Machine Learning Approach for Diagnosis and Prognosis of Cardiac Arrhythmia Condition Using a Minimum Feature Set and Auto-Segmentation-Based Window Optimisation

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***Abstract*—Cardiovascular diseases have become extremely prevalent in the global population. Several accurate classification methods for arrhythmias have been proposed in the healthcare literature. However, extensive research is required to improve the prediction accuracy of various arrhythmia conditions. In this paper, discussion is focussed on two major objectives: optimisation of windows based on our proposed auto-segmentation method for the exact diagnosis of the heart condition within the segment and prediction of arrhythmia progression. For prediction, identification of features is vital. Identified efficient independent feature sets such as RR interval, peak-to-peak amplitude, and unique derived parameters such as coefficient of variation (CV) of RR interval and CV of peak-to-peak amplitude. The progression of arrhythmia includes the following steps such as data preprocessing, time and frequency domain feature extraction, and feature selection using principal component analysis. A hypertuned support vector machine is utilised for accurate diagnosis. Proposed two techniques to predict the progression of arrhythmias: the regression-based trend curve (RBTC) and the fuzzy enhanced Markov model (FEMM). We have effectively evaluated our prediction algorithms using offline Massachusetts Institute of Technology Physio Net database signals, using automatic segmentation with prediction accuracy of 98 %. In terms of accuracy, FEMM outperforms RBTC. Thus, an auto-segmentation algorithm was proposed to classify various arrhythmia signals using a minimal feature set and to predict future conditions using our proposed method, FEMM.**

***Index Terms*—Biomedical monitoring; Decision making; Feature detection; Markov processes.**

I. INTRODUCTION

An electrocardiogram (ECG) signal represents cardiac activity by sensing depolarisation and repolarisation caused by heart contraction and expansion [1], thus generating PQRST waves, with each cycle representing one cardiac cycle, or QRS complex. In healthy individuals, the ECG signal is called the "normal sinus rhythm" (NSR), while deviation in PQRST waves indicates an aberrant ECG signal, also known as arrhythmia [2]. If these arrhythmia conditions are not properly diagnosed and treated in a timely manner, they can lead to life-threatening cardiac problems. Bradycardia (BC), tachycardia (TC), supraventricular tachycardia (SVT), malignant ventricular ectopy rhythm (MVER), and atrial fibrillation (AF) are the five arrhythmia conditions considered the most common causes of cardiac disorder. The primary objective of diagnosing and predicting arrhythmia conditions is to determine the key features. By focusing on these key features and making the right algorithms, it is possible to build classification and prediction models that can successfully analyse ECG data and give valuable insights for making clinical decisions. By using the suggested auto-segmentation method, this method tries to get the most out of the analysis windows. When correctly segmenting the ECG signals, the algorithm can focus on certain segments and perform a more accurate analysis. Machine learning (ML) algorithms, such as support vector machine (SVM), are well suited for tasks requiring feature interpretation. This algorithm can provide insight into the significance and impact of individual classification, as well as prediction features. Deep learning (DL) methods, on the other hand, are a subset of ML that have grown in popularity due to their ability to automatically acquire features from raw data without explicit feature engineering. Convolutional neural networks (CNNs) and recurrent neural networks (RNNs) are examples of DL models that can learn hierarchical representations of the data and immediately extract relevant features from the input. Although DL methods excel at tasks involving image, speech, and natural language processing, their use in ECG analysis and prediction of arrhythmias may require more labelled data and computational resources. In addition, the interpretability of DL models can be more difficult than that of conventional ML algorithms. In the context of the research discussed, ML algorithms have been applied to the identification and interpretation of features of the analysis of arrhythmias.

This paper focusses on the proposed auto-segmentation-based window optimisation algorithm with a minimal feature set for arrhythmia progression using the coefficient of variation (CV) as an important parameter along with Fuzzy Enhanced Markov Model (FEMM)-based arrhythmia prediction, a unique concept that, to the best of our knowledge, has not been previously proposed in the

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literature. The remainder of the paper is structured as follows. In Section II, a concise literature review is provided. Section III describes the methodology, Section IV elaborates on the results and discussions, and Section V concludes with a summary of the work and a discussion of its implications for future research.

II. LITERATURE REVIEW

ECG recordings are utilised for arrhythmia detection. The duration of the recordings deemed essential for an accurate diagnosis. ECG signal segments are transmitted sequentially to the classification system for continuous monitoring. The information derived from these segments can be utilised to predict the progression of an arrhythmia. Consequently, early diagnosis will allow patients to receive opportune treatment, thus reducing the mortality rate. Although there are numerous novel algorithms in active research, signal conditioning, feature extraction, reduction, and detection of ECG for prediction remain formidable obstacles. Initially, noise must be removed efficiently for signal conditioning, which requires a preprocessing stage. Although there are numerous filtering techniques such as wavelet transforms and adaptive filters, we chose band-pass filters because they are superior at eliminating noise from offline signals. After removing the noise from the ECG signal, the next step is to extract essential biomedical features for the classification and prediction of arrhythmias. Despite the fact that numerous characteristics in the time/frequency domain have been proposed in the literature for this purpose, we selected two features using principal component analysis (PCA) [3]. The main aim of feature reduction is to eliminate redundancy and minimise computational complexity during classification. For the classification of arrhythmias, machine learning algorithms such as k-nearest neighbour (k-NN) [4], naive Bayes [5], random forest, and support vector machine (SVM) have been extensively proposed in the literature. The support vector machine-based particle swarm optimisation technique (SVM-PSO) was used in [6] to reduce the lower dimensions (input variables) in the training data to improve the accuracy of the classification algorithm. It has been observed that SVM performs better due to its rapid response and that fuzzy quasilinear SVM reduces overfitting and outliers with reduced error [7]. Compared to quasilinear SVM, clustering-based SVM can be used to effectively separate the hyperplane and devise the appropriate membership function, resulting in model robustness by eliminating outliers. Variations in the QRS complex are identified using the Fourier transform, Hilbert transform, wavelet transform, short-time Fourier transform (STFT), and Hermite transform [8]–[12]. STFT allows for real-time classification based on the energy spectrum [8]. ECG patterns for various arrhythmias have been identified [13] using clustering and window optimisation. Using the discrete wavelet transform and adaptive segmentation, abrupt changes in ECG characteristics have been discovered [10]. In our research, we proposed a novel segmentation technique for determining the optimal window size for every form of arrhythmia.

The progression of an arrhythmia can be predicted by forecasting the characteristics of the ECG. Various methods for prediction have been proposed in the literature, including linear regression, K-NN, the Markov model, and polynomial regression. Heart rate variability (HRV) is an effective predictor of the arrhythmia progression [14]–[16]; however, its convergence time is prolonged. Our proposed FEMM identifies the precise arrhythmia condition with the fewest number of features. Using prior knowledge of the data sets, Bayesian algorithms have been proposed to predict the conditions. In our work, we propose the FEMM, which predicts the arrhythmia condition with fewer features than the aforementioned methods.

The proposed research focusses on feature set minimisation, optimal window based on auto-segmentation for arrhythmia classification, and FEMM-based arrhythmia prediction.

III. METHODOLOGY

The steps involved in the proposed method are given in Fig. 1, which gives the overall scope of the work, which includes data acquisition, preprocessing, auto-segmentation, feature extraction, and minimisation followed by diagnosis and prognosis.

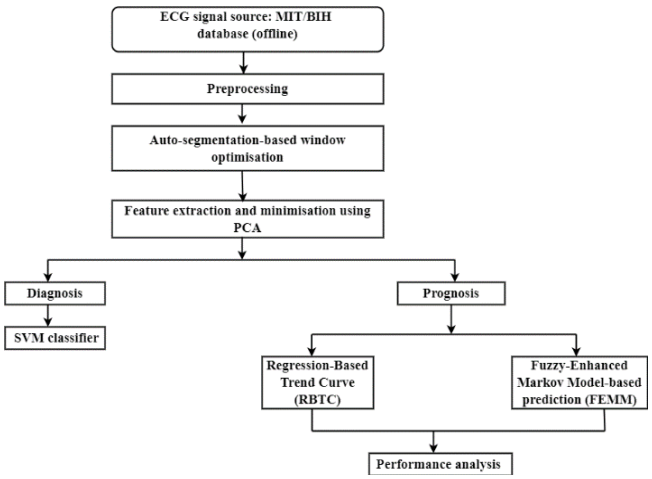


Fig. 1. Flow chart representing the scope of the proposed work.

A. Data Set Collection

The offline signals were obtained from the Physio Net database at MIT-BIH [17] for various arrhythmia conditions, and the obtained records are shown in the Table I.

TABLE I. RECORDS USED IN THE WORK.

Arrhythmia Conditions	Records used	Total number of records
BC	100, 101, 102, 104, 105, 115, 121, 123, 124, 202	10
TC	106, 107, 108, 109, 110, 111, 112, 113, 114, 117	10
NSR	16265, 16272, 16423, 16240, 16420, 16483, 16579, 16773, 16786, 16795, 17052, 16745, 18184, 19140, 19093, 19090, 19088, 18177, 17453, 19830	20
AF	iaf3_afwm, iaf2_tvam, iaf2_svcm, iaf2_ivcm, iaf2_afwm, iaf1_tvam, iaf1_svcm, iaf1_ivcm, iaf1_afwm, cu01, cu02, cu03, cu04, cu05, cu06, cu07, cu08, cu09, cu10	20
SVT	800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 820, 821, 822, 823, 824, 825, 826	20
MVER	428, 429, 430, 602, 603, 605, 607, 609, 610, 611, 614, 615, 427, 418, 419, 420, 421, 422, 423, 424	20

This database contains signals with durations ranging from one minute to several hours. We have segmented the long-duration signals into smaller, uniformly sized windows and generated a larger data set. Before preprocessing, we resampled all of these signals to a homogeneous sampling rate of 360 Hz because they were acquired with varying sampling frequencies. Figure 2(a) depicts the typical NSR signal, while Figs. 2(b) to 2(f) depict numerous arrhythmia signal samples.

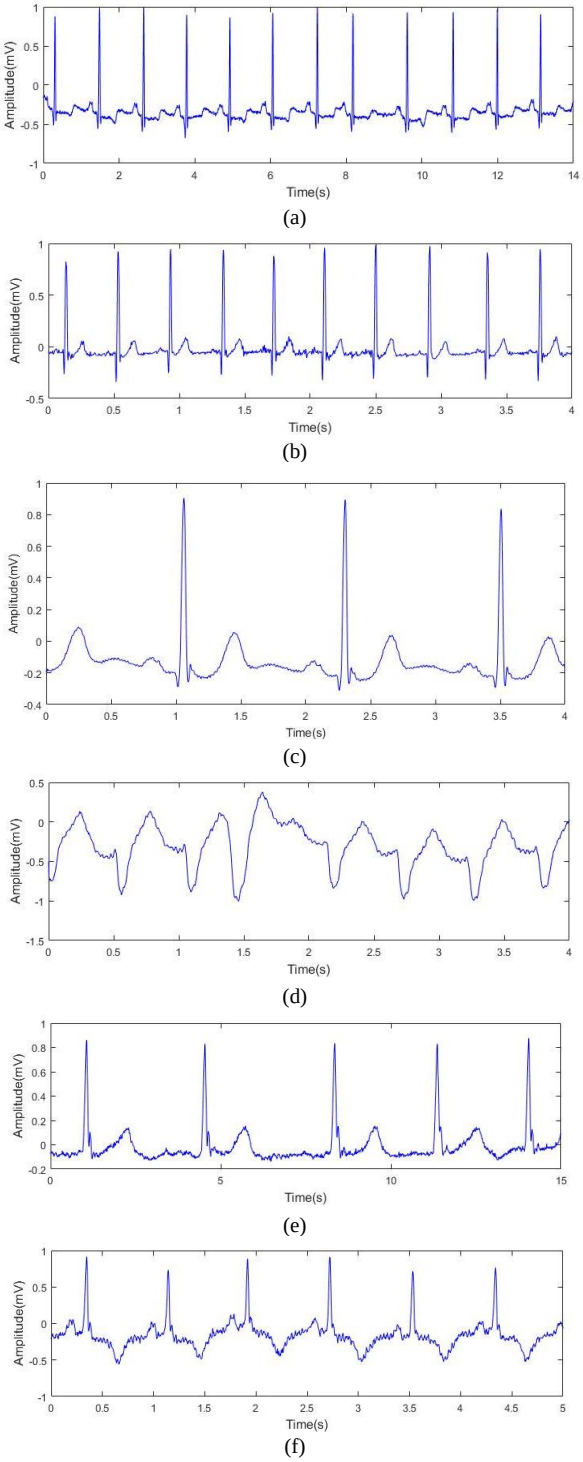


Fig. 2. Various types of arrhythmia considered for classification and prediction: (a) NSR; (b) BC; (c) TC; (d) AF; (e) SVT; (f) MVER.

B. Preprocessing

The sequence of preprocessing operations is depicted in Fig. 3. Passing the signal through a band-pass filter (BPF) with a lower cutoff frequency of 0.4 Hz and an upper cutoff frequency of 40 Hz eliminates noise disturbances such as power line interference and baseline wandering. Then the ECG signal normalises between 0 and 1.

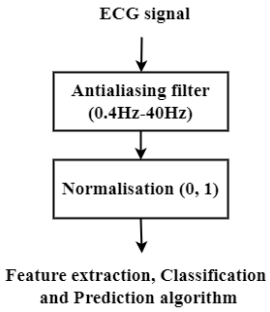


Fig. 3. Preprocessing block.

Here, Fig. 4 shows the preprocessing stages of a normal sinus rhythm.

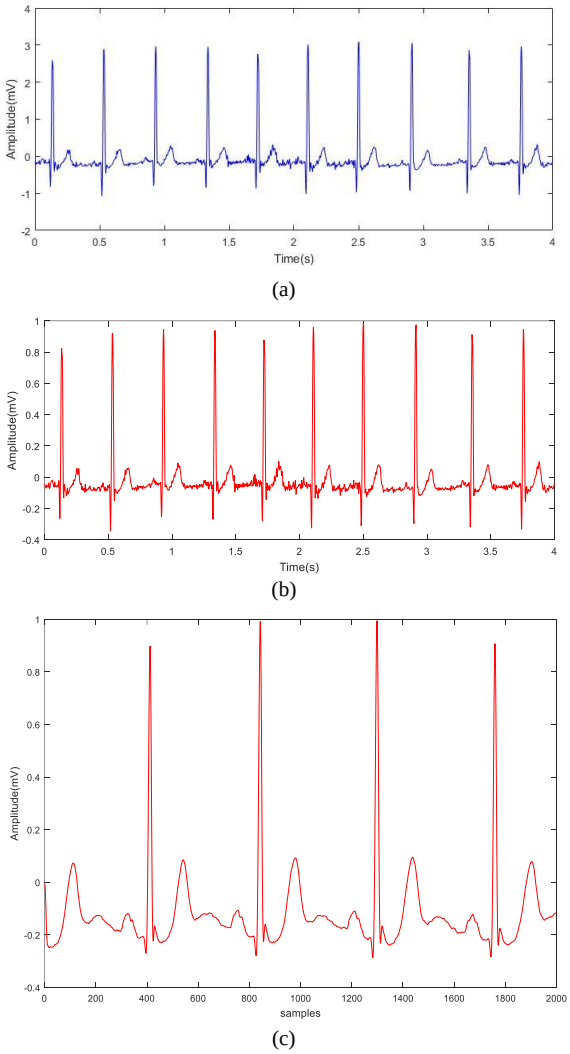


Fig. 4. (a) A portion of the raw ECG signal; (b) Normalised ECG signal; (c) Noise filtered ECG signal.

C. Auto-Segmentation-Based Window Optimisation

Real-time ECG monitoring can be performed continuously or at regular intervals, and diagnosis is based on multiple measurements. The algorithm proposed for optimising the window size based on auto-segmentation is an innovative method. The method seeks to improve the accuracy of

diagnosis and prediction by dynamically adjusting the window size based on the specific type of arrhythmia depicted in Fig. 5. The initial window length size is vast enough. Note that the optimal window size varies depending on the form of the arrhythmia. Therefore, the procedure must be repeated for each form of arrhythmia.

As shown in Fig. 5, choose an initial window L that is of considerably larger length, say one minute or more. The features (RR_{ref} and PP_{ref}) are extracted for this window and stored as references. The allowable tolerances around the reference values are also fixed ($\pm RR_{th}$ and $\pm PP_{th}$) for each type of arrhythmia. Start by reducing the window size by half iteratively and check the features of the reduced window every time. If the features are within the thresholds, we continue with the truncation. If the window size is L_i for the i^{th} iteration, it will be $L_i/2$ for the $(i + 1)^{th}$ iteration. If there is a disparity between the values of the actual features and the reference features, the window length $L_i/2$ is increased by $L_i/4$. Thus, the new window length will be $L_i/2 + L_i/4$.

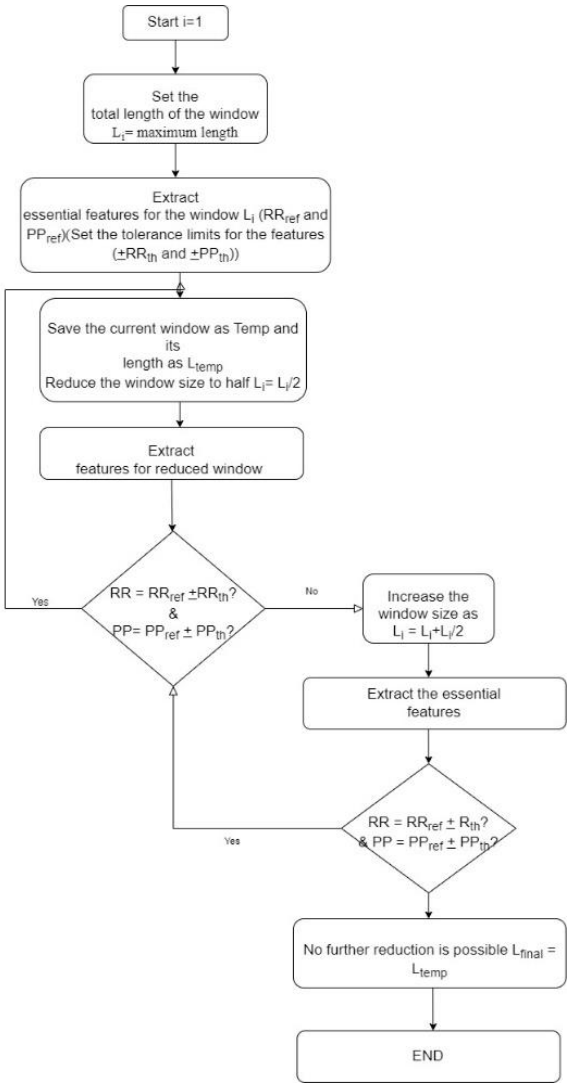


Fig. 5. Auto-segmentation-based window optimisation procedure.

This is considered the new window length, and the procedure is repeated over and over again. Therefore, the optimal window size for each type of arrhythmia is reached as follows:

– LAF = optimal window size for atrial fibrillation;
– LBC = optimal window size for bradycardia;
– LNSR = optimal window size for normal sinus rhythm;
– LTC = optimal window size for tachycardia;
– LSVT = optimal window size for supraventricular tachycardia;
– LMVER = optimal window size for malignant ventricular ectopy rhythm.

Windows are segmented using our suggested method and the derived CV parameter for RR and PP. For classification and prediction, the minimum window size based on auto-segmentation is utilised, as shown in Table II.

TABLE II. WINDOW ANALYSIS FOR VARIOUS ARRHYTHMIA CONDITIONS.

Condition	RR (s)	PP (mV)	Optimal window size (s)
NSR	0.62	0.99	7.8
	0.78	1.00	
	0.70	1	
BC	1.00	0.5	7.56
	0.60	0.79	
	0.95	0.9	
TC	0.68	0.68	9.65
	0.64	0.92	
	0.52	0.73	
AF	1.03	0.2	5.86
	1.60	0.36	
	1.13	0.45	
SVT	1.83	0.65	3.58
	1.06	0.98	
	1.54	0.85	
MVER	0.85	0.9	2.89
	1.01	0.45	
	1.35	0.62	

For some arrhythmia conditions, 5 seconds is adequate for prediction, but in other cases, 5 seconds is insufficient; therefore, 10 seconds was chosen to overcome the tolerance. We analysed 10 min signals obtained from the MIT/BIH Physio Net database, segmented them for durations of 5 s, 10 s, and 60 s, and using these segmented signals, a regression curve was drawn to analyse the patterns and trends of the data. The regression curve provides information on the relationships between various characteristics or variables and facilitates comprehension of the progression of arrhythmia over time. The signal durations of 10 s allow for a comprehensive analysis of arrhythmia patterns over an extended time period. This allows the capture of both short- and long-term trends, which is useful for predicting the progression of arrhythmias. In conclusion, by analysing signals of varying durations and plotting regression curves, the proposed method aims to provide a comprehensive understanding of arrhythmia patterns and facilitate a straightforward prediction based on the selected window sizes. Extended durations of 10 minutes and 30 minutes allow for a more in-depth analysis, whereas 5-second and 10-second window sizes accommodate the variability in various arrhythmia conditions.

D. Feature Extraction

Identification of the R peak is the initial stage in extracting multiple features such as RR, HR, HRV, etc. Adaptive thresholding is carried out using the moving average method, where it is implemented in each window to determine the R peak by comparing the previous window to the current window, with a threshold range of 0.001 mV to 0.8 mV. The

signal that has been normalised over the range [0 mV, + 1 mV] and the R peaks are detected and their amplitudes are calculated using adaptive thresholding. After identifying the R peak, the features are extracted. NSR is identified when the heart rate is between 60 and 100 pulses per minute, the RR interval varies within 0.16 seconds, and the PP of the signal is approximately 1 mV which is shown as their salient features in Table III. 10 distinct time domain features that can be extracted from the ECG signal are identified.

TABLE III. VARIOUS TYPES OF ARRHYTHMIA AND THEIR SALIENT FEATURES*.

Arrhythmia type	HR (BPM)	RR (s)	PP (mV)
BC	20–60	0.6 < x < 1.2	0.2 < x < 0.9
TC	100–160	0.4 < x < 0.7	0.7 < x < 0.95
NSR	70–80	0.6 < x < 1.2	0.4 < x < 1.0
SVT	150–250	0.4 < x < 0.6	0.5 < x < 1.0
AF	350–400	0.8 < x < 0.5	0.1 < x < 0.4
MVER	240–350	0.1 < x < 0.3	0.25 < x < 0.55

*Note: *Referred from the American Heart Association (AHA) standards [10].*

Mean (μ): It is defined as the average amplitude of the ECG signal that is calculated as shown in (1)

$$\mu = \frac{1}{N}\sum_{n=1}^{N} x(n), \tag{1}$$

where μ = mean amplitude, N = total number of samples in the ECG window, and x(n) = the n^{th} ECG sample within the window.

Variance (σ^2): It gives an average of the estimated value shown in (2)

$$\sigma^2 = \frac{\sum\left(x(n)-\mu\right)^2}{N}. \tag{2}$$

Standard deviation (σ): It is defined as the square root of the variance as given in (3)

$$\sigma = \sqrt{\frac{\sum x(n)-\mu}{N}}. \tag{3}$$

Average RR interval (RR): RR is defined as the average difference between the present and successive R peaks as shown in (4)

$$RR = \frac{1}{N-1}\sum_{i=2}^{N} RR_{(i)} - RR_{(i-1)}, \tag{4}$$

where $R_{(i)}$ = present R peak within the window.

Mean Absolute Value (MAV): It is defined as the mod of the ECG sample within the window with respect to the mean value as shown in (5)

$$MAV = \frac{1}{N}\sum_{n=2}^{N}\left|x(n)-\mu\right|. \tag{5}$$

Standard deviation of RR interval (SDNN): It is the root square of the average difference between the R peaks as expressed in (6)

$$SDNN = \sqrt{\frac{1}{N-1}\sum_{i=1}^{N}\left(RR_{(i)} - RR_{(i-1)}\right)^2}. \tag{6}$$

Root mean square of standard deviation (RMSSD): It is defined as the root mean square between successive R peaks as given in (7)

$$RMSSD = \sqrt{\frac{1}{N-1}\sum_{i=1}^{N}\left(RR_{(i+1)} - RR_{(i)}\right)^2}. \tag{7}$$

Heart rate (HR): It is defined as the average of RR with respect to the sampling frequency, as shown in (8)

$$HR = \frac{f_s \times 60}{RR}. \tag{8}$$

Heart rate variability (HRV): It is defined as the variation in the RR interval with respect to the mean. Taking into account the numbering of windows as j = 1, 2, 3, …, $HRV_{(j)}$ is calculated using (9)

$$HRV_{(j)} = HR_{(j)} - HR_{(j-1)}. \tag{9}$$

Peak-to-peak amplitude (PP): It is defined as the difference of the maximum and minimum of normalised amplitude as shown in (10)

$$PP = \max\left(x(n)\right) - \min\left(x(n)\right). \tag{10}$$

Table IV gives the minimum and maximum values of each feature as observed from the ECG signals database that cover all types of arrhythmias. This gives an idea of the limiting values and helps in fixing the thresholds and ranges for classification.

TABLE IV. FEATURES AND THEIR RANGE OF VALUES OBSERVED FOR THE ECG DATA SET (100 SAMPLES)*.

Sl. No.	Feature	Unit	Overall range including all 4 types of arrhythmia
1	Heart rate (HR)	BPM	4–205
2	RR interval (RR)	s	0.6–4.8
3	Peak-to-Peak amplitude (PP)	mV	0.04–1.38
4	Mean absolute value (MAV)	mV	0.06–0.7
5	Heart rate variability (HRV)	--	0.002–0.4
6	Standard deviation of normal to normal inter beat (SDNN)	mV	0.01–30.10
7	Root mean square of standard deviation (RMSSD)	mV	0.003–24.5
8	Mean of amplitude	mV	$9.49e^{-08}$–2.13
9	Standard deviation of amplitude	mV	$1.44e^{-05}$–86.5
10	Variance of amplitude	mV	$2.08e^{-10}$–16.88

*Note: *Data sets as per Table I.*

E. Feature Minimisation Using PCA

Using PCA, the essential features are identified from the 10 extracted features. To eliminate inconsistencies, redundant data, and highly correlated features, PCA extracts the eigen values and eigen vectors of the features to evaluate the

principal components. The number of features can be reduced without affecting the accuracy of the classification or causing overfitting problems [18].

The correlation plot of all features is depicted in Fig. 6. According to the matrix, correlation coefficients of 0.6 or higher are significantly correlated with the PP and RR. Table V displays the percentage of variance derived as a result of PCA, which demonstrates that highly correlated values have low variance and vice versa.

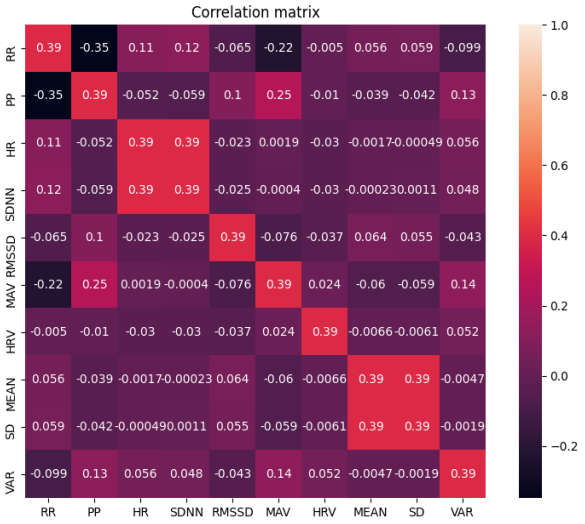


Fig. 6. Correlation matrix of all 10 features extracted from the ECG signal.

TABLE V. VARIANCE PERCENTAGE FOR VARIOUS FEATURES.

FEATURES	VARIANCE %
PP	74
RR	73
MAV	70
HRV	68
HR	63
SDNN	56
RMSSD	53
Mean	50
SD	43
Variance	42

To reduce the number and type of features to an optimal level, independent component analysis (ICA) is conducted, and the corresponding feature weights are displayed in Fig. 7. Initialising the random state to zero, it decomposes the covariance matrix and generates a new set of values until convergence, at which point the weights are generated.

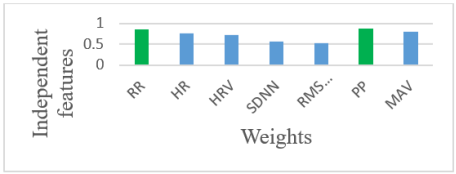


Fig. 7. Plot of weights obtained for various features through ICA.

By identifying independent features and their variations, the method seeks to capture crucial data for precise classification and prediction. However, we propose two additional features for prediction: CV_{RR} and CV_{PP}. For predicting future values, the CV provides the trend of these two characteristics. The four characteristics of our classification and prediction algorithm are as follows:

1. RR - interval of the RR complex;
2. PP - peak-to-peak amplitude;
3. CV_{RR} - coefficient of variation for the RR interval;
4. CV_{PP} - coefficient of variation for the peak-to-peak amplitude.

F. Diagnosis of Various Arrhythmia Conditions

Before prediction, diagnosis is a crucial stage because it sets the groundwork for understanding the arrhythmia condition and customising prediction models accordingly. An accurate diagnosis provides vital information for the effective and individualised prediction of arrhythmia progression. Classification is done based on the range within which each feature lies. The box plots shown in Figs. 8(a) to 8(d) confirm that the RR and PP values exhibit significant and distinct deviations from the mean for each form of arrhythmia. To predict the progression of an arrhythmia, CV_{RR} and CV_{PP} are calculated using (11) and (12), which assess the deviations of RR and PP from their respective means. By evaluating the deviations of RR and PP from their respective means via CV_{RR} and CV_{PP}, the proposed method captures the time-varying variability and dynamics of these features. Higher values of CV_{RR} and CV_{PP} indicate greater fluctuations and irregularities in the RR and PP, respectively, indicating an increased probability of progression of the arrhythmia. This finding suggests that a minimal feature set consisting of RR and PP is effective for classification purposes, which could simplify the classification algorithm and reduce computational cost:

$$CV_{RR} = \sigma(\mathrm{RR})/\mu(\mathrm{RR}), \tag{11}$$

$$CV_{PP} = \sigma(\mathrm{PP})/\mu(\mathrm{PP}). \tag{12}$$

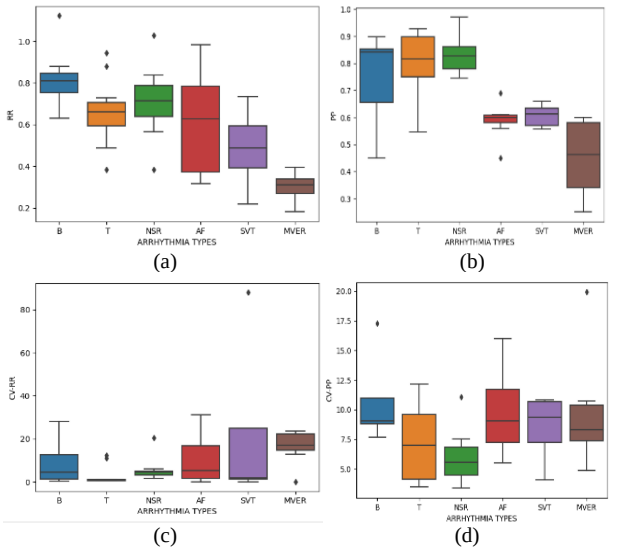
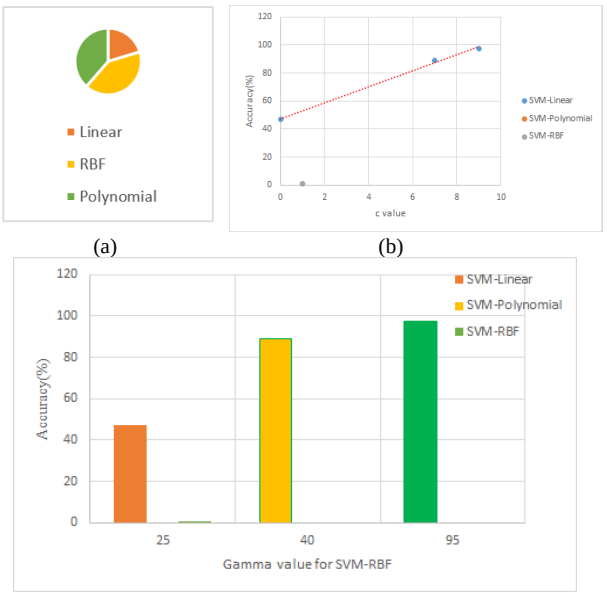


Fig. 8. Box plot: (a) RR, (b) PP, (c) CV_{RR}, and (d) CV_{PP} showing the ranges for different arrhythmia conditions.

G. Support Vector Machine (SVM)-Based Classification with Hyperparameter Tuning

SVM is an efficient classifier that is basically a model of supervised learning algorithms, as it removes outliers from the data set and avoids the overfitting problem. It has three different kernel types: linear function, radial basis function (RBF), and polynomial function. The SVM uses an n-dimensional space (where n is the number of features) and plots the data in the space, with the value of each feature

being the value of a particular coordinate. The hyperplane thus formed separates one class from another by dividing the samples into groups. The hyper parameters in RBF-SVM, namely "C" and "γ" used for this purpose can be tuned for maximum accuracy. "C" is used to reduce the error, and the parameter "γ" is used in the decision boundary. Figure 9(a) shows the accuracy plot with respect to different types of kernels, while Fig. 9(b) shows the optimisation of SVM with respect to the tuning parameter "C" where the SVM-RBF reaches the maximum accuracy when the value of "C" is at 9 compared to other methods. Therefore, the optimal values of "C" and "γ" obtained for the three types of SVM kernels and the classification accuracy obtained are shown in Table VI.



(a) (b)

(c)

Fig. 9. SVM accuracy with respect to (a) kernel type, (b) hyperparameter "C", and (c) hyperparameter "γ".

TABLE VI. OPTIMAL VALUES OF HYPER PARAMETERS OF SVM WITH DIFFERENT KERNEL FUNCTIONS AND THE CORRESPONDING CLASSIFICATION ACCURACY OBTAINED.

Functions	C value	γ value	Training accuracy (%)	Testing accuracy (%)
SVM-Linear	0.0001	25	45	47
SVM-Polynomial	7	40	92	89
SVM-RBF	9	95	98	97.6

Based on the results obtained, the SVM-RBF algorithm with the highest accuracy of 97.6 % as inferred from Fig. 10 is selected for implementation alongside its optimised hyperparameter values. Totally 1600 samples have been given for classification in which 80 % have been given for training set and 20 % have been given for testing to the classification algorithm.

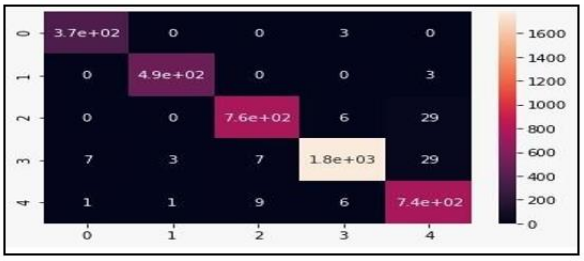


Fig. 10. Confusion matrix for the classification of SVM-based arrhythmias.

Based on our current or historical hypotheses and the data we already possess, our model provides accurate categorisation. From the classification, the classes of arrhythmia conditions are accurately distinguished, but for ECG prediction, segmentation and amplitude are crucial to accurately and simply predict future conditions. The selection of various signal durations and analysis contribute to the improvement of the prediction capabilities and the accuracy of the predictions. It is important to know that ECG prediction and classification are not mutually exclusive. They can work together to create a complete system for tracking and taking care of the heart. Classification helps to make decisions immidiately during ECG analysis, but prediction gives a bigger picture by predicting what will happen in the future and making care proactive.

H. Prediction of Arrhythmia Progression

Two different prediction algorithms are proposed, namely the regression-based trend curve (RBTC) and the fuzzy enhanced Markov model (FEMM) method, for the prediction of arrhythmia progression using segmented windows in continuous monitoring.

I. 1 Regression-Based Trend Curve (RBTC)

The regression-based trend curve (RBTC) predicts a specific characteristic as the n^{th}-order polynomial regression. ECG samples are divided into training and test data sets for the formulation of the RBTC equation. The training data set is used to develop the regression model, while the test data set is used to generate the prediction results. The flow chart of the prognosis algorithm using polynomial regression is given in Fig. 11. A 10-second prediction window for all forms of arrhythmia is used. The actual values are in contrast to the predicted values.

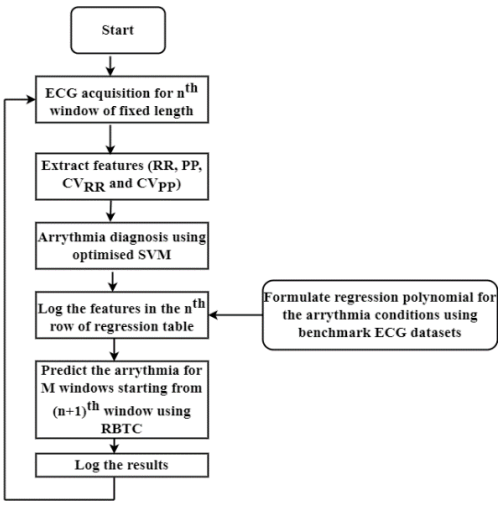
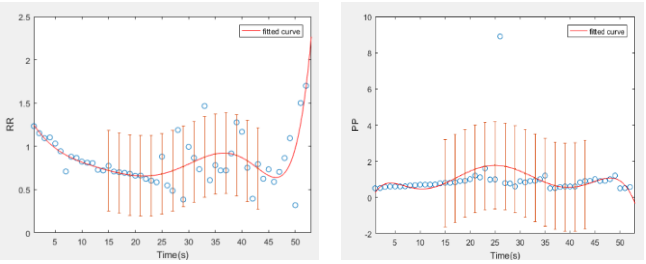


Fig. 11. Polynomial regression-based prognosis algorithm.

They were analysed using a regression diagram for the arrhythmia condition and created a graph. As an example, an RR interval feature set is obtained and plotted using various polynomial orders. As shown in Fig. 12, the analysis led us to the conclusion that polynomial regression of the fifth order best matches the curve for future predictions.

The prediction accuracy is observed to be excellent for the future. However, due to the ambiguity and uncertainty, the prediction fails for the future from the n^{th} window onwards. Randomly, 80 % of the training phase signals were selected,

and for the testing phase, 20 % were from the stored MIT/BIH data set signals. Analysis and prediction were carried out for RR and PP feature sets using the RBTC method, as shown in Fig. 12. Complex relationships involving interactions, nonlinearities, and higher-order effects can be challenging for regression models to capture.



(a) (b)

Fig. 12. Prediction of (a) RR and (b) PP using RBTC.

Typically, regression models are intended for interpolation as opposed to extrapolation. Extrapolation entails making long-term predictions outside the range of the observed data, and in such instances, regression models may not provide accurate predictions. For long-term prediction, probabilistic methods will be more suitable. Therefore, a Markov model-based prediction is proposed. The proposed Markov model-based prediction method provides a probabilistic framework for the long-term prognosis of arrhythmia progression. Incorporating the principles of Markov processes, it provides a method for estimating the probabilities of transitioning between various arrhythmia states and making accurate predictions about future states.

J. 2 Fuzzy-Enhanced Markov Model (FEMM)

When there are more uncertainties in the characteristics of the signal, the regression model cannot accurately predict certain arrhythmia conditions. The primary advantage of the Markov model is that it can accurately predict n steps in the future. The Markov model is made up of a sequence of states that constitute a chain. Changes from one state to another are called "transitions", and changes in state coordinated with probabilities are called "transition probabilities", leading to the formation of a Markov chain. The precision of prediction is determined by the precise formulation of the transition probability matrix, which is designed using RR and PP for various features of the ECG and is also based on the Markov equation for prediction. Since the characteristics of the ECG signal corresponding to different arrhythmia conditions are well understood, it is possible to design Markov equations for accurate prediction. Table VII shows the maximum and minimum range of values extracted from 100 ECG signal samples for the CV_{RR} and CV_{PP} features.

TABLE VII. RANGE OF FEATURES FOR VARIOUS ARRHYTHMIA CONDITIONS.

STATES	CV_{RR} (%)	CV_{PP} (%)
BC	45 < x < 33.3	15.6 <x < 26.68
TC	55 < x < 66.4	121 < x < 135
NSR	50 < x < 52.3	11 < x < 17.4
SVT	87 < x < 94.7	98 < x < 200.9
AF	178 < x < 183	389 < x < 400
MVER	109 < x < 120	189 < x < 220

The Markov model is capable of predicting n steps ahead with acceptable accuracy if the transition probability matrix is formulated properly. Fuzzy logic is then used along with the Markov model to enforce CV_{RR} and CV_{PP} for arrhythmia prediction. This describes the procedure for generating membership functions for ECG parameters. The membership function is generated for CV_{RR} and CV_{PP}. After estimating the features of 100 ECG signals corresponding to known arrhythmia conditions, these membership functions are obtained. The FEMM involves the following steps.

STEP 1: Training and testing data sets: The Markov model is trained and evaluated using multiple data sets that contain relevant features such as the RR and PP intervals. This stage comprises using 80 % of the data for training the model and 20 % for evaluating its performance.

STEP 2: The transition matrix is constructed from the characteristics of the RR and PP intervals. Specifically, the state-space paradigm divides the feature RR into six regions such as low (L), very low (VL), medium (M), high (H), and very high (VH). Each region represents a distinct state or condition associated with the progression of arrhythmia. The state-space model for the parameter RR as an example is given here

$$S = \{VL, L, M, H, VH, DH\},$$

where:

– VL = very low (0.1–0.3) s,
– L = low (0.3–0.5) s,
– M = medium (0.5–0.7) s,
– H = high (0.5-0.7) s,
– VH = very high (0.7–1.0) s,
– DH = dangerously high (1.0–1.2) s.

$$T = \begin{array}{c|cccccc} T & VL & L & M & H & VH & DH \\ VL & 0.76 & 0.11 & 0 & 0.05 & 0.02 & 0.06 \\ L & 0.71 & 0.21 & 0.03 & 0 & 0.02 & 0.03 \\ M & 0.3 & 0.4 & 0.24 & 0.06 & 0 & 0 \\ H & 0.06 & 0.4 & 0.17 & 0.1 & 0.09 & 0.18 \\ VH & 0.2 & 0.5 & 0 & 0.1 & 0.15 & 0.05 \\ DH & 0.09 & 0.43 & 0 & 0.08 & 0.18 & 0.22 \end{array}. \quad (13)$$

Assume

$$X = [1\ 0\ 0\ 0\ 0\ 0]. \quad (14)$$

Calculate

$$X_n = T_0X = T_0X^1 = T_0X^2 = \ldots = T_0X^n. \quad (15)$$

The obtained probability vector "X" is calculated using "T".

$$X^5 = \begin{bmatrix} 0.639 \\ 0.1854 \\ 0.0179 \\ 0.0474 \\ 0.039 \\ 0.07 \end{bmatrix}. \quad (16)$$

STEP 3: Fuzzy rules are formed after obtaining the output

vector from the transition matrix as shown in Table VIII. These fuzzy rules capture the links between the output vectors of RR interval and arrhythmia situations. The fuzzy rules express the patterns detected in the data linguistically. The IF-THEN rules were formulated, and then the Markov model was trained for every given feature, predicting the arrhythmia conditions for the next 10 seconds. Fuzzy rules were formulated based on the triangular and trapezoidal membership functions with the five linguistic variables as two input features for the five different types of arrhythmia conditions as shown in the Table IX. The membership function for the parameters (CV_{RR}, CV_{PP}) is formulated using these specifications and as an example the degree of membership for the CV_{RR} parameter is shown in the Fig. 13.

TABLE VIII. OUTPUT VECTORS FOR THE FEATURE RR FOR EACH WINDOWS ARE CALCULATED USING (15).

T	VL	L	M	H	VH	DH
T_0	1	0	0	0	0	0
T_1	0.76	0.11	0	0.05	0.02	0.06
T_2	0.6681	0.1625	0.0118	0.0498	0.0357	0.0721
T_3	0.6433	0.1811	0.0162	0.0484	0.0394	0.0716
T_4	0.6396	0.1851	0.0175	0.0476	0.0396	0.0705
T_5	0.6399	0.1854	0.0179	0.0474	0.0394	0.07

TABLE IX. SPECIFICATIONS OF THE FUZZY BLOCK FOR THE PREDICTION OF ARRHYTHMIA.

No. of features (inputs)	No. of linguistic variables	Membership function used	No. of output
CV_{RR} and CV_{PP}	5	Triangular and Trapezoidal	NSR, BC, TC, SVT, AF, MVER

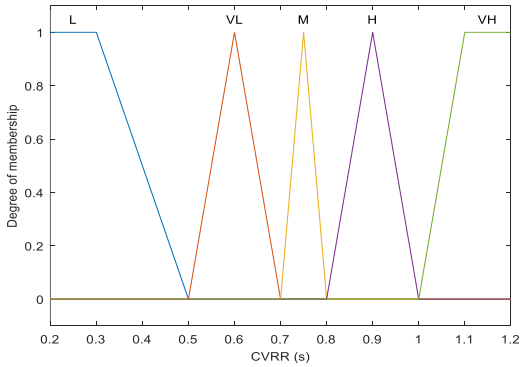


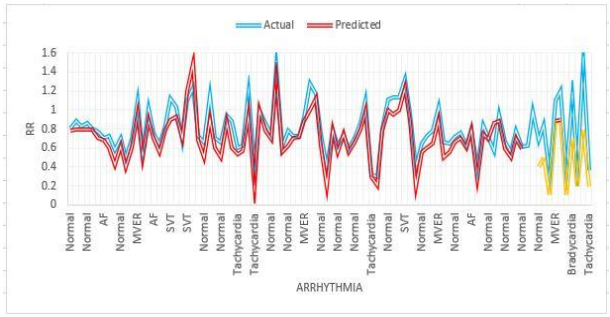
Fig. 13. Membership function of CV_{RR} parameter.

STEP 4: A transition probability matrix T is constructed using the mapped CV_{RR} values and other pertinent parameters. Based on the observed patterns and variances in the input characteristics, this decision matrix shows the probabilities of transitioning between distinct states in Table X.

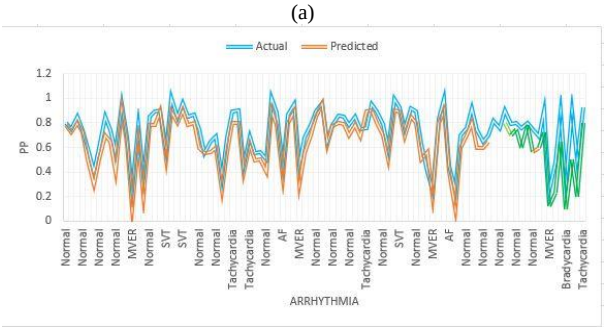
TABLE X. FORMULATION OF RULE MATRIX USING CV_{RR} AND CV_{PP} FOR DETECTION OF ARRHYTHMIA CONDITION.

CV_{RR}/CV_{PP}	L	VL	M	VH	H
L	TC	BC	MVER	MVER	SVT
VL	BC	NSR	MVER	SVT	Other condition
M	TC	TC	MVER	TC	SVT
VH	Other condition	SVT	SVT	Other condition	AF
H	BC	NSR	SVT	AF	AF

STEP 5: After the formulation of the rule matrix, the features extracted from the proposed FEMM were applied individually for each 10-second window. 10-second window was combined into a 10-minute window for the prediction of arrhythmia using the simple moving average technique, which sums up the predictions and divides them by the total number of predictions. The predicted accuracy is evaluated for the 10-minute window based on the 10-second prediction window and the comparison graph for actual versus predicted for the 10-minute window is shown with the colour variation for RR and PP in Fig. 14. The depiction in Fig. 14 is empirical evidence supporting the efficacy of the FEMM method for predicting arrhythmia. It emphasizes the ability of the model to estimate future values with a high degree of similarity to the actual values, reinforcing its potential as a valuable tool for monitoring and forecasting the progression of arrhythmias in clinical settings.



(a)



(b)

Fig. 14. Comparison of actual versus predicted using FEMM for consequent windows (a) RR and (b) PP.

To ensure accuracy and performance, the rule matrix is iteratively developed using past knowledge, and decisions are made according to them. However, under certain conditions, the probability is distributed and determined for each 10 s, making the decision to make a prediction difficult, and FEMM is more accurate than the simple Markov model. Therefore, fuzzy was improved along with the Markov model (FEMM) to determine the set of features and the arrhythmia condition using CV_{RR} and CV_{PP}. Two methods, RBTC and FEMM, were proposed for prediction, and these methods were analysed for varying seconds. RBTCs are only applicable to the feature set for which the Markov model produces accurate predictions for the 10-second window. Figure 14 provides a visual representation of the FEMM prediction results compared to the actual values. The graph demonstrates a close relationship between the predicted values of the FEMM method and the actual values. This conclusion suggests that the FEMM method predicts the progression of arrhythmia with high correlation and precision. The similarity between the predicted and actual values indicates that the FEMM model can capture the

underlying patterns and trends in the data, allowing it to make accurate predictions. The synopsis Table XI presents the performance of the numerous methods discussed previously.

TABLE XI. TECHNIQUES PROPOSED IN LITERATURE AND THE PERFORMANCE CLAIMED BY THE AUTHORS.

References	Features	Classifiers	Arrhythmias	Classification Accuracy	Prediction accuracy
Llamedo and Martínez [19]	RR interval, QRS morphology	SVM + PCA	2	86 %	NA
Devi and Kalaivani [20]	Statistical features	SVM	4	88.9 %	NA
Martis, Rajendra Acharya, and Min [21]	RR interval features	PCA + LS-SVM	5	93.48 %	NA
Martis, Acharya, Mandana, Ray, and Chakraborty [22]	RR interval features	PCA + NN	5	94.5 %	NA
Christov, Gómez-Herrero, Krasteva, Jekova, Gotchev, and Egiazarian [23]	QRS morphology	Matching pursuits algorithm	1	90.7 %	NA
Li, Pan, Li, Jiang, and Liu [24]	RR interval	Hidden Markov model	1	85 %	NA
Ashkezari-Toussi and Sabzevari [25]	Time domain and frequency domain	k-NN	5	NA	95 %
Gawde, Bansal, and Nielson [26]	QRS complex	Markov model	4	NA	91.8 %

Table XII gives the comparison result of various methods used for prediction in the literature, and our proposed work gives 98 % accuracy compared to other methods.

TABLE XII. COMPARISON OF PREDICTION ACCURACY WITH OTHER METHODS IN THE LITERATURE.

Methods	Prediction accuracy (%)
SVM + MM [27] (MIT/BIH Data Sets)	97.1
MM [28] (MIT/BIH Data Sets)	91.8
MM + Rule based [29] (MIT/BIH Data Sets)	97.3
SVM (MIT/BIH Data Sets) [30]	83.24
MM + Fuzzy (FEMM) (MIT/BIH Data Sets)	98

IV. DISCUSSION

Our proposed method is exceptionally efficient for both classification and prediction. Proposed PCA with SVM and obtained 97.6 % classification and 98 % prediction accuracy, respectively. Compared to other techniques proposed and discussed in Table XI, its efficacy is exceptional. Instead of visually observing them, the system extracts statistical characteristics and uses them for classification and prediction. The FEMM state machine and knowledge-based approach play a crucial role in system prediction by reducing the ambiguity of the system. It predicts not only the current 10-second window, but also the succeeding windows concurrently, which may result in 10 min signal prediction. As the initial conditions are based on the assumptions we make, the implementation of the Markov model alone is insufficient for accurate prediction, degrading the system's performance, whereas the fuzzy-based model does not require initial conditions, increasing the accuracy of the prediction. Using this method, the onset of arrhythmia conditions is identified, and early intervention for minutes is also very important for healthcare providers to reduce the severity. For long-term prediction, we must consider the patient's age, gender, and other somatic conditions, in addition to the patient's comorbidities, which are highly effective for hourly predictions. Our methodology has some benefits. It achieved a high level of accuracy with a minimal feature set, which is crucial for the prediction of arrhythmia in real time, whereas the other methods proposed in the literature use a large feature set. Using a minimal feature set and an automatic segmentation method reduces processing time complexity. Although our method is based on traditional techniques, it is active in processing signals in real-time prediction, and the identification of features is crucial for the development so that clinicians can identify arrhythmia conditions in continuous monitoring with ease.

Limitations: The model might require efficient training data sets to estimate the probability of the transition matrix, as well as subject matter knowledge from professionals in the field to construct the decision matrix that may lead to a lack of interpretation.

V. CONCLUSIONS

Our method was effectively implemented with the most important characteristics, including RR and PP, as well as the derived parameters CV_{RR} and CV_{PP}, which are sufficient to detect arrhythmia conditions. These characteristics are essential for accurate signal detection and prediction using our proposed auto-segmentation method. Through the FEMM model, it is also determined that ECG signal segmentation with respect to these features for identifying arrhythmia achieves an accuracy of 97.6 % and a prediction accuracy of 98 %.

Our hardware-efficient algorithm works well for both long- and short-duration signals in continuous monitoring.

Future plans involve working with real-time signals and implementing them in hardware. In addition, we can extend our work by implementing efficient adaptive filters for real-time signal denoising. Adjusting the Markov model and fuzzy design parameters also permits long-term forecasting.

CONFLICTS OF INTEREST

The authors declare that they have no conflicts of interest.

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