Detection of Cardiac Disease with Less Number of Electrocardiogram Sensor Samples using Chebyshev

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Abstract. Cardiac disease detection is a tedious process. Morphology of the electrocardiogram (ECG) sensor signal reveals the presence and severity of the cardiovascular disease. The most important factor that limits the detection of cardiac disease is the rare availability of instances of the abnormal condition collected using ECG sensors. In this work, we address the problem of cardiac disease detection with less number of ECG sensor signals using a Chebyshev function which is termed as Chebfun. The Chebfun approximates the signal with its coefficients. These coefficients known as Chebfun coefficients are used as the features instead of the conventional handcrafted features. With these features of Chebfun, the present work aims to give an interpretation of the features learned by the model for cardiac disease detection. The proposed work makes use of a machine learning algorithm to tackle the problem of better performances using less number of ECG sensor signals. Machine learning algorithms such as SVM, logistic regression, decision tree, and AdaBoost are used in the present work.

Keywords: Less Number of ECG, Chebyshev, Machine Learning.

1. Introduction

Nowadays, cardiac diseases have a wide variety of patterns, which change drastically with respect to the individual. ECG is the most reliable method for the detection of these variations in the diseases. The distinct features of the cardiovascular diseases are captured in the QRS complex, P-wave, and T-wave components of the ECG signal. The ECG is a record of the electrical activity of the heart and thus ECG could capture all anomalies that can happen in the cardiac activities. Therefore, the electrical impulses leave the trace of the abnormal activities in its ECG structure. Numerous conventional feature extraction techniques are available for retrieving the information from the ECG. At the initial stage, Pan et al.[1], proposed the real-time QRS detection algorithm in which they acquired 99.3% accurate QRS complex detection for 24 hours MIT/BIH arrhythmia database. Desai et al.[2] proposed a discrete wavelet transform (DWT) for denoising the signal and independent component analysis (ICA) as a dimensionality reduction technique using a support vector machine (SVM) classifier for arrhythmia classification. In addition to this, they used the Pan-Tompkins algorithm for R peak detection. The SVM quadratic kernel provides the highest classification accuracy of 98.4% and the highest kappa coefficient of 0.9520. Kalidas et al.[3] proposed a stationary wavelet transform along with adaptive thresholding for real-time beat detection. The proposed method was evaluated on MIT–BIH arrhythmia database, QT Database, and American Heart Association (AHA) database. The algorithm acquired sensitivity (SE) of 99.88% and a positive predictive value (PPV) of 99.84% on the MIT-BIH arrhythmia database. The algorithm also gained a sensitivity of 99.80% and PPV of 99.91% on the AHA database and sensitivity of 99.97 % and

PPV of 99.90% on the QT database. Kiranyaz et al.[4] proposed an adaptive implementation of 1-D convolutional neural networks (CNNs) for the classification of arrhythmia. The input of the model is the beat segmented ECG signals using R peak detection. The method acquired less computational complexity, high speed, and it combined the two major processes of feature extraction and classification in machine learning. They utilized the MIT-BIH Arrhythmia dataset on this approach. Xia et al. [5] proposed a 2D CNN for the detection of Atrial fibrillation. They used the short-term Fourier transform (STFT) and stationary wavelet transform (SWT) for converting the 1D features to 2D features. The MIT-BIH atrial fibrillation (MIT-BIH AFIB) data set was used for the performance evaluation of this approach. The CNN model method does not require the detection of P or R peaks or the extraction of handcrafted manual features for cardiac disease detection. 2D CNNs with the input based on STFT has gained a sensitivity of 98.34%, a specificity of 98.24%, and accuracy of 98.29% and DCNNs with the input based on SWT has acquired sensitivity of 98.79%, a specificity of 97.87%, and accuracy of 98.63%.

In all these scenarios, the cardiac disease is detected using the model trained with more numbers of samples. In most of the medical scenarios, there is less availability of unhealthy samples of data. This results in a lack of a sufficient amount of data to train the model. In such cases, where there is less availability of data samples, there is a requirement of capturing the proper disease-specific features that are best suitable for the detection of the diseases. In most conventional feature extraction techniques, they capture the peak information. It cannot be generalized that the cardiac abnormalities are captured only at the peaks. The presence of cardiac disease can change the structural morphology of the ECG signal. But in most cases, the conventional feature extraction technique fails to capture the structural variation that is continuous in nature. The structural variation that is present continuously in ECG is the one which aids the identification of disease. To tackle the problem of lesser samples for cardiac disease detection and to interpret the features learned by the model, we propose the Chebyshev based feature extraction technique.

2. Chebyshev polynomial interpolation

A Chebfun is a function that represents every function in an interval [-1,1]. It is an open-source package available in Matlab. It computes the function with an accuracy of 15 floating-point digits [14]. Chebfun is defined based on the fact that the smooth function can be symbolized by using the polynomial interpolations in Chebyshev points. The number of Chebyshev points is stored automatically to machine precision using an adaptive technique [14]. The Chebfun system only stores minimum Chebyshev points for representing a signal even with a large number of samples.

The Chebyshev points are defined by

$$x_j = -\cos(j\pi/N),\ 0 \le j \le N \tag{1}$$

The polynomial interpolant is defined as a unique polynomial at any data values at the Chebyshev points and a Chebyshev series is defined as an expansion represented as

$$f(x) = \sum_{k=0}^{\infty} a_k\ T_K(x) \tag{2}$$

a_k is known as the Chebyshev coefficients. The peculiarity of the Chebyshev is that we will get a continuous function while using the Chebyshev functions in the MATLAB.

The Chebfun of the signal ‘s’ is computed using the command

f=Chebfun(s) (3)

f is the Cheb function then, the command

$$C=\text{chebcoeffs}(f) \quad (4)$$

returns its Chebyshev coefficient. The truncation of the valid coefficient is computed by using the command

$$t = \text{Chebfun}(f,'\text{trunc}',m) \quad (5)$$

m, represents the number of the coefficients to which the function is to be truncated.

In the literature, the Cheb function (Chebfun) is used in the speech epoch extraction purpose [6] and in the electrical system [7]. B. Ganga et al. [6] used the Chebfun for the accurate epoch extraction of the telephonic speech signal. The proposed method gained an improvement in performance by incorporating changes in the prevailed zero frequency filtering by including the Chebyshev interpolation method. Neethu Mohan et al. [7] proposed a combination of variational mode decomposition and Chebyshev interpolation for the estimation of power system frequency and the amplitude.

3. Dataset Description

ICBHI 2019 scientific challenge cardiovascular disease dataset is used for the proposed work [15]. The SC dataset contains ECG signals and the PCG signals. The ECG sensor signals are collected in controlled clinical surroundings. The dataset contains both generalized normal and abnormal cardiac vascular disease cases. The dataset contains 24 normal cases (negative cases) and 13 abnormal cases (positive cases). The sampling frequency of the signal is 44100Hz.

3.1. Feature Extraction Technique based on Chebfun

The main feature that is considered for this study is the approximated signal that is extracted from the original signal using the Chebfun. The signal is initially downsampled from the sampling frequency of 44100Hz to a sampling frequency of 250 Hz. The signal is then transformed into a Chebyshev function. From the Chebyshev function, the Chebfun coefficients are extracted. The main advantage of the Chebfun is that we don't need to consider the whole signal coefficients. We take the Chebfun obtained from the truncated coefficients of the signal. Depending on the length of each signal the number of coefficients varies in individual ECG signals. To maintain the uniform length of coefficients for all the signals we can either reduce the number of coefficients to the minimum number available or we can zero pad the signal with a number of zeros to match each signal length. Here, the Chebfun coefficients considered are fixed according to the minimum coefficient required for the signal reconstruction.

4. Methodology

The main aim of the present work is to analyze whether the Chebfun feature can replace conventional feature extraction techniques for low resource data. Using the property of Chebfun coefficients to reconstruct the original signal the study also aims to interpret the features learned by the model. For this study, we have considered the feature extraction techniques such as the Pan-Tompkin algorithm [1],

Hamilton algorithm [9], Engelse, and Zeelenberg algorithm [10], Christov algorithm [11], stationary wavelet transform [12], and matched filter [13]. Due to the limitations in the availability of the data we have conducted the analysis using state-of-art machine learning algorithms such as SVM, Logistic Regression, Decision Tree, and AdaBoost. The best model parameters are computed using the grid search. For better validation of the result using a small dataset, instead of conventionally splitting the dataset into training, testing, and validation sets we consider the leave-one-out cross-validation (LOOCV). In this type of validation, the model is validated against each of the data samples. The workflow of the validation set up is that the model is trained for all the available data samples except one. The trained model is tested using untrained data. Similarly, this procedure gets repeated for all the data samples by shifting one after the other. The model accuracy is the average accuracy of the model prediction for all the data samples.

The methodology followed for the study is shown in Fig 1. The features from the ECG signal of the SC dataset is extracted using Chebyshev features, and other conventional features and is fed to the classifiers for making predictions. These prediction predictions are further analyzed for the study.

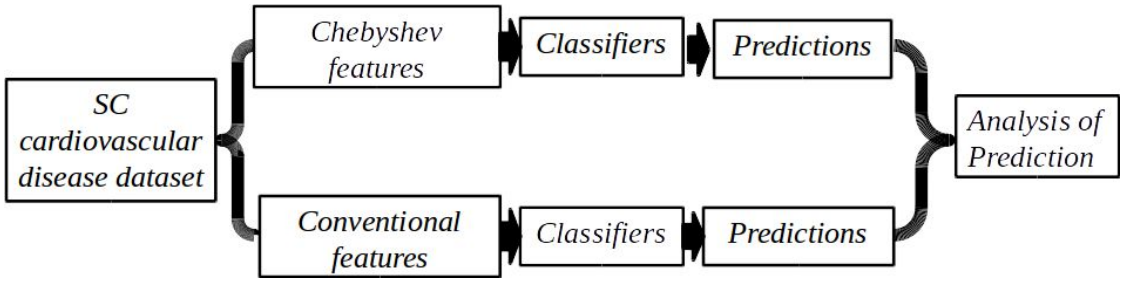

Fig 1. The workflow diagram of the proposed method.

5. Experiments and Results

The proposed work is evaluated using SC cardiovascular disease dataset. The dataset contains 13 abnormal ECG signals and 24 normal ECG signals. To fix the number of coefficients required to capture all the information of the ECG signal we computed the following experiments. Initially, the plot of Chebfun coefficients was analyzed. Fig 2 shows the plot of Chebfun coefficients. From the figure, we could interpret that most of the variations are present from time 0 to time 4000.

The model performance by varying the length of the Chebyshev coefficient was evaluated to finalize the number of coefficients required. The experiments are done by varying the coefficients from feature length 2000 to 7000. Table 1, 2, 3, and 4 shows the performance analysis of the different machine learning algorithms using different feature length of Chebfun coefficients. The number of coefficients is finalized through the evaluation of the model performance using varying coefficients.

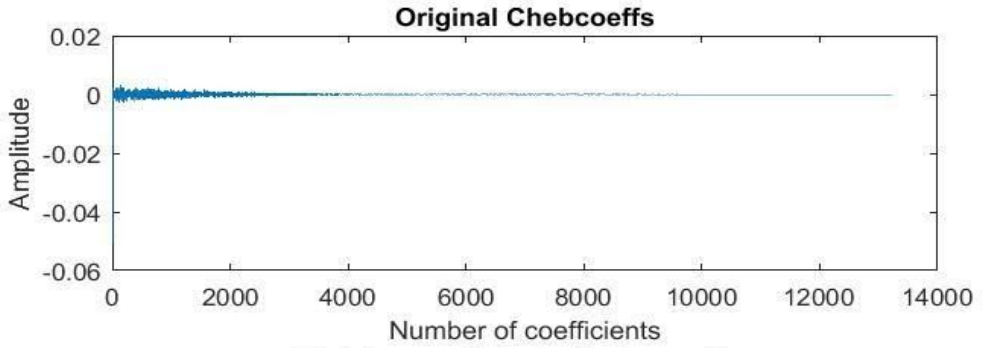

Fig 2. The variation of the Chebfun coefficient for a signal.

Table 1. Performance analysis of Chebyshev features based on the number of coefficients in terms of accuracy (%).

No. Coeff.	2000	2500	3000	3500	4000	4500	5000	5500	6000	6500	7000
SVM	64.86	64.86	78.4	**81.1**	**81.1**	78.37	78.37	78.37	78.37	78.37	**81.1**
LR	64.86	64.86	64.86	**64.86**	**64.86**	64.86	64.86	64.86	64.86	64.86	**64.86**
DT	54.05	62.16	48.6	**59.5**	**59.5**	43.24	56.75	62.16	59.45	56.75	**64.86**
AB	59.45	62.16	67.6	**62.2**	**56.8**	59.45	56.75	56.8	56.8	54.05	**67.6**

Table 2. Performance analysis of Chebyshev features based on the number of coefficients in terms of precision.

No. Coeff.	2000	2500	3000	3500	4000	4500	5000	5500	6000	6500	7000
SVM	0.500	0.500	0.727	**0.800**	**0.800**	0.727	0.727	0.727	0.727	0.727	**0.800**
LR	0.000	0.000	0.000	**0.000**	**0.000**	0.000	0.000	0.000	0.000	0.000	**0.000**
DT	0.00	0.400	0.200	**0.400**	**0.400**	0.000	0.200	0.400	0.250	0.000	**0.500**
AB	0.400	0.500	0.556	**0.444**	**0.333**	0.286	0.143	0.333	0.333	0.250	**0.667**

Table 3. Performance analysis of Chebyshev features based on the number of coefficients in terms of recall.

No. Coeff.	2000	2500	3000	3500	4000	4500	5000	5500	6000	6500	7000
SVM	0.538	0.538	0.615	**0.615**	**0.615**	0.615	0.615	0.615	0.615	0.615	**0.615**
LR	0.000	0.000	0.000	**0.000**	**0.000**	0.000	0.000	0.000	0.000	0.000	**0.000**
DT	0.000	0.154	0.154	**0.308**	**0.308**	0.000	0.077	0.154	0.077	0.000	**0.385**
AB	0.308	0.154	0.385	**0.308**	**0.231**	0.154	0.077	0.231	0.231	0.154	**0.154**

Table 4. Performance analysis of Chebyshev features based on the number of coefficients in terms of specificity.

No. Coeff.	2000	2500	3000	3500	4000	4500	5000	5500	6000	6500	7000
SVM	0.708	0.708	0.875	**0.916**	**0.916**	0.875	0.875	0.875	0.875	0.875	**0.917**
LR	1.00	1.00	1.00	**1.00**	**1.00**	1.00	1.00	1.00	1.00	1.00	**1.00**
DT	0.833	0.875	0.666	**0.750**	**0.750**	0.666	0.833	0.875	0.875	0.875	**0.792**
AB	0.750	0.916	0.833	**0.792**	**0.273**	0.792	0.75	0.75	0.75	0.75	**0.958**

From Tables 1, 2, 3, and 4 we could interpret that among the feature length from 2000 to 7000 the SVM model with a feature length 3500 could gain accuracy of 81.1%, precision of 0.800, recall of 0.615, and specificity of 0.916. The performance of all the other algorithms gained less than the SVM model with 3500 coefficients. When the number of features is increased from 3500 to 4000 SVM, logistic regression and decision tree classifiers could gain the same performance as that of feature length 3500. For the Adaboost classifier, the performance decreased from 62.2 to 56.8, 0.444 to 0.333, 0.308 to 0.231, and 0.793 to 0.273 respectively in terms of accuracy, precision, recall, and specificity while increasing the number of feature length from 3500 to 4000. When the number of feature length increased from 3500 to 7000 again for SVM and the logistic regression classifier the performance remained the same as 81.1%, 0.800, 0.615, and 0.916 and 64.86%, 0.000, 0.000 and 1.00 respectively in terms evaluation metrics. The decision tree has achieved a better performance of 64.86 from 59.5 in terms of accuracy. In terms of precision, recall, and specificity it has improved from 0.400 to 0.500, 0.308 to 0.385, and 0.75 to 0.792 while increasing the number of coefficients from 3500 to 7000. In the case of AdaBoost, it has achieved an improvement of 67.6 from 62.2 in terms of accuracy, it has gained an improvement of 0.667 from 0.444 in terms of precision and has gained an improvement of 0.954 from 0.792 in terms of specificity. In terms of recall, it could not show an improvement in performance as it decreased from 0.308 to 0.154. Hence, from this analysis, we could interpret that while increasing the feature length from 3500 to 7000 there is no improvement in performance in the case of SVM and Logistic regression classifiers. In the case of the decision tree and Adaboost, there is a slight increase in performance yet it did not reach the performance of the SVM classifier. The number of features is fixed to 3500 based on better performance with lesser feature length and minimum time complexity.

As the first step of the analysis, the PSNR value is computed between the original and the reconstructed ECG signal from the truncated Chebfun coefficients. The PSNR value is calculated to validate whether the truncated Chebyshev coefficients could capture all the structural information of the ECG signal. Few samples of the PSNR values that are obtained from the computations for feature length 3500 and feature length 7000 are shown in Table 5 and Table 6 respectively.

Table 5. The PSNR value computed between the original and the ECG signal reconstructed from the truncated Cheb coefficients with a feature length of 3500.

Data	PSNR(dB)	Data	PSNR(dB)
Normal_signal_1	59.79	Abnormal_signal_1	41.901
Normal_signal_2	55.836	Abnormal_signal_2	39.963
Normal_signal_3	55.566	Abnormal_signal_3	38.769
Normal_signal_4	55.011	Abnormal_signal_4	37.911
Normal_signal_5	54.172	Abnormal_signal_5	36.601

Table 6. The PSNR value computed between the original and the ECG signal reconstructed from the truncated Cheb coefficients with a feature length of 7000.

Data	PSNR(dB)	Data	PSNR(dB)
Normal_signal_1	60.755	Abnormal_signal_1	48.872
Normal_signal_2	58.010	Abnormal_signal_2	48.718
Normal_signal_3	57.695	Abnormal_signal_3	48.033
Normal_signal_4	56.662	Abnormal_signal_4	47.938
Normal_signal_5	54.642	Abnormal_signal_5	47.332

The PSNR value of reconstructed ECG signal from the truncated Chebfun coefficients with reference to the original signal ranges from 36.60 to 59.79 for feature-length of 3500 and 47.33 to 60.75 for 7000. From the PSNR value, there is a clear picture portrayed that the reconstruction using the truncated Chebfun coefficient is proper for the ECG signal. The truncated Chebfun coefficient has captured all the required signal information. To validate the proper retrieval of the structural information of the ECG signal, the signal is plotted as an image. The images of the original signal and its reconstruction with the Chebfun for the healthy and abnormal cases are shown in Fig 3 and Fig 4 respectively.

From Fig 3 and Fig 4, it is clear that the Chebfun is able to capture all structural variation of the signal for healthy (Normal) and unhealthy (Abnormal) cases. The reconstruction is proper for the signal with 3500 features. As shown in the figure, we got the same reconstruction of the signal as shown in Fig 3 and Fig 4. While analyzing the reconstruction of the signal with less than 2500 coefficients as shown in Fig 5 we could clearly see that between the timestamp from 800 to 9500 there is an effect of noise. Apart from the reduction in performance, the irregularities occurred while reconstructing the signal restricted us in reducing the number of coefficients below 2500. Thus from this analysis, the number of features(coefficients) is fixed to 3500.

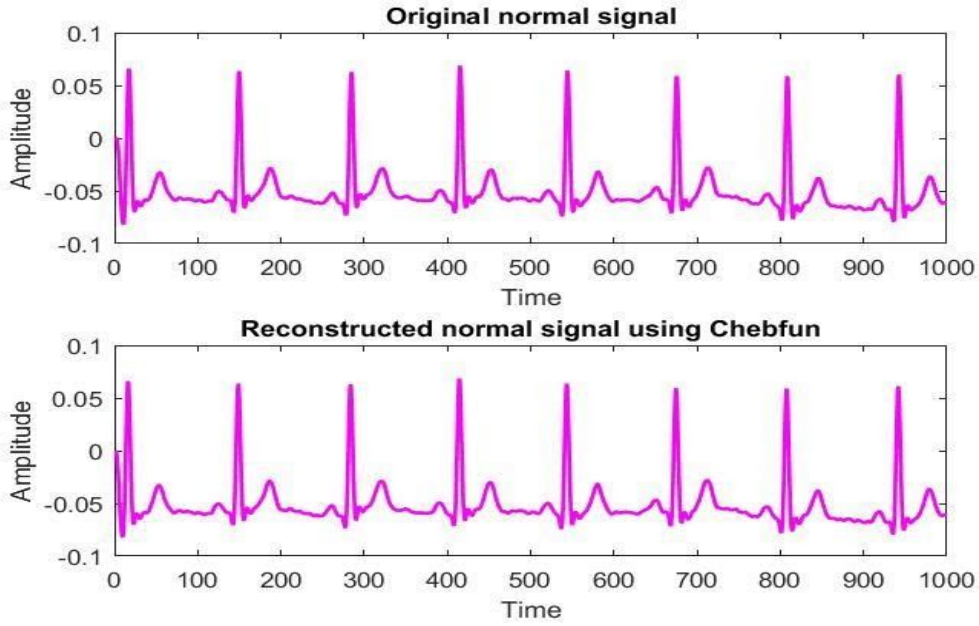

Fig 3. The original normal signal and the reconstructed signal using Chebfun coefficients.

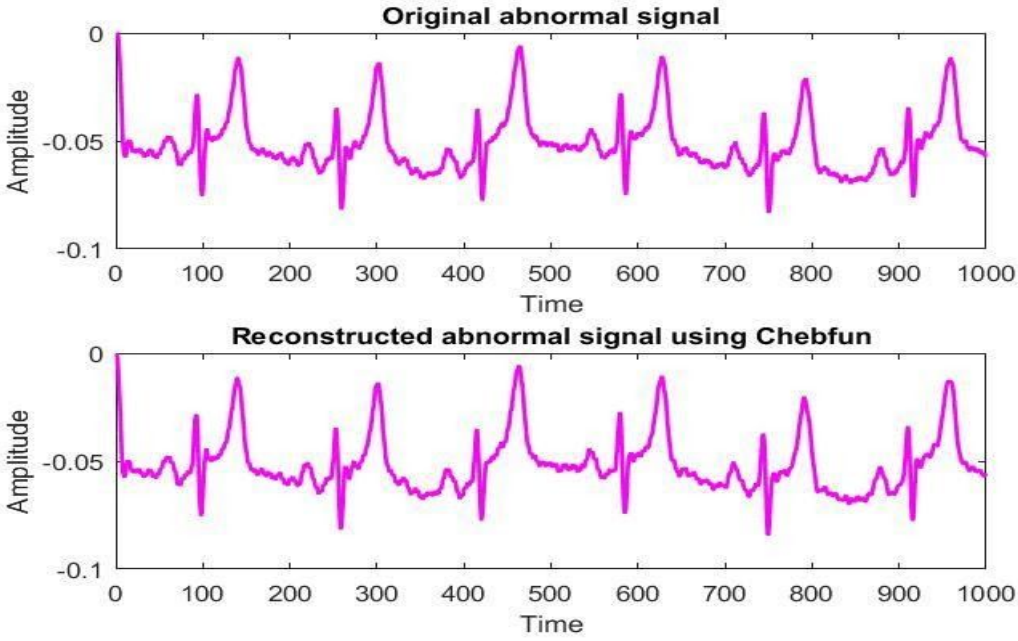

Fig 4. The original abnormal signal and the reconstructed signal using Chebfun coefficients.

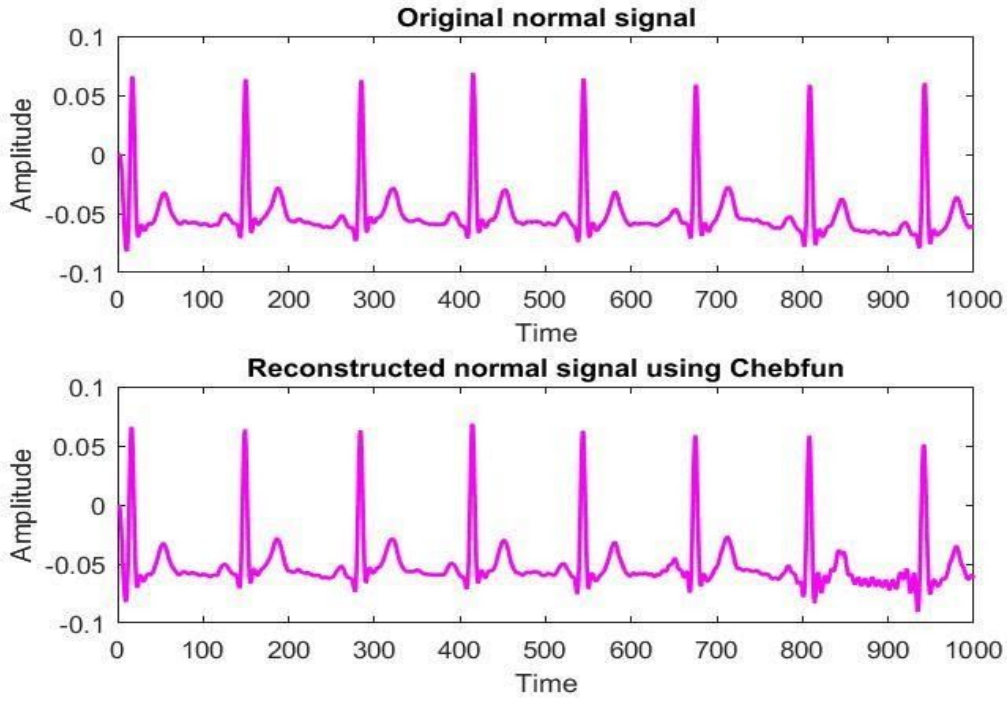

Fig 5. The original abnormal signal and the reconstructed signal using Chebfun coefficients with 2500 features.

The next step is to analyze the performance of the proposed method in comparison with conventional feature extraction techniques. The proposed Chebfun feature extraction technique is compared to the prevailed conventional feature extraction such as the Pan-Tompkin algorithm, Hamilton algorithm, Engelse, and Zeelenberg algorithm (EngZee), Christov algorithm, stationary wavelet transform, and matched filter. The different models used for the analysis are SVM, Logistic Regression, Decision Tree, and AdaBoost. In a biomedical application scenario, validation of disease detection is unacceptable with accuracy measures alone. For a more accurate evaluation of the Chebyshev system, we have considered the accuracy, precision, recall, and specificity as evaluation metrics. Accuracy defines the overall performance. Sensitivity/Recall defines the ability of the model to detect positive cases (diseased cases). Precision defines the ability of the model to detect relevant positive cases. Specificity defines the ability of the model to detect negative cases (healthy cases). Comparison of different conventional features with Chebyshev features for the detection of cardiac disease in SC data by using different machine learning algorithms in terms of accuracy (%), precision, recall, and specificity are shown in Table 7, Table 8, Table 9, Table 10 respectively.

Table 7. Comparison of different conventional features with Chebyshev features for the detection of cardiac disease in SC data by using different machine learning algorithms in terms of accuracy (%).

	Chebyshev	Pan Tompkins	Hamilton	Christov	Engzee	Matched filter	SWT
SVM	81.1	59.5	62.2	59.5	70.3	67.6	64.9
LR	64.86	70.3	67.6	64.9	70.3	64.9	70.3
Decision Tree	59.5	59.5	59.5	45.9	67.6	62.2	73.0
AdaBoost	62.2	62.2	54.1	48.6	67.6	62.2	73.0

In the case of accuracy scores, the SWT feature has scored an accuracy of 73% for the decision tree and AdaBoost classifier. The logistic regression model gained an accuracy of 70.3% by using each of the conventional feature extraction methods such as Pan Tompkins, Engzee, and SWT. These are the top accuracies gained by the logistic regression, Decision tree, and Adaboost. The SVM could gain an accuracy of 81.1% which is higher than other models and other conventional feature extraction techniques.

Table 8. Comparison of different conventional features with Chebyshev features for the detection of cardiac disease in SC data by using different machine learning algorithms in terms of precision.

	Chebyshev	Pan Tompkins	Hamilton	Christov	Engzee	Matched filter	SWT
SVM	0.800	0.333	0.333	0.00	0.750	0.600	0.500
LR	0.000	0.750	0.571	0.000	0.750	0.500	0.625
Decision Tree	0.400	0.429	0.400	0.182	0.556	0.467	0.615
AdaBoost	0.444	0.462	0.000	0.200	0.556	0.444	0.615

Coming to analysis with respect to precision. The SVM classifier has gained a precision 0f 0.800. The logistic regression classifier has gained a precision of 0.750 for Pan Tompkins and Engzee. The decision tree and Adaboost have gained precision of 0.615 respectively for the SWT feature which is best among them. The precision of these conventional feature extraction techniques is much less than the SVM classifier with Chebyshev features.

Table 9. Comparison of different conventional features with Chebyshev features for the detection of cardiac disease in SC data by using different machine learning algorithms in terms of recall.

	Chebyshev	Pan Tompkins	Hamilton	Christov	Engzee	Matched filter	SWT
SVM	0.615	0.154	0.077	0.00	0.231	0.231	0.077
LR	0.000	0.231	0.308	0.000	0.231	0.231	0.385
Decision Tree	0.308	0.462	0.308	0.154	0.385	0.538	0.615
AdaBoost	0.308	0.462	0.000	0.154	0.385	0.308	0.615

In the case of sensitivity score which is considered to be the measure of how the model perfectly predicts the positive cases. The SVM classifier with Chebyshev features, the decision, and the AdaBoost classifier with SWT features gained a recall of 0.615. These are the highest recall score among all other features as classifiers with other conventional features could acquire only a precision score which is less than 0.5.

Table 10. Comparison of different conventional features with Chebyshev features for the detection of cardiac disease in SC data by using different machine learning algorithms in terms of specificity.

	Chebyshev	Pan Tompkins	Hamilton	Christov	Engzee	Matched filter	SWT
SVM	0.916	0.834	0.917	0.917	0.958	0.917	0.958
LR	1.00	0.958	0.875	1.000	0.958	0.875	0.875
Decision Tree	0.750	1.00	0.75	0.625	0.834	0.666	0.833
AdaBoost	0.792	0.708	0.834	0.666	0.834	0.792	0.792

In the case of predicting the normal case, almost all the features have performed pretty well. The decision tree classifier with pan Tompkins features and the logistic regression with Chebyshev and Christov features was able to detect all the normal samples. The logistic regression classifier with Pan Tompkins, Engzee features, and the SVM classifier with Engzee and SWT have gained specificity of 0.958. The SVM classifier with Chebyshev features has gained a specificity of 0.916.

From the results, we can infer that Chebyshev features using SVM classifiers have outperformed all other conventional feature extraction techniques using all other classification algorithms in terms of accuracy, precision, and recall. One other inference is that in case of specificity even though the SVM classifier using Chebyshev features cannot outperform other conventional features, it has equivalent performance with other models.

PREDICTED VALUES		Chebyshev		Pan-Tompkins		Hamilton		Christov		Engzee		Matched filter		SWT	
	0	22	2	20	4	22	2	22	2	23	1	22	2	23	1
	1	5	8	11	2	12	1	13	0	10	3	10	3	12	1
		0	1	0	1	0	1	0	1	0	1	0	1	0	1
		ACTUAL VALUES													

Fig 6. The confusion matrix of the SVM model predictions using the Chebyshev features and conventional features.

For further evaluation of the experiment, we have included the confusion matrix. The confusion metric for the SVM model using Chebyshev features and conventional features is given in Fig 6.

From the analysis and with reference to Fig 3 and Fig 4. we can infer that Chebyshev polynomial approximation can capture all the structural pieces of information of ECG signals which indicate the disease characters. In most cardiovascular diseases, the disease characteristics can be present in other portions of the signal such as Q, S, T waves along with R peak. In the case of other conventional features, they capture only the peak information [9] and so there is a chance of missing out other structural variation that indicates the diseases. In such cases, it leads to the failure of the model to distinguish between normal and abnormal signals. The peculiar characteristics of the Chebfun which exploit the capacity to capture all

the structural information of the disease in the ECG signal help the model to distinguish between the normal and the abnormal cases than the conventional features.

6. Conclusion

In the proposed work, we have analyzed the possibilities of the Chebyshev feature extraction for cardiac disease detection. From the experiments and the result, we could conclude that the Chebyshev features extracted from the ECG signal using the SVM classifier have outperformed all other conventional feature extraction techniques such as Pan-Tompkins, Hamiltion, Engzee, Christov, matched filter and switched wavelet transform. The Chebfun gained an accuracy of 81.1%, precision of 0.800, recall of 0.615, and a specificity of 0.958. From the experiments, it's also possible to infer that the Chebyshev coefficients could capture all the structural variations of the ECG signal for the better identifications of the normal and abnormal ECG signals.

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