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Atrial Fibrillation Detection Through ML Approach: A Comparitive Study

Poonam Chhabra[1], Rosy Madaan[2]

[1]Research Scholar, Manav Rachna International Institute of Research and Studies

[2]Associate Professor, Manav Rachna International Institute of Research and Studies

Abstract: Atrial Fibrillation (AF) is a common "cardiac arrhythmia" with significant health implications. Traditional AF detection methods have limitations in continuous monitoring and data analysis. The emergence of machine learning (ML) offers promising solutions for accurate and timely AF detection. This study aims to explore and evaluate various ML techniques for AF detection, considering data quality, clinical validation, and algorithm performance. A diverse dataset of ECG signals and patient information is collected and pre-processed for training and testing ML models. The study implements supervised and unsupervised learning algorithms, deep learning (DL) architectures, and ensemble methods to compare their effectiveness in AF detection. Results demonstrate the potential of ML-based AF detection to revolutionize diagnosis and management, leading to improved patient care and healthcare outcomes in cardiology. The results of our comparative study demonstrate that all ML approaches achieved impressive results in detecting AF from ECG signals. "The logistic regression classifier achieved an accuracy of 92.48% and sensitivity of 91.89%. The Naïve Bayes classifier achieved an accuracy of 90.26% and sensitivity of 89.27%. The SVM classifier achieved an accuracy of 93.87% and sensitivity of 92.43%. The Decision tree achieved an accuracy of 93.87% and sensitivity of 90.63%. Finally, the Random Forest model attained an accuracy of 95.8% and sensitivity of 92.88%".

Keywords*: Atrial Fibrillation, ML, AF Detection, Cardiac Arrhythmia, Healthcare Innovation.*

1. Introduction

AF is a heart problem summarized by inconsistent and often rapid heartbeats, which can affect an individual's quality of life and increase the risk of severe health complications, including stroke, heart failure, and other cardiovascular diseases (Johnson & Cornia, 2019). For timely intervention to reduce associated health risks early detection of AF is necessary. Traditional methods of AF detection, such as electrocardiograms (ECGs) and Holter monitors, have limitations in terms of continuous monitoring, real-time analysis, and processing vast amounts of data (Young, 2019). However, recent advancements in ML offer promising avenues for developing efficient and reliable AF detection systems.

The use of ML algorithms for medical applications has found considerable support as it has the ability to analyse complex and large-scale data sets (Lippi et al., 2021). ML techniques have demonstrated remarkable prominence in different domains, including image recognition, natural language processing, and finance ((Alhusseini et al., 2020); (Sivanandarajah et al., 2022); (Liaqat et al., 2020)). Applying these cutting-edge techniques to AF detection has the potential to revolutionize how healthcare professionals identify and manage this cardiac condition.

The traditional methods of AF detection have limitations that hinder their ability to provide comprehensive and timely insights(Plaseka & Taborsky, 2019). For instance, standard 12-lead ECGs can only capture brief periods of a patient's cardiac activity, potentially missing intermittent episodes of AF (Ahmed & Zhu, 2020). Holter monitors, while more extended in their monitoring capability, generate vast amounts of data, making manual analysis laborious and time-consuming for healthcare practitioners (Wei et al., 2022).

ML approaches can overcome these limitations by enabling continuous monitoring of heart rhythm through wearable devices or implantable cardiac monitors (Roithinger, 2020). These devices can collect a wealth of data over extended periods, providing a comprehensive picture of a patient's cardiac activity. ML algorithms can then process this data in real-time or retrospectively, accurately detecting AF episodes and helping healthcare professionals make informed decisions about patient care (Liaqat et al., 2020).

Despite the immense promise of ML in AF detection, several challenges need to be demonstrated for its successful implementation in clinical practice. Firstly, the quality and reliability of data obtained from wearable devices and monitors are crucial for accurate AF detection. Noise, artifacts, and motion interference may affect the data, leading to false positives or negatives. Ensuring data accuracy and developing robust preprocessing techniques are essential in mitigating these issues. Secondly, the interpretation of ML results requires validation and integration with clinical expertise. ML models can yield highly accurate predictions, but their effectiveness in a real-world clinical setting must be carefully evaluated and compared with existing standards of AF detection.

The primary objective of this study is to explore and evaluate various ML techniques for AF detection, considering their potential advantages and limitations. Specifically, the main contribution of this study involves:

(a) Collect and preprocess a diverse dataset of ECG signals and related patient information for training and validating ML models.

(b) Implement and compare various ML algorithms for AF detection, including supervised and unsupervised methods, DL architectures, and ensemble techniques.

(c) Assess the performance and robustness of the developed models on the dataset and evaluate their potential for real-world deployment in clinical settings.

2. Literature Review

This comprehensive review assesses the applicability of ML models, specifically Naïve bias, SVM, Random Forest, decision tree, and Logistic regression, in Atrial Fibrillation detection and diagnosis.

(Tison et al., 2018) investigates the feasibility of passive AF detection using consumer-grade smartwatches equipped with photoplethysmography sensors. The authors employ ML algorithms to analyse wrist-worn optical sensor data and accurately detect AF episodes in real-time. The study demonstrates the potential of wearable devices combined with ML for continuous and non-invasive AF monitoring. (Hannun et al., 2019) proposes a DL approach for AF detection using ambulatory ECG. The deep neural network achieves cardiologist-level accuracy in detecting various arrhythmias, including AF. The study emphasizes the potential of DL algorithms in improving the accuracy and efficiency of AF detection in clinical settings.

In the study by (Attia et al., 2019), an AI based ECG algorithm is developed to detect AF during sinus rhythm. The algorithm utilizes ML methods to predict AF presence based on standard 12-lead ECG recordings. The research highlights the potential of AI-powered algorithms for early AF detection and outcome prediction. In the study, (Ghrissi et al., 2022) proposes using ML to automatize the identification of atrial fibrillation's spatiotemporal dispersion electrograms. They compared different data formats and found promising results with VGG16-based transfer learning for real-time deployment. However, due to class imbalance, precision and F1 score were relatively low, but data augmentation addressed the issue effectively. The Apple Heart Study, sponsored by Apple Inc., used the Apple Watch's heart-rate pulse sensor to detect atrial fibrillation. Findings by (Stanford Medicine, 2019) showed promising potential for wearable technology in detecting health conditions.

(Torres-Soto & Ashley, 2020) presented DeepBeat, a multitask DL model, greatly enhances atrial fibrillation detection from wearable photoplethysmography devices. Two-stage training improves performance, addressing unbalanced data challenges in biomedical applications. High sensitivity, specificity, and F1 score are achieved in real-time monitoring.

(Michel et al., 2021) The γ-metric filter approach for feature selection in atrial fibrillation detection using short ECG recordings showed satisfactory results, with high stability and accuracy for models with fewer features. New methodological avenues are opened for clinical decision making.

3. Methods

3.1. Methodology

An electrocardiogram (ECG) serves as a vital diagnostic tool, capturing the heart's electrical activity. Its primary purpose lies in evaluating the heart's rhythm and identifying potential irregularities indicative of cardiac conditions (Mathews, 2022). To generate the ECG signal, electrodes are strategically placed on the chest, arms, and legs (Serhani et al., 2020). These electrodes detect the heart's electrical signals and transmit them to a recording device, displaying a waveform that represents the heart's activity over time.

The ECG waveform comprises distinct waves and intervals, each corresponding to a different phase of the heart's electrical cycle. Medical professionals utilize the ECG signal to diagnose an array of heart conditions, including arrhythmias, conduction disorders, and heart attacks ((Mousavi et al., 2021); (Merdjanovska & Rashkovska, 2022); (Park et al., 2022)). By meticulously analysing the shape and timing of the various waves and intervals, doctors can gain valuable insights into the heart's health and functionality.

3.2. Preprocessing of ECG signals

Preprocessing of ECG signals plays a critical role in signal analysis and classification, involving a various technique to optimize signal quality, eliminate noise and artifacts, and ready the signal for subsequent processing (Sikorska et al., 2022). Below are some common preprocessing techniques commonly applied to ECG signals:

Baseline wander removal: ECG signals are frequently affected by low-frequency noise, known as baseline wander (Venkatesan et al., 2018). This interference can be effectively eliminated by applying high-pass filtering or subtracting a moving average of the signal (Karnewar & Shandilya, 2022).

Filtering: ECG are susceptible to different noise, such as powerline interference, muscle artifacts, and electrode motion artifacts. To address these issues, filtering techniques like bandpass and notch filters are employed to effectively remove these noise components (Rahman et al., 2019).

Signal normalization: ECG signals often exhibit variations in amplitude and polarity between individuals and recordings (Luz et al., 2016). Signal normalization techniques, such as normalization to the mean or standardizing to a fixed amplitude range, are utilized to establish a consistent baseline for the signal.

Resampling: ECG signals are typically recorded at a high sampling rate, which can be computationally demanding for further analysis. To alleviate this, resampling techniques like decimation or interpolation are applied to reduce the sampling rate while preserving the essential features of the signal (Singh et al., 2021). This aids in making the subsequent analysis more efficient without losing crucial information.

3.3. Atrial Fibrillation (AF) ECG signal

Atrial Fibrillation (AF) ECG signals can undergo classification based on various extracted features from the ECG waveform (Budeus et al., 2007). Below are commonly utilized features for AF classification:

(a) RR Interval Analysis:

RR interval variability: Quantitative assessments of variances in the consecutive RR intervals (Castells et al., 2007).

Mean RR interval: The average duration of RR intervals.

Heart rate: Mean heart rate per minute derived from RR interval data.

(b) Frequency-domain Analysis:

Power spectral density: Analyzing the power distribution of the signal across different frequency bands (Guaragnella et al., 2019).

LF/HF ratio: The ratio of LF power to HF power, providing information about the balance in the autonomic nervous system.

(c) P-wave Analysis:

P-wave duration: Difference of the P-wave component in the ECG signal.

P-wave morphology: Assessing the shape and characteristics of the P-wave, including amplitude, slope, and presence of notches or abnormal morphologies (Gupta & Mittal, 2020).

(d) QRS Complex Analysis:

QRS duration: The length of the QRS complex in the ECG signal.

QRS morphology: Evaluating the shape and characteristics of the QRS complex (An & Stylios, 2020).

(e) Heart Rate Variability (HRV) Analysis:

Time-domain HRV measures: It involves the evaluation of variability in consecutive RR intervals, employing measurements such as the standard deviation of RR intervals or the root mean square of successive RR intervals.

Frequency-domain HRV measures: Analyzing power spectral density of RR intervals.

(f) Morphological Analysis:

Morphological features related to waveform characteristics, such as presence of irregular or chaotic patterns in the ECG signal (Ganesh et al., 2021).

These features are extracted from the ECG signal using signal processing techniques and then fed as inputs to a classification model, such as “Support Vector Machines (SVM), Random Forest (RF), or DL models like Convolutional Neural Networks (CNN), to classify AF ECG signals”.

3.4. Classification Methodology

3.4.1. Logistic Regression

Logistic regression stands as a prevalent statistical technique employed in binary classification tasks, wherein the target variable assumes one of two possible values, usually represented as 0 or 1 (Sperandei, 2014). This method finds broad application across multiple domains, encompassing machine learning, statistics, and social sciences, owing to its straightforwardness, interpretability, and efficacy in addressing classification challenges (Austin & Merlo, 2017).

The logistic regression model applies the logistic or sigmoid function to the result of a linear combination of input features. The sigmoid function effectively defines any real-valued number to a range spanning from 0 to 1, making it well-suited for expressing probabilities (Ghavamipour et al., 2022). This transformation ensures that the predicted probability lies within the valid probability range, allowing us to interpret the model's output as the likelihood of the positive class (class 1) occurring. Mathematically, the logistic regression model can be expressed as:

$$p(y=1|x) = \frac{1}{1+e^{-(\beta_0+\beta_1 x_1+\beta_2 x_2+\cdots+\beta_n x_n)}} \quad (1)$$

where: $p\left(y=\frac{1}{x}\right)$ represents the probability of the positive class (class 1) given the input features x; β_0, β_1, β_2, ..., β_n are the coefficients (also known as weights) of the model that determine the effect of each input feature on the estimated probability; x_1, x_2, ..., x_n are the input features (Scott et al., 1991). The coefficients are estimated during the model training process using optimization techniques like maximum likelihood estimation, reducing the variance in the estimated probabilities and the actual binary outcomes in the training data.

To make predictions with logistic regression, a threshold (usually 0.5) is applied to the predicted probabilities (Ahmadini, 2022). One of the key benifits of logistic regression is its interpretability. The model coefficients provide insights into the influence of each input feature on the likelihood of the positive outcome.

3.4.2. Naive Bayes

"Naive Bayes represents a widely embraced and uncomplicated classification algorithm rooted in Bayes' theorem, a fundamental principle in probability theory (Chen et al., 2020). Its utility extends prominently to machine learning and natural language processing tasks, especially in situations characterized by an abundance of intricate features. At its core, Naive Bayes relies on Bayes' theorem, which elucidates the process of updating the probability of a hypothesis based on fresh evidence (Ressan & Hassan, 2022). In the context of classification, it empowers us to compute the probability associated with a specific class given the input features. The "naive" aspect of Naive Bayes posits that all input features are conditionally independent, signifying that the presence or absence of one feature exerts no influence on the presence or absence of any other feature (Foo et al., 2022). This simplifying assumption significantly mitigates computational complexity and renders the algorithm highly scalable, even in scenarios characterized by a profusion of features."

Consider a dataset comprising input features X1, X2, ..., Xn, with the goal of predicting the class label Y, which represents the target variable. In the Naive Bayes methodology, the algorithm calculates the likelihood of each class given the input features and subsequently designates the class with the highest probability as the predicted category (Kim & Lee, 2022). Mathematically, for a specific class denoted as c, the probability of observing the features X1, X2, ..., Xn can be determined using Bayes' theorem as expressed below:

$$P(Y = c|x_1, x_2, \dots, x_n) = \frac{P(Y=c)P(x_1|Y=c)P(x_2|Y=c)\dots P(x_n|Y=c)}{P(x_1, x_2, \dots, x_n)} \quad (2)$$

In the formula provided, P(Y=c) denotes the prior probability associated with class c, signifying the relative frequency of class c instances within the training data. P(Xi|Y=c) represents the conditional probability of feature Xi given class c, and this can be estimated from the training data. P(X1, X2, ..., Xn) represents the probability of observing the input features, serving as a normalization factor that remains consistent across all classes. During the classification process, this term can be disregarded as it does not impact the comparative likelihood of different classes (Kim & Lee, 2022).

During the training phase, Naive Bayes calculates the prior probabilities and conditional probabilities from the labelled training data. For discrete features, such as word occurrences in text classification, the probabilities can be estimated using simple frequency counting(Xu, 2018). For continuous features, common probability distributions like Gaussian (for continuous numeric features) or multinomial (for count data) are often used to estimate the probabilities.

3.4.3. SVM

SVM is a potent ML algorithm for classification and regression tasks, widely used in pattern recognition, image classification, text categorization, and bioinformatics due to its versatility (Huang et al., 2017). It seeks to discover the optimal hyperplane in a high-dimensional feature space to effectively separate different class data points, enhancing classification accuracy. In binary classification, this hyperplane serves as the decision boundary, creating a clear divide between two classes (Chandra & Bedi, 2021).

During the training phase, SVM aims to minimize the classification error while maximizing the margin. It does this by formulating a cost function that penalizes misclassification and accounts for the margin width (Zeng et al., 2019). The optimization process involves finding the Lagrange multipliers associated with the support vectors to determine the hyperplane coefficients. SVM offers several advantages, including:

(a) Flexibility: The use of various kernel functions allows SVM to handle data that might not be linearly separable in the original feature space.

(b) Robustness: SVM's reliance on support vectors makes it less sensitive to outliers, improving generalization performance.

(c) High-dimensional spaces: SVM is well-suited for problems with a large number of features, as it operates effectively in high-dimensional spaces.

(d) Interpretability: The support vectors are key components of the model, allowing for better understanding and interpretation of the classification boundaries.

3.4.4. Decision Tree

Decision Tree, a widely used ML algorithm for classification and regression, builds a hierarchical, interpretable tree-like structure from data (Lee et al., 2022). It repeatedly divides data into subsets using the most informative feature, aiding in clear decision-making. Internal nodes represent feature-based decisions, while leaf nodes contain final predictions for data subsets (Charbuty & Abdulazeez, 2021).

In Decision Trees, the decision process begins at the root node and follows a path down the tree based on input data's feature values. At each internal node, a choice is made using a feature-specific threshold or condition (Kotsiantis, 2013). This continues until a leaf node is reached, providing the final prediction. Building the tree involves selecting the best feature and split point at each node, which is determined by criteria like Gini impurity (Alcolea & Resano, 2021), and MSE or MAE errors for regression.

Decision Trees are interpretable, with a visualizable tree structure that represents rules for predictions. They work with numerical and categorical features and manage missing values automatically.

3.4.5. Random Forest

Random Forest, an hybrid ML method, enhances both classification and regression tasks by combining multiple Decision Trees for more accurate and stable predictions (Schonlau & Zou, 2020). Its versatility in handling complex data, reducing overfitting, and ensuring reliability makes it a key ML tool. The core concept involves creating numerous Decision Trees during training, then aggregating their predictions (Sekulić et al., 2020). Each tree is trained on random subsets of data and features, introducing diversity that bolsters model robustness against overfitting (Bai et al., 2022).

"During training, each tree in a Random Forest uses a bootstrap sample (randomly drawn with replacement) from the original dataset for training. Moreover, at each tree node, only a random subset of features is considered for splitting (Baba & Sevil, 2020). This diversity ensures that each tree captures different data perspectives and patterns. When making predictions, each tree independently classifies input data, and the final prediction is based on majority voting (for classification) or averaging (for regression). This aggregation minimizes noise and mitigates individual Decision Trees' biases, enhancing prediction accuracy and stability."

Random Forest has several advantages:

(a) Robustness: The aggregation of multiple Decision Trees reduces the risk of overfitting and makes the model more resilient to noisy data.

(b) Versatility: Random Forest can handle both categorical and numerical features, as well as missing values, without requiring extensive data preprocessing.

(c) Interpretability: Although Random Forest models may not offer the same level of interpretability as individual Decision Trees, they can offer insights into feature significance, aiding in the comprehension of which features wield the most influence in shaping predictions.

Scalability: Random Forest can efficiently handle large datasets and high-dimensional feature spaces.

4. Result and Discussion

Physionet Challenge 2017 Atrial fibrillation database used to detect AF. The sample of these dataset is represented in fig. 1. The PhysioNet Challenge 2017 Atrial Fibrillation Database, often referred to as the "AF Challenge 2017," was a competition organized by PhysioNet, an online repository of physiological data. The challenge aimed to promote research and development in the field of AF identification from ECG recordings.

The challenge provided a dataset of ECG recordings collected from a variety of sources. The dataset was diverse in terms of patient demographics, recording conditions, and ECG machine types.

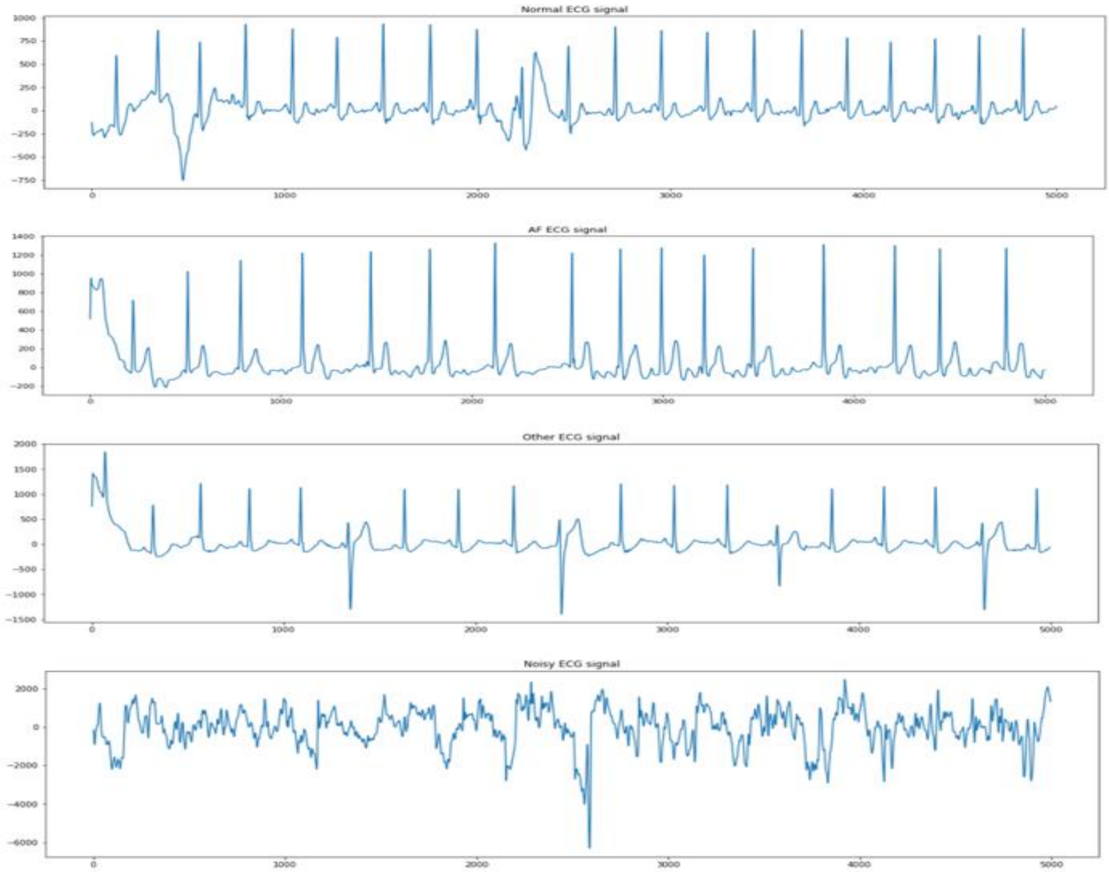

Fig. 1: ECG Signal

For cleaning and removal of noise from the initial signal the ECG signals are pre-processed using high pass, low pass and notch filter. The pre-processed signal is represented in fig. 2.

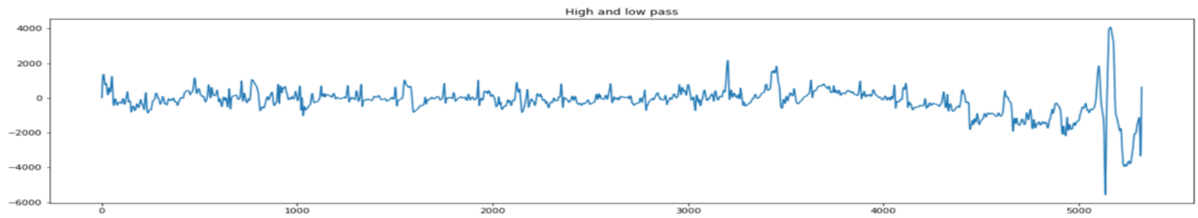

Fig. 2: Pre-processed Signal

Further the signal is conditioned by using butter high pass, butter lowpass and notch filter and their resultant is shown in fig. 3.

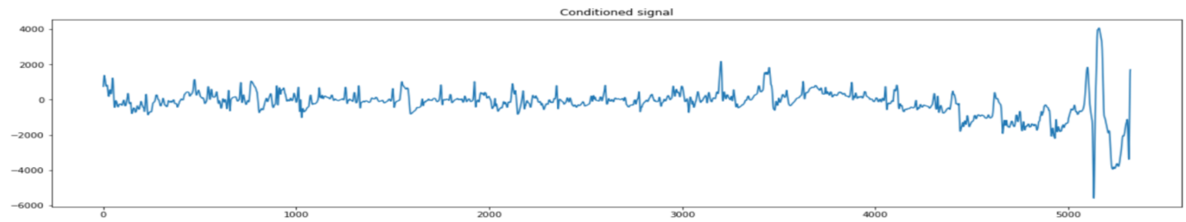

Fig. 3: Conditioned Signal

After the conditioning of signal the signal smoothened by converting the conditioned signal into its frequency domain. This signal is further transverse using IIR filter and the followed steps are shown in fig. 3.

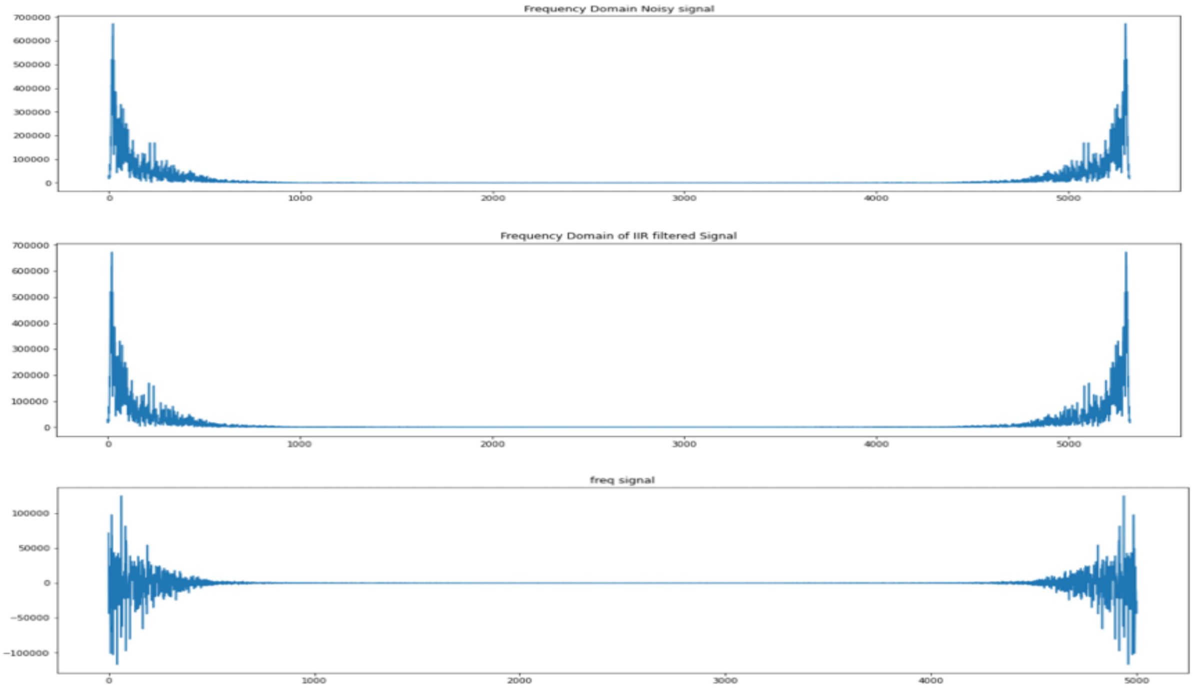

Fig. 4: Conditioned Signal

After applying the applicable filters, the final variation in the ECG signals is reported and are shown in Fig. 5.

Our comparative study reveals that all five ML approaches excel in detecting AF from ECG signals. Logistic regression achieved 92.48% accuracy and 91.89% sensitivity, Naïve Bayes reached 90.26% accuracy and 89.27% sensitivity, SVM attained 93.87% accuracy and 92.43% sensitivity, Decision tree delivered 93.87% accuracy and 90.63% sensitivity, and Random Forest outperformed with 95.8% accuracy and 92.88% sensitivity. Figure 6 illustrates the prediction accuracy levels.

The SVM model demonstrated robust performance, with relatively balanced sensitivity and specificity. Its ability to find the optimal hyperplane for separating classes and handling non-linear relationships between features and the target variable contributed to its success in AF detection.

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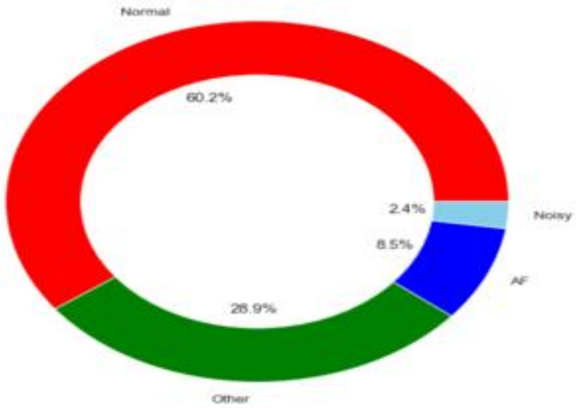
The Random Forest model's ensemble nature provided improved generalization and resilience to overfitting, leading to competitive results. The model's capability to process large datasets efficiently and handle missing values makes it an attractive choice for real-world applications. Despite the promising outcomes, some limitations merit consideration. The comparative study relies on a specific dataset, and performance may vary with different datasets or sample sizes. Additionally, feature engineering plays a critical role in model performance; thus, more advanced feature selection techniques could further improve the results.



	0	1	2	3	4	5	6	7	8	9	...	4991	4992	4993	4994	4995	4996	4997	4998	4999	5000
0	-127	-162	-197	-229	-245	-254	-261	-265	-268	-268	...	24	26	28	29	31	34	37	42	48	Normal
1	128	157	189	226	250	257	262	265	268	269	...	-54	-53	-52	-52	-53	-53	-54	-55	-57	Normal
2	56	73	85	93	100	107	113	117	118	117	...	-476	-479	-480	-481	-482	-483	-483	-484	-484	Normal
3	519	619	723	827	914	956	955	934	920	900	...	-32	-30	-28	-26	-25	-24	-24	-24	-24	AF
4	-188	-239	-274	-316	-356	-374	-380	-384	-387	-389	...	-31	-28	-25	-22	-19	-15	-12	-8	-4	AF
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
8073	-104	-127	-144	-154	-160	-164	-168	-170	-172	-172	...	14	13	13	13	12	12	11	11	10	Normal
8074	-121	-197	-288	-390	-496	-600	-693	-775	-848	-907	...	187	191	195	198	206	215	225	236	247	Other
8075	-202	-235	-272	-305	-325	-339	-344	-340	-334	-330	...	-4	-3	-3	-3	-4	-5	-7	-10	-12	Normal
8076	-227	-297	-374	-449	-505	-527	-539	-549	-557	-554	...	34	41	48	56	64	71	79	89	104	Normal
8077	-237	-286	-338	-390	-425	-437	-443	-445	-442	-435	...	-13	-12	-12	-12	-11	-11	-10	-9	-7	Normal

	heart_rate	mean_rr	std_rr	rmssd	qrs_duration	lppower	hppower	class
0	0.254977	235.315789	8.553563	7.749552	1.148	183.938194	32154.167841	Normal
1	0.206517	290.533333	54.853583	67.778526	1.148	343.889142	19525.825996	Normal
2	0.264931	226.473684	14.932721	17.824764	1.148	20.485827	29467.179102	Normal
3	0.196937	304.666667	57.899530	75.401307	1.148	3438.387991	44069.158571	AF
4	0.372842	160.925926	61.107026	75.453756	1.148	217.340560	47721.871918	AF
...	...	...	...	...	...	...	...	...
5544	0.218380	274.750000	78.031644	128.858320	1.148	462.736906	23128.264936	AF
5545	0.230665	260.117647	8.337600	13.495370	1.148	173.505130	3740.629067	Normal
5546	0.250988	239.055556	16.567948	10.975909	1.148	368.447748	30459.947834	Normal
5547	0.324544	184.875000	34.312671	50.846743	1.148	9.149812	47073.710725	Normal
5548	0.206754	290.200000	6.155756	7.750576	1.148	356.620903	18106.544478	Normal

Fig. 5 Proportion of signal variations

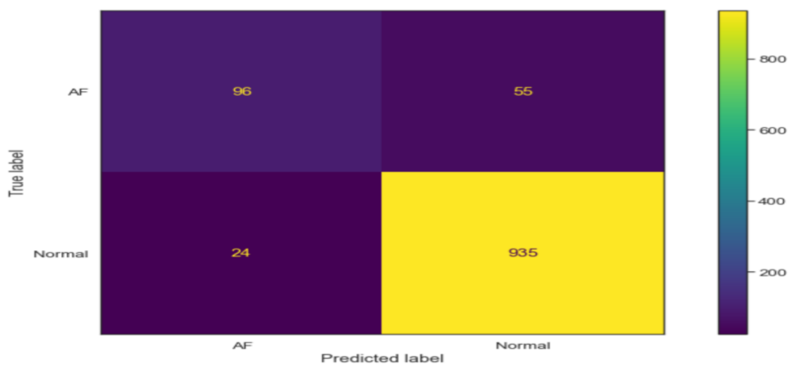


Fig. 6: Detection label

5. Conclusion

In summary, the utilization of ML techniques in AF detection offers significant promise in reshaping the landscape of diagnosing and managing this prevalent cardiac arrhythmia. Our study, addressing outlined challenges and objectives, seeks to contribute to the growing knowledge base that can lead to improved patient outcomes and more efficient cardiology healthcare practices.

Our comparative study underscores the potential of ML approaches as valuable tools for detecting AF from ECG signals. Logistic regression, Naive Bayes, SVM, Decision Trees, and Random Forest models all demonstrate high accuracy and robustness, indicating their potential integration into clinical practice for timely AF diagnosis. The choice of the most suitable method should consider specific needs, such as interpretability, computational complexity, and dataset characteristics. Future research could explore combining multiple classifiers or DL models to enhance AF detection accuracy and further advance automated cardiology diagnosis.

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