are due to HA and stroke.<sup>[2]</sup> This has led to heart attacks becoming the most important health problem in both developing and developed countries. HA is a potentially fatal disease that occurs with severe chest pain due to complete or partial narrowing of the coronary arteries of the heart, which

deprives the cells in the heart muscle of nutrition and oxygen.<sup>[3-4]</sup>

Electrocardiograms (ECG), echocardiograms, and blood tests are frequently used by physicians and experts to diagnose a HA. The most often used diagnostic approach is ECG, in which electrical impulses travelling through the human heart are recorded using electrodes placed to the patient's chest, and these signals are aberrant if the heart is sick. As a result, if the patient has a heart attack, the signals will be irregular, and this is a late intervention that will be unsuccessful in saving lives. Furthermore, individual differences in the structure of the heart, as well as pre-existing cardiac ailments, accidents, and procedures such as coronary artery bypass surgery, alter

the specificity of the ECG. As a result, it cannot be a case of early diagnosis.<sup>[6-7]</sup> Echocardiogram, on the other hand, is used to evaluate whether any region of the heart is injured by employing sound waves to create pictures. It has nearly the same drawbacks as EKG. As a result of these drawbacks, an echocardiography cannot be used as an early detection technique for HA. Both of these approaches are not favoured because to their drawbacks, and the accuracy of recognizing HA is totally dependent on the doctor's expertise and experience with these methods. These approaches are time-consuming and labor-intensive, and the accuracy of detecting AMI is totally dependent on the doctors' experience.<sup>[8]</sup>

The only approach to reduce HA-related mortality and morbidity is to intervene early. It is less costly, quicker, and more objective to detect HA signs in the blood. Some proteins and enzymes, such as brain natriuretic peptide (BNP), troponin myoglobin, and creatine kinase isoenzymes, which can be identified by blood tests, slowly seep into the blood before a HA. CK-MB isoenzyme, a type of creatine kinase found specifically in heart muscle cells, increases in the blood, particularly in heart diseases. Furthermore, another cardiac biomarker, troponin, is generated when the heart muscle is injured, as in a HA, and the more damage to the heart happens, the more troponin is seen in the blood. Based on the variations in these, it may be feasible to predict the risk of HA with great accuracy. As a result, a diagnosis can be done to diagnose a HA early and commence treatment.<sup>[9]</sup> It may be important to utilize a machine rather than a human to diagnosis HA. Data sciences have become more important in the twenty-first century in order to automatically identify illnesses. ML technologies are becoming increasingly significant in the diagnosis of patients. ML has played an important role in heart disease research as it has in other diseases. Finding the difference between healthy and heart-diseased

individuals in existing clinical data has been a powerful approach in classification work. Being able to predict and classify heart disease will help doctors make quick decisions. This provides a critical basis for the treatment of sick individuals, and more lives will be saved with this approach.<sup>[10]</sup> Despite the promising performance of ML, data on its use in a real-world clinical environment and explainable risk prediction models to aid illness prognosis is limited. Due to the "black-box" nature of ML algorithms, it is difficult to explain why certain predictions about patients should be made; that is, what specific attributes of the patient lead to a given forecast.<sup>[11]</sup>

To solve these drawbacks, this work combined the advanced ML algorithm with a framework based on LIME. Thus, in this study, it was aimed to classify patients with and without HA, and to determine the personalized risk factors associated with HA, using an open-access dataset including patients' demographic characteristics and blood values.

## MATERIAL AND METHODS

### Data description

The dataset utilized in the current study, which includes details of people who have and have not had a HA, was gathered in the cardiology center in the Erbil area of Iraq in 2018. The dataset consists of 1319 patients and has eight input variables and one output variable. The output variable has two categories: negative and positive. The negative category denotes the absence of HA, while the positive category denotes the presence of HA. Age, blood sugar (glucose), heart rate (impulse), systolic blood pressure (pressurehigh), diastolic blood pressure (pressurelow), CK-MB (kcm), and troponin data make up the input variables.<sup>[12]</sup> All nine variables in the dataset are included in Table 1, along with any associated datatypes and a brief explanation.

**Table 1: The names, Kinds and Descriptions of the variables in the dataset.**

Variable	Description	Type
Age	Patient age in the year	Quantitative
Gender	Gender of the patient (1= Male, 0= Female)	Qualitative
Heart Rate (impulse)	Maximum heart rate achieved 10 to 160-180	Quantitative
Systolic blood pressure (Pressurehigh)	Resting systolic blood pressure (in mm Hg on admission to the hospital) (70-190).	Quantitative
Diastolic blood pressure (Pressurelow)	Resting diastolic blood pressure (in mm Hg on admission to the hospital) (40-100).	Quantitative
Blood sugar (Glucose)	(Blood sugar >120 mg/dl) (1-900 mg/dl)	Quantitative
CK-MB (kcm)	Enzyme CK-MB (Creatine Kinase Enzymes)	Quantitative
Troponin	Enzyme troponin (0.0-0.014)	Quantitative
Class	Negative HA/ Positive HA	Qualitative

### Biostatistics analysis

Qualitative data from the variables in the data set used in the study were summarized with numbers (percentage). The conformity of the quantitative data to the normal distribution was evaluated with the Kolmogorov-Smirnov test. Since the data did not show normal distribution, they were summarized as median

(minimum-maximum). Also, Mann-Whitney U test was used for statistical analysis. The  $p < 0.05$  value was considered statistically significant in the applied statistical analyzes. Statistical analyzes were performed using IBM SPSS Statistics 26.0 for Windows (New York; USA).

### Model development

With the dataset used, the extreme gradient boosting (XGBoost) model, which is a model created using tree-based learners, was trained to predict patients with and without HA during the modeling phase. Chen and Guestrin proposed the XGBoost algorithm.<sup>[13]</sup> It is a supervised ML technique that was designed as an improved version of the gradient boosting algorithm. The XGBoost method uses additive approaches to build a powerful learning model by combining the predictions of weak learners. In addition to its speed and great performance, the XGBoost classifier avoids overfitting and makes maximum use of computing resources. These benefits stem from simplifying the goal functions, which allow for the integration of regularization and predictive terms, as well as parallel execution in the training phase.<sup>[14]</sup> According to the XGBoost algorithm's processes, the first learner is fitted to the full dataset. The second student is then equipped with the previous learner's faults. This procedure is repeated indefinitely until a stopping condition is reached, at which time the final prediction model is generated by combining the predictions of all learners.<sup>[15]</sup> The data is divided into 70% training data and 30% test data. To confirm model validity, the n-fold cross-validation approach, one of the resampling methods, was used in this study. In The method of n-fold cross-validation. The dataset will be divided into k subsets, with one of the k subsets serving as the test set and the remaining k-1 subsets acting as the training set. As a consequence, each data point appears exactly once in the test set and k-1 times in the training set. The results of the k folds will be averaged to create a

single guess. Because it is the most commonly used standard value in research, k=10 was picked.<sup>[16]</sup>

Because it is difficult to explain why an algorithm gives correct predictions for a certain patient cohort, ML models are frequently regarded as black boxes; hence, in this study, the LIME method was used for the interpretability of the ML model. LIME is an open source framework that Ribeiro published in 2016 with the goal of establishing trust in the use of ML models by shedding light on the decision-making process of ML models.<sup>[17]</sup> Every model must be linear on a local scale, according to the foundational tenet of LIME. Therefore, it applies a local linear model to the real data and then generates new, slightly modified data points around it to explain specific predictions. Local Interpretable Model-Agnostic Explanations is also known as LIME. Local refers to the analysis of certain observations using the framework. It describes how a particular observation is classified rather than providing a general explanation for why the model acts in a certain way.<sup>[18]</sup>

On the test set, the completed model was evaluated using ACC, b-ACC, SE, SP, ppv, npv, and F1-score.

All analyzes and calculations were performed using Python Version 3.6.5 (sklearn, xgboost, and lime packages).

Figure 1 shows a graphical summary of the biostatistical analysis and modeling development used in the study.

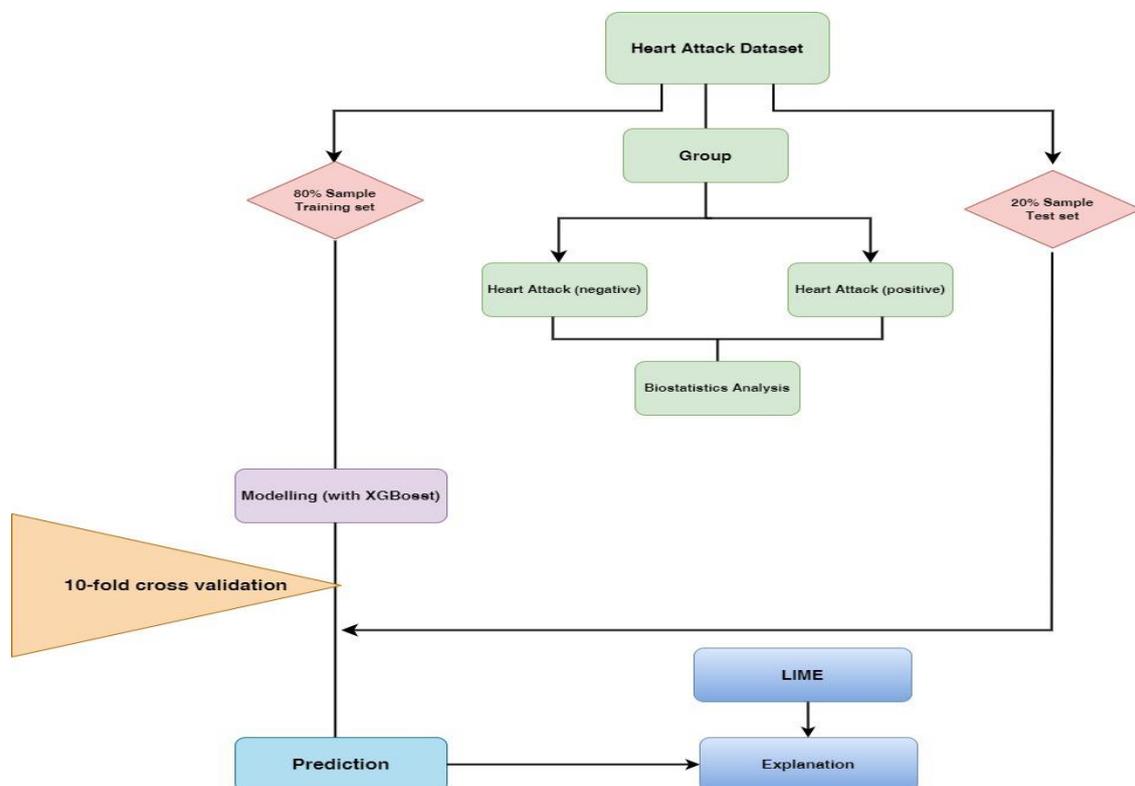


Figure 1: The flow of analysis for model Development and Assessment.

## RESULTS

The data set used in the study consists of 1319 people, of whom 810 (61.4%) had a heart attack, and 509 (38.6%) did not have a heart attack. There are 449 (34%) female and 870 (66%) male individuals. The mean age is  $56.19 \pm 13.647$  and the median is 58(14-103).

When patients negative HA and positive HA were compared on input variables age, impulse, pressurehigh,

pressurelow, glucose, kcm, and troponin, there was a statistically significant difference in age, CK-MB (kcm), and troponin. Other factors, however, were not statistically significant. In addition, there is a statistically significant relationship between gender variable and dependent/target variable (class) groups ( $p < 0.05$ ). Table 2 displays the findings of the analyses.

**Table 2: The statistical comparison of the independent variables.**

Variables	Class		p
	Negative HA	Positive HA	
Age	52(14-91)	60(19-103)	<0.001*
Heart rate (Impluse)	75(20-111)	74(20-111)	0.966*
Systolic blood pressure (Pressurehigh)	125(42-223)	122(65-223)	0.185*
Diastolic blood pressure (Pressurelow)	72(40-128)	71(38-154)	0.775*
Blood sugar (Glucose)	117(60-541)	116(35-541)	0.515*
CK-MB (kcm)	2.31(0.321-7.02)	3.775(0.353-300)	<0.001*
Troponin	0.006(0.001-10)	0.044(0.003-10.3)	<0.001*
gender	Male n(%)	202 (39.69)	0.001**
	Female n(%)	307 (60.31)	

Data are given as count (percentage) or median (minimum–maximum); \*Mann Whitney U test, \*\*:Pearson chi-square test

## Modelling results

Table 3 shows the values of the performance measures derived by modeling with XGBoost using persons with and without a heart attack.

**Table 3: Values of performance measures acquired after modeling.**

Performance Metrics	Performance Metrics Value (%) [Confidence Interval]
ACC	98.5 (97.3-99.7)
b-ACC	98.6 (97.5-99.8)
SE	99.3 (96.4-100)
SP	97.9 (95.3-99.3)
ppv	96.8 (92.7-99)
npv	99.6 (97.7-100)
F1-score	98.1 (96.7-99.4)

Table 4 shows the table of the variable importance value that was produced as a consequence of the modeling.

**Table 4: The variable importance value from the XGBoost model.**

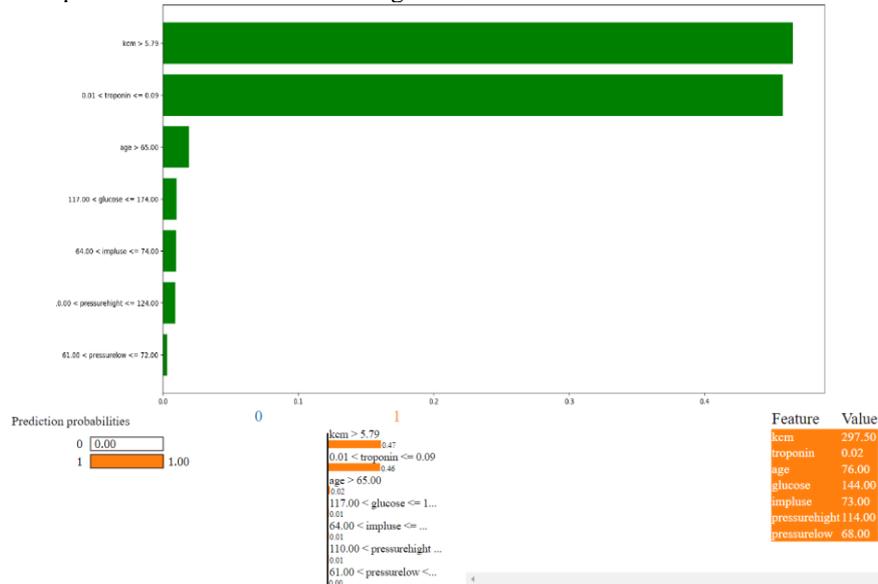
Variables	Variable Importance Value
Troponin	100
kcm	54.345
Age	3.831
Gender	0.4
Systolic blood pressure	0.2
Heart rate	0.166
Diastolic blood pressure	0.13
Glucose	0

The most important variables obtained from the variable importance obtained as a result of the XGBoost model are troponin, kcm, age, gender, systolic blood pressure, heart rate, diastolic blood pressure, respectively. Using

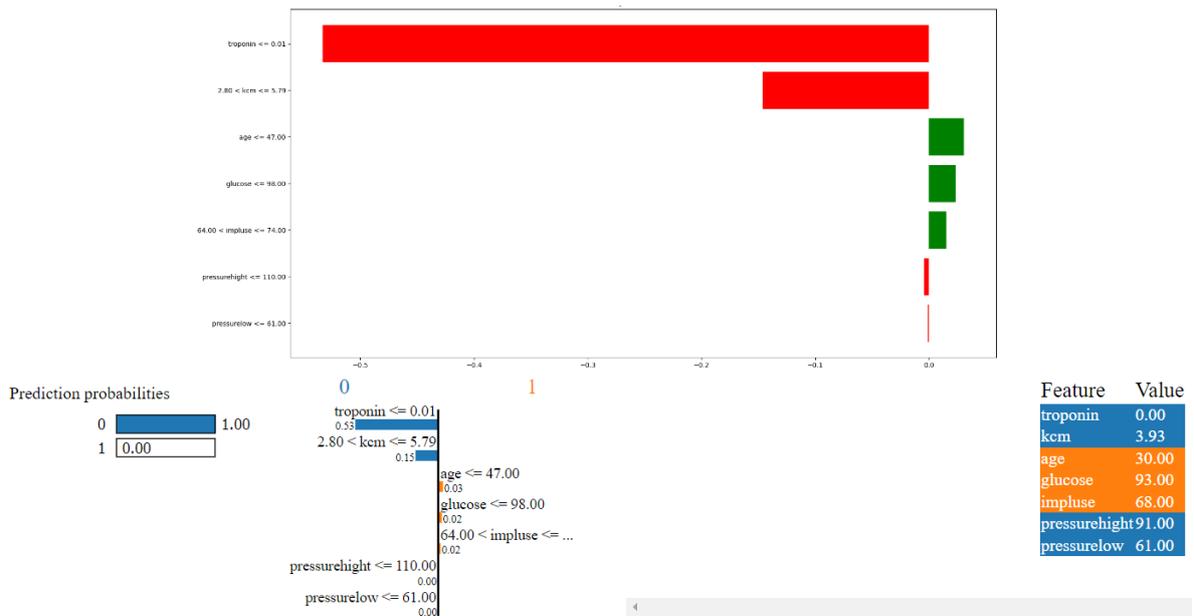
the LIME method, which is an explainable artificial intelligence method, these variables are used to show which intervals are risk factors for a few patients.

**LIME results**

The results of the first 5 patients in the test data set are given below.



**Figure 2: Patient 1 in the test dataset.**



**Figure 3: Patient 2 in the test dataset.**

Patient 3 in the test data set

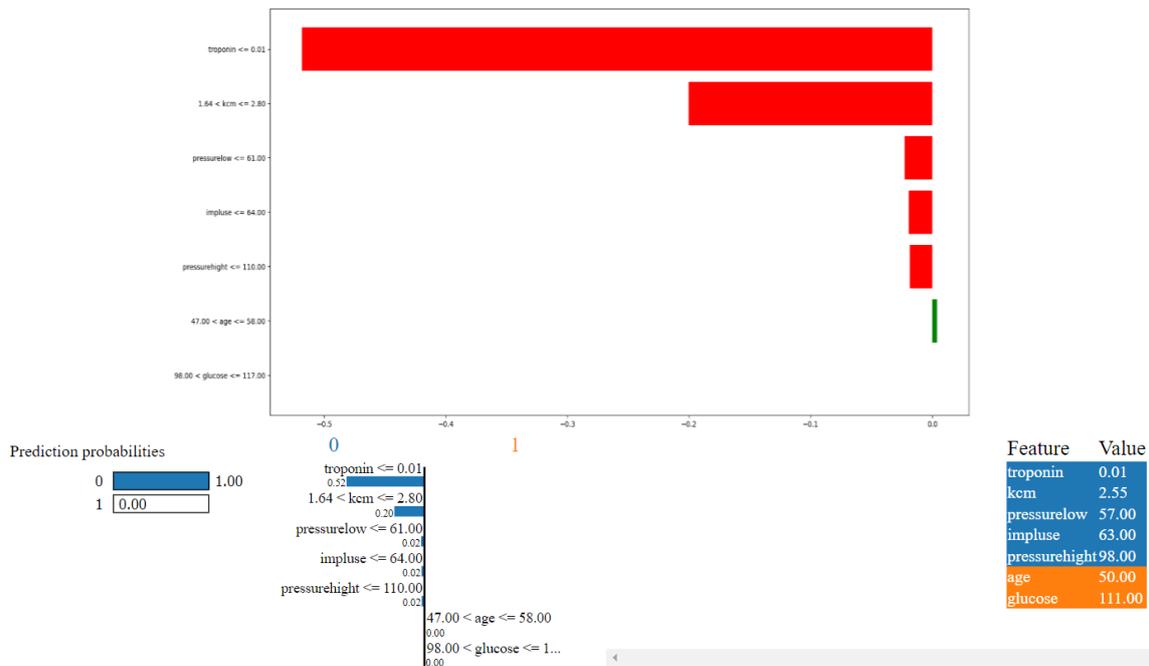


Figure 4: Patient 3 in the test dataset.

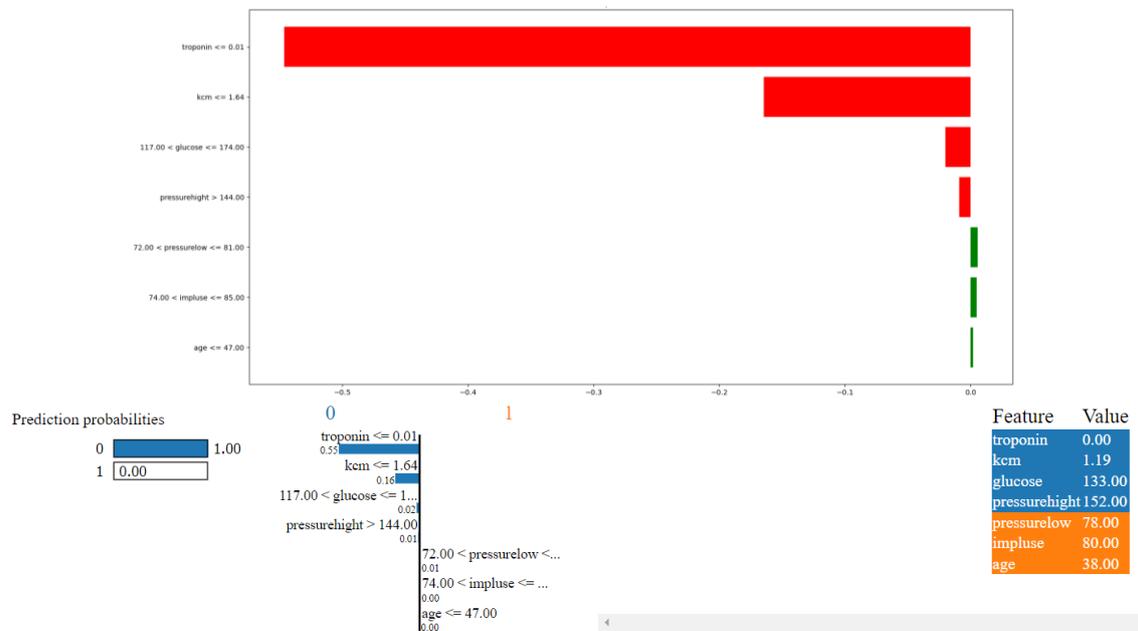
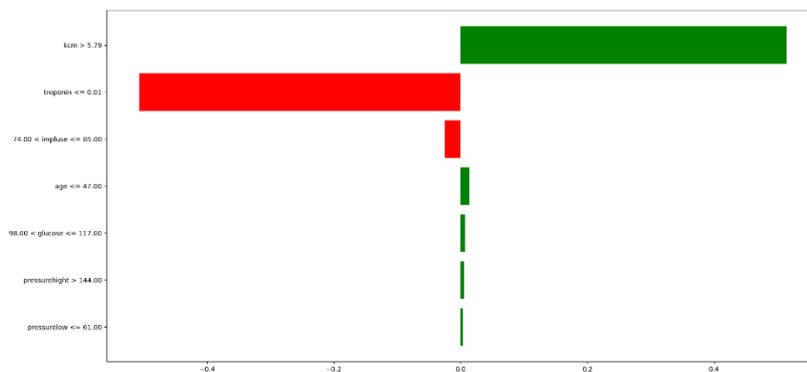


Figure 5: Patient 4 in the test dataset.



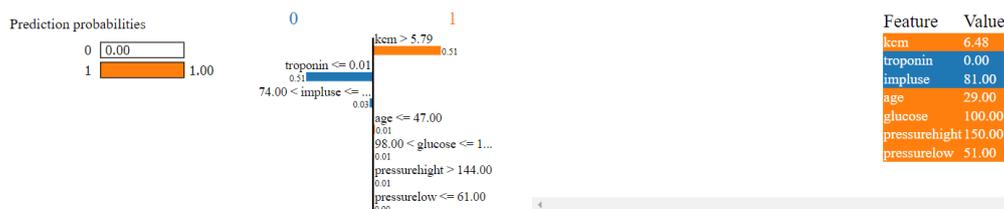


Figure 6: Patient 5 in the test dataset.

Considering the LIME results, with 100% probability for patient 1 positive heart attack were presumed. The "kcm > 5.79, 0.01 < troponin <= 0.09, age > 65.00, 117.00 < glucose <= 174.00, 64.00 < impluse <= 74.00, 110.00 < pressurehigh <= 124.00, 61.00 < pressurelow <= 72.00" values positively affected the probability of predicting this patient as a heart attack with a 100% probability. In addition, with 100% probability for patient 2 negative heart attack were presumed. While the "troponin <= 0.01, 2.80 < kcm <= 5.79, pressurehigh <= 110.00, pressurelow <= 61.00" negatively affected the probability of predicting this patient, and "age <= 47.00, glucose <= 98.00 and 64.00 < impluse <= 74.00" positively affected. Results for other patients will be interpreted similarly. Additionally, with 100% probability for patient 5 positive heart attack were presumed. While the "troponin <= 0.01 and 74.00 < impluse <= 85.00" negatively affected the probability of predicting this patient, and "kcm > 5.79, age <= 47.00, 98.00 < glucose <= 117.00, pressurehigh > 144.00, pressurelow <= 61.00" positively affected. Results for other patients will be interpreted similarly.

## DISCUSSION

CVD are among the leading causes of mortality in today's world, and they are especially prevalent in Western countries. According to studies, the global death rate from cardiovascular disorders would rise from 28.9% to 36.3% between 1990 and 2020. A HA is the most frequent kind of CVD.<sup>[19]</sup>

According to the WHO, heart attacks are the primary cause of 31% of fatalities globally.<sup>[20]</sup> The number is greater, at 46%, among nations that make up the Gulf Cooperation Council, including the Kingdom of Saudi Arabia.<sup>[21]</sup> According to a statement made on World Heart Day in 2015 by the Turkish Society of Cardiology, 125,000 heart attacks in Turkey result in death for every 300,000 that occur there.<sup>[22]</sup> In addition, more than a quarter of a million Americans pass away from heart attacks every year. According to statistics, the yearly expense of heart disease alone in the US is above \$200 billion. The American Heart Association also predicts that by 2030, the expense of treating heart disease will have doubled.<sup>[23]</sup> HA is a significant public health issue since it is relatively widespread, particularly in the productive age group of society, creates substantial issues owing to complications in the post-acute phase, and can even end in mortality in late stages. Despite advances in illness detection and treatment procedures in recent years, it remains one of the leading causes of

morbidity and death in our nation and industrialized civilizations.<sup>[29]</sup>

The evaluation of the incidence and case mortality of HA, regarded as one of the most important components of the cardiovascular disease burden, will be critical in reducing coronary disease mortality. As a result, the demand for diagnostic markers that can predict HA is growing. Some isoenzymes are known to rise in the blood prior to a HA. Physical examination, electrocardiography (ECG) with Q waves, and the findings of tests such as creatinine kinase, Myoglobin, and Troponin are the most often used diagnostic procedures in the diagnosis of HA.<sup>[24]</sup> Creatine kinase and troponin enzymes in the study's data set have been used to accurately diagnose HA for many years Physical examination, electrocardiography (ECG) with Q waves, and the findings of assays such as creatinine kinase, myoglobin, and troponin are the most often used diagnostic procedures in the diagnosis of HA. Creatine kinase and troponin enzymes in the research data set have been utilized consistently in the diagnosis of HA for many years.<sup>[25]</sup> As a result, the availability of a diagnostic model based on these enzymes will be able to recognize the risk of HA at an early stage and limit the mortality that may ensue. Moreover, heart attack is critical to recognize the condition at an early stage and conduct out the necessary analysis and therapies to avoid the complications that may ensue.<sup>[26]</sup> Because most people today are ignorant of how things might turn deadly, there is a need to develop a solution that can readily assist them in comprehending and forecasting heart attacks, while also being inexpensive in comparison to typical testing and treatments. Artificial intelligence (AI), particularly ML, may play a critical role in quickly analyzing and displaying results.<sup>[27]</sup> Despite the fact that ML models have been constructed in line with data science theory and performance requirements, their acceptance in clinical practice by healthcare practitioners remains minimal.<sup>[28]</sup> The explanation might be based on the "black-box" nature of ML techniques. categorization models with great performance have minimal transparency, which means that the recipients of the results have little insight into the reasoning underlying the specific categorization. This creates barriers in the realm of healthcare for a variety of reasons. Because a forecast may be the catalyst for action, inaccurate predictions can have serious implications. Explaining the categorization results enables the healthcare provider to uncover faulty thinking and, as a result, avoid undesirable implications

for the patient.<sup>[29]</sup> LIME is a recently developed framework that can be used with any black-box classification model in order to obtain an explanation for one specific instance. It operates by providing a local explanation of the classification and providing the fewest features that lead to the highest likelihood of the specified class outcome for one observation.<sup>[17]</sup> Despite the fact that LIME has previously been used to clinical classification models, research on the acceptance and interpretability of LIME explanations among clinical healthcare practitioners is lacking.<sup>[19]</sup>

HA can be diagnosed using cardiac markers. In this study, it was aimed to predict HA with an ML-based model for early diagnosis and prediction of risk factors with the help of a dataset containing cardiac markers, and to identify risk factors that may be associated with HA and to make these factors more interpretable with the help of LIME, a locally explainable method.

The statistical analysis indicated a statistically significant difference between the positive HA and negative HA groups in gender, age, CK-MB, and, troponin variables, but no statistical differences in other variables.

The values of ACC, b-ACC, SE, SP, ppv, npv, and F1-score performance metrics obtained according to the prediction model results made with the XGBoost method were 98.5%, 98.6%, 99.3%, 97.9%, 96.8%, 99.6%, and 98.1%. Considering the predictive model performance results obtained in this study, it appears that a machine learning-supported risk classification technique used for the diagnosis of HA is a qualified study in terms of categorizing patients and guiding future research. Furthermore, when the variable importance values generated from the modeling were investigated, it was discovered that troponin and CK-MB were the most relevant factors related with HA. On the other hand age, gender, systolic blood pressure, heart rate, diastolic blood pressure, and glucose variables, appear to have little influence on HA. Modeling results are consistent with the literature. The literature also supports that the risk of HA can be evaluated with troponin and CK-MB, which is the creatine kinase isoenzyme. What makes this study different from the literature is that it examines HA-related risk factors obtained as a result of modeling with LIME on an individual basis. When we look generally at the individual-based results obtained with LIME of the patients in the test data set, troponin  $\geq 0.01$ , kcm  $> 5.79$ ,  $117.00 < \text{glucose}$ ,  $58.00 < \text{age}$ ,  $72.00 \leq \text{pressurelow}$ ,  $\text{pressurehigh} > 144.00$  values increase the risk of being HA positive.

With the LIME method, which contributes to the lack of interpretation in modeling on an individual basis, risk factors for HA are revealed with threshold values in each individual. With these results, patients can be handled on an individual basis by healthcare professionals and individual-specific treatment strategies can be developed to ensure optimal effect of the treatment.

## REFERENCES

1. G. Özdemir Bakırhan, Ö. Bilen, and S. C. Ateş, "Hastane Aciline Gelenlerde Kalp Krizi Risk Olasılığının Belirlenmesi için Bir Karar Destek Sisteminin Oluşturulması," *Duzce University Journal of Science & Technology*, 2022; 10.
2. T. Y. Gurel, "Hemşirelik Öğrencilerinin Kardiyovasküler Hastalıklar Risk Faktörleri Bilgi Düzeylerinin Belirlenmesi," *Samsun Sağlık Bilimleri Dergisi*, 2023; 8: 103-112.
3. W. H. Organization, "Cardiovascular diseases (cvds)," <http://www.who.int/mediacentre/factsheets/fs317/en/index.html>, 2009.
4. Available: <https://www.nhs.uk/conditions/heart-attack/diagnosis/#:~:text=An%20ECG%20machine%20records%20these,about%205%20minutes%20to%20do>
5. S. Arslankaya and M. T. Çelîk, "Prediction of heart attack using fuzzy logic method and determination of factors affecting heart attacks," *International Journal of Computational and Experimental Science and Engineering*, 2021; 7: 1-8.
6. Z. Liu, D. Meng, G. Su, P. Hu, B. Song, Y. Wang, et al., "Ultrafast Early Warning of Heart Attacks through Plasmon-Enhanced Raman Spectroscopy using Collapsible Nanofingers and Machine Learning," *Small*, 2023; 19: 2204719.
7. P. J. Zimetbaum and M. E. Josephson, "Use of the electrocardiogram in acute myocardial infarction," *New England Journal of Medicine*, 2003; 348: 933-940.
8. D. Y. Leung, P. M. Davidson, G. B. Cranney, and W. F. Walsh, "Thromboembolic risks of left atrial thrombus detected by transesophageal echocardiogram," *Am J Cardiol*, 1997; 79: 626-9, 1.
9. Z. Liu, D. Meng, G. Su, P. Hu, B. Song, Y. Wang, et al., "Ultrafast Early Warning of Heart Attacks through Plasmon-Enhanced Raman Spectroscopy using Collapsible Nanofingers and Machine Learning," *Small*, 2023; 19: e2204719.
10. C. M. Bhatt, P. Patel, T. Ghetia, and P. L. Mazzeo, "Effective heart disease prediction using machine learning techniques," *Algorithms*, 2023; 16: 88.
11. S. M. Lundberg, B. Nair, M. S. Vavilala, M. Horibe, M. J. Eisses, T. Adams, et al., "Explainable machine-learning predictions for the prevention of hypoxaemia during surgery," *Nature biomedical engineering*, 2018; 2: 749-760.
12. M. Anshori and M. S. Haris, "Predicting Heart Disease using Logistic Regression," *Knowledge Engineering and Data Science*, 2022; 5: 188-196.
13. T. Chen and C. Guestrin, "Xgboost: A scalable tree boosting system," in *Proceedings of the acm sigkdd international conference on knowledge discovery and data mining*, 2016; 22: 785-794.
14. I. Sharafaldin, A. H. Lashkari, S. Hakak, and A. A. Ghorbani, "Developing realistic distributed denial of service (DDoS) attack dataset and taxonomy," in

- 2019 *International Carnahan Conference on Security Technology (ICCST)*, 2019; 1-8.
15. H. A. Alamri and V. Thayananthan, "Bandwidth control mechanism and extreme gradient boosting algorithm for protecting software-defined networks against DDoS attacks," *IEEE Access*, 2020; 8: 194269-194288.
  16. P. Sonkar, "Application of supervised machine learning to predict the mortality risk in elderly using biomarkers," 2017.
  17. M. T. Ribeiro, S. Singh, and C. Guestrin, "" Why should i trust you?" Explaining the predictions of any classifier," in *Proceedings of the ACM SIGKDD international conference on knowledge discovery and data mining*, 2016; 22: 1135-1144.
  18. J. Dieber and S. Kirrane, "A novel model usability evaluation framework (MUSE) for explainable artificial intelligence," *Information Fusion*, 2022; 81: 143-153.
  19. Z. Tunc, I. BalıkcıCicek, and E. Guldogan, "Performance evaluation of the deep learning models in the classification of heart attack and determination of related factors," *The Journal of Cognitive Systems*, 2020; 5: 99-103.
  20. WHO. *WHO Cardiovascular Diseases*. Available: [https://www.who.int/health-topics/cardiovascular-diseases#tab=tab\\_1](https://www.who.int/health-topics/cardiovascular-diseases#tab=tab_1)
  21. K. F. Alhabib, M. A. Batais, T. H. Almigbal, M. Q. Alshamiri, H. Altaradi, S. Rangarajan, et al., "Demographic, behavioral, and cardiovascular disease risk factors in the Saudi population: results from the Prospective Urban Rural Epidemiology study (PURE-Saudi)," *BMC public health*, 2020; 20: 1-14.
  22. D. Schneeberger, K. Stöger, and A. Holzinger, "The European legal framework for medical AI," in *International Cross-Domain Conference for Machine Learning and Knowledge Extraction*, 2020; 209-226.
  23. E. J. Benjamin, S. S. Virani, C. W. Callaway, A. M. Chamberlain, A. R. Chang, S. Cheng, et al., "Heart disease and stroke statistics—2018 update: a report from the American Heart Association," *Circulation*, 2018; 137: e67-e492.
  24. G. Özdemir, Ö. Bilen, and S. C. Ateş, "Hastane Aciline Gelenlerde Kalp Krizi Risk Olasılığının Belirlenmesi için Bir Karar Destek Sisteminin Oluşturulması," *Düzce Üniversitesi Bilim ve Teknoloji Dergisi*, 2022; 10: 2093-2106.
  25. M. Yöntem, B. S. Erdoğan, M. Akdoğan, and S. Kaleli, "Akut miyokard infarktüsü tanısında kardiyak markörlerin önemi," *Online Türk Sağlık Bilimleri Dergisi*, 2017; 2: 11-17.
  26. A. Menshawi, M. M. Hassan, N. Allheeb, and G. Fortino, "A Hybrid Generic Framework for Heart Problem diagnosis based on a machine learning paradigm," *Sensors*, 2023; 23: 1392.
  27. J. S. Rose, P. M. Bruntha, S. Selvadass, and M. Rajath, "Heart Attack Prediction using Machine Learning Techniques," in *2023 International Conference on Advanced Computing and Communication Systems (ICACCS)*, 2023; 9: 210-213.
  28. M. Jabbar, S. Samreen, and R. Aluvalu, "The future of health care: Machine learning," *International Journal of Engineering & Technology*, 2018; 7: 23-25.
  29. N. B. Kumarakulasinghe, T. Blomberg, J. Liu, A. S. Leao, and P. Papapetrou, "Evaluating local interpretable model-agnostic explanations on clinical machine learning classification models," in *2020 IEEE 33rd International Symposium on Computer-Based Medical Systems (CBMS)*, 2020; 7 – 12.