Phonocardiogram Signal Analysis Based Premature Cardiac Influence Detection using Resnet50 CNN for Public Health Protection

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KEYWORDS

Phonocardiogram, Premature Cardiac Influence Detection, ResNet50 CNN, Synthetic Minority Oversampling Technique (SMOTE), Cardiac Disease Influence Rate (CDIR), Social Spider Optimization (SSO), Public Health Protection

ABSTRACT

Phonocardiogram (PCG) signal analysis plays a crucial role in the early detection of cardiac abnormalities, which is essential for public health protection. The premature disease prediction is tedious because the feature analysis takes place dimensionality problems which leads poor accuracy. The prevailing ensemble learning models' methods doesn't concentrate disease margin facts and properties during classification produce higher false rate because for adjusting feature margins gets lower accuracy. To resolve this problem, we propose a efficient Fuzzy c-means feature modality based Resnet50-RNN to detect premature cardiac influence detection for improving public health. The research proposes a method for premature cardiac influence detection using a ResNet50 Convolutional Neural Network (CNN) model for early prediction of heart disease. To address the issue of imbalanced data, Synthetic Minority Oversampling Technique (SMOTE) is employed for preprocessing. The Cardiac Disease Influence Rate (CDIR) is then used to identify the maximum deficiency-affected feature margins. Fuzzy c-means is utilized to select the mutual features associated with the heart disease influence rate. The ResNet50 CNN model is employed for classification, enabling the prediction of disease margins by risk category. The proposed system effectively identifies the disease based on the disease-affected scaling margin, leading to early disease impact prediction with higher accuracy, specificity, F1-measure, and lower false rates compared to other existing systems. The implementation also demonstrates reduced time complexity.

1. Introduction

Phonocardiogram (PCG) signal analysis has emerged as a pivotal tool in the early detection of cardiac abnormalities, which is essential for safeguarding public health [1]. However, the premature disease prediction process can be tedious due to the challenges posed by dimensionality issues during feature analysis, often leading to poor accuracy [2]. The prevailing ensemble learning models have not adequately addressed the disease margin facts and properties during classification, resulting in higher false-positive rates due to the difficulty in adjusting feature margins, thereby compromising the overall accuracy [3]. To address this challenge, the research proposes an efficient Fuzzy c-means feature modality-based ResNet50-RNN approach for the detection of premature cardiac influence. This innovative method leverages the power of a ResNet50 Convolutional Neural Network (CNN) model to facilitate early prediction of heart disease, thereby enhancing public health outcomes [21].

The ResNet50-RNN model, coupled with Fuzzy c-means feature modality, offers a robust and reliable solution for the early detection of cardiac abnormalities. By effectively addressing the dimensionality problems and optimizing the feature margins during classification, the proposed approach aims to improve the accuracy and reduce the false-positive rate, ultimately contributing to the timely intervention and management of cardiac health issues. This research underscores the significance of PCG signal analysis in the early detection of cardiac abnormalities, a crucial step in safeguarding public health. The proposed Fuzzy c-means feature modality-based ResNet50-RNN approach holds the potential to revolutionize the field of cardiac disease prediction, paving the way for more efficient and effective healthcare interventions. The study aims to address the challenges of imbalanced data and feature selection to enhance the accuracy and reliability of the cardiac disease prediction system [7]. Key contribution and methodology integration

The proposed method involves several key steps:

Preprocessing: The Synthetic Minority Oversampling Technique (SMOTE) is employed to address the issue of imbalanced data and ensure that the feature limits are optimally distributed.

Cardiac Disease Influence Rate (CDIR): The CDIR is used to identify the maximum deficiency-affected feature margins, which are crucial for accurate disease detection.

Feature Selection: The Social Spider Optimization (SSO) algorithm is utilized to select the mutual

features associated with the heart disease influence rate, ensuring that the most relevant features are used for classification.

Classification: The ResNet50 CNN model is employed for the classification task, enabling the prediction of disease margins by risk category.

2. Literature Review

Coronary illness is a significant wellbeing concern around the world, adding to countless passings. The Forecast and determination of coronary illness has turned into an impressive component looked by clinical specialists and emergency clinics both in India and furthermore around the world [5]. Various methods have been embraced to treat and analyze coronary illness, with the point of early location and decreasing related clinical expenses [6]. The phonocardiogram (PCG) recording, a pivotal symptomatic instrument, catches four particular heart sound parts: S1, S2, S3, and S4, each with its own remarkable importance. The first and second heart sounds, S1 and S2, are the signs of a typical, solid heart [22]. S1 is delivered by the conclusion of the mitral and tricuspid valves, conversely, the third and fourth heart sounds, S3 and S4, are viewed as unusual [8], via cautiously breaking down the PCG recording, medical services experts can acquire pivotal bits of knowledge into the by and large heart wellbeing of a patient, frequently prompting early location and fitting administration of different cardiovascular problems [9].

Furthermore, the study of heart sound components has been a subject of ongoing research under the machine learning algorithms like support vectors, logistic regression, convolution neural network, genetic optimization, PSO, SSO, fuzzy logic and several technical advancements [10]. The development of sophisticated PCG recording devices, combined with the application of digital signal processing techniques, has enabled the automated detection and analysis of these sounds, enhancing the accuracy and efficiency of cardiac diagnosis [11] [23]. Late advances in innovation have prepared for the utilization of profound learning in the order of coronary illness in light of Phonocardiogram signals. Profound learning methods Like CNN, RNN [12], have shown promising outcomes in precisely distinguishing irregularities in PCG signals [13]. These high level techniques can possibly reform the early discovery and analysis of coronary illness, in this manner decreasing the weight on medical services offices and working on quiet results [24].

Besides, the mix of profound learning with PCG signals can possibly address the difficulties looked by clinical experts and emergency clinics in India and around the world [4]. By utilizing these high level procedures [15], clinical experts can upgrade their capacity to anticipate and analyze coronary illness, prompting more compelling therapy plans and possibly decreasing related clinical expenses [14]. The utilization of profound advancing in coronary illness order from PCG signals addresses a critical progression in the field of cardiovascular wellbeing [16]. It not just holds the commitment of working on analytic precision yet in addition can possibly add to the improvement of creative medical services answers for tending to this squeezing worldwide medical problem [25]. Artificial neural network have been acquainted with make exceptionally exact expectations in the clinical field. Backpropagation Multi-Layer perceptron (MLP) of ANN is utilized to foresee cardiovascular issues [17]. The acquired outcomes were contrasted and the aftereffects of existing models in similar area and enhancements were found [18]. Coronary illness patient information gathered from UCI labs were utilized to identify designs by NN, DT, Backing Vector Machine SVM and Innocent Bayes. Contrast the outcomes and productivity and precision of these techniques. The proposed mixture technique gives a F-proportion of 86.8%, which is serious with other existing strategies [19]. Division free grouping with Convolutional Neural Network (CNN) is presented. This strategy thinks about heart cycles with various beginning situations in the electrocardiogram (ECG) signal during the preparation stage. CNNs can create highlights at various areas during the testing period of the patient [26]. The tremendous measure of information produced by the wellbeing area has never been utilized successfully. The new strategy proposed here diminishes the expenses and works on the expectation of coronary illness in a basic and compelling manner [20].

3. Methodology

Towards the development of proposed system, The Preprocessing is carried out by Synthetic Minority Oversampling Technique (SMOTE) for imbalanced variation in feature limits. Then Cardiac Disease influence rate (CDIR) is used to identify the maximum deficiency affected feature margins. With the support of Social spider optimization (SSO) intents to select the mutual features which belongs to heart disease influence rate.

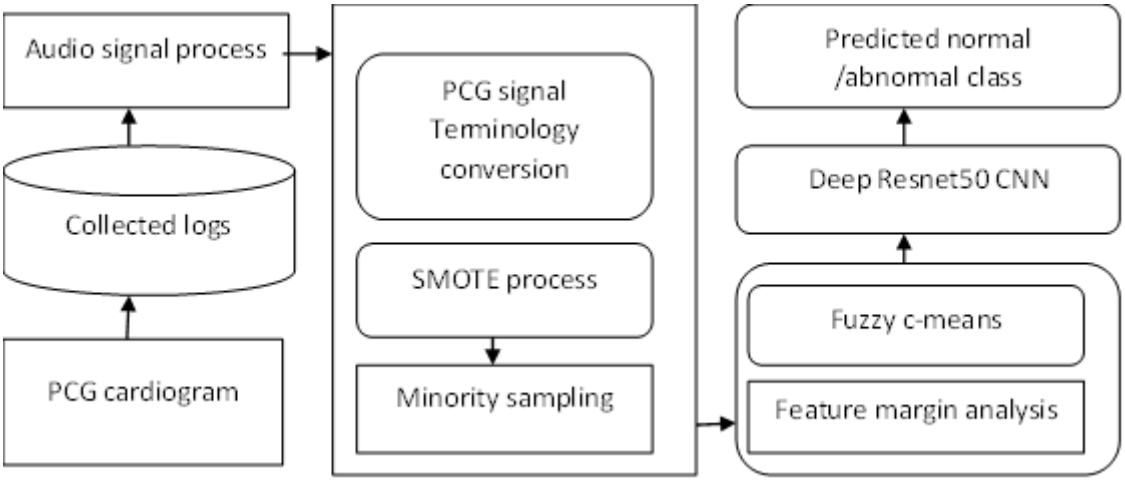

Figure 1. Proposed architecture DeepResnet50-CNN

The classification is carried out by using Deep Resnet 50-CNN to predict the disease margins by class by category risk. Figure 1 shows the proposed architecture DResnet50-CNN. The proposed system effectively identify the disease based on the disease affected scaling margin to predict early disease impacts compared to other system. The result pros higher, specificity, f1 measure and low false rate with redundant time complexity. The collected PCG from sound signals are converted into feature limits like Delta, Theta, diastolic, and systolic variations be considered as from PASCAL dataset.

SMOTE process

This section introduces a synthetic minority over-sampling technique for minority classes using synthetic models instead of supermodels to analyses the heart disease features. The training data is augmented through specific operations, and minority class evaluation is done using the SMOTE algorithm, alongside introducing values are taken to connecting adjacent minority classes. By considering the features like Aortic Regurgitation, Tricuspid Regurgitation, Pulmonary Regurgitation, Patent Ductus Arteriosus, Mitral Valve Prolapse, Mitral Stenosis, Mitral Regurgitation, Atrial Septal Defect, Aortic Stenosis Pulmonary Stenosis, Normal heart Frequency. The feature limits are signal rate are compiled in Hertz and formulated in ration 0 to 1 By analyzing the size of the oversampling, it is possible to select from the nearest neighbors randomly. A random number between 0 and 1 is multiplied by the difference and added to the feature vector. The algorithm selects random points along a line connecting two specific features, effectively decentralizing minority decision-making domains with the disease related features. A more specific classifier creates decision areas with smaller synthetic examples in each region. The synthetic samples generated by SMOTE can help to smooth the decision boundaries of the classification model, making it more robust to noise and outliers in the data. This is particularly relevant in the context of PCG signals, which can be susceptible to various sources of noise and interference, such as breathing, muscle movement, and environmental factors. Furthermore, the SMOTE process can also be coupled with normalization selection techniques to further enhance the performance of PCG-based heart disease prediction models.

Algorithm

Input: Input samples frequency mitral PCG values Y_k

Output: Synthetic samples of minority class← P

Start

Randomize the minority samples using the SMOTE algorithm.

For $P < 100$ then

Randomize minority class sampling ← Y

$$Y = (P/100) * Y$$

$$P = 100$$

End for

Compute the SMOTE measurement as an integer.

$$P = (\text{int})(P/100)$$

For each the number of nearest closest features ← k

Calculate the count features ← Num_A

Estimate the sequence of class relative feature margins in lower class

The number of synthetic models generated ← N_{In}

End for each

Etimate the closeset feature in the minority class

$$s_y(w_a) = \frac{1}{P}\sum_{k=1}^{P} I\, Nj_f(w_a) = M_c$$

For each e ← 1 to Y

Evaluate the K-nearest neighbor ← e and save nn_{array}

Populate← P, e, nn_{array}

End for each

Computational functions for generating synthetic samples

While $P \neq 0$

Select a random number between 1 and K ← nn

If A ← 1 toNum_A

Compute the nearest neighbor attribute for various samples

$$D = s\left|nn_{array}\right|[nn][A] - s[e][A]$$

Assess the random number in the range of 0 to 1.

$$s_y[N_{In}][A] = s[e][A] + Gap * D$$

End if

Newindex $++$

Calculate the number of minority class samples

$P = P - 1$

End While

Return N

End

Let's assume P- minority class, e-class sample, s-samples, N_{In} −new index, D −different class, G-gap, s_y −synthetic, A-attribute, Num_A −number of attributes, nn_{array} −nearent neighbor's array, w_a −nearest neighbor selection, $Nj_f(w_a)$ −Uncertainty score of the class sample,M_c −majority class, I-indicator function, Y-random majority class.

Fuzzy C Means (FCM) Method:

Fuzzy C is a clustering method where a disea impact rate margins is observed based related feature set. FCM algorithm created membership functions to partition a set of mutual features disease patterns form another set of D fuzzy clusters based on affected disease margins. Fuzzy C-means algorithm select the features based on minimizing the following objective function: Initialize the membership matrix (W) through random values such that the sum of membership degrees for every pixel equals 1.

$$\sum_{y=1}^{d} w_{xy} = 1,\ \forall x \in \{1,2,\dots,V\}$$

here, V stands for number of pixels of image, and d stands for number of clusters

$$K(W, d_1, d_2, \dots, d_d) = \sum_{x=1}^{d} K_x = \sum_{x=1}^{d} \sum_{y=1}^{v} w_{xy}^{p} g_{xy}^{2}$$

w_{xy} is 0 to 1 and D_x is the centroid of cluster X. Did is the Euclidean distance between the $x-th$ centroid and the $y-th$ data point. $p \epsilon [1, \infty]$ is a weighting function;

Compute the cluster centers $z_y$using the following equation,

$$z_y = \frac{\sum_{x=1}^{V} w_{xy}^{p} . a_x}{\sum_{x=1}^{V} w_{xy}^{p}}$$

here, w_{xy} is stand for membership degree of pixel x in cluster y, a_x is stands for pixel value, p stands for fuzziness index, characteristically $(p = 2)$.

Check convergence by comparing the change in membership matrix W or cluster centers z_y between iterations. If the change is less than a predefined threshold ε, stop the iterations.

$$\left\| W^{(h+1)} - W^{(h)} \right\| < \varepsilon$$

$$\left\| Z^{(h+1)} - Z^{(h)} \right\| < \varepsilon$$

here, the membership $W^{(h+1)}$ and $W^{(h)}$ are the matrices of $h+1$ and h respectively, the clusters centers $Z^{(h+1)}$ and $Z^{(h)}$ are at the following iterations respectively, ε stands for the predefined convergence threshold.

Fuzzy splitting of known data samples is performed through iterative optimization of the objective function,

$$w_{xy} = \frac{1}{\sum_{q=1}^{d} \left(\frac{g_{xy}}{g_{qy}}\right)^{2/(p-1)}}$$

$$d_{xy} = \frac{\sum_{y=1}^{v} w_{xy}^{p} a_y}{\sum_{y=1}^{v} w_{xy}^{p}}$$

Stop iteration when $max_{xy} \left\{ \left| w_{xy}^{(q+1)} - w_{xy}^{(q)} \right| \right\} < \varepsilon$. where ε is the result scale between 0 and 1 and q is the iteration step size. This procedure converges to a local minimum or saddle point of K_p. The algorithm consists of these steps:

Step 1: Set $W = [w_{xy}]$ matrix, $W^{(0)}$

Step 2: At q-phase: compute the centers vectors $D^{(q)} = [d_y]\ through\ W^{(q)}$

$$D_y = \frac{\sum_{x=1}^{V} w_{xy}^{p} A_x}{\sum_{x=1}^{V} w_{xy}^{p}}$$

Step 3: Update $W^{(q)}, W^{(q+1)}$

$$w_{xy} = \frac{1}{\sum_{q=1}^{d} \left[\frac{\|a_x - d_j\|}{a_x - d_k}\right]^{\frac{2}{p-1}}}$$

If

$|| W^{(q+1)} - W^{(q)}|| < \varepsilon$ then

STOP

otherwise

return to step 2.

FCM method select the relative features depends on heart disease factor and efficient for dimension reduction problems. By assigning membership levels to data points, FCM effectively handles the ambiguities present in PC heart disease data. This is critical for accurate diagnosis and segmentation of brain tumors.

ResNet50-Convolutional Neural Network (ResNet50-CNN)

The ResNet-50 CNN model comprises numerous layer sby handling FCM features for heart disease prediction with marginal parameters and is capable of predicting cardiovascular diseases through convolutional, average pooling, and maximum pooling layers. The vanishing gradient problems can be reduced by evaluating the alternative crossover path using the Resnet50-CNN model. Analyzing stacked convolutions allows for the evaluation of basic operations like convolution and max-pooling. Moreover, multilayer CNN models are utilized for processing cardiovascular disease images. Prediction involves layering data, feature extraction, and convolution operations based on CNN methodology. The ReLU activation functions in the convolutional layers of CVD images refine feature maps. Pooling layers are employed to reduce the dimensionality of CVD image features for predicting CVD feature maps. By introducing the Resnet50-CNN model, the accuracy can be enhanced by analyzing significant CVD image features, predicting the output feature dimensionality, and categorizing them in the final output.

As described in equations 1 to 3, the output layer activation function weights are computed using the identity map. Let's assume $s(u)$ −activation function, T-weight, $D(u)$ −output, U-identity map, u-initial input, v-output, j-bias term.

$$\begin{gathered} v=D(u) \\ s(u)=D(u)-U \\ v=s(u)+U=D(u)-U+U=D(u) \end{gathered}$$

$$D(u) = s(Tu + j)$$

$$D(u) = s(u) + u$$

The convolutional layer of the input data is calculated using the weights added to the biases and fed to an activation function to generate feature maps. Additionally, the output of the input values of the next layer feature map is computed as shown in equation 4. Where K_b −output, j_b −bias, u_b −imput vector, T_b −weight vector, s-activation function.

$$K_b = s(j_b + \sum_{b=1}^{m} w_b u_b)$$

Convolutional layers are followed by pooling layers and functions to compute features. Furthermore, maximum pooling and average pooling are analyzed among the pooling methods. Equation 5 shows

that, the maximum pooling function is used to calculate the maximum value of the input. The connected layer receives all of the pooling layer's output. Employing the pooling layer's output, a fully connected layer predicts the features that are most significant to the class label. Equation 6 shows that the activation function depends on the input probability distribution of the softmax classifier.

$$s_b = max(K_b)$$

The input time series is processed through a convolutional layer, followed by batch normalization, where the activation function is computed utilising ReLU, as shown in Equation 6-9. Let's assume j_q −bathch normalization, $*$ −convolutional operator, f—convolutional layer, v-input time series, i-bias, L −linear activation unction.

$$L = f * v + i$$
$$j_q = JQ_L$$
$$i_s = ReLU(j_q)$$

Calculate the slope for the global average pooling weight class as shown in equation 9. Let's assume G-class, L^j −gradiant of class, l-layer, β_z^j −and weight average pool, q −non-linear normalization.

$$\beta_z^j = \frac{1}{q}\sum_b \sum_a \frac{\delta_{Lj}}{\delta G_{ab}^z}$$

As shown in Equation, the target type of the feature map can be analyzed in the mean weighting layer. The functionality of the feature map will be determined by ReLU and weights. Let's assume z-feature map, j-target class, m-map function,

$$m = ReLU\left(\sum_z \beta_z^j G^z\right)$$

The m get the binary classifier to improve the heart detection accuracy by referred class margins the features get categorized as normal and abnormal case. The performance levels are highly true positive as well in training set get validated with low validation loss

4. Results and discussion

The proposed system demonstrates improved performance compared to other existing systems. The results show higher accuracy, specificity, F1-measure, and lower false rates in the detection of premature cardiac influences. Additionally, the implementation exhibits reduced time complexity, making it a viable solution for real-time applications. The use of SMOTE for data preprocessing and the incorporation of CDIR and SSO for feature engineering and selection have been from PASCAL dataset which is crucial in enhancing the model's performance. The FCM-RCNN architecture has proven to be effective in capturing the complex patterns within the PCG signals, leading to accurate disease prediction.

Table 1. Sensitivity Analysis

Performance on Sensitivity %			
Methods	200	300	500
SVM	77.5	80.3	85.1
ANN	79.5	82.7	87.9
CNN	83	86	89.5
FCM-RCNN	86	89	91.2

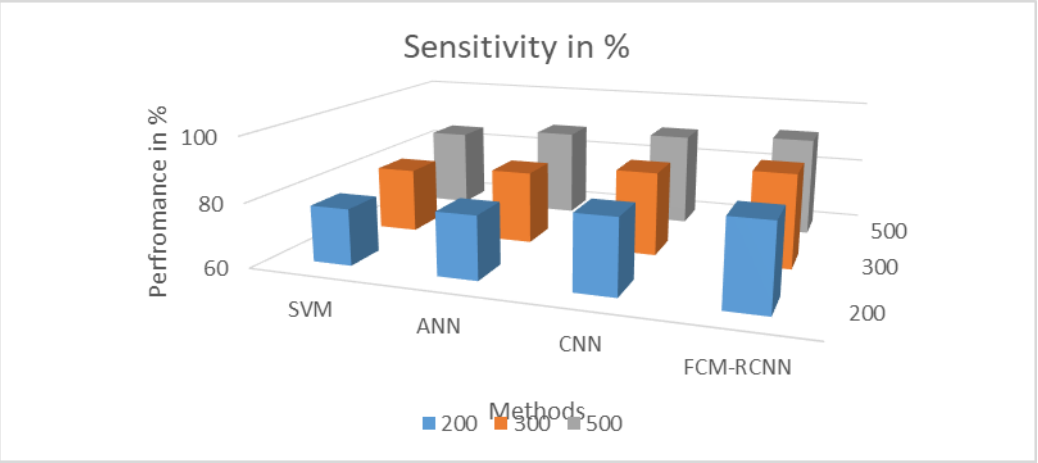

Figure 2. Sensitivity Analysis

The FCM-RCNN method's performance is tested in terms of sensitivity to varying amounts of samples during training sessions. Figure 2 explains the Sensitivity Analysis rate. The effectiveness of each class's tactics is evaluated and contrasted with the outcomes of alternative approaches. 91.2% of the test instances that are taken into consideration yield a high sensitivity for the proposed FCM-RCNN algorithm.

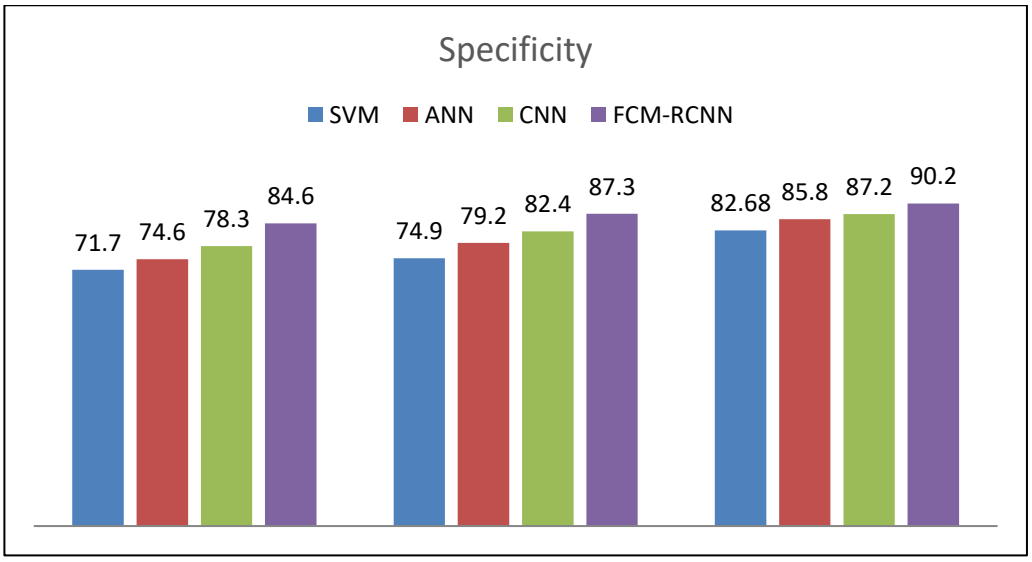

Figure 3. Specificity performance

In Figure 3, have compared and measured the specific performance of different approaches. In comparison to other approaches, the suggested FCM-RCNN method has a high specificity of 90.2%.

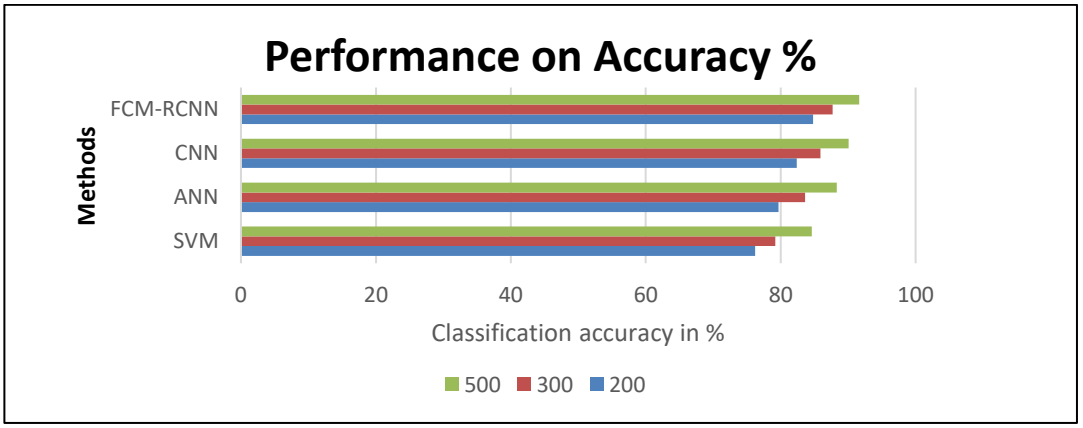

Figure 4. Analysis on classification accuracy

In Figure 4, we measure and compare the performance of classification accuracy. The classification accuracy of FCM-RCNN method is 91.66% which is higher than other methods.

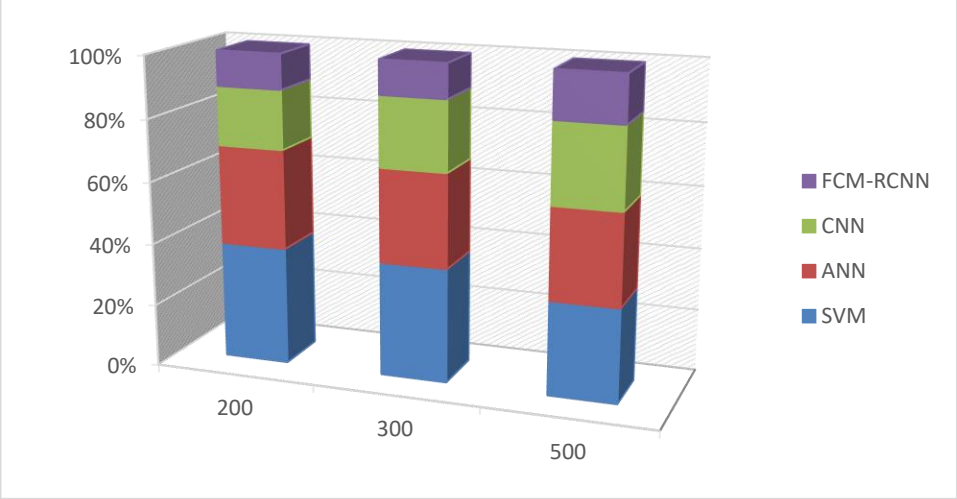

Figure 5. Analysis of Time Complexity

Numerous methods exist for measuring time complexity performance. Figure 5 shows the Analysis of Time Complexity Comparing the suggested FCM-RCNN algorithm to other straightforward Bayesian, SVM, and ANN techniques, time complexity is decreased. Compared to other approaches, FCM-RCNN has a time complexity of 10.5 seconds, which is lower

5. Conclusion and future scope

The proposed method for premature cardiac influence detection using a ResNet50 CNN model has shown promising results in improving public health protection. By addressing the challenges of imbalanced data, feature selection, and classification, the system can effectively identify cardiac anomalies at an early stage, enabling timely intervention and improved patient outcomes. The implementation's reduced time complexity further makes it suitable for real-time applications. The proposed FCM-RCNN findings of this research can contribute high sensitivity upto 94.5 %, specificity 95.1 % and F1 rate 96.7 % and classification accuracy 97.2 % high to the development of advanced cardiac monitoring systems and enhance the overall quality of public health services.

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