

Risk Factors and Prediction of ST-segment Elevation Myocardial Infarction

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Abstract

Studies have shown that the mortality rate due to ST-segment elevation myocardial infarction (STEMI) has drastically increased in developed and developing countries. The purpose of this study is to develop a diagnostic support tool to help classify STEMI patients and validate the predictive risk factors associated with STEMI using an ensemble learning approach. In this retrospective data-mining study, the data are retrieved from electronic health records of an urban emergency department between January 2017 and August 2020. A Random Forest model is trained to classify non-acute coronary syndrome (non-ACS) etiologies and STEMI patients using 38 features. Of the study cohort, 411 patients with chest pain fulfilled inclusion criteria, of whom 225 (55%) are STEMI, and 186 (45%) are non-ACS etiologies patients. The proposed framework successfully classifies the non-ACS etiologies and STEMI patients with recall and area under the receiver operating characteristic (AUROC) values of 73% and 90%, respectively.

Keywords

Acute coronary syndrome, ST-segment Elevation Myocardial Infarction, Prediction, BorutaShap, and Machine Learning.

1 Introduction

Cardiovascular disease (CVD) is a group of illnesses that comprise both heart and blood vessels (Mendis *et al.* 2011), including coronary heart disease (CHD) and coronary artery disease (CAD), and acute coronary syndrome (ACS). Although health professionals often use the terms CAD and ACS interchangeably with CHD, they are not equivalent. ACS is a subcategory of CAD, while CHD is an outcome of CAD. ACS typically comprise three manifestations of

ischemic heart disease (Danish 2016) – (i) ST-segment elevation myocardial infarction (STEMI), (ii) Non-ST-segment elevation myocardial infarction (NSTEMI), and (iii) Unstable angina (UA).

STEMI, usually resulting from thrombotic obstruction of a coronary artery, is a fatal cardiovascular emergency requiring early diagnosis and rapid reperfusion therapy. Clinical trial and registry data have shown that individuals with STEMI, and its counterpart NSTEMI, have differing short-term prognoses and responses to treatments (Cox *et al.* 2006; Abbott *et al.* 2007). Given the aging US population and the growing populace burden of obesity and diabetes, the attributes of hospitalization for acute myocardial infarction (AMI) patients have changed during recent years (Mokdad *et al.* 2001; Floyd *et al.* 2009). According to (Garoufalidis *et al.* 1998), the frequency of AMI used to be as low as 2–6% but has increased in recent times due to the increased predominance of risk factors for CAD, such as earlier onset glucose resistance and obesity, in adolescence (Sinha *et al.* 2002). Early acknowledgment and risk factor modification are crucial to mitigating AMI's risk (Jamil *et al.* 2013).

The existing predictive models for mortality prediction following STEMI comprise the Thrombolysis in Myocardial Infarction (TIMI) score and the Global Registry of Acute Cardiac Events (GRACE) scores. These scores permit risk stratification, identification of high-risk patients, and appropriate treatment (Fox *et al.* 2006; Addala *et al.* 2004; Morrow *et al.* 2000). However, these predictive models are based on a conventional statistical approach which conveys inherent limitations, conceivably impeding performance (Breiman 2001; Shouval *et al.* 2014). In current practice, standard statistical methods for prediction depend on parametric regression methods. However, progressions in Computer Science, particularly in machine learning (ML), allow for the development of complex predictive models exposed to risk factors. ML techniques like the random forest, neural network, and support vector machines have been presented in epidemiologic studies for predictive analytics (Peng *et al.* 2010; Kruppa *et al.* 2012; Gurm *et al.* 2013). This study aims to develop a diagnostic support tool to help classify STEMI patients and validate the predictive risk factors associated with STEMI using an ensemble learning approach.

The rest of the paper proceeds as follows. After reviewing related literature in section 2, we propose a dynamic decision support tool in section 3. We then presented our findings from our results and gave insights in section 4. Finally, section 5 includes concluding remarks.

2 Literature Review

Machine learning (ML) is a technique of data analysis that automates logical model building. Utilizing algorithms that iteratively learn from data, ML permits computers to discover hidden insights without being expressly programmed about where to look. Thus, ML offers an alternative methodology for the development of prediction models. ML is scientific research standing at the convergence of statistics and computer science, relying on proficient computing algorithms. The significance of ML has been perceived through the difficulties of building statistical models from massive data sets, which required computational strategies (Deo 2015). ML may detect the intricate and non-linear interactions between variables by limiting the error between predicted and observed outcomes (Karthik *et al.* 2014).

Data mining (DM) utilizes ML algorithms for knowledge discovery and predictive modeling in massive datasets (Shouval *et al.* 2014; Deo 2015). DM applications are continuously entering clinical use in everyday medicine and cardiology (Arsanjani *et al.* 2015; Gurm *et al.* 2014; Hsich *et al.* 2011; Shouval *et al.* 2015). As opposed to the standard statistical approach, ML does not begin with a pre-defined model; instead, it allows the data to develop the model by identifying underlying patterns.

DM is significant for various kinds of issues. Predicting a reliant variable from the implications of independent variables is one of the utilizations of this technique. Healthcare is one of the fields with big data accessible freely from various sources, and DM could be the best way to handle it. As per the Centers for Disease Control and Prevention (CDC), 647,457 people died of coronary illness in the US as of (2017) [Source: CDC, National Center for Health Statistics]. One reason for casualty due to heart disease is that risks are either not classified or distinguished distinctly later. In the present circumstance, ML could be the best way to deal with this issue and forecast at the beginning phase.

Several ML methods have effectively been applied for prediction. A portion of the methods utilized for such prediction problems is support vector machines (SVM), neural networks, decision trees, regression, and naive Bayes classifiers. SVM was perceived as the best predictor and precision, followed by neural networks with improved accuracy, and decision trees introduced a diminished accuracy. Chest pain, age, smoking, hypertension, and diabetes were estimated

to be the risk factors of heart disease (Latha and Jeeva 2019). Studies on DM techniques for CAD prediction uncover that neural networks, decision trees, and naive bayes are instrumental in predicting coronary illness.

Scott *et al.* (2002) examined the estimations and quality checking of care for patients with acute coronary syndromes. Massad *et al.* (2008) assessed the present state of the art of logical applications in clinical diagnosis. Quteishat and Lim (2008), in their paper, examined the intelligent DM techniques like min-max neural networks to medical diagnosis. They also chose real-life clinical records from which suspected ACS patients, mainly STEMI, are gathered and utilized for their analysis. Although, the utilization of DM when tackling the issue of forecasting in-hospital outcomes in ACS has not been investigated broadly in the existing literature (Velicki *et al.* 2014; Mihajlović *et al.* 2011).

3 Methods

The primary purpose of this research is to propose a framework capable of classifying STEMI and non-ACS etiologies in the emergency department (ED) and recognizing the leading risk factors contributing to this classification. The proposed framework is built on three phases. The first phase, data preprocessing, comprises feature engineering (i.e., cleaning the data, data imputation, and standardization). The second phase, feature selection, reduces the dimension of the dataset by identifying the most suitable features. The final phase, model training, and evaluation starts with 10-fold cross-validation to provide a robust evaluation of the performance for the trained model (i.e., Random Forest) based on metrics such as the AUROC, recall, precision, F1-score, and accuracy. Figure 1 below depicts the architecture of the proposed framework.

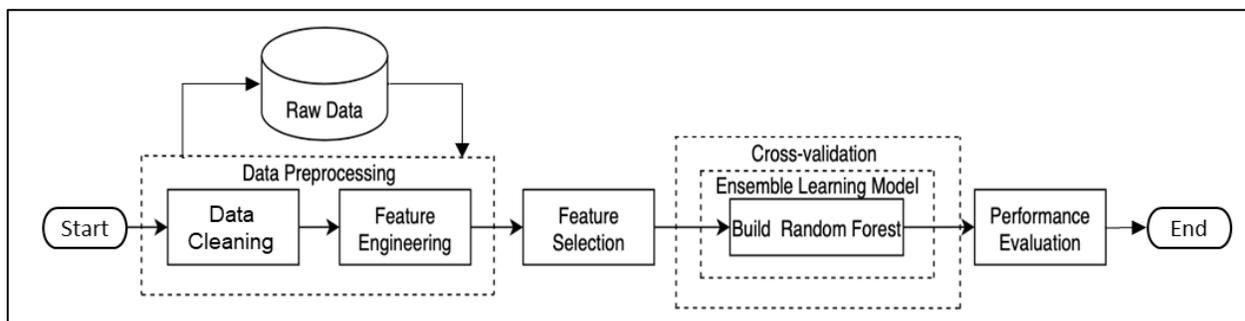


Figure 1: Architecture of proposed framework

3.1 Data Collection

The data used for the study analysis is extracted from the electronic health record (EHR) made available by Henry Ford Health Systems. A total of 411 patients with chest pain were selected for this study, of which 225 (55%) had STEMI and 186 (45%) had non-ACS etiologies of chest pain. 38 variables are selected after a broad literature search and following discussions with medical experts. Then, all available features, including demographic and clinical factors, are retrieved from the EHRs.

3.2 Data Preprocessing

This includes two main steps: i) data cleaning and ii) feature engineering

3.2.1 Data Cleaning

Data cleaning eliminates incorrect, corrupted, incorrectly formatted, duplicate, or incomplete data within a dataset. The following stages are performed during our analysis. (i) *Eliminating redundant data*: missing data values and inconsistencies can negatively impact the integrity of the dataset; redundant data points are dropped. (ii) *Data imputation*: this is achieved through the use Multiple Imputations by Chained Equations (MICE) approach (Schafer and Graham 2002). MICE is a robust, informative method of handling missing data in datasets. The approach addresses the issue of missing data in a dataset through an iterative series of predictive models.

3.2.2 Feature Engineering

This process includes using space information to extricate variables from a dataset. The following stage is performed during our analysis. (i) *One-hot encoding*: to supplant encoded categorical features with recently created binary factors.

3.3 Feature Selection

Feature Selection is the way toward diminishing features to those contributing the most to the output (Shaikh 2018). To distinguish the features with the most commitment in boosting the performance of a classification algorithm, BorutaShap (Keany 2020) is introduced. BorutaShap is a wrapper feature selection technique that merges the Boruta feature selection algorithm with SHAP (SHapely Additive exPlanations). SHAP links game theory with local explanations to create the only consistent and accurate explainer. From an exceptionally high level, SHAP analyses the average marginal contributions for each feature across all permutations at a local level. As this method is additive, the average value of these marginal contributions can then accomplish global feature importance. Furthermore, since most feature selection methods are biased towards continuous or categorical data, BorutaShap becomes suitable for this type of problem. It takes care of this limitation; thus, leading to our implementation in this study.

3.4 Ensemble Model

In statistics and ML, ensemble methods utilize several learning algorithms to acquire better predictive performance than any constituent learning algorithms alone (Maclin and Opitz 2011; Rokach 2010). In contrast to a statistical ensemble in statistical mechanics, which is usually endless, an ML ensemble comprises only a particular finite set of alternative models. Notwithstanding, it ordinarily permits a considerably more flexible structure to exist among those other options. The classifier utilized stated in the proposed framework is Random Forest. Random forests or random decision forests are ensemble learning techniques for classification and regression problems. A random forest is operated by building many decision trees at training time and outputting the class that is the mode of classification or regression of the individual trees (Ho 1995, 1998). In addition, random decision forests correct for decision trees' propensity for overfitting to their training set (Hastie *et al.* 2001).

4 Results and Discussion

4.1 Descriptive Statistics

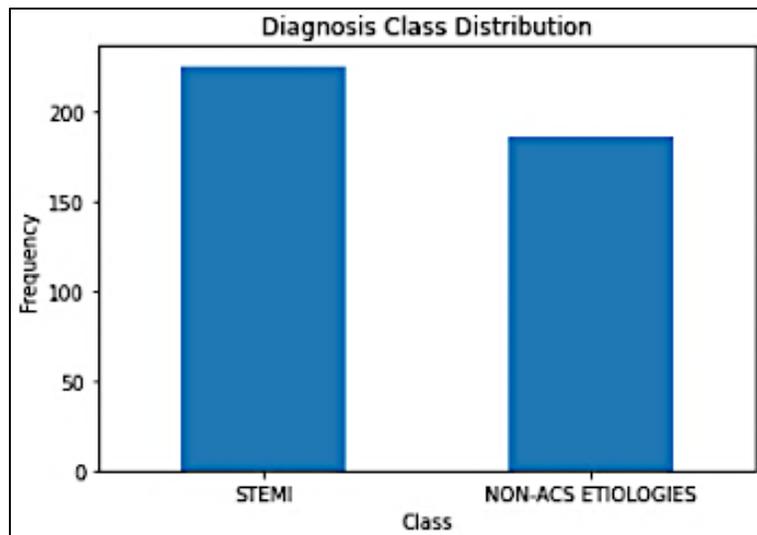


Figure 2: Diagnosis class distribution

Table 1 shows the characteristics baseline of patients with STEMI and non-ACS, where all measurable tests are two-tailed at a significant level of 5%. The mean age of the patient groups is 60.43 ± 12.71 and 50.83 ± 16.61 years for STEMI and non-ACS etiologies, respectively. The ratio of female patients seems to be lower in STEMI (38%) compared to non-ACS (46%). Furthermore, dominance of coronary artery disease (69% vs 24%), chronic heart failure (28% vs 24%), chronic heart disease (29% vs 24%), cardiovascular disease (56% vs 39%), hypertension (78% vs

55%), heart attack (69% vs 12%), and diabetes (37% vs 25%) are observed in STEMI patients. Figure 2 shows the diagnosis class distribution.

Table 1: Baseline characteristics of selected variables

<i>Variables</i>		<i>STEMI</i>	<i>Non-ACS</i>	<i>p-value</i>
<i>Demographic</i>	<i>Age (years)</i>	60.43±12.71	50.83±16.61	<0.001
<i>Sex</i>	<i>Female</i>	0.38	0.46	0.126
	<i>Male</i>	0.62	0.54	
<i>Ethnicity</i>	<i>Decline</i>	0.02	0.03	0.127
	<i>Do not know</i>	0.06	0.02	
	<i>Hispanic/Latino</i>	0.04	0.04	
	<i>Not Hispanic/Latino</i>	0.88	0.91	
<i>Comorbidities</i>	<i>Abdominal aortic aneurysm</i>	0.00	0.02	N/A
	<i>Atrial fibrillation</i>	0.09	0.10	0.470
	<i>Alcoholism</i>	0.09	0.12	0.165
	<i>Anemia</i>	0.13	0.29	<0.001
	<i>Asthma</i>	0.06	0.21	<0.001
	<i>Breast cancer</i>	0.02	0.02	0.995
	<i>CAD</i>	0.69	0.24	<0.001
	<i>CHF</i>	0.28	0.24	0.521
	<i>CHD</i>	0.29	0.24	0.376
	<i>Chronic liver disease</i>	0.07	0.10	0.325
	<i>Chronic lung disease</i>	0.16	0.32	<0.001
	<i>CKD</i>	0.26	0.32	0.106
	<i>COPD</i>	0.11	0.21	0.005
	<i>CVD</i>	0.56	0.39	0.008
	<i>Diabetes</i>	0.37	0.25	0.024
	<i>Type-2 diabetes</i>	0.38	0.25	0.019
	<i>Hypertension</i>	0.78	0.55	<0.001
	<i>History of hemoglobinopathies</i>	0.00	0.02	0.158
	<i>History of hypertension</i>	0.78	0.55	<0.001
	<i>Lipid disorder</i>	0.00	0.00	N/A
	<i>Nephrotic syndrome</i>	0.00	0.00	N/A
	<i>Noncardiac atherosclerosis</i>	0.00	0.00	0.997
	<i>Peripheral vascular disease</i>	0.08	0.04	0.164
<i>Heart attack</i>	0.69	0.12	<0.001	
<i>Liver disease</i>	0.00	0.00	N/A	
<i>CAD risk factors</i>	0.00	0.00	N/A	
<i>Obesity</i>	0.22	0.21	0.818	
<i>Vital Signs</i>	<i>SBP</i>	140.31±32.82	137.38±25.56	0.446
	<i>DBP</i>	85.22±22.25	79.65±18.82	0.014
	<i>HR</i>	84.74±21.63	87.83±17.70	0.022
	<i>Temperature</i>	97.77±1.32	98.23±0.59	<0.001
	<i>RR</i>	19.63±4.94	18.10±2.42	0.004
	<i>Oxygen saturation</i>	97.82±2.84	97.68±7.41	0.936

4.2 Feature Engineering

After performing one-hot encoding on our dataset, we had a total of 75 features. This is due to the method producing vectors with lengths equal to the number of categories in the data set. We can see this increase from 38 to 75 features, as illustrated in Figure 3.

4.3 Feature Selection

Figure 3 displays the output values from the feature selection algorithm, BorutaShap, where the green, yellow, and red bars symbolize accepted, uncertain, and rejected features, respectively. A total of 11 variables, including age, anemia, cardiovascular disease, chest pain, chronic lung disease, chronic obstructive pulmonary disease, coronary artery disease, diastolic blood pressure, heart attack, systolic blood pressure, and temperature level, are reported as significantly contributing.

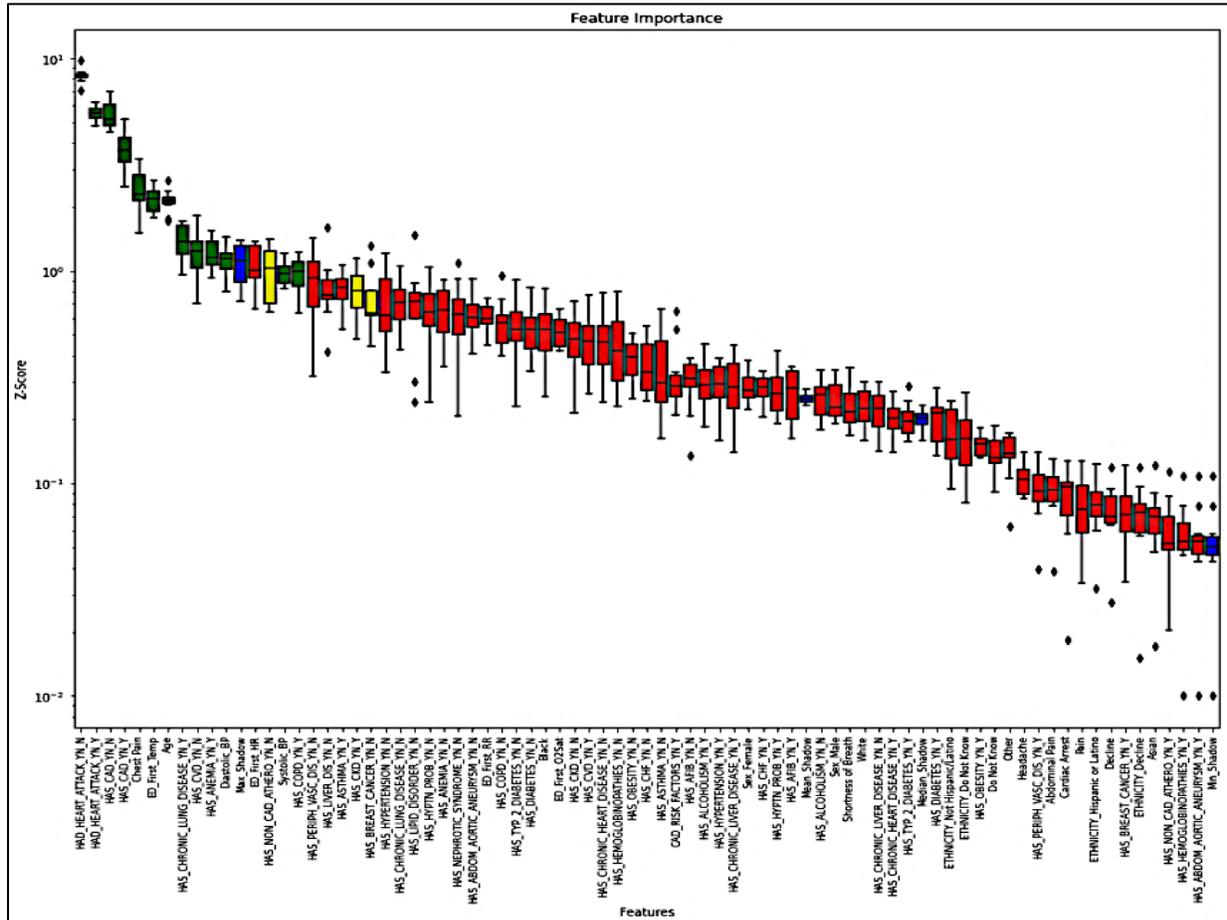


Figure 3: Selection of potential variables by BorutaShap

4.4 Model Performance

Given the impacts of the features on the performance of the random forest model, the features recommended by the BorutaShap algorithm are compared to eleven random selections of features. The performances of the classification model based on different sets of features are presented in Figure 4. As displayed in Figure 4, the features suggested by BorutaShap are indeed the most significant. Furthermore, Table 2 fully illustrates the evaluation criteria for each feature subset.

Table 2: Evaluation criteria for the feature subsets

<i>Feature Subsets</i>	<i>Accuracy (%)</i>	<i>Precision (%)</i>	<i>Recall (%)</i>	<i>F1-score (%)</i>	<i>AUC (%)</i>
<i>BorutaShap Subset</i>	82	83	73	82	90
<i>Subset 1</i>	62	58	63	63	70
<i>Subset 2</i>	61	59	60	62	66
<i>Subset 3</i>	67	70	54	66	72
<i>Subset 4</i>	56	52	53	57	59

<i>Subset 5</i>	56	73	7	42	53
<i>Subset 6</i>	64	60	61	64	68
<i>Subset 7</i>	77	74	78	77	83
<i>Subset 8</i>	75	72	71	74	81
<i>Subset 9</i>	65	62	61	65	72
<i>Subset 10</i>	68	65	67	69	74
<i>Subset 11</i>	65	63	62	65	71

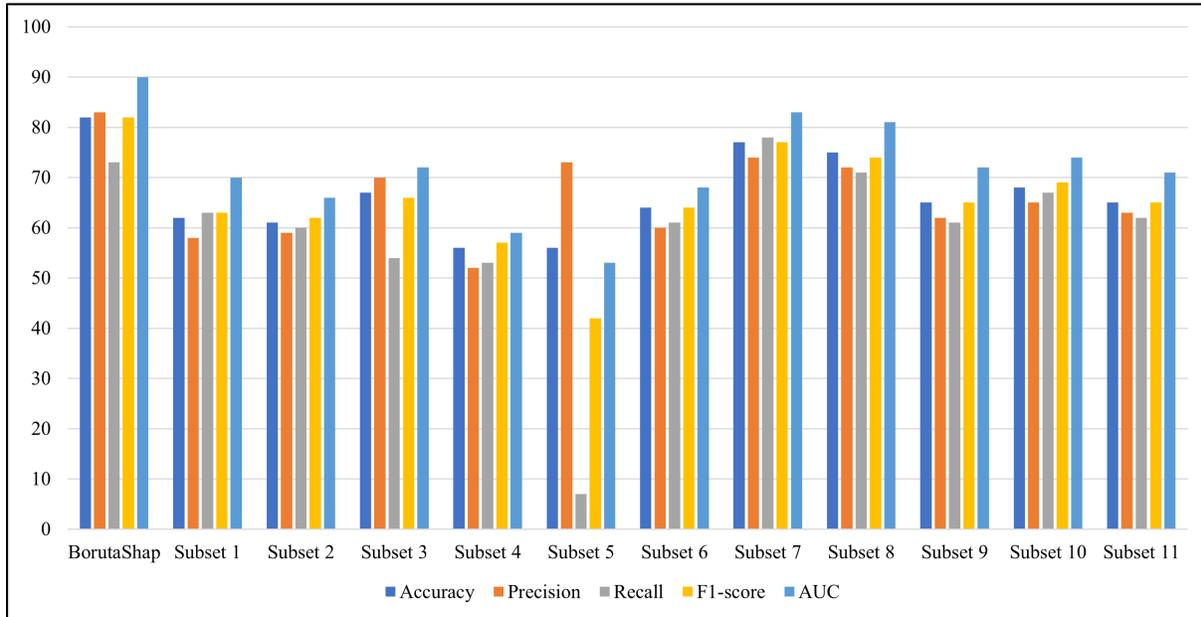


Figure 4: Bar chart comparing the ensemble learning methods

The BorutaShap selected features outperformed other features based on all the evaluation criteria from our proposed approach. The BorutaShap selected features have accuracy, precision, recall, F1-score, and AUROC values of 82%, 83%, 73%, 82, and 90%, respectively. Therefore, the AUROC curve for BorutaShap selected features is illustrated below in Figure 5.

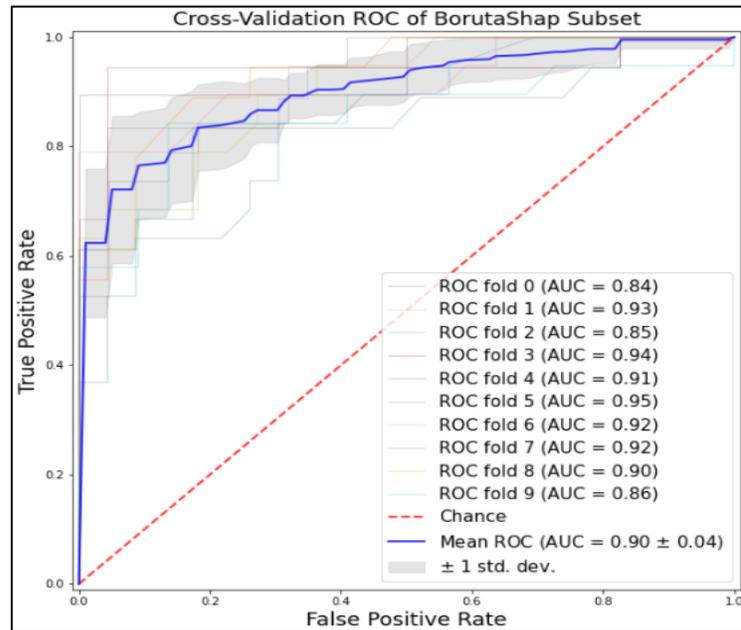


Figure 5: ROC for Random Forest on the BorutaShap selected features

The feature selection process in our current study merged data-driven systems and domain knowledge ensuing comprehensive clinical variables. From prior related works, several risk factors, such as age, coronary artery disease, cardiovascular disease, are exceptionally connected with STEMI. This result correlates well with 8 out of 11 features selected being clinically understood as typical risk factors of STEMI. This study also showed that having a history of heart attack is a strong indicator of STEMI cases. Prior related works have demonstrated that advanced age is associated with more significant morbidity than younger patients (Zorbozan *et al.* 2018). Additionally, anemia, chest pain, chronic lung disease, chronic obstructive pulmonary disease, and systolic blood pressure were regarded as strong indicators of STEMI case prediction (Bailey *et al.* 2003; Goedemans *et al.* 2020; Granot *et al.* 2019). Furthermore, diastolic blood pressure and temperature were also distinguished as indicators, showing their influence on the disease spectrum.

Our findings show that ML can effectively help diagnose patients with STEMI from non-ACS etiologies given clinical information. Not only can the proposed framework classify these diseases with high accuracy, but it can also detect the leading features that essentially add to the classification process. Though our proposed framework shows high accuracy, and AUROC scores, the combination of the physicians' remarks may further improve the performance of our proposed framework. What's more, the proposed framework has not been implemented in actual clinical practice yet, but the potential variables identified would probably update clinical dynamics and improve the well-being of the designated patients.

5 Conclusion

Our findings support our proposed model to distinguish the significant variables and diagnose STEMI and non-ACS with high accuracy. With these features identified, it will enhance treatment decisions for STEMI patients requiring medical intervention. Physicians will not only have to rely on electrocardiogram readings, but with the inclusion of the selected variables, they may enhance decision-making in evaluating ACS. Future analysis may also be enhanced by considering more extensive free-text data in the EHR, as it could aid in uncovering hidden patterns and improve our predictive performance.

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