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RESEARCH ARTICLE

Machine Learning-Based Acute Myocardial Infarction Detection from 12-Lead ECG: Model Development and Validation

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Abstract: ***Background:*** Acute Myocardial Infarction (AMI) remains a major cause of morbidity and mortality worldwide. Early and accurate diagnosis is critical to implementing timely treatment strategies and improving patient outcomes. Traditional ECG interpretation can be time-consuming and prone to human error, highlighting the need for automated diagnostic solutions. This study aims to develop and evaluate a machine learning-based system for the automated detection of AMI using 12-lead Electrocardiogram (ECG) recordings obtained from real-world hospital data. ***Methods:*** A observational study was conducted using ECG data collected from hospital. The study focuses on leveraging machine learning algorithms to differentiate between normal and AMI-affected ECGs. The proposed system includes a robust signal preprocessing pipeline capable of extracting clean, one-dimensional ECG signals from images or PDF files. Feature extraction techniques were applied to the preprocessed signals, followed by classification using an ensemble machine learning model. The ensemble integrates Support Vector Machine (SVM), K-Nearest Neighbors (KNN), Random Forest (RF), Gaussian Naive Bayes (GNB), and Logistic Regression. Performance metrics, including accuracy, sensitivity, and specificity, were calculated to evaluate the model. ***Results:*** The ensemble model achieved an average classification accuracy of 80%. Notably, the model demonstrated high sensitivity in detecting myocardial infarction, achieving a sensitivity rate of 96%, while also effectively identifying normal ECG cases. ***Conclusion:*** The findings suggest that machine learning can significantly enhance the rapid and accurate diagnosis of AMI, supporting clinical decision-making and potentially improving patient outcomes. The proposed system demonstrates promise for integration into real-world healthcare settings, offering automated and reliable ECG analysis.

Keywords: Acute Myocardial Infarction, ECG, Machine Learning, Signal Processing, Ensemble Learning, Diagnostic Aid.

INTRODUCTION

Acute Myocardial Infarction (AMI), commonly known as a heart attack, occurs due to prolonged obstruction of blood flow to a portion of the heart, leading to tissue injury or myocardial cell death [1]. The 12-lead Electrocardiogram (ECG) is a fundamental, non-invasive diagnostic tool for AMI, capturing the heart's electrical activity and providing essential insights into its physiological condition. Nevertheless, accurate ECG interpretation requires a high level of expertise and is often complicated by subtle variations, individual differences, and the large volume of clinically relevant recordings. These complexities can lead to diagnostic delays or misinterpretations, negatively impacting patient care and management [2,3,4]. The advent of machine learning (ML) presents new opportunities for the automated and intelligent interpretation of complex medical data, including ECGs. ML algorithms are capable of recognizing patterns and correlations in ECG signals that human analysts may overlook, thereby improving diagnostic accuracy and efficiency [4,5,6,7]. While numerous studies have explored ML-based methodologies for ECG analysis, a substantial demand remains for robust models empirically validated against real clinical data, particularly those that address the complexities of signal acquisition and variability [8,9,10]. This study details the development and validation of a machine learning-based system for detecting AMI from 12-lead ECGs. Our approach emphasizes a comprehensive signal preprocessing pipeline that efficiently manages raw ECG data, often presented in PDF or image formats, in conjunction with a sophisticated ensemble learning model. We evaluate the performance of the proposed model using metrics crucial for medical diagnosis, with a particular focus on its accuracy in identifying cases of myocardial infarction.

MATERIAL AND METHODS

2.1. Dataset

The present study utilized a real hospital dataset that included 12-lead electrocardiogram (ECG) recordings. To ensure reproducibility and generalizability, a comprehensive description of patient demographics, along with the distribution of myocardial infarction (MI) and normal case instances, is essential. Specifically, the dataset incorporated 120 ECG recordings designated for training purposes, with an additional 40 recordings allocated for validation and another 40 for testing within both the normal and MI classifications. This approach guarantees that model development and evaluation are conducted using a clinically representative and balanced dataset. All ECG recordings were provided in PDF or image format, necessitating the application of advanced image processing techniques.

Ethical Approval and informed consent : The study was conducted in accordance with the principles of the Declaration of Helsinki. Ethical approval for the use of hospital ECG data was obtained from the Institutional Ethics Committee under reference number 102/01/2025. All patient data were anonymized prior to analysis to ensure confidentiality and privacy. Written informed consent was obtained from all participants or their legal guardians prior to inclusion in the study.

2.2. Signal Preprocessing Techniques

The raw electrocardiogram (ECG) data, often saved in PDF or image format, necessitated a multi-stage pre-processing pipeline to produce clean and quantifiable one-dimensional signals. This pipeline was meticulously designed to minimise noise, normalise the signal, and prepare it for subsequent feature extraction. The steps involved are outlined below:

1. PDF/Image to Image Conversion: The initial step addresses the widespread practice of storing ECGs as PDFs. The PyMuPDF (fitz) and PIL (Pillow) libraries were employed to convert the ECG PDFs into high-resolution images, such as PNG format. This conversion facilitates the uniform application of subsequent image-processing steps.

2. Grayscale Conversion: To expedite image processing while highlighting intensity variations, the colour ECG images were converted to grayscale using cv2.cvtColor. This modification reduces the dimensionality of the image data without compromising essential waveform details.

3.Thresholding (Binarisation): Otsu's thresholding algorithm (cv2.THRESH_BINARY + cv2.THRESH_OTSU) was implemented to distinguish the ECG waveform from the background grid and accompanying text. This adaptive thresholding method automatically determines an optimal threshold value, thereby maximising the variance between foreground and background pixels and generating a binary image with a clear delineation between the waveform (black pixels) and background (white).

4. Noise Reduction: Visual noise present in scanned or digitised ECGs can significantly impede signal extraction. The application of cv2.fastNlMeansDenoising serves to mitigate this noise. This non-local means denoising technique is particularly effective at preserving edges while smoothing homogeneous regions, which is critical for maintaining the integrity of the ECG waveform.

5. Boundary Noise Cleanup: Although overall noise reduction is achieved, isolated black pixels (speckles) may persist. A specialised local window filtering method was employed to eliminate these artifacts. This approach involved examining the binary image and removing black pixels that lacked sufficient neighbouring black pixels within a defined small window, thereby rectifying isolated artifacts without distorting the primary signal.

6. Signal Extraction (1D Trace): The pre-processed binary image underwent extraction of the one-dimensional ECG waveform by scanning the black pixels column-wise. In each column, the position of the black pixel (or the centroid of black pixels in the case of multiple pixels due to waveform thickness) was documented, resulting in a discrete one-dimensional representation of the ECG signal for each lead.

7. Sampling Frequency Estimation: Accurate ECG interpretation requires knowledge of the sampling frequency. In the absence of direct digital sampling information, an estimation method was formulated based on the ECG grid—the cv2.HoughLinesP function was employed to detect vertical grid lines, which typically indicate fixed time intervals (e.g., 200 ms or 40 ms). By calculating the average pixel distance between these identified lines, the pixels per millimetre (or per time unit) could be approximated, leading to an estimate of the sampling frequency of the digitized signal.

8. Bandpass Filtering: To eliminate baseline wander (low-frequency noise) as well as high-frequency muscle artifacts or power line interference, a Butterworth bandpass filter was implemented. The filter's cutoff frequencies were established at 0.5 Hz and 40 Hz, which are considered standard for clinical ECG analysis—the scipy.signal. The butter function was utilised for designing filter coefficients, and scipy.signal.filtfilt was applied for zero-phase filtering to prevent signal distortion.

9. R-Peak Detection: R-peaks, characterised as the most considerable deflections within the QRS complex, serve as critical fiducial points for various ECG analyses, including heart rate variability and feature extraction. The detection of R-peaks employed scipy.signal.find_peaks with dynamic thresholding to accommodate variations in R-peak amplitudes both within and among different ECGs.

2.3. Feature Engineering

A fixed-length one-dimensional signal was extracted from each of the twelve preprocessed ECG leads. These twelve individual one-dimensional signals were then concatenated to form a single, comprehensive feature vector for each ECG sample. For instance, if each lead produced a signal of length L (such as 255 samples derived from a fixed window or interpolation), the total feature vector for a twelve-lead ECG would amount to 12×L. In this study, the feature vector was defined as having a dimensionality of 3060 per sample, which indicates that L equals 3060/12, resulting in 255 samples per lead. This concatenation technique effectively preserves the spatial relationships between the leads in the feature space.

2.4. Model Architecture and Training

The foundation of our AMI detector is an ensemble machine-learning model designed to leverage the strengths of multiple classifiers.

1. Type: This model employs a Classic Ensemble Machine Learning approach utilizing a Soft Voting Classifier. It computes the average of probabilistic estimates from individual base classifiers, assigning greater weights to more confident predictions. This methodology generally yields more accurate and robust outcomes compared to using single classifiers alone.

2. Components: The ensemble model comprises five heterogeneous classifiers:

i. Support Vector Machine (SVM): This classifier excels in high-dimensional data scenarios and is particularly effective at identifying optimal hyperplanes for data separation.

ii. K-Nearest Neighbors (KNN): A non-parametric, instance-based learning algorithm, KNN classifies data points based on the majority class among its k-nearest neighbors.

iii. Random Forest (RF): This ensemble technique constructs multiple decision trees and derives the mode of the class predictions (for classification) or the mean predictions (for regression) from these individual trees. Random Forest is known for its resilience against overfitting and its effectiveness with high-dimensional datasets.

iv. Gaussian Naive Bayes (GNB): This probabilistic classifier is rooted in Bayes' theorem and operates under the assumption of feature independence. Its simplicity often leads to commendable performance in various applications.

v. Logistic Regression: This linear model is employed for binary classification, producing outputs in the form of probabilities. This ensemble approach not only enhances prediction accuracy but also contributes to the overall robustness of the AMI detector.

3.Model Input Preprocessing

i. StandardScaler for Feature Normalization: In this analysis, the feature vectors comprising 3060 dimensions were processed using StandardScaler. This technique transforms the features to conform to a standard normal distribution characterized by a mean of 0 and a variance of 1. Normalization of features is crucial, especially for machine learning algorithms such as Support Vector Machines (SVM) and K-Nearest Neighbors (KNN), as it mitigates the risk that features with larger numerical ranges will disproportionately influence the model's performance.

ii. PCA for Dimensionality Reduction: Given the high dimensionality of the feature vectors (3060 dimensions), there is a significant concern regarding computational inefficiency alongside the risk associated with the curse of dimensionality. To address these challenges, Principal Component Analysis (PCA) was employed to condense the feature space while preserving a substantial portion of the variance. Through PCA, the data was transformed into a new set of orthogonal principal components, from which 133 components were selected. This selection process successfully retained approximately 95% of the variance from the original dataset, thereby significantly alleviating computational demands and reducing the likelihood of model overfitting.

4.Optimization:

a) GridSearchCV for Hyperparameter Optimization: To identify the optimal hyperparameters for the foundational classifiers—Support Vector Machine (SVM), K-Nearest Neighbors (KNN), and Random Forest (RF)—GridSearchCV was employed extensively. This method comprehensively investigates a defined hyperparameter grid, evaluating each possible combination through cross-validation.

b) Three-Fold Cross-Validation: In conjunction with GridSearchCV, a three-fold cross-validation approach was implemented. This technique partitions the training dataset into three segments, wherein the model is trained on two segments and evaluated on the remaining segment. This process is iterated across all possible combinations, facilitating a more accurate assessment of model performance while mitigating the risk of overfitting to any single train-test partition.

2.5. Model Training Steps

The overall training process followed a systematic sequence outlined as follows:

1. ECG Image to 12-lead 1D Signal to Combined Feature Vector: This initial step involves a comprehensive signal preprocessing pipeline, as delineated in Section 2.2, which transforms raw ECG images into well-structured numerical feature vectors.

2. Normalisation Using StandardScaler: The extracted feature vectors were normalised using the StandardScaler to ensure uniform scaling across all features.

3. Dimension Reduction via PCA: Principal Component Analysis (PCA) was applied to the normalised features

to reduce dimensionality to 133 components, effectively capturing 95% of the variance in the data.

4. Data Partitioning (70% Training, 30% Testing): The dimension-reduced and preprocessed dataset was divided into training (70%) and testing (30%) sets. The training set was utilised for model training, while the unseen testing set was reserved to evaluate the model's generalisation performance.

5. Training the VotingClassifier with Optimal Parameters from GridSearchCV: The VotingClassifier was trained on the training dataset. Hyperparameters for the individual base classifiers—Support Vector Machine (SVM), K-Nearest Neighbors (KNN), and Random Forest (RF)—were assigned optimal values identified during an initial tuning process using GridSearchCV.

6. Evaluation of Classification Report: The performance of the trained model was assessed on the unknown test set using a comprehensive classification report, which provides metrics such as accuracy, precision, recall (also known as sensitivity), and F1-score for each class.

7. Serialisation of the Final Model: The trained ensemble model was serialised using the pickle library, facilitating its deployment and reuse without the need for retraining.

3.Statistical Analysis:
Descriptive and inferential statistics were employed to evaluate the performance of the proposed machine learning model. Continuous variables, such as feature vectors extracted from ECG signals, were summarized using mean ± standard deviation (SD) where applicable. Categorical outcomes, including class labels (Normal vs. Myocardial Infarction), were expressed as counts and percentages.

Metrics:
Accuracy: Calculated as the proportion of correctly classified ECG samples (both MI and Normal) to the total number of samples.
Sensitivity (Recall): Defined as the proportion of true positive cases correctly identified, with emphasis on MI detection due to clinical significance.
Precision: Calculated as the ratio of correctly predicted positive cases to the total predicted positive cases.
F1-Score: The harmonic mean of precision and sensitivity, providing a balanced measure of model performance, particularly useful in imbalanced class scenarios.

Validation Approach:
The dataset was divided into training (70%) and testing (30%) subsets. Three-fold cross-validation was applied during hyperparameter optimization with GridSearchCV to prevent overfitting and ensure robust performance estimation. Statistical analyses were performed using Python libraries, including scikit-learn, NumPy, and SciPy. Differences in model predictions between MI and Normal classes were considered significant based on performance metrics, emphasizing high sensitivity to minimize false negatives in clinical diagnosis.

4. Performance Metrics
The performance of the trained machine learning model was measured with standard metrics for classification, with a special emphasis given to those metrics that are most important for medical diagnosis, particularly for diseases such as MI, where false negatives are particularly disastrous.

1. Accuracy: The percentage of instances overall that were accurately classified (both MI and Normal).
Accuracy: 80%

2. Sensitivity (Recall): The model's capacity to accurately predict all positive cases (true positives). In the MI case, high sensitivity is paramount to reduce the likelihood of an AMI diagnosis being missed.
MI: 96%
Normal: 53%

3. Precision: The ratio of correct identifications to total identifications. For MI, high precision means that when the model says MI, it is highly likely to be accurate.
MI: 78%
Normal: 89%

4.F1-Score: Harmonic mean of the precision and sensitivity. It provides a balanced estimate of the model's performance, which is particularly valuable when the class is imbalanced.
MI: 0.86
Normal: 0.67

RESULT AND DICSUSSION

The implemented machine learning framework yields promising results in detecting Acute Myocardial Infarction (AMI) from 12-lead ECGs using real-world hospital data. An average accuracy of 80% reflects a solid performance across both classification categories. Notably, the sensitivity for myocardial infarction stands at 96%, which is a critical outcome. In clinical settings, minimizing false negatives for AMI is essential, as missed diagnoses can lead to significant morbidity and mortality. The model's ability to accurately identify 96% of true MI cases underscores its potential as an effective screening diagnostic tool. The high recall for MI is particularly reassuring, indicating that the system is unlikely to overlook genuine MI instances. The accuracy rate for diagnosing MI at 78% signifies that when the model predicts an MI, it is correct 78% of the time. While 100% accuracy would be ideal, 78% accuracy is a strong starting point, especially considering the emphasis on high sensitivity. This implies that while some MI predictions may turn out to be false positives requiring clinical reassessment, the model still performs well in detecting the majority of true positive cases compared to lower-precision alternatives. In terms of the "Normal" class, the sensitivity is recorded at 53%, with a precision of 89%. The low sensitivity for normal cases indicates that a significant proportion of true normal ECGs could be classified as MI (false positives). This trade-off is common in medical diagnostic models, where the primary objective is to mitigate false negatives for life-threatening conditions.

However, the high precision observed in normal cases (89%) suggests that when the model categorizes a case as "Normal," it is highly likely to be correct. The MI F1-score of 0.86 indicates a commendable balance between precision and sensitivity for the disease in focus. In contrast, the Normal F1-score of 0.67 is less ideal, primarily due to the lower sensitivity associated with this classification. The combination machine learning strategy, which integrates the strengths of algorithms such as SVM, KNN, Random Forest, Gaussian Naive Bayes, and Logistic Regression, likely contributed to the model's robust performance. Additionally, rigorous preprocessing methods, including image-to-signal transformation and noise removal, were instrumental in converting raw ECG data into a consistent and analyzable format. The implementation of StandardScaler and PCA effectively addressed issues related to high dimensionality and varied scales among features through feature scaling and dimensionality reduction. The utilization of GridSearchCV with 3-fold cross-validation ensured that the individual models were finely tuned and that results were not overly optimistic due to specific data splits.

We successfully developed and validated a machine learning-based methodology for the automated diagnosis of Acute Myocardial Infarction (AMI) from 12-lead ECGs utilizing real-world hospital data. Our comprehensive signal preprocessing pipeline effectively transforms raw ECG images into one-dimensional signals, making them suitable for analysis. The conventional ensemble machine learning approach demonstrated impressive sensitivity (96%) in detecting myocardial infarction. While challenges remain, particularly in improving sensitivity for normal cases, our findings underscore the significant potential of machine learning as a valuable tool for clinicians, facilitating timely and accurate diagnosis of AMI and ultimately contributing to the preservation of patient lives.

Limitations:

1.The presence of artifacts that are not adequately addressed by the current preprocessing pipeline, such as baseline wander and electrode detachment artifacts, may still influence performance outcomes.

2. Furthermore, while the existing model exhibits superior sensitivity for myocardial infarction (MI), enhancing its sensitivity for normal conditions without significantly compromising MI sensitivity represents a valuable direction for future research.

3. The explainability of ensemble models poses challenges, which constitutes a significant concern for their application in clinical settings.

Future Work:

Future research will focus on expanding the dataset's size and diversity to include a broader range of heterogeneous patient populations and various models of ECG machines. An exploration of state-of-the-art deep learning architectures, such as Convolutional Neural Networks (CNNs) and Recurrent Neural Networks (RNNs), applied to raw or minimally preprocessed two-dimensional ECG images, may facilitate the identification of more intricate spatial and temporal patterns. Incorporating clinical metadata, including sex, age, and symptoms, alongside ECG features could further enhance diagnostic performance. Additionally, applying explainable AI methodologies to identify which features or segments of the ECG contribute to the model's predictions would foster greater trust and acceptance among clinicians.

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