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Acil servis hastalarında troponin ve trombosit düzeyleri arasındaki ilişkinin incelenmesi: Akut koroner sendrom üzerine yapay zekâ tabanlı çalışma

Investigation of the relationship between troponin and platelet levels in emergency patients: AI-based study on acute coronary syndrome

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ABSTRACT

Aim: Advancements in Artificial Intelligence (AI) and Machine Learning (ML) have revolutionized the field of medical diagnostics, offering new possibilities for early detection and risk assessment of critical conditions. This study utilizes machine learning models to predict acute coronary syndrome (ACS) and evaluate its association with key biomarkers, specifically Troponin T, Platelet (PLT), and Mean Platelet Volume (MPV). The primary objective is to assess the efficiency of ML algorithms in identifying high-risk patients based on laboratory parameters and improving early intervention strategies.

Materials and Methods: A retrospective analysis was conducted on 4092 patients admitted to the emergency department, of whom 3640 survived and 452 deceased. The study population consisted of 2427 male and 1665 female patients. Feature importance analysis using the Random Forest algorithm identified Troponin T, PLT, and MPV as the most critical biomarkers for predicting ACS and mortality risk. To enhance predictive accuracy, three machine learning models-Gradient Boosting, XGBoost, and Decision Tree—were implemented and evaluated. The Gradient Boosting model achieved an accuracy of 73.99% and an ROC AUC score of 0.6058, demonstrating the best overall performance. The XGBoost model followed closely with an accuracy of 69.11% and an ROC AUC score of 0.6054. The Decision Tree model exhibited the highest accuracy of 77.29%, but its ROC AUC score of 0.5623 suggested weaker sensitivity in distinguishing ACS cases. Each model was assessed based on accuracy, ROC AUC scores, confusion matrices, and classification reports.

Results: The findings indicate that Gradient Boosting and XGBoost models demonstrated strong predictive capabilities, with Gradient Boosting achieving the highest classification accuracy at 73.99%. Despite having the highest accuracy, the Decision Tree model exhibited a lower ROC AUC score of 0.5623, suggesting limitations in its ability to differentiate between ACS-positive and ACS-negative cases. The results further reinforce that patients with abnormal Troponin T, MPV, and PLT levels were at a significantly higher risk of developing ACS, highlighting their potential as key diagnostic markers in cardiac risk assessment.

Conclusion: This study underscores the importance of artificial intelligence in predicting acute coronary syndrome and emphasizes the critical role of Troponin T, PLT, and MPV as biomarkers. By integrating machine learning models into emergency healthcare settings, clinicians can identify high-risk ACS patients with greater accuracy, enabling timely interventions and reducing mortality rates. Future research should focus on incorporating advanced ensemble learning techniques (Random Forest, XGBoost, Deep Learning) and additional clinical variables to enhance predictive performance further. AI-driven diagnostic models can play a vital role in improving early ACS detection, optimizing patient care, and transforming emergency medicine with data-driven decision-making.

ÖZ

Amaç: Yapay Zekâ (YZ) ve Makine Öğrenmesi (MÖ) alanındaki gelişmeler, tıbbi tanı süreçlerini kökten değiştirmiş olup kritik durumların erken tespiti ve risk değerlendirmesi için yeni olanaklar sunmaktadır. Bu çalışma, makine öğrenmesi modellerini kullanarak Akut Koroner Sendrom (AKS) öngörüsünü yapmayı ve Troponin T, Trombosit (PLT) ve Ortalama Trombosit Hacmi (MPV) biyobelirteçleriyle ilişkisini değerlendirmeyi amaçlamaktadır. Temel hedef, laboratuvar parametrelerine dayalı olarak yüksek riskli hastaların belirlenmesinde MÖ algoritmalarının etkinliğini incelemek ve erken müdahale stratejilerini geliştirmektir.
Gereç ve Yöntem: Acil servise başvuran toplam 4092 hasta retrospektif olarak incelendi. Bunların 3640'ı sağ kaldı, 452'si ex oldu. Çalışma popülasyonu 2427 erkek ve 1665 kadından oluştu. Random Forest algoritmasıyla yapılan özellik önem analizi sonucunda, AKS ve mortalite riskini öngörmede en kritik biyobelirteçler Troponin T, PLT ve MPV olarak belirlendi. Tahmin doğruluğunu artırmak için üç makine öğrenmesi modeli—Gradient Boosting, XGBoost ve Karar Ağacı-uygulandı ve değerlendirildi. Gradient Boosting modeli %73,99 doğruluk ve 0,6058 ROC AUC değeri ile en iyi genel performansı gösterdi. XGBoost modeli %69,11 doğruluk ve 0,6054 ROC AUC değeri ile yakın sonuç verdi. Karar Ağacı modeli %77,29 doğruluk oranına sahip olsa da, 0,5623 ROC AUC değeri AKS olgularını ayırt etmede zayıf duyarlılık gösterdi. Tüm modeller doğruluk, ROC AUC değerleri, karışıklık matrisleri ve sınıflandırma raporlarına göre değerlendirildi.

Bulgular: Gradient Boosting ve XGBoost modelleri güçlü öngörü yetenekleri sergiledi; Gradient Boosting en yüksek sınıflandırma doğruluğunu (%73,99) elde etti. Karar Ağacı modeli en yüksek doğruluk oranına ulaşmasına rağmen, ROC AUC değerinin düşük olması (0,5623) nedeniyle AKS pozitif ve negatif vakaları ayırt etmede sınırlı kaldı. Ayrıca, Troponin T, MPV ve PLT değerlerinde anormallik olan hastaların AKS gelişim riski anlamlı derecede yüksek bulundu.

Sonuç: Bu çalışma, akut koroner sendromun öngörülmesinde yapay zekânın önemini vurgulamakta ve Troponin T, PLT ile MPV'nin kritik biyobelirteçler olduğunu göstermektedir. Acil servislerde makine öğrenmesi modellerinin entegrasyonu, yüksek riskli AKS hastalarının daha doğru belirlenmesine olanak sağlayarak erken müdahale ve mortalite oranlarının düşürülmesine katkı sağlayabilir. Gelecek araştırmaların, ileri topluluk öğrenme yöntemleri (Random Forest, XGBoost, Derin Öğrenme) ve ek klinik değişkenlerin entegrasyonu ile tahmin performansını daha da artırması beklenmektedir. YZ tabanlı tanısal modeller, acil tıpta erken AKS tespitini geliştirerek hasta bakımını optimize etmede ve veri odaklı karar vermede kritik bir rol oynayabilir.

ARTICLE INFO/MAKALE BİLGİSİ

Key Words: Artificial intelligence, machine learning, acute coronary syndrome, Troponin T, predictive

Anahtar Kelimeler: Yapay zekâ, makine öğrenmesi, akut koroner sendrom, Troponin T, tahminleme

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INTRODUCTION

The integration of Artificial Intelligence (AI) and Machine Learning (ML) in healthcare has revolutionized the landscape of medical diagnostics, particularly in the early detection and management of life-threatening conditions (1-4). Among these conditions, Acute Coronary Syndrome (ACS) remains one of the leading causes of mortality worldwide, necessitating rapid and accurate diagnostic tools to improve patient outcomes (5-7). Traditional diagnostic approaches rely heavily on clinical symptoms, electrocardiographic findings, and biomarker levels, but these methods often fail to detect ACS at an early stage or in atypical cases (8). AI-powered predictive models have the potential to enhance early risk assessment, diagnostic accuracy, and personalized treatment strategies, ultimately improving survival rates and reducing healthcare burdens (9,10).

In cardiovascular medicine, biomarkers such as Troponin T, Platelet (PLT) count, and Mean Platelet Volume (MPV) play a crucial role in assessing myocardial damage and predicting patient prognosis (11,12). Troponin T is widely recognized as the gold standard biomarker for myocardial injury, while alterations in PLT and MPV levels have been linked to thrombotic activity, inflammation, and increased cardiovascular risk. Despite their clinical significance, these biomarkers are often evaluated in isolation, limiting their predictive power in real-time decision-making (13,14). Leveraging machine learning algorithms can provide a more comprehensive and dynamic risk stratification, integrating multiple biomarker patterns to enhance predictive performance and reduce diagnostic uncertainties (15).

Machine learning models, particularly Gradient Boosting, XGBoost, and Decision Trees, have demonstrated remarkable success in various medical applications, ranging from disease classification to outcome prediction (16-19). These models excel at detecting complex relationships within high-dimensional datasets, making them particularly suitable for predicting ACS based on biomarker profiles. In this study, we employed feature importance analysis using Random Forest, which identified Troponin T, PLT, and MPV as the most significant predictors of ACS. Subsequently, we developed and compared three supervised machine learning models- Gradient Boosting, XGBoost, and Decision Tree- to assess their ability to predict ACS and classify high-risk patients. Each model was evaluated based on accuracy, ROC AUC scores, confusion matrices, and classification reports to determine the most effective approach.

Given the critical nature of ACS, early detection and timely intervention can significantly impact patient survival and long-term prognosis. By integrating AI-driven predictive models into emergency healthcare settings, clinicians can rapidly identify patients at high risk, prioritize urgent care, and optimize treatment decisions. This study aims to contribute to the growing field of AI-assisted cardiology, demonstrating how machine learning techniques can enhance the accuracy and efficiency of ACS diagnosis and risk stratification. Future advancements in ensemble learning, deep learning architectures, and real-time clinical AI integration hold the potential to further refine these predictive capabilities, paving the way for a new era of personalized and data-driven cardiovascular care.

Materials and Methods

Study Design and Setting

This study was designed as a retrospective cohort study conducted at SBÜ Diyarbakır Gazi Yaşargil Training and Research Hospital, a tertiary-level education and research hospital. The study covered the period between January 1, 2024, and December 31, 2024. The research protocol was approved by the institutional ethics committee (Approval Date: 28.02.2025, Approval Number: 373). The study included adult patients (≥18 years old) who presented to the emergency department (ED) with a preliminary diagnosis of acute coronary syndrome (ACS) and were admitted to the resuscitation unit for further evaluation. Only patients whose Troponin T test results indicated significant levels suggestive of ACS were included in the study.

Study Population and Data Collection

A total of 4092 patients met the inclusion criteria, comprising 3640 survivors and 452 deceased individuals (Figure 1).

The study population consisted of 2427 male and 1665 female patients (Figure 2).

The age distribution of the study population is as follows (Figure 3):

- 28.3% (1157 patients) were aged 65-74 years
- 18.0% (738 patients) were aged 75-84 years
- 17.2% (702 patients) were aged 55-64 years
- 14.5% (592 patients) were aged 45-54 years
- 7.6% (310 patients) were aged 85+ years
- 7.6% (309 patients) were aged 35-44 years
- 6.9% (284 patients) were aged 18-34 years

The selection criteria required patients to have both Troponin T and a complete blood count (CBC) panel, which included 16 hematological parameters. Special attention was given to Mean Platelet Volume (MPV) and Platelet Count (PLT) due to their potential role in vascular endothelial damage and coronary events.

Patient data, including laboratory test results and clinical outcomes, were retrospectively extracted from the electronic hospital information system (HIS). Blood samples were collected upon emergency admission and prior to resuscitation unit transfer. The clinical course of each patient, including survival or mortality status, was also documented based on hospital discharge records. Patients younger than 18 years were excluded from the study.

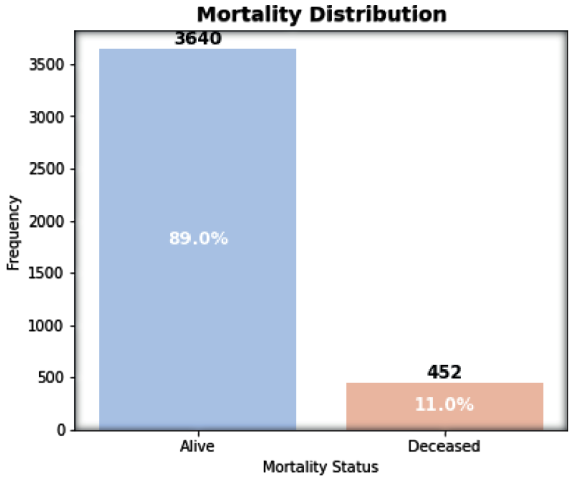

Fig 1. Mortality distribution

Machine Learning Models and Implementation

This study employed machine learning algorithms to develop a predictive model for ACS risk stratification. Three supervised learning models were implemented:

- Gradient Boosting
- XGBoost
- Decision Tree

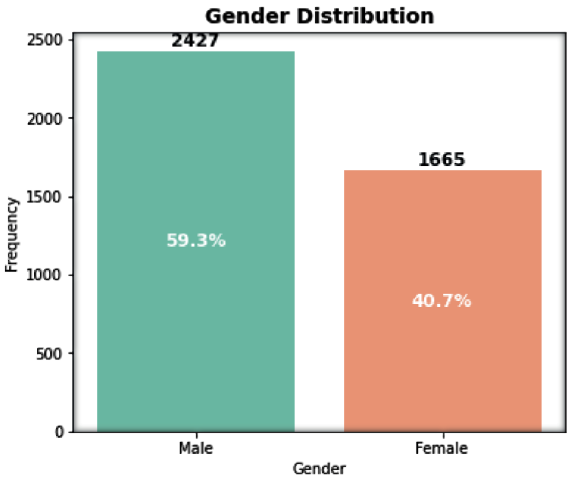

Fig 2. Gender distribution

The Python programming language was used for data preprocessing, model training, and evaluation. The implementation involved various machine learning and data science libraries, including Scikit-learn, Pandas, NumPy, and XGBoost. Data visualization tools such as Matplotlib and Seaborn were used to analyze feature distributions and correlations between biomarkers.

Data Preprocessing and Feature Engineering

To ensure data quality and improve model performance, the dataset underwent extensive preprocessing and feature selection:

Handling Missing Data: Patients with missing Troponin T values were excluded. Missing values for other features were imputed using the mean method.

Feature Scaling: Continuous numerical variables, including biomarker concentrations and hematological parameters, were standardized using StandardScaler to normalize feature distributions.

Feature Selection: A Random Forest-based feature importance analysis was conducted to identify the most predictive laboratory markers. Troponin T, MPV, and PLT emerged as the most significant features in ACS risk assessment.

Data Splitting: The dataset was divided into training (80%) and testing (20%) sets using stratified sampling to maintain proportional class distribution.

Balancing Data: Since ACS mortality cases were underrepresented, Synthetic Minority Over-sampling Technique (SMOTE) was applied to the training set to address class imbalance and improve generalizability.

Model Training and Performance Evaluation

Each of the three machine learning models was trained using the training dataset and tested on the unseen test dataset. Hyperparameter tuning was performed using GridSearchCV to optimize model performance. Model evaluation metrics included accuracy, precision, recall, F1-score, and ROC AUC scores. Confusion matrices and classification reports were generated to assess model classification capabilities.

Visualization and Statistical Analysis

Descriptive statistical analyses and visualizations were conducted to explore the relationships between Troponin T, MPV, and PLT levels in patients diagnosed with ACS. Heatmaps, histograms, and scatter plots were used to visualize correlations between biomarkers and ACS risk. Feature importance rankings were visualized using bar plots to highlight the most predictive hematological parameters.

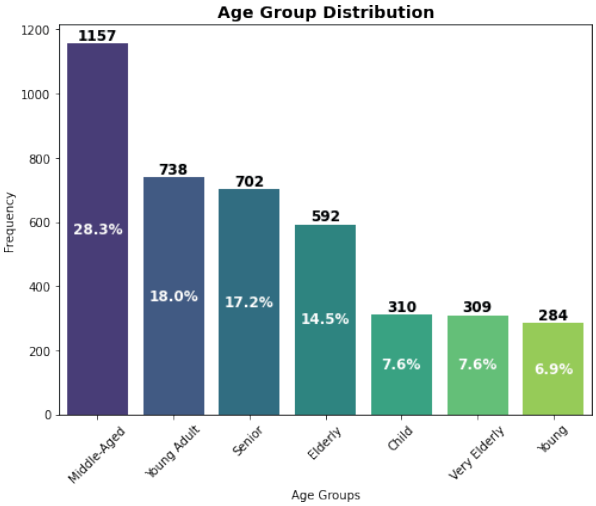

Fig 3. Age distribution

This methodological approach integrates machine learning and statistical modeling to improve ACS risk prediction and mortality assessment, supporting the potential role of AI-driven diagnostic tools in emergency medicine.

RESULTS

The mortality distribution was analyzed based on gender and age groups to determine patterns of survival and mortality in the study population.

Mortality by Gender

The dataset included 1,665 female and 2,427 male patients. Among the female patients, 1,476 (88.7%) survived, while 189 (11.3%) deceased. Among male patients, 2,164 (89.2%) survived, while 263 (10.8%) deceased (Table 1).

Gender	Mortality	Count
Female	Alive	1476
	Deceased	189
Male	Alive	2164
	Deceased	263

Table 1. Mortality by gender

These findings suggest a slightly higher mortality rate in female patients compared to male patients; however, the difference appears marginal. The results align with previous studies indicating that gender may have a minor but notable influence on cardiovascular and ischemic stroke-related mortality. However, additional factors such as comorbidities, access to medical care, and lifestyle differences should be considered when interpreting these findings.

Mortality by Age Group

A detailed breakdown of mortality across different age groups is as follows:

Age Group	Mortality	Count
Child	Alive	278
	Deceased	32
Elderly	Alive	522
	Deceased	70
Middle-Aged	Alive	1027
	Deceased	130
Senior	Alive	622
	Deceased	80
Very Elderly	Alive	273
	Deceased	36
Young	Alive	260
	Deceased	24
Young Adult	Alive	658
	Deceased	80

Table 2. Mortality by age group

Youngest age groups (Children and young adults) exhibited the lowest mortality rates. For instance, among children, only 32 out of 310 (10.3%) deceased, while among young adults, 80 out of 738 (10.8%) deceased. Middle-Aged and Senior patients had a higher proportion of mortality, with 130 deaths among 1,157 middle-aged individuals (11.2%) and 80 deaths among 702 senior patients (11.4%). Elderly and Very Elderly patients showed the highest mortality rates, where 70 out of 592 elderly patients (11.8%) and 36 out of 309 very elderly patients (11.7%) deceased.

These findings indicate that age plays a significant role in mortality risk, with older populations experiencing higher mortality rates. This is consistent with the well-documented association between aging, cardiovascular risk factors, and reduced physiological resilience.

The statistical summary of MPV, PLT, and Troponin T provides insights into their distribution and variability. Troponin T exhibits the highest variability (Mean: 117.89, Std Dev: 369.47), with values ranging from 0 to 7101.5, indicating significant outliers and a right-skewed distribution. MPV has a mean of 10.19 fL with a relatively lower standard deviation (1.75), while PLT has a mean of 252.17 × 10⁹/L with a wider spread (Std Dev: 98.06). The median values for MPV (10.3 fL), PLT (244 × 10⁹/L), and Troponin T (23.78 ng/L) suggest that the distribution is asymmetric, particularly for Troponin T, which shows extreme upper values (Table 3).

Statistic	MPV	PLT	Troponin T
Count	4076	4076	4092
Mean	10.192583	252.171184	117.896508
Std Dev	1.755444	98.06599	369.474453
Min	0	0	0
25% (Q1)	9.5	195	7.9175
50% (Median)	10.3	244	23.78
75% (Q3)	11.1	302	78.349375
Max	17.2	1416	7101.5

Table 3. Statistical Summary of MPV, PLT, and Troponin

The correlation analysis reveals weak relationships between the biomarkers. MPV and Troponin T have a slight positive correlation (0.063), suggesting a minor link between platelet activity and cardiac injury, while PLT and Troponin T show an almost negligible negative correlation (-0.0065), indicating independent behavior. The weak correlation between MPV and PLT (0.0466) suggests minimal direct association between platelet volume and count. These findings highlight that while Troponin T remains the strongest predictor, MPV and PLT may contribute to risk assessment in a supportive role, reinforcing the need for advanced predictive modeling to identify nonlinear interactions between these biomarkers (Table 4).

Feature	MPV	PLT	Troponin T
MPV	1	0.046617	0.063027
PLT	0.046617	1	-0.006567
Troponin T	0.063027	-0.006567	1

Table 4. Correlation analysis

The correlation heatmap provides a visual representation of the relationships between different features in the dataset (Figure 4), with values ranging from -1 to 1. Red shades indicate strong positive correlations, while blue shades represent strong negative correlations. Light colors suggest weak or no correlation.

1. MPV (Mean Platelet Volume) shows weak correlations with PLT (0.05) and Troponin T (0.06), indicating that platelet volume has minimal impact on platelet count and Troponin levels.
2. PLT (Platelet Count) has a weak negative correlation with Troponin T (-0.01) and Age (-0.01), suggesting platelet count does not vary significantly with Troponin levels or age.
3. Troponin T, a critical biomarker for cardiovascular events, exhibits a weak positive correlation with Mortality (0.08), confirming its role as a predictor of adverse outcomes.
4. Mortality shows weak relationships with MPV (0.02) and PLT (-0.04), but has a stronger association with Troponin T (0.08), reinforcing its importance in patient prognosis.
5. Age is moderately correlated with Age Group_Elderly (0.44), Age Group_Senior (0.30), and Age Group_Very Elderly (0.42), which is expected given that these categorical variables represent age subgroups.
6. Gender has a weak negative correlation with Age (-0.20) and Mortality (-0.20), suggesting minor differences in mortality risk between male and female patients.
7. Age Group_Elderly has a moderate positive correlation (0.44) with Age, confirming it captures older patient characteristics.
8. Age Group_Young and Age Group_Young Adult show strong negative correlations (- 0.39) with Age, which aligns with their classification of younger individuals.

The application of Artificial Intelligence (AI) and Machine Learning (ML) models in predicting Acute Coronary Syndrome (ACS) has shown promising results, with Gradient Boosting, XGBoost, and Decision Tree being evaluated for their predictive performance. Among these models, Decision Tree achieved the highest accuracy (0.77), indicating strong classification ability. However, its ROC AUC score (0.56) suggests weak discriminatory power, likely due to overfitting. In contrast, Gradient Boosting and XGBoost performed more consistently, with accuracies of 0.74 and 0.69, respectively, and identical ROC AUC scores of 0.61, demonstrating better generalizability (Figure 5).

Despite these differences, all models exhibited low F1-scores (ranging from 0.21 to 0.26), indicating challenges in correctly predicting positive cases, likely due to class imbalance in the dataset. While Decision Tree appears to be the most accurate model, the more stable performance of Gradient Boosting and XGBoost suggests they may be better suited for balanced classification. Future improvements, such as hyperparameter tuning, class balancing techniques (e.g., SMOTE), and feature selection refinement, could enhance the models' reliability and predictive accuracy.

The feature importance analysis highlights the most influential variables in predicting

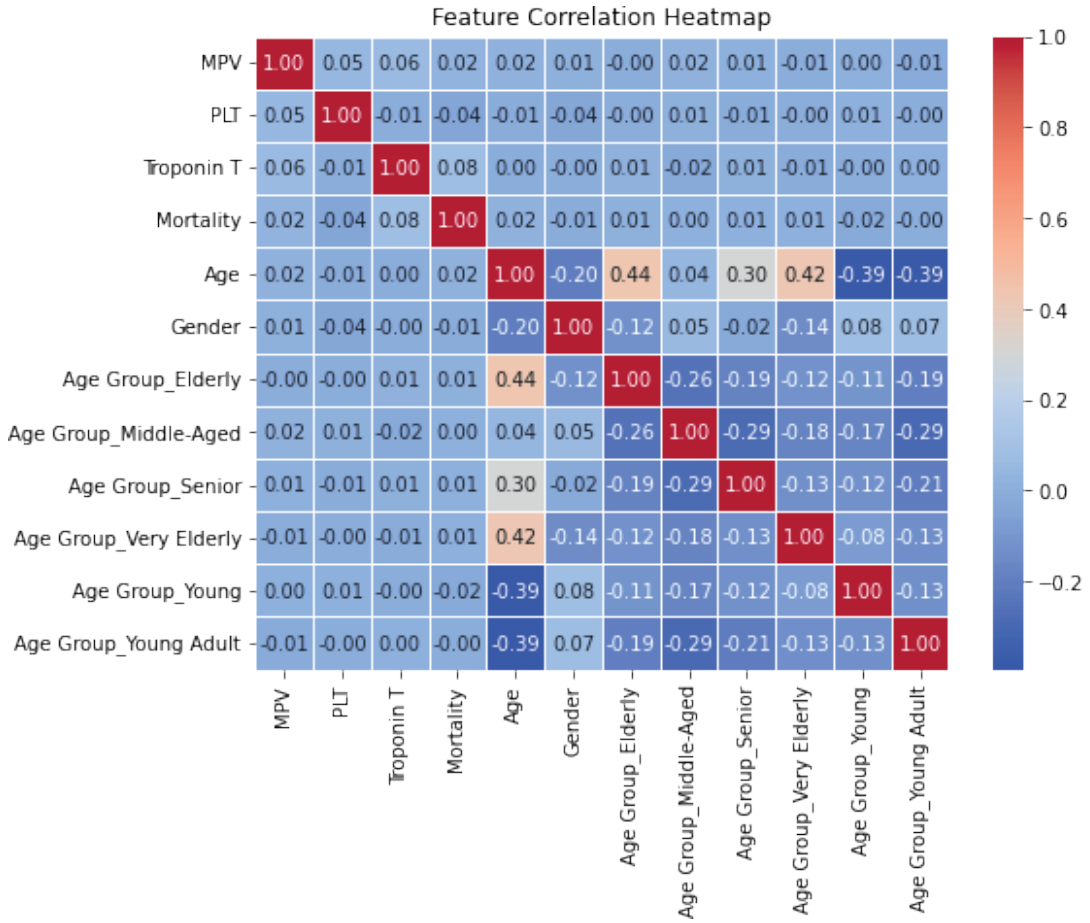

Fig 4. Correlation heatmap

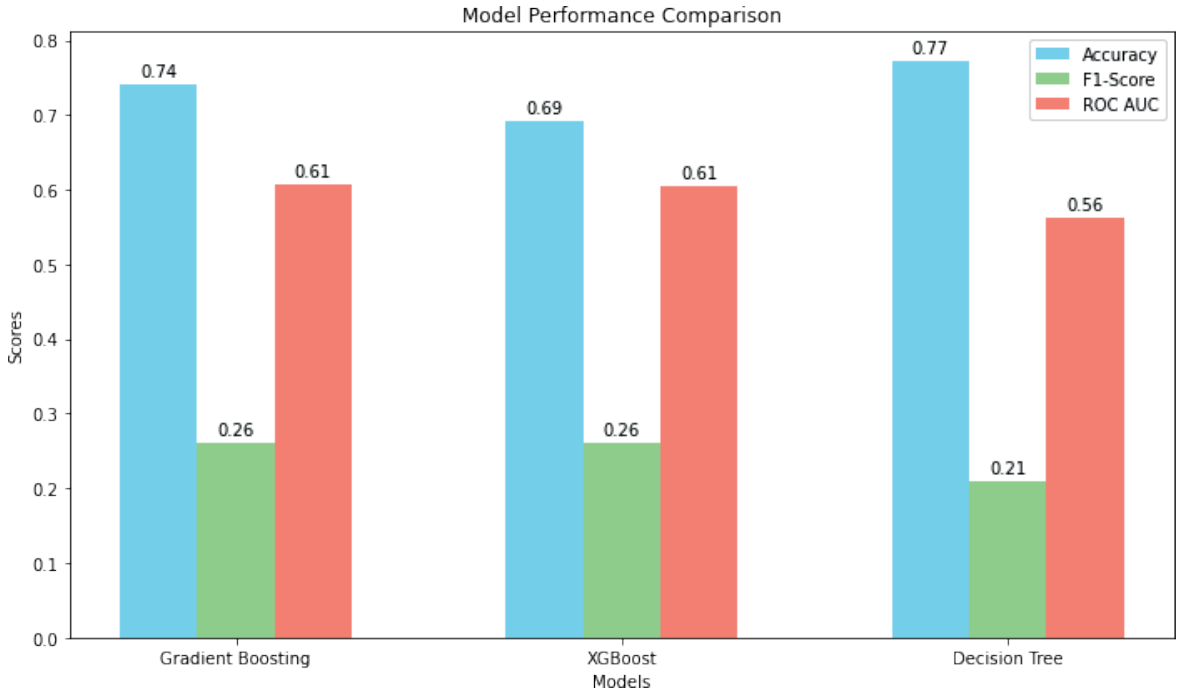

Fig 5. Model performance comparison

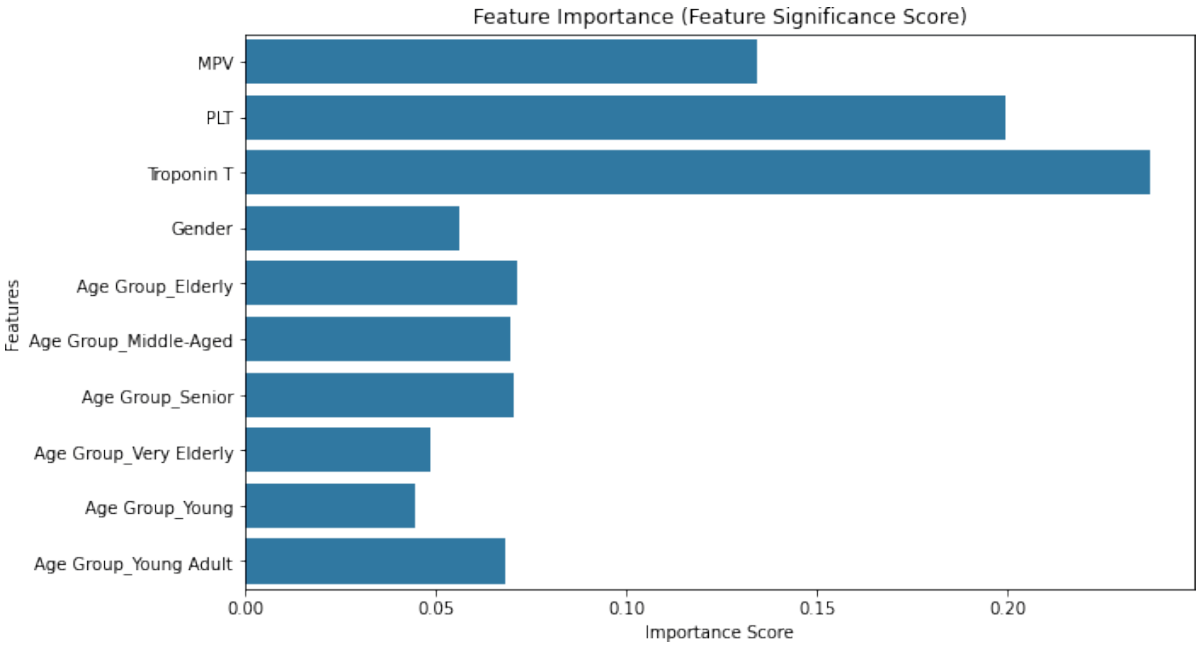

Fig 6. Feature Importance

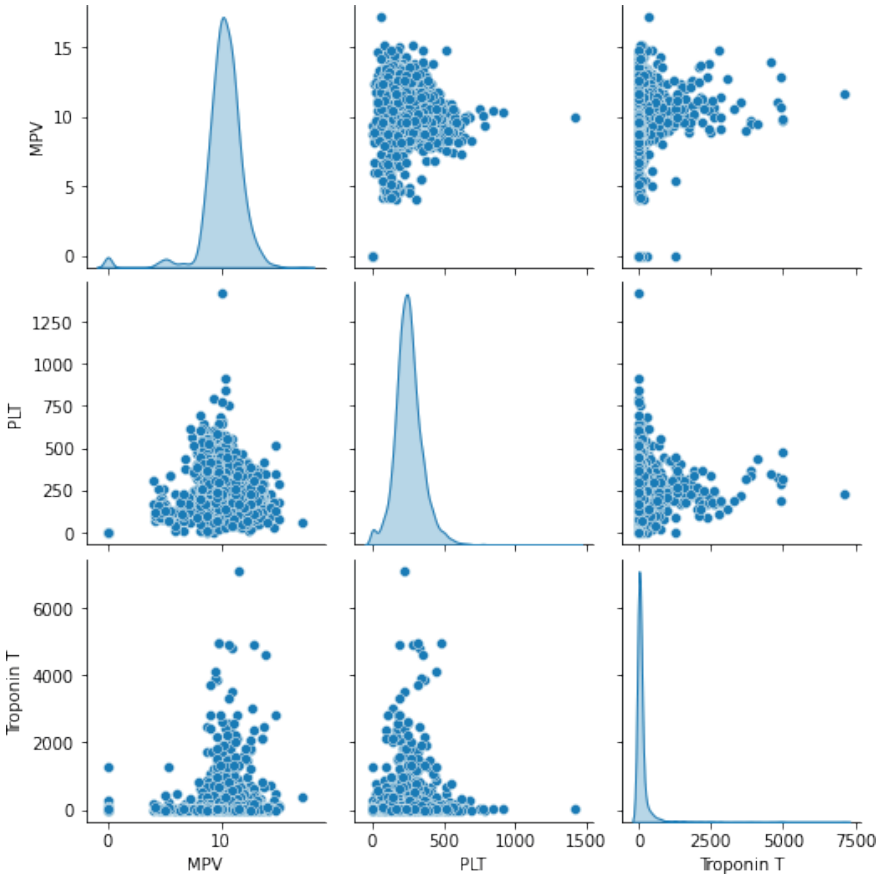

Fig 7. Distribution of MPV, PLT, and Troponin T

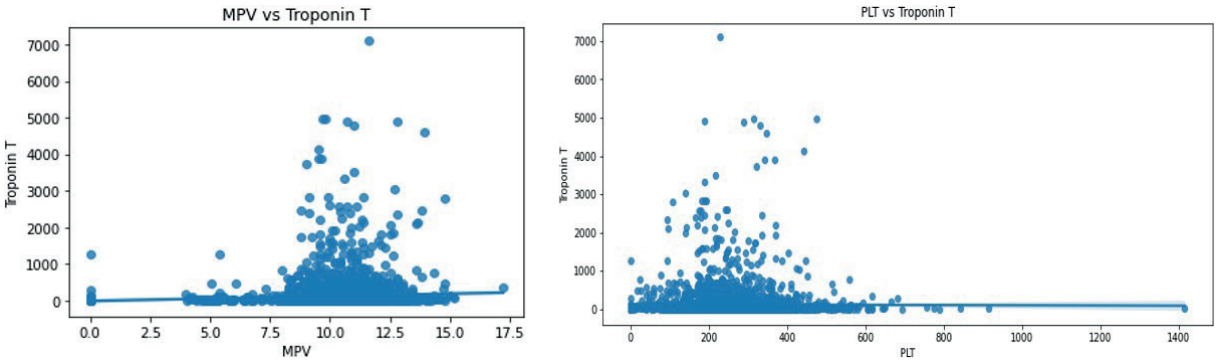

Fig 8. The scatter plots illustrating the relationships between Troponin

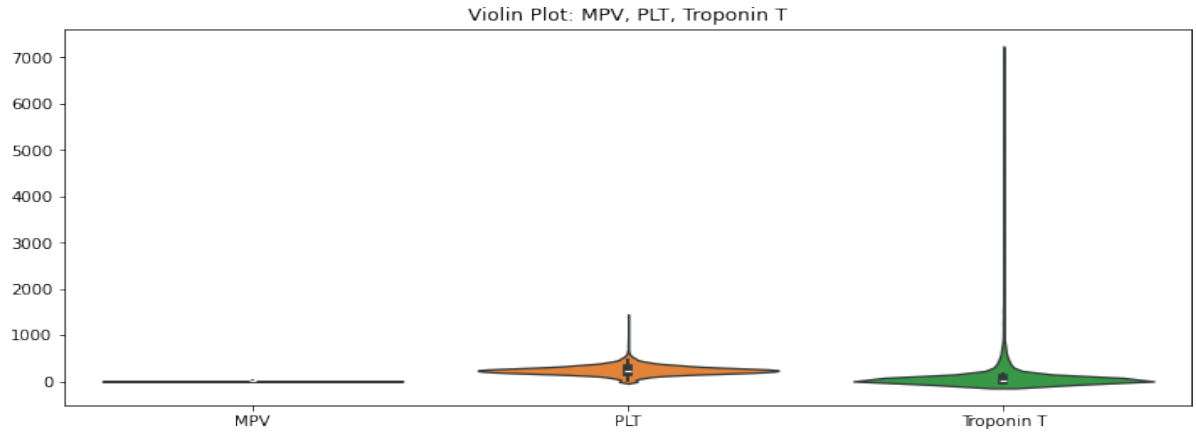

Fig 9. Violin plot visualizing the distribution of three variables, likely MPV, PLT, and Troponin

Acute Coronary Syndrome (ACS) using machine learning models. The results indicate that Troponin T is the most critical predictor, reinforcing its well-established role as the primary biomarker for myocardial injury. Mean Platelet Volume (MPV) and Platelet Count (PLT) also show significant importance, suggesting that platelet-related parameters contribute to ACS risk assessment, albeit to a lesser extent than Troponin T. Additionally, age-related features, including Elderly, Middle-Aged, and Senior groups, play a notable role, confirming the association between aging and increased cardiovascular risk. In contrast, gender and other hematological parameters exhibit lower importance, indicating a comparatively weaker impact on ACS prediction. These findings emphasize that Troponin T remains the dominant biomarker, while platelet indices and demographic factors provide additional predictive value. Future model refinements could involve feature selection techniques to enhance performance by prioritizing the most relevant variables, ensuring more accurate and efficient AI-driven risk stratification in clinical settings.

The figure presents the distribution of MPV, PLT, and Troponin T, highlighting their statistical characteristics. The MPV and PLT histograms (top two plots) exhibit normal-like distributions, indicating that these variables are symmetrically distributed around a central value.(Figure 7). In contrast, the Troponin T histogram (bottom-left) shows a highly right-skewed distribution, suggesting

that most values are concentrated near zero, with a few extreme outliers. This trend is also observed in the Mortality histogram (bottom-right), reinforcing the presence of a class imbalance. These insights indicate the need for data preprocessing techniques such as normalization or resampling to enhance machine learning model performance and predictive accuracy.

The scatter plots illustrate the relationships between Troponin T and MPV (left) and Troponin T and PLT (right) (Figure 8). In the MPV vs. Troponin T plot, most data points are concentrated near lower Troponin T values, with a few extreme outliers indicating significantly higher Troponin levels. This suggests that while there is some variation, MPV does not strongly correlate with Troponin T, as most values remain clustered near the baseline. Similarly, in the PLT vs. Troponin T plot, a negative trend is observed, where higher PLT values correspond to lower Troponin T levels, though the relationship is not strongly defined. The presence of extreme outliers in both plots highlights the highly skewed distribution of Troponin T, reinforcing its critical role as a key biomarker for cardiovascular risk. These insights suggest that while MPV and PLT may contribute to ACS prediction, Troponin T remains the dominant predictor, and further analysis is needed to explore potential nonlinear relationships.

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