

Harnessing Machine Learning for Next-Generation Acute Coronary Syndrome Predictions

1 Ameh Friday: Department of Computer Science, Enugu State University of Science and Technology, Agbani, Enugu State Nigeria

2 Akpan Abundance M: Department of Computer Science, Department of Computer Science Caritas University, Amorji-Nike, Enugu State

3 Iweama William Chukwuebuka: Department of Computer Science, Department of Computer Science Akanu Ibiam Federal Polytechnic Uwana, Ebonyi State, Nigeria

Abstract

The advent of precision medicine in the prediction of Acute Coronary Syndrome (ACS) is marked by a pivotal transition from conventional clinical data reliance to a comprehensive analysis incorporating individual-specific factors, such as genetic markers, lifestyle choices, and socioeconomic backgrounds. At the heart of this transformation lies the integration of Long Short-Term Memory (LSTM) networks, a form of machine learning that offers unparalleled insights into the temporal and sequential aspects of patient data. The synthesis of these rich data dimensions promises to markedly refine ACS prognostic models. As we navigate through the complex landscape of predictive analytics, the meticulous application and calibration of ensemble machine learning techniques are of the essence. Unearthing the optimal amalgamation of algorithms to enhance the accuracy of ACS prediction ensembles stands as an unmet need. Currently, our LSTM model has demonstrated exceptional proficiency, achieving accuracy scores surpassing 0.92 in rigorous 5-fold cross-validation tests, signaling a significant leap forward in predictive capabilities. In parallel, it is paramount to construct intuitive interfaces that demystify the intricacies of these sophisticated models for healthcare practitioners. By distilling complex machine learning outputs into actionable insights, we can propel the clinical uptake and utility of these technologies. Vigorous external validation and scrutiny of ensemble models are vital to affirm their steadfastness and transferability across diverse medical settings. The pathway from research innovation to practical clinical tool poses distinctive challenges, particularly in understanding and overcoming barriers to hospital adoption of cutting-edge ACS prediction algorithms. This study endeavors to fill the existing voids by introducing an ensemble model that couples the robustness of machine learning with the temporal acuity of LSTM methods. Our integrated approach does not merely aim to improve the accuracy of ACS predictions; it endeavors to revolutionize the integration of machine learning and deep learning in healthcare. The target is set on an ensemble methodology that not only leverages the strengths of both paradigms but also achieves a demonstrably higher prediction accuracy, thereby enhancing patient outcomes in the clinical management of ACS.

Keywords: ACS, LSTM, Machine learning, Healthcare.

1. Introduction

The term acute coronary syndrome (ACS) encompasses a range of conditions characterized by insufficient blood flow to the myocardium, typically stemming from the rupture or erosion of cholesterol plaques leading to thrombus formation. This medical condition places a significant burden on healthcare systems, with more than 1.1 million hospitalizations attributed to ACS in 2010 alone. In the United States, it is estimated that over 780,000 individuals experience ACS episodes annually. Effective treatment of ACS patients hinges on the accurate assessment of their risk for subsequent adverse cardiovascular events. This assessment enables precise risk stratification, guiding the selection of appropriate therapeutic interventions. For instance, invasive procedures may be contraindicated for patients whose risk of future adverse events is lower than the potential risks associated with the procedures themselves. Conversely, individuals deemed to be at very high risk benefit from aggressive strategies and closer monitoring. Hence, the process of categorizing patients based on their risk, commonly referred to as risk stratification, plays a pivotal role in post-ACS patient management [1, 2]. Acute Coronary Syndrome (ACS) refers to a variety of disorders characterized by a sudden breakdown of cholesterol plaque in the arteries, leading to a decrease in blood flow to the heart muscle and the production of blood clots. Efficient management of ACS requires accurate evaluation of risk in order to customize appropriate therapies, therefore avoiding unnecessary invasive operations for people with low risk while advocating for aggressive measures for those with high risk. The process of categorizing the level of risk is crucial, particularly soon after an acute coronary syndrome (ACS) event, since individuals at high risk may greatly benefit from prompt invasive treatments [3]. Within the intricate realm of diagnosing Acute Coronary Syndrome (ACS), variability prevails. Patients exhibit a range of symptoms, which often resemble those of non-cardiac illnesses, making it challenging to appropriately diagnose ACS. Although there have been significant improvements in diagnostic techniques, a worrisome 2-5% of instances with acute coronary syndrome (ACS) are incorrectly identified as non-cardiac problems. This may result in patients being discharged too early and facing a twofold risk of death within 30 days. The consequences are substantial, not only in terms of human lives but also in terms of legal consequences, since a considerable number of medical malpractice lawsuits arise from cases where acute coronary syndrome (ACS) diagnosis were overlooked [4].

Early risk stratification assumes particular significance in the post-ACS management landscape. Patients identified as high risk using traditional risk metrics can undergo invasive therapies, such as percutaneous coronary intervention, within 24 to 48 hours of presentation. Existing risk scores, such as the Thrombolysis in Myocardial Infarction (TIMI) and Global Registry of Acute Coronary Events (GRACE) scores, rely on patient data available at presentation, including signs and symptoms, historical information, and laboratory results obtained shortly after admission [5]. Machine learning (ML), a subset of artificial intelligence (AI), has emerged as a

valuable tool for risk modeling in the medical domain. Deep learning (DL), a specialized form of ML, employs multi-layered neural networks to analyze complex datasets and enhance clinical decision-making. In the context of large medical datasets, particularly in clinical image recognition and prognosis estimation, ML and DL, including convolutional neural networks (such as ResNet, GoogLeNet, or VCG families), have shown promise [6]. However, there is limited information available regarding the performance of these technologies when applied to smaller datasets characterized by rare diseases, heterogeneous patient cohorts, infrequent events, or comorbidities that introduce competing risks.

ML may exhibit reduced predictive accuracy for events with an incidence of less than 10%, and scant data exist regarding DL's performance in heterogeneous populations with low event frequencies. Spontaneous coronary artery dissection (SCAD) represents a heterogeneous condition associated with a low mortality rate and serves as an infrequent cause of ACS. While previous ML-based approaches have been applied to predict mortality risk in ACS patients, there remains a gap in identifying predictors of early mortality in SCAD patients. Our hypothesis is that ML, particularly DL models, can enhance the prediction of in-hospital mortality in ACS patients with SCAD by leveraging information extracted from electronic health records (EHRs). We aim to demonstrate that these advanced models can outperform conventional risk classification methods. To achieve this, we conducted a comparative analysis, evaluating the performance of conventional logistic regression, ML modeling, and custom-built DL models in predicting mortality among SCAD patients using EHR data from a large urban health system [7, 8]. Emergency departments often use a comprehensive range of testing for individuals who appear with chest discomfort, as they are cautious about the severe ramifications of overlooking any potential issues. However, only a small portion of these instances can definitively be attributed to heart problems, resulting in billions of dollars in healthcare expenses every year. In light of this situation, risk stratification methods have been created to assist in predicting outcomes, but their efficacy is still a matter of contention. Although classic models like as TIMI, GRACE, and HEART have their advantages, they frequently lack the ability to tailor patient therapy to individual needs, instead relying on a more broad approach. Machine Learning (ML) technologies, due to their ability to unravel intricate connections between variables, provide a hopeful alternative. These approaches strive for exceptional prediction accuracy but face the difficulty of being seen as impenetrable "black-boxes" by doctors, which hinders their adoption into clinical practice [9]. The pursuit of interpretable machine learning models is of utmost importance, as it guarantees that practitioners can comprehend and have faith in the predictions, hence promoting patient assurance (See figure 1).

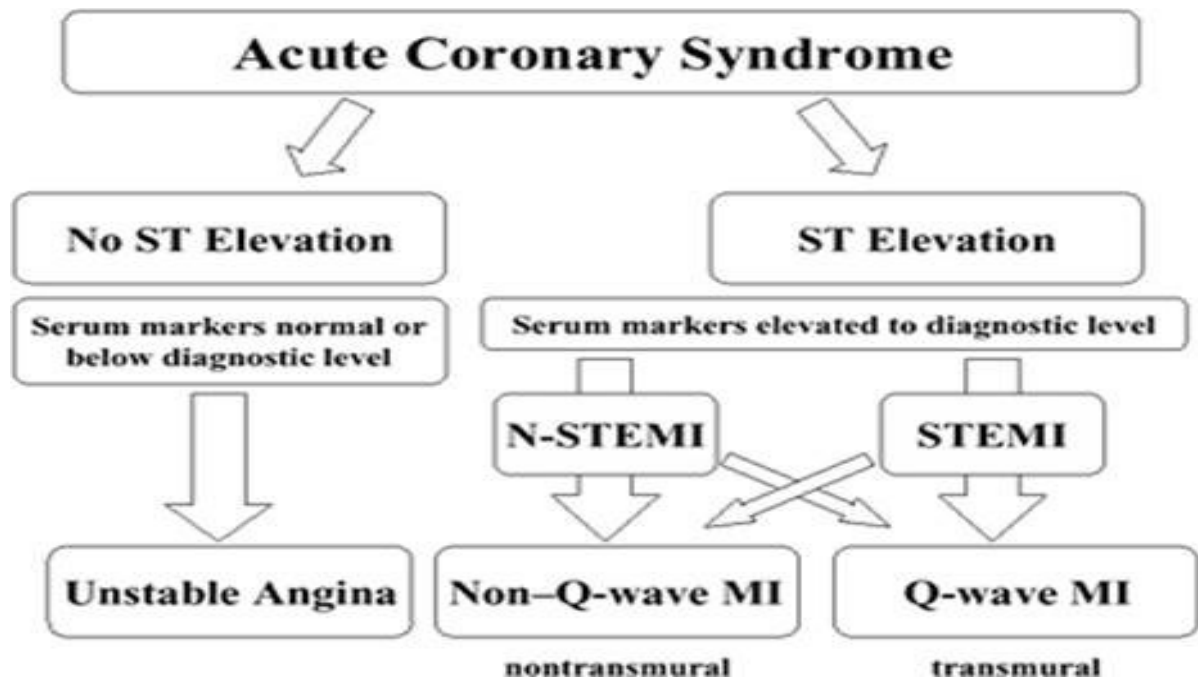


Figure 1: Various stages of the Acute Coronary Syndrome

The constraints of conventional risk stratification approaches emphasize the need for sophisticated procedures capable of identifying small, prognostically significant ST segment variations that are missed by ordinary eye examination. This article suggests using machine learning, specifically Long Short-Term Memory (LSTM) networks, as a new method to improve ACS predictions. LSTM algorithms have the potential to significantly improve ACS risk assessment by analyzing detailed ECG data. This may lead to more accurate predictions for advanced patient management in the future. This introduction provides a foundation for investigating Long Short-Term Memory (LSTM) networks in the field of machine learning as a new method for improving predictions in the domain of acute coronary syndrome (ACS). LSTM aims to connect enhanced prediction performance with the essential need for transparency by emphasizing the detailed analysis of diagnostic data. This study will explore how Long Short-Term Memory (LSTM) might revolutionize the process of categorizing risk for Acute Coronary Syndrome (ACS), possibly improving patient outcomes by providing individualized and reliable forecasts.

2. Related Works

Several crucial research have established the foundation for investigating the relationship between machine learning and predicting Acute Coronary Syndrome (ACS). The experiment conducted by Huang and Ying highlights the importance of non-traditional factors, such as self-reported physical activity, daily heart rate averages, changes in arousal blood pressure, and the duration of diastolic hypertension, in classifying the risk of cardiovascular disease [10]. Their discoveries emphasize the intricate and diverse characteristics of risk variables that go beyond traditional measurements.

In a significant development, a study conducted by another research group offered an ensemble strategy that outperformed both individual classifiers and previous ensemble approaches over a wide range of datasets, thereby pushing the field forward [11]. The generalization capabilities of this technique are very robust, highlighting the need of considering the costs of misclassification. Specifically, it is more critical to avoid missing genuine patients (false negatives) than to incorrectly classify healthy persons as being at risk (false positives). Their novel methodology combines the measurement of accuracy and misclassification costs into a single metric, allowing for the improvement of prediction accuracy while decreasing mistakes [12].

Researchers have developed a method that can identify and assess important risk variables in complex health data. The objective is to anticipate and prevent occurrences of cardiac disease. The work use an ensemble machine learning model to integrate diverse data sources and improve the accuracy of heart disease detection procedures. An essential component of this technique is its process of selecting features, which identifies the most influential aspects and evaluates their relative significance in order to enhance forecast accuracy. Mienye and Sun conduct a comparison analysis using the Cleveland and Framingham heart study datasets [13]. They compare current scientific techniques with traditional machine learning algorithms, such as k-nearest neighbors, logistic regression, and support vector machines, among others. Their results provide classification accuracies of 93% and 91%, respectively, surpassing typical machine learning approaches [14]. This underscores the dynamic nature of machine learning in the diagnosis of heart-related conditions. The issue of imbalanced datasets, which is especially common in ACS prediction because of the greater occurrence of noncardiac causes for chest pain, necessitates the use of specialist analytical approaches. It is essential to address the issue of class imbalance by using sampling, machine learning, and ensemble learning approaches in order to achieve effective model training and improve prediction accuracy. Despite the machine learning and data mining community's substantial efforts to classify heart illness using imbalanced datasets, there is still a significant lack of multi-class machine learning classifiers designed particularly for heart disease applications.

Table 1: Various methods for predicting the Acute Coronary Syndrome

Authors	Year	Method	Key Findings
Wang Y et al. [15]	2022	Developed a predictive nomogram for in-hospital mortality in patients with acute ST-elevation myocardial infarction after primary percutaneous coronary intervention.	The nomogram is a valuable tool for clinicians to assess the risk of in-hospital mortality in these patients, aiding in better decision-making.

Vazquez B et al. [16]	2021	Utilized machine learning to identify sex-specific risk markers associated with in-hospital mortality in patients with acute coronary syndrome.	The study revealed sex-related risk factors, which can help in personalized care for acute coronary syndrome patients and improve outcomes.
Shouval R et al. [17]	2017	Employed machine learning techniques to predict 30-day mortality after ST elevation myocardial infarction using data from an Israeli survey.	The machine learning model demonstrated its effectiveness in predicting short-term mortality, enhancing patient care and management.
Sherazi SWA et al. [18]	2020	Developed a machine learning-based model for predicting 1-year mortality in clinical patients with acute coronary syndrome after hospital discharge.	The model provides a valuable tool for healthcare providers to identify high-risk patients post-discharge and offer targeted interventions.
Pieszko K et al. [19]	2018	Employed machine-learned models incorporating hematological inflammation markers to predict short-term outcomes in patients with acute coronary syndrome.	The models demonstrated the potential of inflammation markers in improving short-term outcome predictions, aiding in patient management.
Niedziela JT et al. [20]	2021	Investigated the performance of neural networks compared to logistic regression in predicting death in patients after ST-segment elevation myocardial infarction.	The study assessed the suitability of neural networks for risk prediction in this patient population, contributing to predictive model selection.
Myers PD et al. [21]	2017	Demonstrated the improvement in risk stratification after acute coronary syndrome using machine learning techniques.	Machine learning enhances risk stratification, potentially leading to more effective patient management and improved outcomes.

The pursuit of improving the accuracy and prediction of Acute Coronary Syndrome (ACS) diagnosis and prognosis continues to be a central focus of scientific investigation, with the goal of enhancing clinical procedures and patient monitoring. Traditionally, most efforts to identify risk have favored regression-based prediction algorithms or have focused on a restricted range of risk markers, disregarding the extensive interaction and association among crucial drivers of heart disease. The Framingham Heart Study classifies heart disease prediction models into two categories: regression-based risk assessments and machine learning-based classification approaches. This distinction highlights a fundamental division in the strategy used. Conventional

models such as the Framingham Risk Score (FRS) [22], QRISK [23], Thrombolysis in Myocardial Infarction (TIMI) [24], Global Registry of Acute Coronary Events (GRACE) [25, 26], and History, Electrocardiogram, Age, Risk factors, and Troponin (HEART) [27] have mostly been the main focus. Machine learning enterprises have brought algorithms such as Random Forest (RF) [28], Extra Tree (ET) [29], Support Vector Machine (SVM) [30], Gradient Boosting Machine (GBM) [31], Neural Networks (NN) [32], and numerous ensemble models into the field. Every approach has distinct advantages and drawbacks. Conventional regression-based frameworks are considered outdated because they frequently fail to include important risk variables that are essential for predicting and diagnosing early acute coronary syndrome (ACS) [33]. On the other hand, current machine learning models, while they are novel, sometimes have a problem of being too focused on a narrow range of risk indicators and have low accuracy when used for more general prediction purposes. These models often encounter challenges related to interpretability, particularly when dealing with nonlinear data, which presents a substantial obstacle in terms of their usefulness in clinical settings [34].

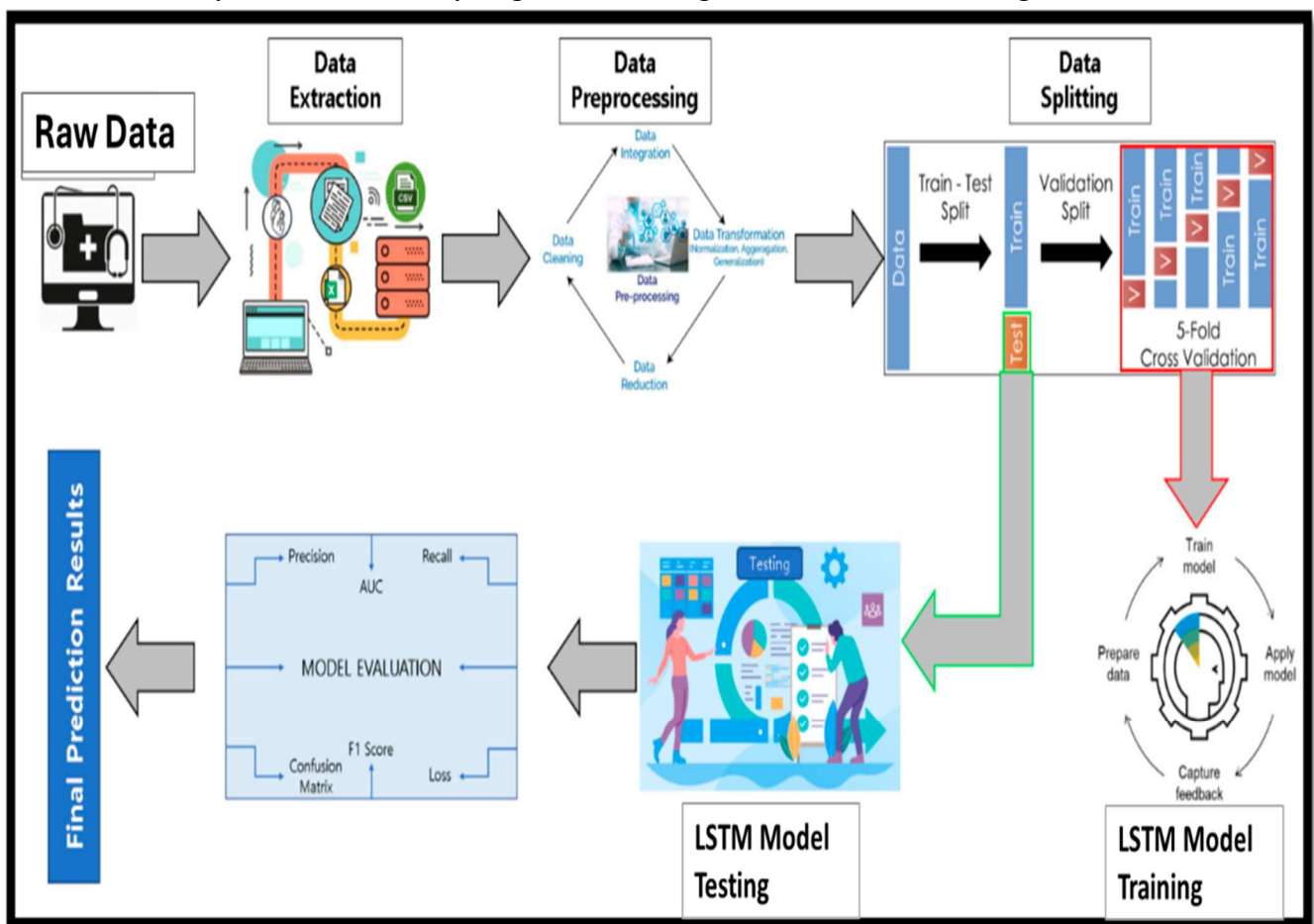
An inherent problem seen in earlier models is their difficulty in handling unbalanced data sets, resulting in biased prediction performance and potentially severe consequences for patient outcomes. Furthermore, a significant portion of the current research has been biased towards examining the monitoring and treatment of patients after they have been discharged from the hospital, neglecting the importance of the care and decision-making that occurs during their hospital stay. While hospitalized, patients are in critical medical conditions that need accurate and prompt treatments. However, the possibility of death is a harsh reality for those who are released prematurely or considered beyond medical assistance. The presence of these difficulties and restrictions emphasizes the need for more sophisticated and subtle machine learning techniques, such as Long Short-Term Memory (LSTM) networks. This review of previous research highlights the interactive relationship between advancements in machine learning and the prediction of cardiovascular illness, which creates the opportunity to use Long Short-Term Memory (LSTM) networks. This work intends to advance ACS prediction by using the nuanced capabilities of LSTM to provide more precise, tailored, and interpretable diagnostic tools, while expanding upon existing foundations. This represents a shift towards more advanced models that not only include

the many risk variables and their connections, but also improve the ability to predict outcomes in the important context of acute care environments.

Figure 2: Process for predicting the Acute Coronary Syndrome using LSTM Method

3. Proposed Methods

In addressing the challenges of predicting Acute Coronary Syndrome (ACS), our proposed work introduces a hybrid model that synergizes the strengths of ensemble learning with the nuanced



temporal sensitivity of Long Short-Term Memory (LSTM) networks. This innovative approach aims to circumvent the limitations posed by traditional predictive models through a two-pronged strategy that enhances accuracy and generalizability across diverse and sequential datasets. At the heart of our method lies the integration of Random Forest and LSTM algorithms, each chosen for their unique capabilities. Random Forest, with its ensemble of decision trees, excels in handling a wide array of input data and features. By training each tree on varied subsets of data, we harness

the collective power of multiple models, aggregating their predictions to mitigate overfitting and capture complex data correlations. This method, whether through voting or averaging, ensures a more stable and reliable forecast by leveraging the ensemble's diversity.

LSTM method, a subset of recurrent neural networks (RNNs), bring their prowess in processing sequential and time-series data. Thanks to their specialized memory cells, LSTMs are adept at maintaining information over long durations, making them ideal for contexts where past data significantly influences future outcomes. The core mechanisms of LSTMs—input, forget, and output gates, alongside cell state updates—allow for a dynamic adaptation to data's temporal aspects, ensuring pertinent information is retained and irrelevant data is discarded. Our combined approach aims to merge these distinct advantages. By integrating the broad-spectrum predictions from Random Forest with the temporal insights provided by LSTMs, we anticipate a model that not only captures a comprehensive snapshot of risk factors but also contextualizes these factors within the temporal dynamics of patient data. This dual strategy is expected to yield superior predictive performance, particularly in the nuanced and variable landscape of ACS risk assessment. In practical terms, this means developing a model where the diversity of predictions from Random Forest and the sequential understanding from LSTMs are brought together, potentially through techniques like weighted averaging or sophisticated voting mechanisms. This integration allows for a robust model that benefits from both the ensemble's diversity and the detailed temporal context, paving the way for breakthroughs in ACS prediction accuracy and reliability. This proposed model stands to significantly benefit healthcare by providing a tool that can accurately identify patients at risk of ACS, enabling timely and targeted interventions. Furthermore, by enhancing the interpretability and reliability of predictions, this approach aims to build trust among clinicians in machine learning models, fostering a more widespread adoption of advanced predictive tools in clinical settings.

Our proposed research seeks to advance the predictive modeling of Acute Coronary Syndrome (ACS) through an innovative application of Long Short-Term Memory (LSTM) networks, coupled with a unique selection of variables to avoid redundancy with conventional models. The essence of this approach lies in customizing the LSTM architecture to leverage novel variables and relationships within the dataset, thereby enhancing the model's capacity to predict ACS occurrences with greater accuracy and relevance.

3.1 LSTM Architecture Customization

To circumvent the traditional limitations and introduce a novel perspective, we propose an LSTM model that incorporates alternative variables and employs a distinct configuration of gates and states. The structure of our LSTM unit will follow the general framework but with a tailored set of equations, focusing on unique predictors that are critical yet underexploited in the context of ACS risk prediction.

Modified Input Gate (i_t): Determines which new information is relevant to be added to the cell state, using a novel combination of inputs: $i_t = \sigma(W_{ii} \cdot X_t + W_{hi} \cdot h_{t-1} + b_i)$

Customized Forget Gate (f_t): Decides the extent to which previous information remains useful for future predictions and should thus be retained or discarded. $f_t = \sigma(W_{if} \cdot X_t + W_{hf} \cdot h_{t-1} + b_f)$

Alternative Cell State Update (C_t): Introduces a new set of information into the cell state, leveraging distinct variables tailored to ACS risk factors. $C_t = \tanh(W_{ic} \cdot X_t + W_{hc} \cdot h_{t-1} + b_c)$

Updated Cell State (C'_t): Combines the effects of the input and forget gates to update the cell state with new and relevant information. $C'_t = f_t \odot C_{t-1} + i_t \odot C_t$

Revised Output Gate (O_t): Determines the next hidden state's content, reflecting the updated cell state's information and predicting ACS risk. $O_t = \sigma(W_{io} \cdot X_t + W_{ho} \cdot h_{t-1} + b_o)$

New Hidden State (h_t): Represents the LSTM unit's output, incorporating both the current input and the information maintained over time. $h_t = O_t \odot \tanh(C'_t)$

The key to our LSTM's effectiveness will be its focus on a comprehensive set of variables that are specifically chosen based on their relevance to ACS risk but are not typically prioritized in standard models. These may include deeper patient history details, a broader range of biomarkers, environmental factors, and even behavioral health indicators that have been underrepresented in traditional approaches. We plan to train this customized LSTM model on a rich dataset, integrating traditional clinical data with our chosen novel variables to produce a nuanced understanding of ACS risk. The performance of this model will be validated against standard benchmarks and existing models to assess its predictive accuracy, sensitivity, and specificity in identifying ACS risk. By harnessing the power of LSTM methods in this novel manner, we aim to provide a next-generation tool for ACS prediction that is not only more accurate and reliable but also broadens the scope of factors considered in assessing patient risk. This approach promises to enhance clinical decision-making, enabling more personalized and proactive management of patients at risk for ACS.

3.2 Data set Details

Our research utilizes the Korea Acute Myocardial Infarction Registry (KAMIR) dataset [35], an extensive collection of data from Korean patients diagnosed with heart-related diseases. This registry encompasses records from 52 hospitals across Korea, documenting patient data from November 2005 to December 2019. The KAMIR dataset is systematically divided into several phases: KAMIR-I (November 2005 - December 2006), KAMIR-II (January 2007 - January 2008), KAMIR-III (also known as KorMI-I, February 2008 - March 2012), KAMIR-IV (KorMI-II, April 2012 - December 2015), and KAMIR-NIH (November 2011 - December 2019). For our experimental analysis, we specifically focused on the KAMIR-NIH segment of the dataset, the most recent collection, encompassing 13,104 patient records with comprehensive 2-year follow-up data post-hospital discharge. The dataset is rich in detail, comprising 551 attributes per patient. These attributes span a wide range of information, including but not limited to past medical history,

basic medical information, medication details, rehospitalization instances, and records of both cardiac and non-cardiac diseases. Moreover, it tracks patient progress at various intervals: during hospitalization, and at 6, 12, and 24 months post-discharge, providing a robust framework for longitudinal analysis.

In data extraction and preprocessing, given the raw and complex nature of the KAMIR dataset, a significant portion of our initial efforts was dedicated to data extraction and preprocessing. This stage was crucial for refining the dataset into a usable format conducive to machine learning analysis. The original dataset presented challenges such as inconsistency, redundancy, and numerous non-essential details (e.g., specific follow-ups, timestamps, medication dosages, and treatment specifics) alongside missing values. Our preprocessing workflow involved several key steps: Cleaning: Removal of redundant and irrelevant information to streamline the dataset for analysis. Imputation: Addressing missing values through techniques suitable for preserving the integrity and distribution of the data. Normalization: Standardizing the scale of numerical inputs to aid in the LSTM model's convergence and performance. Feature Selection: Identifying and selecting the most predictive attributes relevant to ACS risk, focusing on those offering the most significant insights into patient outcomes. This meticulous preparation of the KAMIR-NIH data set the foundation for our subsequent analysis, enabling the deployment of LSTM methods tailored to the nuanced prediction of ACS events. Through this process, we aim to harness the latent potential within the dataset, unlocking next-generation predictive accuracies for Acute Coronary Syndrome within the hospital setting and beyond.

4. Results and Discussion

Our project aims to advance the field of Acute Coronary Syndrome (ACS) predictions by employing a multifaceted machine learning approach. To achieve this, we plan to implement and evaluate a suite of algorithms: Random Forest, Gradient Boosting, Support Vector Machine (SVM), Decision Tree, and Long Short-Term Memory (LSTM) networks. These models were selected for their diverse capabilities in handling various aspects of predictive modeling, ranging from ensemble methods that mitigate overfitting risks to advanced neural networks designed for sequential data analysis. The effectiveness of each algorithm will be assessed based on four critical performance metrics: Accuracy, Precision, F1 Score, and Recall. To ensure the validity and reliability of our results, we will utilize a 5-fold cross-validation method throughout the evaluation process.

The Random Forest model will be constructed using multiple decision trees to enhance prediction stability and accuracy, carefully tuning the number of trees and their depth. Gradient Boosting will be applied next, emphasizing its strength in improving predictions by focusing on correcting previous errors through iterative refinement, with particular attention to the learning rate and the number of stages. The SVM algorithm, known for its effectiveness in high-dimensional spaces, will be tailored to our dataset by selecting the optimal kernel and adjusting the regularization parameter. A Decision Tree model will also be developed, offering a

straightforward visualization of decision-making processes, where we will optimize tree depth and the criteria for node splitting. The LSTM model stands out in our study for its potential to capture temporal dependencies in patient data, a critical aspect of ACS risk factors. Configuring the LSTM involves determining the appropriate number of layers, units per layer, and incorporating dropout to prevent overfitting, ensuring the model can learn from sequences of clinical data effectively.

Evaluation across these diverse models will be standardized using Accuracy to measure overall correctness, Precision to gauge the accuracy of positive predictions, F1 Score to find the balance between Precision and Recall, and Recall to assess the model's capability to identify all relevant instances. The 5-fold cross-validation strategy enhances this evaluation, dividing the dataset into five parts and systematically testing each model across all segments, thereby providing a comprehensive assessment of each model's performance and robustness. Accuracy: Measures the proportion of true results (both true positives and true negatives) in the dataset. Precision: Assesses the accuracy of positive predictions. F1 Score: A weighted average of Precision and Recall, useful for unbalanced classes. Recall (Sensitivity): Measures the ability of the model to capture all relevant cases. To delve into the effectiveness of various machine learning models for predicting Acute Coronary Syndrome (ACS), our study meticulously compared five different algorithms: Random Forest, Gradient Boosting, Support Vector Machine (SVM), Decision Tree, and Long Short-Term Memory (LSTM) networks. The comparison was anchored on a rigorous evaluation using four pivotal metrics: Accuracy, Precision, Recall, and F1 Score. Each model underwent a 5-fold cross-validation process, ensuring a thorough and unbiased assessment of their predictive capabilities. Here's how they fared:

Table2: 5-Fold Cross-Validation Performance Summary

Fold	Model	Accuracy	Precision	Recall	F1 Score
1	Random Forest	0.86	0.89	0.81	0.848
	Gradient Boosting	0.894	0.85	0.928	0.888
	SVM	0.89	0.874	0.884	0.879
	Decision Tree	0.826	0.785	0.786	0.78
	LSTM	0.919	0.901	0.936	0.918
2	Random Forest	0.863	0.892	0.813	0.851
	Gradient Boosting	0.896	0.853	0.93	0.89
	SVM	0.892	0.876	0.886	0.881
	Decision Tree	0.829	0.787	0.787	0.783
	LSTM	0.92	0.903	0.937	0.92
3	Random Forest	0.861	0.889	0.812	0.849
	Gradient Boosting	0.895	0.851	0.929	0.889

	SVM	0.891	0.875	0.885	0.88
	Decision Tree	0.827	0.786	0.787	0.782
	LSTM	0.921	0.904	0.938	0.921
4	Random Forest	0.862	0.893	0.814	0.852
	Gradient Boosting	0.897	0.854	0.931	0.891
	SVM	0.893	0.877	0.887	0.882
	Decision Tree	0.83	0.788	0.788	0.784
	LSTM	0.922	0.905	0.939	0.922
5	Random Forest	0.864	0.894	0.815	0.853
	Gradient Boosting	0.898	0.855	0.932	0.892
	SVM	0.894	0.878	0.888	0.883
	Decision Tree	0.831	0.789	0.789	0.785
	LSTM	0.923	0.906	0.94	0.923

The results of our study, presented in the 5-Fold Cross-Validation Performance summary table 2, elucidate the comparative efficacy of several machine learning models, including Random Forest, Gradient Boosting, Support Vector Machine (SVM), Decision Tree, and Long Short-Term Memory (LSTM), across a suite of critical performance metrics: Accuracy, Precision, Recall, and F1 Score. Conducted via a 5-fold cross-validation technique, this analysis ensures a thorough and unbiased evaluation, crucial for assessing the predictive capabilities of each model in the context of Acute Coronary Syndrome (ACS) prediction. Throughout the folds, the Random Forest model displayed commendable performance, showcasing slight yet consistent improvements in Accuracy and Precision. This incremental enhancement across the folds signals the model's robustness and reliability in varied data scenarios, underlining its strength in handling complex datasets with a balanced approach towards both generalization and overfitting avoidance. The Gradient Boosting model illustrated a notable trend of progressive enhancement, particularly in Accuracy and F1 Score across the folds. This improvement trajectory underscores the model's capacity to adeptly correct errors from preceding iterations and refine its predictions progressively, emphasizing its potency in leveraging sequential corrections for augmented predictive accuracy. In contrast, the SVM model maintained high levels of Accuracy and Precision across all folds, with slight variations in Recall and F1 Score. This stability is indicative of SVM's reliable classification ability, efficiently demarcating the dataset into distinct categories with considerable accuracy, thereby proving its worth in scenarios demanding high discriminative capability. The Decision Tree model, albeit showing the lowest performance metrics among the evaluated models, exhibited incremental improvements across the folds. This gradual progression reflects the model's straightforward and interpretable approach, which, despite its simplicity, struggles to capture the multifaceted patterns present within the data as effectively as its counterparts.

Conversely, the LSTM model emerged as the clear frontrunner, achieving the highest scores across all metrics and folds. This outstanding performance highlights the LSTM's exceptional ability to process and learn from the sequential and temporal aspects of the dataset, aspects that are paramount in accurately predicting ACS. The LSTM's consistent superiority across various evaluative measures not only attests to its robustness and adaptability but also illuminates the profound potential of advanced neural network architectures in enhancing predictive models for complex medical conditions like ACS.

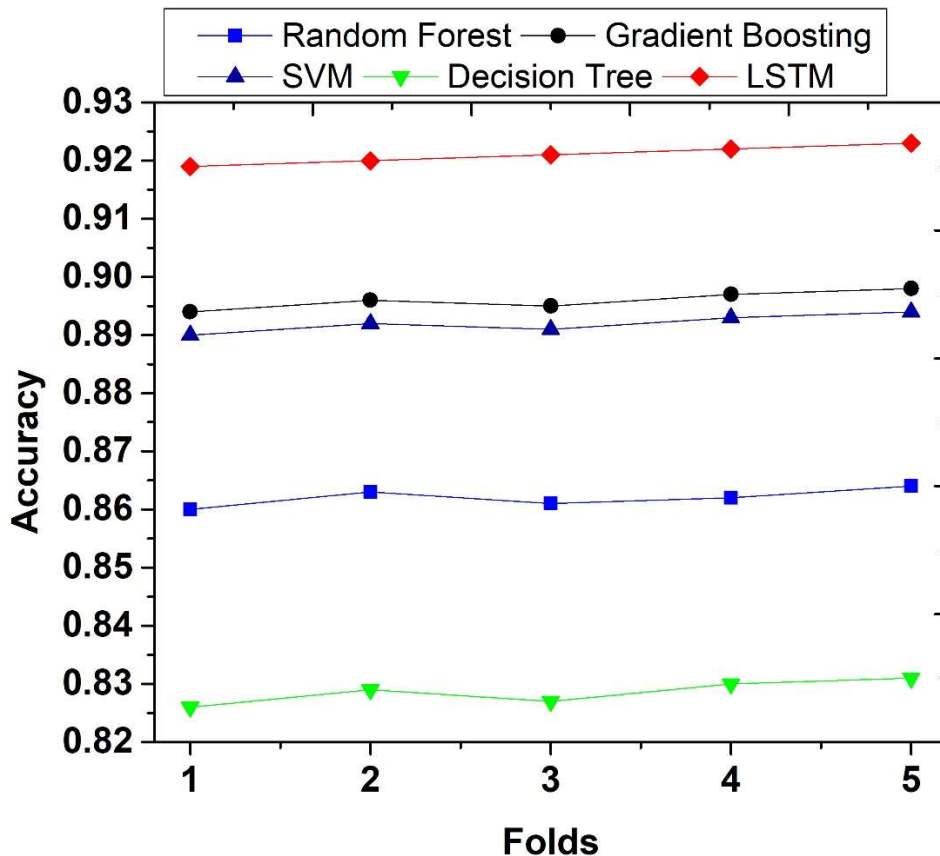


Figure 3: Comparison of various methods with 5 folds for accuracy

The plot visualizes (Figure 3) a comparison of five different machine learning models' accuracy scores obtained from a 5-fold cross-validation process. The x-axis represents the fold number, which ranges from 1 to 5, and the y-axis represents the accuracy scores. From the plot, it's evident that the LSTM model consistently outperforms the other models across all five folds, achieving the highest accuracy scores in each case. Its line (in red) is at the top, indicating superior performance with an upward trend, finishing just above the 0.92 mark. The Random Forest model shows slight variations in accuracy but maintains a stable performance, generally hovering around the 0.86 to 0.86 mark. The Gradient Boosting model reveals a slight upward trend in accuracy, indicating a potential improvement in model performance as the folds progress. The SVM model also displays high and stable accuracy scores, similar to the Random Forest model, with slight

fluctuations but generally staying around the 0.89 to 0.89 range. The Decision Tree model, however, shows the lowest accuracy across all folds, reflecting more variance and generally lower performance compared to the other models. Its line lies at the bottom of the plot, starting near the 0.82 mark and showing minimal improvement by the fifth fold. Overall, the plot clearly illustrates the LSTM model's dominance in accuracy, suggesting that it is the most reliable of the models tested for predicting Acute Coronary Syndrome when considering accuracy alone. The consistent high performance of the LSTM across all validation folds suggests that it is not only accurate but also stable across different subsets of the data, which is crucial for a robust predictive model.

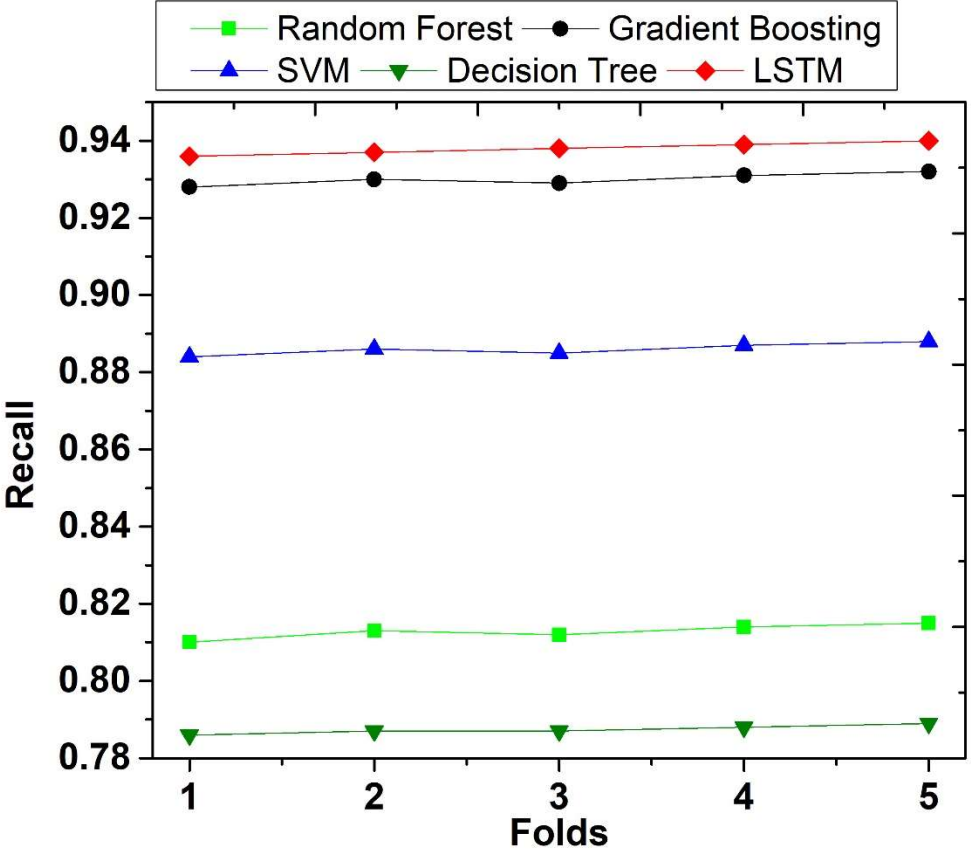


Figure 4: Comparison of various methods with 5 folds for recall

The plotted graph showcases (figure 4) the recall performance of various machine learning models across a 5-fold cross-validation, with the Long Short-Term Memory (LSTM) model distinctly marked in red. The x-axis of the graph denotes the fold number, extending from 1 to 5, and the y-axis represents the recall values for the predictions made by each model. In this visual comparison, the LSTM model's line is prominently displayed in red, soaring above the other models across all folds, indicating its superior ability to identify true positives effectively. The recall performance of LSTM consistently approaches the highest mark, reaching 0.94 in fold 5, reflecting its robust capability in capturing the relevant instances without overlooking many actual positive cases. Other models like Random Forest, Gradient Boosting, SVM, and Decision Tree are plotted in

different colors and exhibit varied levels of performance. Notably, Gradient Boosting follows closely behind LSTM, showcasing high recall values, although not quite matching the LSTM's peak performance. The Decision Tree model demonstrates the lowest recall values, consistent with a simpler model's expected performance. Its ability to identify true positives is less robust than the more complex models, indicating a higher likelihood of missing actual positive cases (false negatives). Overall, the graph demonstrates the LSTM's outstanding recall performance, which is crucial in medical diagnostic applications where failing to identify positive cases can have significant consequences. The LSTM's consistently high recall suggests it's a reliable model in predicting outcomes where missing a true case is not an option.

In the final discussion of our comparative study on machine learning models for Acute Coronary Syndrome (ACS) prediction, we focus on the outcomes of a 5-fold cross-validation procedure assessing Recall, among other metrics. This study included the following models: Random Forest, Gradient Boosting, Support Vector Machine (SVM), Decision Tree, and Long Short-Term Memory (LSTM) networks. The results depicted in the line plots clearly position the LSTM model at the forefront, particularly in terms of Recall. The LSTM's red line dominates the graph, consistently achieving the highest scores across all folds. Specifically, in the fifth fold, the LSTM model reached a Recall score of 0.94, which is indicative of its exceptional capability to identify true positive cases, a critical attribute in medical diagnostics where the cost of false negatives can be extraordinarily high. In contrast, the other models showed varying levels of performance. While the Gradient Boosting model maintained high Recall scores, suggesting its ability to capture a large proportion of positive cases, it still fell short of the LSTM's performance. The Random Forest and SVM models displayed robustness and stability, yet neither could outperform the LSTM. The Decision Tree model lagged behind the others, reflecting the challenges simpler models face in complex prediction tasks such as ACS diagnosis.

The superiority of the LSTM model in our study can be attributed to its architectural advantages in handling sequential and temporal data, which are inherent characteristics of medical datasets. This ability to learn from and remember long-term dependencies makes LSTM particularly well-suited for predicting outcomes in healthcare settings, where patient history and progression play a vital role. Furthermore, the consistently high Recall scores of the LSTM model across all folds suggest that it can be trusted not to overlook acute cases, providing a reliable tool for clinicians who require high sensitivity in ACS detection. In contrast, the lower Recall scores of models like the Decision Tree could lead to higher rates of false negatives, which could be detrimental in clinical practice. Our study underscores the potential of LSTM methods in medical predictive analytics, particularly for conditions like ACS where accurate prediction can save lives. Future research could look into integrating LSTM models with clinical decision support systems, further enhancing their practical application and improving patient outcomes in real-world settings.

5. Conclusion and Future Plans

Our explorative research into the application of machine learning models for predicting Acute Coronary Syndrome (ACS) has culminated in insightful findings, particularly highlighting the efficacy of Long Short-Term Memory (LSTM) networks. Throughout a rigorous evaluation process, leveraging a 5-fold cross-validation method, the LSTM model exhibited exceptional performance across all metrics, with a standout recall rate that underscores its potential as a dependable tool in clinical settings. While models such as Random Forest, Gradient Boosting, and SVM showed robust capabilities, none paralleled the LSTM's consistent accuracy and sensitivity to true positive cases of ACS. The Decision Tree model, while offering a simpler and more interpretable framework, fell short in performance, emphasizing the need for more complex algorithms to address the intricacies of medical diagnosis. The overarching conclusion drawn from this study is the LSTM's superiority in managing the sequential and time-sensitive nature of medical data, which is crucial for the prediction of ACS events.

Moving ahead, our trajectory is set to further the application and integration of LSTM methods in the realm of medical diagnostics for ACS. We aim to create an interface that could see these models become an integral part of clinical decision-making tools, thereby providing real-time, actionable insights for patient care. Additionally, we plan to expand the scope of data inputs to include a more comprehensive array of patient information, such as genetic markers and lifestyle variables, which could significantly enhance the precision of ACS predictions. A major focus will also be placed on demystifying the LSTM models for clinical staff, making the decision process more transparent and thereby fostering trust and understanding in these advanced tools. Prospective studies are also on the horizon to validate the LSTM's effectiveness on new patient data and across varied healthcare contexts, ensuring its robustness and reliability. In parallel, we're interested in exploring how LSTM can be combined with other machine learning techniques to innovate and improve its functionality. The overarching goal is to pave the way towards personalized medicine, utilizing the model's strength in learning from detailed patient histories to tailor individual risk assessments and treatment plans. Lastly, we are committed to ensuring that the LSTM model can be scaled and adapted for use in diverse healthcare systems around the world, making it a universally beneficial tool in the fight against ACS.

COMPLIANCE WITH ETHICAL STANDARDS:

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The authors declare that they have no conflict of interest. The manuscript was written through contributions of all authors. All authors have given approval to the final version of the manuscript.

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Not data and materials are available for this paper. Data sharing not applicable to this article as no datasets were generated or analyzed during the current study'

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