Predicting the Likelihood of Acute Myocardial Infarction (AMI) Diagnosis in ICU Patients Using Machine Learning Approaches

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Introduction

Acute Myocardial Infarction (AMI), commonly known as a heart attack, is one of the leading causes of morbidity and mortality worldwide (WHO, n.d.). It occurs when blood flow to a portion of the heart is blocked, leading to irreversible damage to the heart muscle. Common symptoms include chest pain or discomfort, shortness of breath, nausea, cold sweats, and fatigue. However, in critically ill patients admitted to the Intensive Care Unit (ICU), these symptoms are often masked by other comorbid conditions, complicating timely diagnosis (Shameer et al., 2018).

Early and accurate prediction of AMI is crucial because delays in recognition and treatment significantly increase the risk of death and long-term complications. Studies show that timely interventions, such as percutaneous coronary intervention or thrombolytic therapy, within the first few hours of symptom onset dramatically improve patient outcomes (Thygesen et al., 2018). Despite this, AMI remains one of the most error-prone diagnoses, often misdiagnosed or overlooked, particularly in ICU settings where patients present with atypical or overlapping symptoms (Giannitsis et al., 2013).

Machine learning (ML) has emerged as a powerful tool to address these challenges, offering the potential to analyze complex datasets and identify subtle patterns that may elude traditional diagnostic methods. Previous models in the field have utilized various clinical features, including patient demographics, comorbidities, vital signs, and lab results, to predict AMI. Notably, some studies achieved promising results using biomarkers like troponin, a cardiac-specific protein that is a definitive indicator of myocardial injury (Doudesis et al., 2023). However, the inclusion of troponin in early prediction models introduces the risk of data leakage, as its levels rise only after cardiac damage has occurred (Shameer et al., 2018). Such practices may result in overly optimistic model performance during training but fail to provide meaningful predictions in real-world, pre-diagnostic scenarios.

This project builds upon prior research while addressing its limitations. By leveraging the MIMIC-III database, which contains extensive ICU patient records, including demographics, diagnostic codes, procedures, and lab results, we aim to develop robust machine learning algorithms capable of early AMI prediction (Beam & Kohane, 2018). Unlike traditional approaches, this study focuses on excluding troponin from early predictive models to prevent data leakage and instead emphasizes the use of features available on the earliest admission, such as admission characteristics, patient demographics, and non-cardiac lab tests.

Through this research, we aim to advance the field by providing interpretable and effective models that can assist clinicians in identifying high-risk patients early. This approach has the potential to enable timely interventions, reduce diagnostic errors, and ultimately improve patient outcomes in ICU settings.

Materials and Methods

Literature Review

Early identification of AMI is essential for initiating timely interventions, such as reperfusion therapy, which significantly improves patient outcomes. Delayed diagnosis can lead to complications such as cardiogenic shock, arrhythmias, and heart failure, increasing both morbidity and mortality rates (Thygesen et al., 2018). Traditional diagnostic tools, such as electrocardiograms (ECGs) and cardiac biomarkers, including troponin, are highly specific but may not be available during the early stages of symptom onset, limiting their utility for early prediction (Shameer et al., 2018).

Recent advancements in machine learning (ML) have shown significant potential in improving the early detection and diagnosis of AMI. ML algorithms are capable of analyzing complex and high-dimensional data, such as Electronic Health Records (EHR), to uncover patterns that may not be evident to clinicians. For instance, predictive models leveraging patient demographics, clinical symptoms, comorbidities, and early diagnostic test results have demonstrated promising results in identifying high-risk patients (Beam & Kohane, 2018).

Shameer et al. (2018) reviewed the application of machine learning in cardiovascular medicine, emphasizing its ability to enhance diagnostic accuracy and support clinical decision-making. Models incorporating clinical and demographic features, such as age, gender, comorbidities, and admission vital signs, have been shown to predict AMI risk with reasonable accuracy. However, challenges such as data quality, feature selection, and model interpretability remain critical barriers to implementation in clinical practice (Goldstein et al., 2011).

Among the biomarkers associated with AMI, troponin is widely regarded as the gold standard for diagnosis due to its high specificity and sensitivity for myocardial injury (Giannitsis & Katus, 2013). Elevated troponin levels confirm myocardial damage, making it an invaluable diagnostic tool in clinical settings. However, its inclusion in ML models for early prediction is controversial due to the risk of data leakage. Troponin elevation occurs only after myocardial injury, meaning its availability as a predictor in models aimed at preemptive diagnosis could lead to overfitting and unrealistic performance estimates (Antman et al., 2000). Addressing this issue is critical to ensuring that predictive models reflect real-world clinical scenarios where troponin data may not yet be available.

Several studies have explored predictive modeling for AMI diagnosis. For example, the TIMI risk score is a widely used clinical tool that incorporates age, risk factors, and ECG findings to stratify patients with chest pain into low, intermediate, and high-risk categories (Antman et al., 2000). While effective, such models rely on structured clinical inputs and may not fully leverage the rich, unstructured data available in EHRs.

The emergence of large-scale databases, such as the MIMIC-III critical care database, has provided researchers with an unprecedented opportunity to develop data-driven models for AMI prediction. The MIMIC-III database includes detailed patient information, diagnoses, procedures, and laboratory results, enabling the development of comprehensive predictive models (Johnson et al., 2016). Studies leveraging this database have shown that integrating clinical and demographic features with temporal data, such as lab test trends and vital sign trajectories, can significantly enhance predictive performance (Shameer et al., 2018).

While significant progress has been made, challenges remain in developing robust and clinically applicable predictive models for AMI. Key areas for improvement include handling missing data, ensuring generalizability across diverse patient populations, and integrating real-time predictive analytics into clinical workflows. Additionally, the interpretability of ML models is critical for gaining clinician trust and facilitating adoption in clinical settings (Beam & Kohane, 2018).

In conclusion, the integration of machine learning into AMI prediction holds great promise for improving early diagnosis and patient outcomes. By leveraging rich datasets, such as MIMIC-III, and addressing challenges like data leakage and feature selection, this research aims to develop clinically relevant and interpretable models that can assist in the timely identification of high-risk patients in ICU settings.

Data Description

The Medical Information Mart for Intensive Care III (MIMIC-III) database is a publicly available critical care dataset that contains comprehensive information on over 40,000 ICU admissions at the Beth Israel Deaconess Medical Center between 2001 and 2012. The database integrates diverse types of data, enabling researchers to conduct detailed analyses of ICU patient outcomes and healthcare processes. Key components of the dataset are shown as follows:

- DIAGNOSES_ICD: Includes International Classification of Diseases (ICD) codes for primary and secondary diagnoses.
- PROCEDURES_ICD: Contains ICD codes for medical procedures performed during ICU stays.
- PATIENTS: Provides demographic information such as age, gender, and ethnicity.
- ADMISSIONS: Captures admission-specific details, including admission and discharge times, admission type, and insurance information.
- LABEVENTS: Contains laboratory test results linked to patient admissions, including test names, results, and timestamps.
- Lab_Item_Codes.txt: Offers descriptions or categories of laboratory items, aiding in the interpretation of lab test results.

- Error-Prone Codes: Lists diagnosis codes associated with outcomes that are prone to errors in recognition or treatment.

The MIMIC-III dataset is particularly suited for AMI prediction due to its inclusion of rich temporal data, such as lab results, diagnostic codes, and treatment procedures. By analyzing trends and patterns within this data, ML models can identify early indicators of AMI risk. The inclusion of demographic and admission details further enables stratification of risk based on patient-specific factors.

Data Processing and Cohort Construction

The data preprocessing and cohort construction process involved several methodical steps to ensure a clean and balanced dataset suitable for machine learning analysis. First, the Admissions file was utilized to extract the earliest admission date for each patient. This step ensured that all subsequent analyses were based on each patient's initial hospitalization.

Next, the first admission dataset was merged with the Patients file to compute the age of each individual at their first admission. The age was calculated using the patient's Date of Birth and the admission date. Records indicating patients aged 120 years or older were excluded to eliminate approximately 2,000 erroneous entries. This filtration ensured data accuracy and reliability for downstream analysis.

The Diagnoses dataset was then analyzed to identify patients diagnosed with Acute Myocardial Infarction (AMI). AMI cases were filtered using ICD-9 codes starting with "410", which are specific to this condition. The filtered dataset was merged with the Admissions file to identify the earliest admission date for each MI case. These cases were further enriched with demographic details by merging them with the Patients file, resulting in a case cohort containing 4,671 MI cases.

To create a balanced dataset, a control cohort was constructed by identifying patients in the Admissions file who were not part of the MI cohort. A random sample of 4,671 patients from this control cohort was selected, matching the size of the MI case cohort. The MI and control cohorts were then combined into a single dataset, with a binary label assigned to indicate the group: 1 for MI cases and 0 for controls.

The length of hospital stay, denoted as the STAYTIME feature, was computed for each patient in the combined cohort. This feature was calculated as the difference in days between the Discharge Time (DISCHTIME) and Admission Time (ADMITTIME). Additionally, the dataset was streamlined by retaining only 11 relevant columns from an initial set of 33 columns, focusing on features critical for the training process.

For the procedural data, the Procedures dataset was preprocessed using one-hot encoding to

transform the 2009 procedure codes into binary features. This step enabled the inclusion of procedural information in the machine learning models. Similarly, the Labevents dataset was processed by mapping lab item codes to descriptive names using the Lab Item Codes text file. The data was then pivoted so that each lab test item became a column, with the corresponding maximum value (VALUENUM) for each test serving as the feature value.

The preprocessed Procedures and Labevents datasets were merged with the case-control cohort to create a comprehensive dataset that included procedural, lab, and demographic information. Finally, remaining categorical variables such as ADMISSION_TYPE, ADMISSION_LOCATION, DISCHARGE_LOCATION, MARITAL_STATUS, ETHNICITY, and GENDER were converted into binary features through one-hot encoding. Lab test variables related to “Troponin I” and “Troponin T" were excluded to prevent data leakage and align with the goal of early detection of this project.

The final training data includes 9342 records for two case-control cohorts and 2464 predictor variables (excluding ‘SUBJECT_ID’, ‘HADM_ID, and ‘LABEL’).

	SUBJECT_ID	HADM_ID	STAYTIME (day)	LABEL	Age_at_First_Admission	ICD9_10	ICD9_11	ICD9_12	ICD9_13	ICD9_14	...	ETHNICITY_PATIENT DECLINED TO ANSWER	ETHNICITY_PORTUGUESE	ETHNICITY_UNABLE TO OBTAIN	ETHNICITY_UNKNOWN/NOT SPECIFIED	ETHNICITY_WHITE
0	3	145834	10	1	77.0	0.0	0.0	0.0	0.0	0.0	...	False	False	False	False	True
1	21	109451	13	1	87.0	0.0	0.0	0.0	0.0	0.0	...	False	False	False	False	True
2	24	161859	2	1	39.0	0.0	0.0	0.0	0.0	0.0	...	False	False	False	False	True
3	25	129635	3	1	59.0	0.0	0.0	0.0	0.0	0.0	...	False	False	False	False	True
4	37	188670	5	1	69.0	0.0	0.0	0.0	0.0	0.0	...	False	False	False	False	True
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
9337	19988	141007	3	0	0.0	0.0	0.0	0.0	0.0	0.0	...	False	False	False	False	True
9338	99229	150893	27	0	78.0	0.0	0.0	0.0	0.0	0.0	...	True	False	False	False	False
9339	24541	157578	4	0	67.0	0.0	0.0	0.0	0.0	0.0	...	False	False	False	False	True
9340	10992	145405	6	0	83.0	0.0	0.0	0.0	0.0	0.0	...	False	False	False	False	True
9341	18836	168022	8	0	75.0	0.0	0.0	0.0	0.0	0.0	...	False	False	False	True	False

9342 rows × 2467 columns

Figure 1: Final Dataset for Training

This systematic preprocessing approach ensured that the final dataset was balanced, clinically relevant, and free from potential biases, providing a robust foundation for developing predictive models aimed at identifying patients at risk of Acute Myocardial Infarction (AMI).

Model Selection and Training

To develop robust and interpretable predictive models for identifying Acute Myocardial Infarction (AMI) in ICU patients, three machine learning algorithms were selected: XGBoost, Histogram Gradient Boosting, and Random Forest. These models were chosen based on their proven performance in handling high-dimensional datasets, accommodating missing values, and achieving high accuracy and AUC scores in classification tasks using healthcare datasets, including MIMIC-III.

- Widely recognized for its efficiency and accuracy, XGBoost is an optimized gradient-boosting algorithm that performs exceptionally well on structured data. It utilizes second-order gradients for optimizing loss functions and includes L1/L2 regularization to control overfitting. Its ability to handle missing data by learning optimal splits makes it ideal for healthcare datasets where incomplete data is common. Prior studies, such as Johnson et

al. (2018) and Purushotham et al. (2018), have demonstrated its effectiveness in predicting critical outcomes in ICU settings using MIMIC datasets.

- Histogram Gradient Boosting method bins continuous features into discrete intervals, significantly reducing computational complexity while maintaining predictive accuracy. Its speed and scalability make it particularly suited for large datasets and high-dimensional spaces. Histogram Gradient Boosting has shown excellent performance in clinical prediction tasks, including Zhu et al. (2020), which highlighted its ability to efficiently process ICU patient data.
- Random Forest, a robust ensemble learning method, builds multiple decision trees using bootstrapped datasets and random feature subsets. Its inherent feature selection and bagging process reduce the risk of overfitting, while its interpretability allows clinicians to understand model predictions. It has been extensively used in ICU patient outcome studies, achieving high sensitivity and specificity (Che et al., 2017).

The training pipeline followed a structured approach to evaluate these models' performance across multiple metrics. These metrics comprehensively assessed the models' diagnostic performance.

- Accuracy: Accuracy is the ratio of properly identified samples to the total number of samples. It's computed as:

$$\text{Accuracy} = \frac{(TP+TN)}{(TP+TN+FP+FN)}$$

- Sensitivity (Recall): Sensitivity, also known as recall, is the proportion of real positive samples that the model properly identifies. It’s provided by:

$$\text{Sensitivity} = \frac{(TP)}{(TP+FN)}$$

- Specificity refers to the fraction of real negative samples properly detected by the model. It's computed as:

$$\text{Specificity} = \frac{(TN)}{(TN+FP)}$$

Where TP, TN, FP, and FN represent true positives, true negatives, false positives, and false negatives, respectively.

- Area Under the Curve (AUC): The area under the receiver operating characteristic (ROC) curve, or AUC, relates the true positive rate (sensitivity) to the false positive rate (1 - specificity). A higher AUC implies improved model performance.

A 5-fold cross-validation scheme was employed to split the dataset into training and testing subsets. The dataset was partitioned into Train and Test sets for each fold (k = 1,2,...,5) . This method ensured reliable performance evaluation by mitigating overfitting and exposing the

models to varied data subsets.

The AUC score, representing the model's discriminatory power, was calculated for each fold and aggregated to report the mean AUC. For each fold, the true positive rate (TPR) and false positive rate (FPR) were calculated to construct ROC curves.

Results

The performance of the three selected models—XGBoost, Histogram Gradient Boosting, and Random Forest—was evaluated across five folds using metrics such as accuracy, AUC, sensitivity, specificity, PPV, and NPV. Below, we detail the findings for each model, highlighting their strengths and limitations in predicting Acute Myocardial Infarction (AMI) in ICU patients.

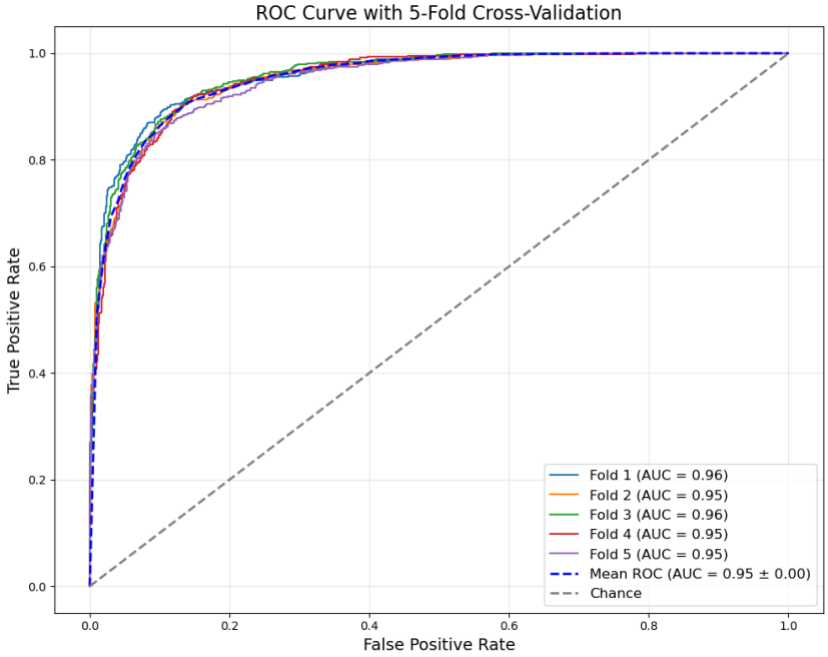

Figure 2: XGBoost Validation Results

	Fold	Accuracy	AUC	Sensitivity	Specificity	PPV	NPV
0	1	0.893526	0.957572	0.894118	0.892934	0.893162	0.893891
1	2	0.880685	0.952122	0.882227	0.879144	0.879402	0.881974
2	3	0.883833	0.957403	0.888651	0.879015	0.880170	0.887568
3	4	0.885974	0.952625	0.890792	0.881156	0.882291	0.889730
4	5	0.876874	0.948714	0.868308	0.885439	0.883442	0.870526

XGBoost demonstrated exceptional performance, achieving an AUC range of 0.95–0.96 across the five folds. The average AUC was 0.95, reflecting its robust discriminatory power between MI and non-MI cases. Other metrics also indicated balanced performance:

- Mean Accuracy: 0.8842
- Mean Sensitivity: 0.8848
- Mean Specificity: 0.8835
- Mean PPV: 0.8837
- Mean NPV: 0.8847

These results suggest that XGBoost is equally adept at identifying MI cases and ruling out non-MI cases. Its high PPV and NPV values indicate strong predictive reliability for both positive and negative classifications. This model's ability to consistently handle high-dimensional ICU data and missing values makes it a strong candidate for AMI prediction tasks.

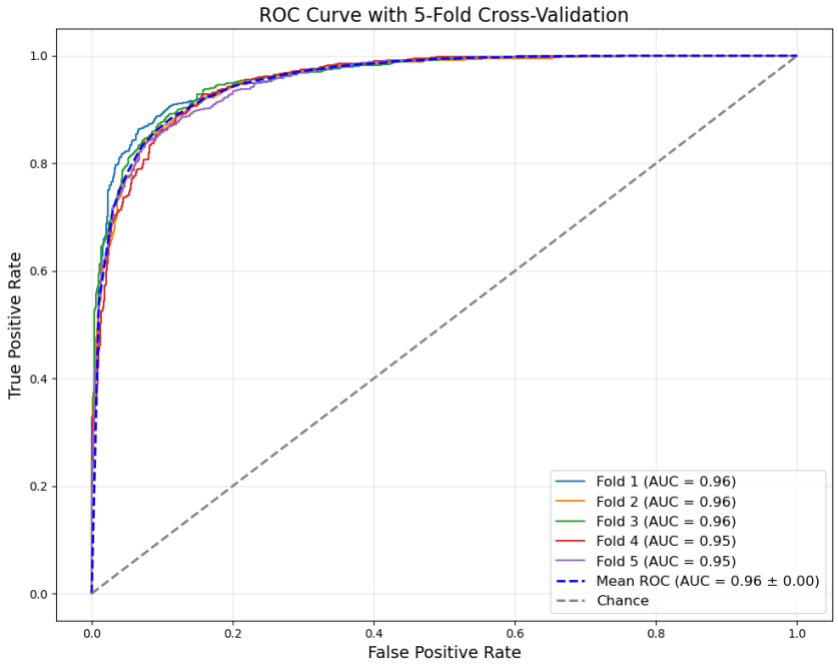

Figure 3: Histogram Gradient Boosting Validation Results

	Fold	Accuracy	AUC	Sensitivity	Specificity	PPV	NPV
0	1	0.896736	0.961150	0.898396	0.895075	0.895522	0.897959
1	2	0.883360	0.955471	0.883298	0.883422	0.883298	0.883422
2	3	0.888116	0.959531	0.898287	0.877944	0.880378	0.896175
3	4	0.879015	0.953931	0.870450	0.887580	0.885621	0.872632
4	5	0.879015	0.953881	0.869379	0.888651	0.886463	0.871849

Histogram Gradient Boosting also exhibited strong performance, with an AUC range of 0.95–0.96 across folds and a slightly higher average AUC of 0.96, outperforming XGBoost in terms of discriminatory power. Its metrics were as follows:

- Mean Accuracy: 0.8852
- Mean Sensitivity: 0.8840
- Mean Specificity: 0.8865
- Mean PPV: 0.8863
- Mean NPV: 0.8844

The model's higher specificity compared to XGBoost suggests a slight advantage in accurately ruling out non-MI cases. Histogram Gradient Boosting's computational efficiency and ability to handle large, complex datasets reinforce its applicability in clinical settings. Its performance closely parallels that of XGBoost, making both models nearly interchangeable for this task.

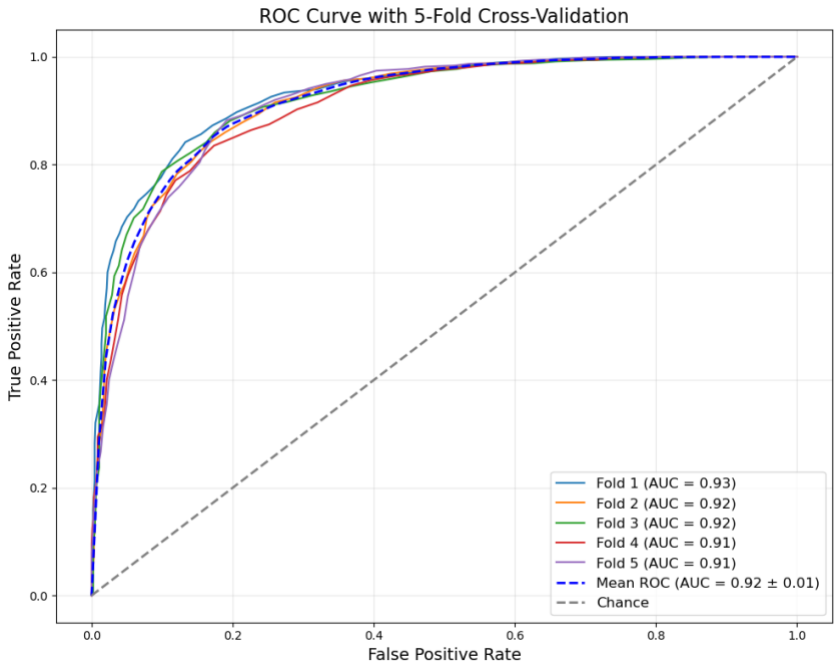

Figure 4: Random Forest Validation Results

	Fold	Accuracy	AUC	Sensitivity	Specificity	PPV	NPV
0	1	0.804708	0.930620	0.640642	0.968951	0.953822	0.729251
1	2	0.766185	0.916642	0.579229	0.952941	0.924786	0.693925
2	3	0.711991	0.920899	0.441113	0.982869	0.962617	0.637500
3	4	0.668630	0.908399	0.356531	0.980728	0.948718	0.603823

4 5 0.752141 0.914443 0.555675 0.948608 0.915344 0.681015

Random Forest, while performing well in specificity (mean of 0.9668) and PPV (mean of 0.9411), lagged behind the other two models in overall performance. The AUC ranged from 0.91–0.93, with an average AUC of 0.92, lower than that of XGBoost and Histogram Gradient Boosting. Other metrics included:

- Mean Accuracy: 0.7407
- Mean Sensitivity: 0.5146
- Mean NPV: 0.6691

The model's relatively low sensitivity (0.5146) indicates a limited ability to correctly identify MI cases, despite its strong performance in ruling out non-MI cases. This imbalance in performance suggests that Random Forest is less suitable for scenarios where the priority is to maximize true positive identification of MI cases. However, its high specificity and PPV may still make it valuable in confirming negative diagnoses.

Understanding the predictors driving model decisions is essential for interpreting machine learning outcomes in clinical settings. XGBoost’s feature importance ranking provides insight into the most influential variables contributing to the identification of Acute Myocardial Infarction (AMI) in ICU patients. Below, we analyze the top 20 features ranked by their importance scores, reflecting the relative contribution of each feature to the model’s predictive power.

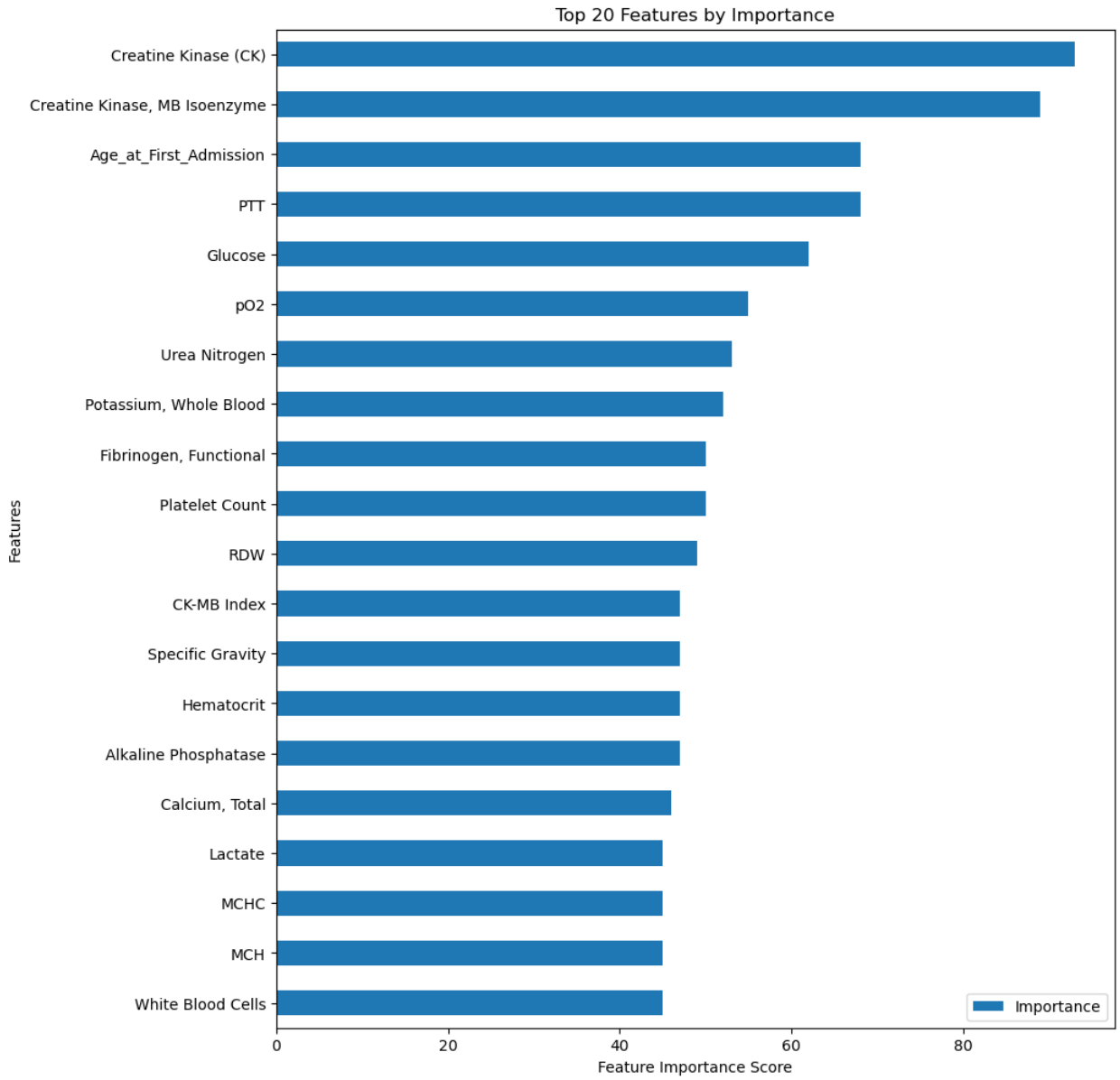

Figure 5: Top 20 Features by XGBoost Model

Conclusion

This project on early prediction of acute myocardial infarction (AMI) has demonstrated the effectiveness of advanced machine learning models, particularly XGBoost and Histogram Gradient Boosting, in predicting AMI risk. Both models outperformed Random Forest in terms of overall predictive ability, with Histogram Gradient Boosting achieving the highest Area Under the Curve (AUC) of 0.96, indicating superior discrimination between classes. Both XGBoost and Histogram Gradient Boosting exhibited nearly identical accuracy rates of approximately 0.88, showcasing its potential as a strong predictive tool. Random Forest, while demonstrating high specificity (0.97), struggled with limited sensitivity (0.51), undermining its utility in effectively detecting AMI cases.

From a clinical perspective, the results emphasize the need for careful model selection based on

the diagnostic priorities of healthcare providers. For tasks that require a balance between correctly identifying both AMI and non-AMI cases, XGBoost and Histogram Gradient Boosting are ideal. In settings where ruling out non-MI cases is critical, Histogram Gradient Boosting or Random Forest may offer significant value. Furthermore, these models offer valuable insights into the underlying factors contributing to AMI risk, such as key biomarkers like Creatine Kinase (CK), age, glucose levels, fibrinogen, and other clinical parameters. These factors provide a foundation for future research aimed at refining AMI prediction models and exploring new strategies for prevention and treatment optimization.

Looking ahead, future work could explore the potential of combining these models through ensemble methods to further enhance predictive performance. By incorporating multiple models, we could potentially improve overall accuracy and reliability, making early AMI prediction more robust and clinically actionable. There is still room to apply the LSTM deep learning model to the time series sequential data. However, tree-based and ensemble models also perform well in predicting the diagnosis, with less complexity in layers and computation. Additionally, XGBoost offers greater interpretability through feature importance extraction.

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