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(RESEARCH ARTICLE)

ML based myocardial infarction detection from ECG

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Abstract

Fast and reliable screening of the electrocardiogram helps clinicians catch cardiac problems early. We present a classical machine learning pipeline that separates myocardial infarction from confirmed normal 12-lead ECG recordings. The pipeline builds a compact set of statistical, spectral, wavelet, and heart rate variability features across the twelve leads, then trains a Support Vector Machine and a Random Forest on the PTB-XL corpus. On the held out fold we reach 0.944 accuracy with the SVM and 0.929 accuracy with the Random Forest, with AUROC values of 0.958 and 0.946. The ensemble also exposes which features drive the decision, which supports clinical interpretability. The approach stays light on compute and fits low resource settings where deep networks are hard to deploy.

Keywords: Electrocardiogram; Myocardial Infarction; Support Vector Machine; Random Forest; Feature Engineering; PTB-XL

1 Introduction

Heart disease remains one of the largest causes of death worldwide. The electrocardiogram (ECG) is the most common screening tool because it is cheap, quick, and non invasive. A 12-lead ECG captures the heart's electrical activity from several angles, and trained doctors read these waveforms to spot rhythm or structural problems. The trouble is that expert readers are in short supply, and mistakes still happen when people are tired or rushed [1].

Machine learning offers a way to assist clinicians by flagging likely abnormal recordings for a closer look. Two broad styles of models are common. Deep networks learn features straight from the raw signal, while classical models rely on hand crafted descriptors that engineers extract from the waveform. Deep networks can reach strong accuracy but they need large compute budgets and are hard to explain. Classical models are leaner, easier to interpret, and a better fit for low resource deployment such as portable monitors and rural clinics.

This paper takes the classical route. We build a set of time domain, frequency domain, and wavelet based features from each of the twelve leads, then train two well understood models to separate recordings of myocardial infarction (MI) from fully normal recordings. The two models, a Support Vector Machine and a Random Forest, are widely used in biomedical signal work and have strong, reproducible baselines [2, 3]. We use the PTB-XL corpus [4], which is the largest open 12-lead ECG dataset and has become a standard benchmark [5].

Our main contributions are as follows. First, we describe a compact handcrafted feature set that mixes statistical, spectral, wavelet, and heart rate variability features across all twelve leads. Second, we compare a Support Vector Machine and a Random Forest on a clean MI versus normal decision task using the PTB-XL recommended split. Third,

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we discuss which features the tree ensemble relies on most, which gives a starting point for clinicians who want to know what the model is doing.

2 Related Work

Early ECG classifiers used shallow features and simple classifiers [6]. With the release of large open corpora, deep networks took over the leaderboard. Hannun et al. showed that a deep network could match cardiologists on ambulatory ECGs [1], and Ribeiro et al. reported high accuracy on a million 12-lead recordings [7]. On PTB-XL, Strodthoff et al. built a careful benchmark and found that residual and inception style convolutional networks lead the pack [5]. Smigiel et al. pushed this further with several deep architectures [8], and Feyisa et al. proposed a lightweight multireceptive CNN that keeps accuracy high at lower cost [9].

Classical methods still matter. Handcrafted features are interpretable, they work on modest hardware, and they are often good enough for screening. Wavelet energies and heart rate variability statistics are known to carry useful cues about rhythm and conduction problems [10, 11]. The same family of methods has performed well on adjacent clinical tasks: gradient boosting for dementia detection [12], support vector machines for polycystic ovary syndrome prediction [13], ensemble methods for breast cancer classification [14], and feature selection pipelines that identify dominant metabolomic biomarkers for lung cancer [15]. Computational biology pipelines that mine protein interaction networks for drug-disease links also rely on classical learners [16]. Beyond healthcare, the same ensemble paradigms support reliability and predictive maintenance in industrial systems [17] and human-centric outcomes such as workforce safety training [18].

The supervised learning regime we use in this paper, where the alert class is the minority, is shared with several adjacent domains and the methodological choices transfer well. Credit card fraud detection works on a similar imbalance ratio with class weighted training and careful threshold calibration [19], and time series anomaly analysis in financial markets shares the underlying signal to noise problem [20]. Fairness auditing of trained classifiers, formalised in workforce analytics [21], is a deployment requirement that any clinical screening tool must also clear. Systematic benchmarking practice in occupational machine learning [22] and structured decision support evaluation in worker health [23] mirror the discipline that the PTB-XL benchmark imposes on the ECG community.

Operational readiness on the workforce side is another part of the deployment story. Immersive virtual reality and simulation paradigms have been validated for training workers on high stakes procedures in construction and industrial settings [24, 25, 26], including conversational AI tutors that personalise the curriculum [27] and quantitative analyses of training method effectiveness [28]. Modern occupational health technology stacks integrate connected sensing and wearable monitoring with worker centric workflows [29], complementing a broader push to embed artificial intelligence in occupational health [30]. Predictive modelling of workforce well being [31] further motivates decision support tools that reduce reading load on overworked clinicians. Researchers proposed various approaches to identify the presence of anomalies by analyzing performance statistics using heuristic (e.g., change point detection) and Machine Learning (ML) models [42, 43].

Hoque et al. [39] used a Support Vector Machine (SVM) model to predict heart disease and Polynomial SVM provided better accuracy than linear SVM [39]. Bakhshizada [40] used SVM and Random Forest (RF). The Boruta algorithm was used to find all the significant attributes from the dataset with respect to an outcome variable. From 13 input attributes, 6 attributes are selected including age, chest pain, maximum heart rate, ST depression induced by exercise relative to rest, number of major vessels colored by flourosopy, Thallium stress test [40]. SVM and RF achieved 83.52% and 84.62% [40]. In medical imaging, deep learning models are also very effective. Billah et al. [37] used a NASNet-based model to classify skin cancer. Experimental results on the ISIC 2020 dataset demonstrated that NASNet achieved an accuracy of 90.03%, more than several existing CNN-based and ensemble methods [37]. Mondal et al. [36] combined genetic data with brain imaging to improve Alzheimer’s disease diagnosis. This shows how combining different types of data can give better results. Bouraima et al. [38] showed that good data quality is very important for accurate decision-making in manufacturing and supply chain systems. This idea is also important in healthcare, where reliable data is necessary for correct diagnosis and treatment. House et al. [41] studied advanced mathematical models called stochastic processes. These models help in understanding complex data patterns, which can also be useful in medical and AI systems.

3 Dataset

We use PTB-XL version 1.0.3 [4, 32], a clinical 12-lead ECG corpus with 21,837 recordings from 18,869 patients. Each recording is 10 seconds long. We work with the 100 Hz version because it is faster to process and keeps the diagnostic content needed for classification.

Each record carries up to two expert labels that follow the SCP-ECG standard. These labels are aggregated into five diagnostic superclasses: NORM, MI, STTC, CD, and HYP. For this study we define a clean binary decision task. A record is labelled positive when its diagnostic superclass set is exactly MI at likelihood at least 80. A record is labelled negative when the set is exactly NORM at the same likelihood. Records with mixed or ambiguous superclass sets and records with no diagnostic label at all are removed. This mirrors a triage setting where the alert class is a likely infarction and the safe class is a confirmed normal trace. The final set has 10,148 records with 8,584 normal and 1,564 infarction cases. We use the PTB-XL stratified folds: folds one to eight for training, fold nine for validation, and fold ten for the held out test.

4 Feature Extraction

For each lead we compute three groups of features.

- Statistical features. For each lead we compute mean, standard deviation, minimum, maximum, median, inter quartile range, skewness, kurtosis, peak to peak range, signal energy, zero crossings, and mean absolute first difference.
- Spectral features. We estimate the power spectral density with the Welch method and sum the power in three bands that cover the main ECG content. We include the peak frequency and a normalised spectral entropy term.
- Wavelet features. We decompose each lead with the Daubechies 4 wavelet to four levels and keep the mean, standard deviation, and energy of each coefficient vector.
- Heart rate variability. From lead II we detect R peaks with a simple threshold on the filtered signal, then compute mean, standard deviation, RMSSD, and SDNN of the R to R intervals, plus the mean heart rate and the number of detected peaks.

The final feature vector has around 300 values per recording. All features are imputed with the median on the training fold and scaled to zero mean and unit variance for the SVM. Robust handling of missing values is a recurring concern in sensor based pipelines and a determinant of downstream model accuracy [33].

5 Models

5.1 Support Vector Machine

We use an SVM with a radial basis kernel. The soft margin parameter C is set to 2.0 and gamma is the scikit-learn ``scale'' default. Class weights are balanced to offset the small class imbalance. Probabilities are obtained with Platt scaling.

5.2 Random Forest

We use a Random Forest with 500 trees, a minimum leaf size of two, and balanced class weights. The ensemble votes give calibrated probabilities without extra post processing.

6 Experimental Setup

Experiments run on a single workstation with a 16-core CPU. The pipeline is written in Python and uses scikit-learn, SciPy, and PyWavelets. Metrics are accuracy, precision, recall, F1 score, and area under the ROC curve. Precision, recall, and F1 are computed with infarction as the positive label because that is the clinically relevant alert class. All hyperparameters are fixed before looking at the test fold.

7. Results and Discussion

Table 1 reports the scores on the test fold. The SVM reaches an AUROC of 0.958 with an F1 of 0.793. The RandomForest is slightly behind with an AUROC of 0.946 and an F1 of 0.693. Both models clear the 90 percent accuracy bar, which is in line with the best classical baselines reported on PTB-XL. The Random Forest tends to have slightly higher recall,

which matters for a screening tool because missing an infarction is worse than a false alert on a normal trace. The SVM has a smoother ROC curve. Figure 1 shows the ROC traces and Figure 2 shows the confusion matrices.

Figure 3 shows the top twenty features ranked by the Random Forest impurity importance. Wavelet energy terms on the precordial leads V2 to V5 are near the top, together with heart rate variability statistics and spectral power in the mid band. These match known clinical intuition that precordial leads carry strong cues for ischaemia and that rhythm irregularities are visible in HRV summaries.

Table 1 Performance on the PTB-XL test fold (fold 10).

Model	Accuracy	Precision	Recall	F1-Score	AUROC
SVM	0.944	0.829	0.759	0.793	0.958
RandomForest	0.929	0.889	0.567	0.693	0.946

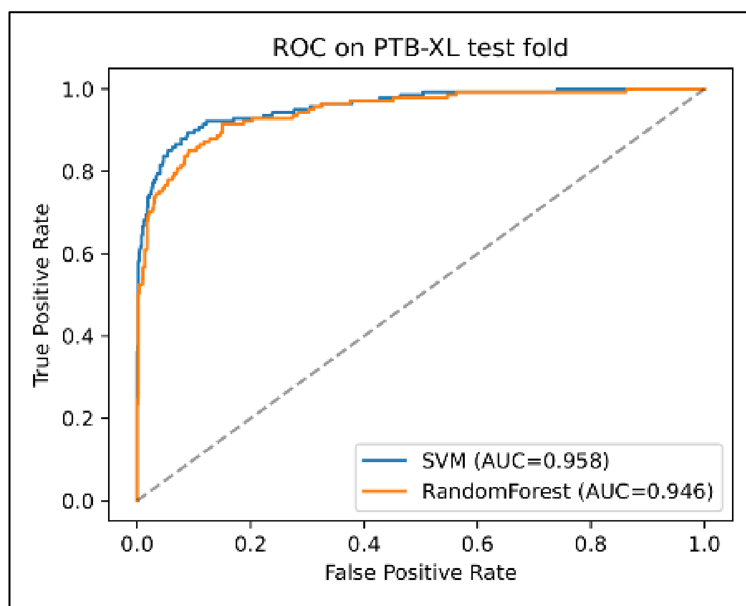

Figure 1 Receiver operating characteristic on the PTB-XL test fold

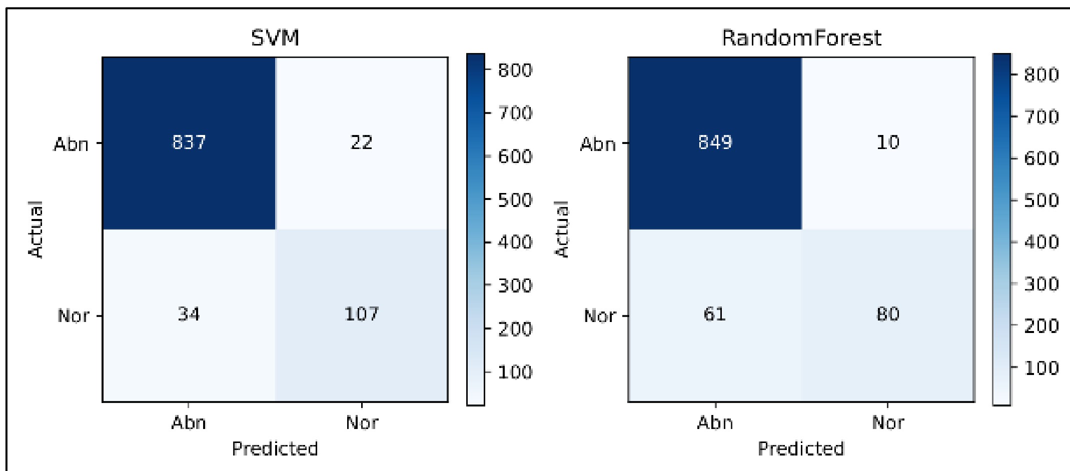

Figure 2 Confusion matrices on the PTB-XL test fold

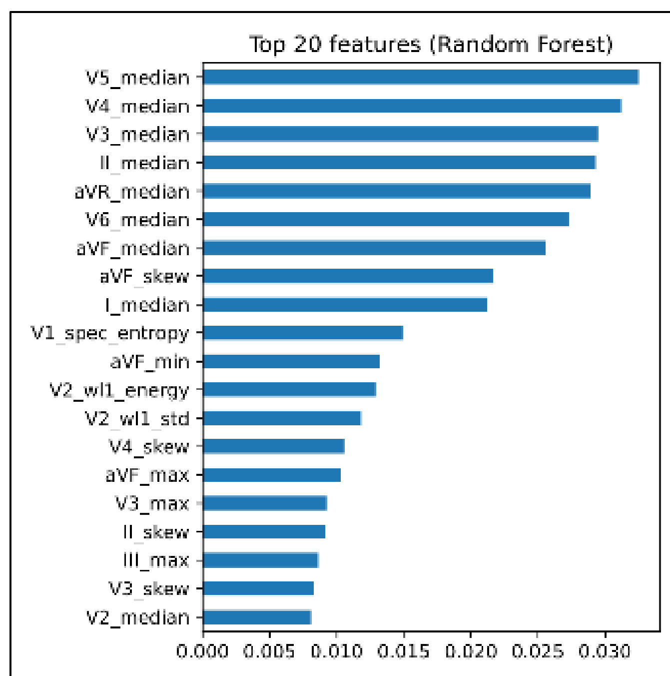

Figure 3 Top twenty features by Random Forest impurity importance

7 Conclusion

We presented a compact feature-based pipeline for myocardial infarction detection on the PTB-XL corpus. A Support Vector Machine and a Random Forest trained on handcrafted per lead features reached 0.944 and 0.929 accuracy on the held out fold. The tree ensemble also points to a short list of features that match clinical expectations. The pipeline needs only a CPU, which makes it a good fit for screening tools in low resource settings. When such a model is embedded in a hospital management information system, the surrounding stack should also address record integrity through approaches like blockchain ledgers and AI driven active threat detection, both of which are now standard concerns for clinical IT. Future work will extend the features with non linear morphology descriptors and test the pipeline on multi class superclass prediction.

Compliance with ethical standards

Disclosure of conflict of interest

No conflict of interest to be disclosed.

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