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HDPSANN: An Efficient Heart Disease Prediction System using A Soft Swish Artificial Neural Network Based on ECG Signals

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Abstract: In the human body, the heart is the most significant organ. The major role of the heart is to circulate blood, nutrients, along with oxygen all over the body. The heart's function might get affected owing to a range of reasons. For identifying along with preventing sudden cardiac death, anomalous heart conditions must be detected in the earlier stage itself. To identify heart abnormalities, a non-invasive methodology termed Electrocardiogram (ECG) is utilized. The Electrical Activity (EA) of the blood circulatory system's (heart) center is handled by this. For automatic Heart Disease Prediction (HDP), various Machine Learning (ML) and Deep Learning (DL) methodologies have been employed. Nevertheless, the diagnostic accurateness is affected owing to the influence of the external environment like signals' poor quality along with inappropriate features. Furthermore, the classification of the sorts of cardiac disease was not done successfully by the prevailing methodologies. Thus, regarding ECG signals, an effectual HDP System (HDPS) has been proposed here by utilizing Patch wise Logistic Tanh SegNet (PLT-SegNet) along with Sinusoidal Chaotic JellyFish search hinged Softswish Artificial Neural Network (SCJFSANN) methodologies. Initially, from the openly accessible dataset, the input ECG signals are extracted. Then, the pre-processing is performed. After that, by utilizing Cosine Similarity adapted Hilbert Transform (CSHT), the signal peak values are identified. Next, the PLT-SegNet is utilized to partition the signals. Subsequently, by employing Shannon Entropy adapted Linear Discriminant Analysis (SELDA), the features are extracted along with the dimensionality is mitigated. Lastly, for classification, the SCJFSANN is provided with the dimensionality reduced features. The experiential outcomes displayed that the highest performance was achieved by the proposed methodology than the prevailing methodologies.

Keywords: *Heart Disease Prediction (HDP), Electrocardiography (ECG), Segmentation, Artificial Neural Network (ANN), Band Pass Filter (BPF), Normalization, Linear Discriminant Analysis (LDA).*

1. Introduction

The most complicated organ in our body is the heart. Pumping blood into the circulatory system is the heart's function [1]. For a healthy person, the heart rate ranges from 60 to 100 beats a minute, whereas at 0.8 sec, a cardiac cycle occurs [2]. Cardiovascular disease (CVD) is occurred owing to any abnormity in the cardiovascular system as the heart pumps blood to the circulatory system [3]. CVD is one of the dangerous diseases that frighten human life. Among all reasons of death till date, the mortality rate of CVD ranks at the top, as per the world health organization's report [4]. Ischemic stroke, hemorrhagic stroke, heart failure, heart attacks, and various types of problems linked with arrhythmia and heart valves are several types of CVDs [5]. To identify the CVDs earlier, a classification model is used, which helps to minimize death rates [6]. The fatal risk can be lowered for the person who suffers from a heart attack if the proper treatment is done within an hour [7]. The leading cause of death is heart-related diseases irrespective of the development of medical technology [8]. To find out the dissimilarities in the heart signals and the dissimilarities in the number of heartbeats per unit time, heart rate variability is utilized. To detect the heart pulses, ECG is one of the technologies used [9]. Examining ECG signals to detect heart conditions is the general method, and this method is the fundamental method to prevent CVDs [10]. Figure 1 depicts the ECG waveform and its characteristic patterns.

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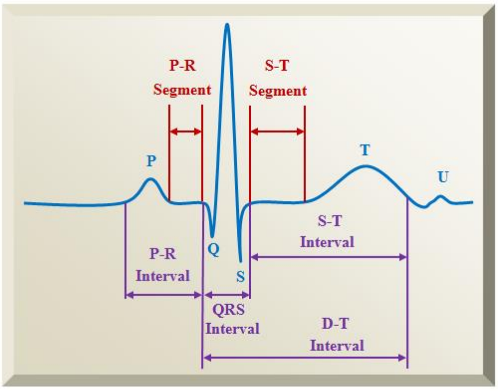

Fig 1: ECG waveform and its characteristics

The electrical activity of a heart is identified and recorded by the ECG via small metal electrode patches, which are attached to the chest, arms, along with legs of a person's skin [11]. From different angles along with positions, the heart's electrical potential is obtained by the ECG; this shows the disease state through the waveforms or rhythm irregularities [12]. The establishment of differences in the morphological and geometric variations in the elements helps to detect the irregularities in the ECG [13]. In an ECG signal, the heart's various areas are indicated by various waves. The P-Wave, T-Wave, PR Interval, QT Interval, U-wave, ST-Segment, and QRS Complex are the waveforms' constituents [14]. The electrical current in the heart's upper cavity is indicated by the P wave. The electrical activity from the Sinusoidal Node (SA) that propagates completely through the atrial is indicated by the P wave [15]. At the time of ventricular depolarization, the QRS complex arises, which forms from the Q, R, and S waves. During the repolarization of ventricles, the T wave occurs as the preparation of the upcoming heartbeat [16]. Currently, for the identification of heart diseases, the most powerful equipment utilized is the ECG. The utilization of ML algorithms to detect ECG signals automatically has become more important nowadays [17]. As the waveforms and variations are different in these signals, it is difficult for the ECG signals to automatically identify the heart diseases [18]. In this area, to identify and classify heart diseases, several ML algorithms are utilized by the researchers. The identification accuracy is affected owing to the presence of electromagnetic interference, power frequency interference, random noise, interference from the human body, breath sounds, and lung sounds. Moreover, decomposition methodologies, which have mode mixing problems, are utilized by some models in which the ECG signals have different frequencies; thus, affecting the detection rate. Therefore, utilizing PLT-SegNet and SCJFSANN techniques, an efficient HDP system centered on ECG signals is proposed in this paper.

The paper's remaining parts are structured as: grounded on the proposed work, the literature survey is presented in section 2, in section 3, the proposed technique is described, the results and its discussions are explained in section 4, and finally, in section 5 the paper is concluded along with future work.

2. Literature Survey

Felipe Meneguitti Dias *et.al* [19] presented an automated model to detect arrhythmias by utilizing single-lead ECG signals. Firstly, for minimizing the baseline wander noise, a filtering process was adopted by amalgamating ‘2’ moving average filters. After that, by employing the R-wave’s position, the heartbeats were segmented with an artificially created jitter. Furthermore, regarding morphological values, RR intervals, along with higher-order statistics, an amalgamation of features was extracted as of every single beat. Lastly, by utilizing a linear discriminant classifier, the arrhythmias were classified with the features being extracted. The outcomes displayed that when analogized with other prevailing methodologies, the presented model obtained competitive outcomes. Conversely, the classes of cardiac diseases were not addressed by this system.

Sheryl Oliver *et.al* [20] introduced a Regressive Learning-centric Neural Network Classifier (RLNNC) model to classify heart disease types earlier. Signal pre-processing was the first step. With the wavelet transformation model’s aid, segmenting the heart disease signal was the second step. Lastly, to extract the output signal’s features, the RLNNC was wielded. The evaluation displayed that a higher accuracy along with efficacy was attained by the RLNNC than the prevailing methodologies. However, here, the detection accuracy was affected since it utilized irrelevant features along with did not focus on the ECG signal’s noise removal.

Wei Zeng et.al [21] elucidated a mechanism for detecting cardiac arrhythmia automatically with one-lead ECG signals. Primarily, by employing the Tuneable Q-factor Wavelet Transform (TQWT) methodology, the

ECG signals were decomposed into a set of frequency sub-bands. Secondly, to decompose the ECG signals' sub-band into varied intrinsic modes, Variational Mode Decomposition (VMD) was deployed. Thirdly, the reference variable's phase space was reconstructed. After that, to derive features, the 3D Phase Space Reconstruction (PSR) combined with Euclidean distance was utilized. Next, to detect and classify normal along with arrhythmia ECG signals, Neural Networks (NNs) were utilized. The outcome displayed that in the automatic detection of myocardial dysfunction, a better performance was attained by the presented model than the prevailing methodologies. Nevertheless, handling massive ECG signals together with their overlapping characteristics was time-consuming as well as complex; thus, resulting in errors.

Varun Gupta *et.al* [22] implemented Chaos theory along with the Auto-regressive Time-Frequency Analysis (ARTFA) model to detect several sorts of arrhythmias present in an ECG signal automatically, accurately, along with effortlessly. Initially, by utilizing Savitzky Golay Digital Filtering (SGDF), the actual ECG signal was filtered. Next, regarding PSR, an optimal trajectory detection step was developed in chaos theory. After that, for finding the extracted features' spectral components utilizing chaos theory, the ARTFA had been wielded, which was also utilized to identify the autoregressive coefficients together with time-frequency description. The outcomes demonstrated that the positive predictive value, sensitivity, and accuracy were enhanced by the presented methodology; thus, ameliorating the identification of arrhythmias. However, the heart dynamics indicated by the heart rate variability along with the cardiac activity's other aspects were not determined precisely.

Tejas Radhakrishnan *et.al* [23] developed a time-frequency domain deep learning-centric model for identifying Atrial fibrillation (AF), in addition, classified terminating along with non-terminating AF episodes by employing ECG signals. Here, by deploying the Chirplet transform, the ECG signals' Time-Frequency Representation (TFR) was assessed. For detecting along with classifying AF episodes utilizing time-frequency images of ECG signals, the 2D deep convolutional Bidirectional Long Short-Term Memory (BLSTM) NN model was deployed. The outcomes displayed that when analogized with the prevailing methodologies, a better AF detection performance was attained by the presented approach. However, the model's detection accuracy was affected owing to the existence of noise in the ECG signal.

3. Proposed Hdps^{3}an^2 Framework

In the human body, the most vital organ is the heart. In today's world, one of the most critical health issues is heart disease. In the process of predicting heart diseases, the highly common along with fundamental methodology utilized is the ECG. ECG, which aids in identifying any disorder of rhythm, heart rate, or alteration in morphological pattern, is the representation of the heart's EA. To save human life, predicting heart diseases earlier is highly significant. Still there occur certain complications even though various research models have been employed with the HDPS. Thus, by utilizing PLT-SegNet along with SCJFSANN methodologies, an effectual HDPS has been proposed regarding ECG signals to overcome the aforementioned complications. (i) Pre-processing, (ii) Signal peak detection, (iii) Signal separation, (iv) Feature extraction, (v) Dimensionality reduction, and (vi) Classification are the phases undergone by the proposed methodology. Figure 2 exhibits the block diagram of the proposed HDPSANN model.

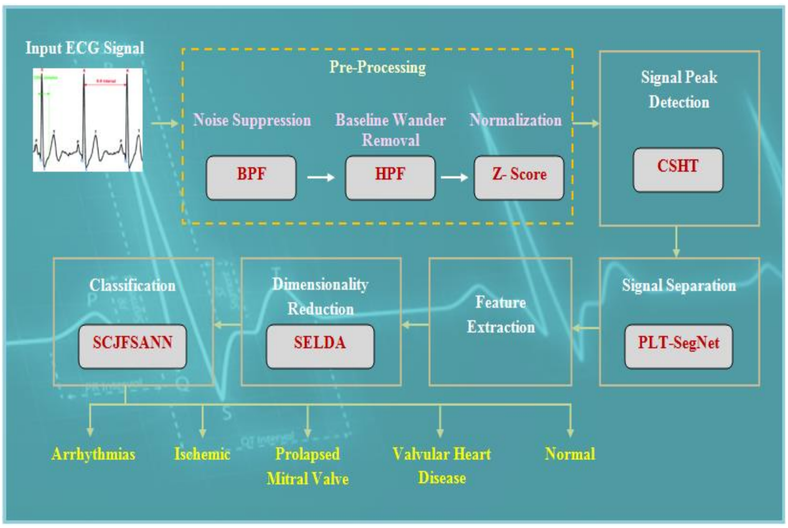

Fig 2: Block diagram of the proposed HDPSANN model

3.1 Preprocessing

Initially, as of the openly accessible dataset, the input ECG signals are obtained. Rather than the heart's electronic signals, the input signals, which are mostly influenced by electrical interference or noise, are recorded as of the other sources. The pre-processing is performed primarily to remove noisy ECG signals. Several noises, which disrupt the fiducial point detection along with heartbeat classification, are eliminated by pre-processing the raw ECG signals. To eradicate signal noises, the Band Pass Filter (BPF) is utilized; similarly, to remove baseline wander, the High Pass Filter (HPF) is wielded. At time t, the input ECG signal $(x(t))$ is formulated as,

$$x(t) = \kappa * i(t) + n(t) \tag{1}$$

Where, the attenuation parameter is specified as κ, the ECG signal is signified as $i(t)$ and the noise present in the signal is notated as $n(t)$.

3.1.1 Noise Suppression through BPF

In general, artefacts will be introduced into the signals whilst recording the ECG signals. Electrode contact noise, power line interference, and baseline wander are the artefacts mainly presented in the signals. The ECG recordings are affected by the power line interference. The loose contact betwixt the skin and the electrodes causes contact noise. The BPF is utilized to take off these artefacts. The BPF is the amalgamation of Low Pass Filter (LPF) along with HPF; in addition, it has a frequency range up to 5-15 Hz. Thus, the noise caused by power line interference, baseline drift, muscle noise, et cetera is attenuated by this filter effectually.

3.1.2 Baseline Wander Removal by HPF

Baseline wander, which is developed as of respiration together with body movements, is a lower-frequency artefact in the ECG signal. The crucial information in the ECG signal is masked by this noise; thus, it should be removed for predicting heart disease. In this, to eliminate the baseline wander noise, the HPF is utilized. Signals with a frequency higher than a specific cut-off frequency are passed by the HPF; furthermore, here, the signals with frequencies lower than the cut-off frequencies are attenuated. For every single frequency, the amount of attenuation relies on the filter design. The HPF's transfer function $(\zeta(x))$ is expressed as,

$$\zeta(x) = \frac{-1 + 32 \cdot (x)^{-1} + (x)^{-32}}{1 - (x)^{-1}} \tag{2}$$

The amplitude response $\zeta(\omega T)$, where $x = \omega T$ $(\omega - frequency, T - time)$, is modelled as,

$$|\zeta(\omega T)| = \frac{\left\langle 256 + \sin^2(16\omega T)\right\rangle^{0.5}}{\cos\left(\frac{\omega T}{2}\right)} \tag{3}$$

Consequently, the noise-free signal is attained, which is then normalized for further process.

3.1.3 Normalization

To trounce the amplitude variations that occurred in the input signal, the noise-removed ECG signals are normalized. The input signal's accuracy along with integrity is enhanced by normalization. To normalize the noise-free signals, the Z-score normalization model is utilized. It is modelled as,

$$x^*(t) = \frac{x'(t) - mean\,of\ x'(t)}{s\tan dard\ deviation} \tag{4}$$

Where, the noise-free signal is specified as $x'(t)$ and the normalized signal is signified as $x^*(t)$. Thus, the normalized higher-quality signals free of baseline wander along with other sorts of noises are attained after pre-processing; the obtained signals are then utilized for detecting the respective signal's peak values.

3.2 Signal Peak Detection with CSHT

In general, P wave, QRS wave, and T wave are utilized for the composition of an ECG cycle. The edges' precise locations, that is to say, the '3' waves' peak positions are needed to segment the ECG signals. Therefore, in the proposed methodology, to segment the signals effectually, the waves' peak positions are detected by utilizing the CSHT. To analyze the instantaneous amplitude along with the signal's frequency, one of the renowned transforms utilized is Hilbert Transform (HT) in which to obtain the required outcome, the signal's phase angles are transformed. Regarding amplitude along with frequency, the instantaneous values of time series ECG signals are computed; thus, making HT better apt for the longer-term processing of ECG signals. Here, the ECG signal's envelope is detected effectually. Generally, by squaring the differentiated ECG, the envelope in HT is computed. Such calculation has certain drawbacks, that is, here, in the transform's output, the normal QRS peaks with smaller magnitude along with wider arrhythmic peaks with reduced slope are minimized. Thus, to compute the envelope, the Cosine Similarity (CS) is utilized here. Consequently, the altered model is termed CSHT. Figure 3 depicts the CSHT peak detected signal.

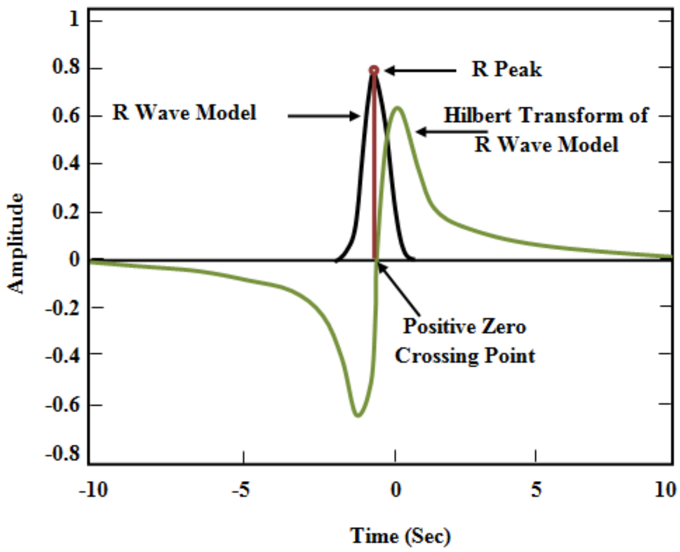

Fig 3: Peak value detected signal using CSHT

Step 1: The pre-processed ECG signal $\left(x^*(t)\right)$ is inputted to the CSHT. The QRS complex peaks have to be computed in this. The input's HT is expressed as,

$$\mathrm{H}\left(x^*(t)\right) = \frac{1}{\pi}\int_{-\infty}^{\infty} x^*(\tau) * (t-\tau)^{-1}\, d\tau \tag{5}$$

Thus, the signal's HT is the convolution betwixt the signal and its phase angle (π); moreover, the phase shift angle is notated as τ . The independent variable is not altered regarding the transformation; thus, the time dependency's property is exhibited here.

Step 2: Then, by utilizing the CS formula, the signal's $\left(x^*(t)\right)$envelope $(\hat{e})$ is computed as,

$$\hat{e} = \frac{x^*(t) * \mathrm{H}\left(x^*(t)\right)}{\sqrt{\left(x^*(t)\right)^2} * \sqrt{\left(H\left(x^*(t)\right)\right)^2}} \tag{6}$$

Step 3: After that, to attain positive peaks irrespective of the QRS complexes' polarity, the signal is passed via a non-linear transformation $\left(\varphi(t)\right)$.

$$\varphi(t) = \arctan\left(\frac{\mathrm{H}\left(x^*(t)\right)}{x^*(t)}\right) \tag{7}$$

Subsequently, the signal's respective peaks are identified by extricating the zero-crossing points in the transformed signal's positive direction.

3.3 Signal Separation by means of PLT-SegNet

To detect heart symptoms along with the effects of cardiac medications effectively, the signals are segmented regarding the detected peak values of the QRS complexes, p and T waves of ECG signal. The process of extracting individual ECG waves as of longer recordings is termed segmentation. Fixed-length segmentation is utilized in the prevailing segmentation methodologies; in addition, they are centered on RR intervals. There might occur morphological information loss in the fixed-length segmentation around the R peak. Thus, to obtain efficient outcomes, a deep learning-centric segmentation technique is employed here by utilizing PLT-SegNet. For semantic segmentation, SegNet, a deep-layered architecture, is utilized. An encoding network, a decoding network, and a final classification layer are encompassed in this architecture. Figure 4 depicts the architecture of PLT-SegNet.

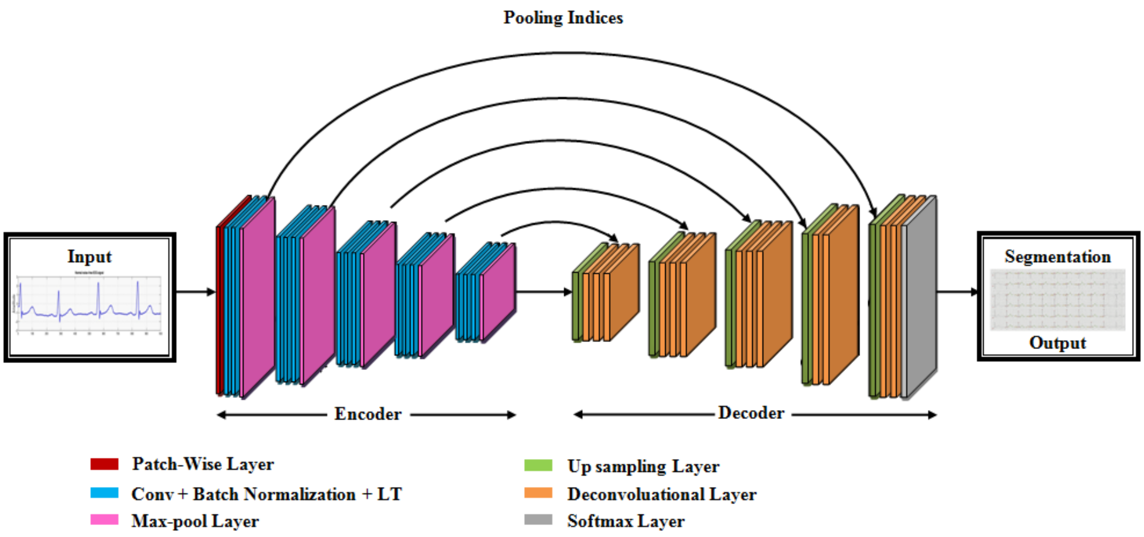

Fig 4: PLT-SegNet architecture

As per figure 4, 5 encoders with ‘13’ Convolutional Layers (CLs) were included in the SegNet architecture. Evert single encoder layer has a respective decoder layer; in addition, ‘13’ layers were subsumed in the decoder network. To generate class probabilities independently, the final decoder output is inputted to a multi-class Softmax Classifier (SMC). To produce a set of feature maps, every single encoder in the encoder network conducts convolution with a filter bank; in such feature maps, batch normalization along with Rectified Linear Unit (ReLU) activation are adopted. Then, the max-pooling is executed; subsequently, the output obtained is sub-sampled. Nevertheless, to train the model, the SegNet desires additional CPU memory if the input signal is extremely large. Additionally, the most significant details might be ignored in the signal’s specific regions. Therefore, the non-overlapping PLT-SegNet is utilized to trounce the aforementioned issues. The input signal is split into non-overlapping patches by utilizing the patch-wise SegNet so the trained network can focus highly on local details in a patch; thus, helping in better localization along with utilizing lesser memory. Furthermore, to learn complex information with higher accuracy levels, instead of ReLU, the Logistic Tanh activation is wielded. The PLT-SegNet’s encoder layer is fed with the peak detected ECG signals; then, the convolutional operation is performed. Let the peak detected ECG signal be η_s . Initially, these signals are partitioned into varied patches $\left(p^i\left(1=1,2,\ldots\ldots,N\right)\right)$. Afterward, let a Q number of different filters in the filter bank be $\lambda_q^b=\left(\lambda_1^b,\lambda_2^b,\ldots\ldots,\lambda_Q^b\right)$; similarly, the number of CLs is specified as $\left(b=1,2,\ldots\ldots,B\right)$. The input patched signal $\left(p^i\right)$ is convolved with the filters $\left(\lambda_q^b\right)$ in the encoder layer. The convolution result $\left(\psi\right)$ is modelled as,

$$\psi = p^i\left(b-1\right)*\lambda_q^b \tag{8}$$

Where, the patched signal in the $\left(b-1\right)^{th}$ CL is demonstrated by $p^i\left(b-1\right)$. Then, the activation function is implemented as,

$$lt\left(\psi\right)=\frac{e^{-\psi}-1}{\left(e^{-\psi}+1\right)^2} \tag{9}$$

Where, the output’s logistic tanh activation is specified as $lt\left(\psi\right)$. In addition, to accelerate the convergence speed along with to avoid the gradient from disappearing, the Batch normalization $\left(\psi^*\right)$ is applied as,

$$\psi^* = \frac{\psi-e^{\psi}}{\sqrt{\operatorname{var}\left(\psi\right)}}$$

(10)

Here, the signal’s variance is signified as $\operatorname{var}\left(\psi\right)$. After that, in the max-pooling layer, the output’s resolution is mitigated. The max-pooling result $\left(\phi\right)$ is,

$$\phi=\frac{\left(1+\lambda^{b-1}-Q^b\right)}{g}$$

(11)

Where, the linear filter in the b^{th} layer is specified as Q^b and the scaling factor to minimize the resolution is notated as g . Then, at the decoder side, the signal’s subsampling is performed by the pooling layer; thus, mitigating the amount of data processed along with retaining the useful data. It is formulated as,

$$\hat{\psi} = lt\left(\psi * \lambda_q^b + B\right) \tag{12}$$

Here, the sub-sampled signal is denoted as $\hat{\psi}$, the bias term at the decoder is indicated as B. In such a manner, the PLT-SegNet network, which splits the ECG signal into QRS, P, and T waves, performs the segmentation process; subsequently, obtains the segmentation outcomes. Finally, to detect heart diseases, features are extracted as of the segmented waves.

3.4 Feature Extraction

For accurate classification, the most vital feature, which elucidates the heart rate, is extracted as of several peaks together with segments. QRS amplitude value, heart rate variability parameter, beat correlation, R-peak identification, fractal dimension, et cetera are the handcrafted features extracted as of the ECG signal's segmented waves. From the ECG signal, the m-number of features $\left(x^k\right)$ extracted are demonstrated as,

$$x^k = x^1, x^2, \ldots\ldots, x^m \tag{13}$$

3.5 Dimensionality Reduction using SELDA

By utilizing the SELDA, dimensionality reduction is performed following the feature extraction process. In this process, to mitigate the number of variables in the training data, the data in the higher dimensional space is transformed into the lower-dimensional representation. One of the most famous supervised dimensionality reduction methodologies is Linear Discriminant Analysis (LDA). Here, the input features are partitioned into 2 or more classes; then, for every single feature, the mean value is estimated; subsequently, to make predictions, variants are calculated by assuming a Gaussian distribution. Nevertheless, an inaccurate dimensionality reduction outcome might be produced if the information is not in the classes of computed means. Thus, by utilizing the Shannon Entropy (SE) measure, the mean computation is altered. SE is nothing but the measure of randomness in processed information. The modification in the traditional LDA is proffered as SELDA.

Step 1: By wielding the linear transformation matrix $\left(T\right)$, the m number of extracted features $\left(x^k\right)$ in the $d-$dimensional feature space be transformed into the lower-dimensional feature space D. Firstly, x^k is partitioned into M-number of subsets $\left(\tau^s\right)$, where $s = 1,2,\ldots,\mathrm{M}$.

Step 2: Next, every single feature's SE along with the subsets is gauged. SE $\left(S^e\right)$ for the input x^k is mathematically formulated as,

$$S^e = -\frac{1}{\log(m)} \sum_k \rho\left(x^k\right) * \log\left\langle \rho\left(x^k\right)\right\rangle \tag{14}$$

Here, the probability of features is represented as $\rho\left(x^k\right)$. Similarly, the SE for τ^s is demonstrated as S^τ.

Step 3: Then, the with-in class $\left(C^w\right)$, between-class $\left(C^b\right)$, and total-class $\left(C^t\right)$ scatter matrix are estimated as,

$$C^w = \sum_{s=1}^{\mathrm{M}} \sum_{k=1}^{m} \left(x^k - S^\tau\right)\left(x^k - S^\tau\right)^T \tag{15}$$

$$C^b = m * \sum_{k=1}^{m} \sum_{s=1}^{\mathrm{M}} \left(S^\tau - S^e\right)\left(S^\tau - S^e\right)^T \tag{16}$$

$$C^t = \sum_{k=1}^{m} \left(x^k - S^e\right)\left(x^k - S^e\right)^T \tag{17}$$

Where, the matrix values' transpose is illustrated as T.

Step 3: By utilizing a transformation matrix $\left(\Gamma\right)$, the lower-dimensional feature space is obtained following the computation of the scatter matrix. The Eigen vectors of $\left(C^w\right)^{-1} C^b$ is computed to estimate Γ. Then, C^b as well as C^w is expressed as,

$$C^b = \Gamma^T C^b \Gamma \tag{18}$$

$$C^w = \Gamma^T C^w \Gamma \tag{19}$$

The features extracted in the $d-$dimensional feature space are converted into D dimensional lower space by employing the transformation matrix. The N-number of dimensionality reduced features $\left(f^i\right)$ is signified as,

$$f^i = f^1, f^2, \ldots\ldots, f^N \tag{20}$$

3.6 Disease Prediction via SCJFSANN

Here, to predict various sorts of heart diseases, the ECG signals' dimensionality reduced features $\left(f^i\right)$ are fed to the SANN classifier. In general, the biological neurons' function in the human brain is imitated by the ANN, a computational learning system. A set of processing elements termed artificial neurons is included in this. In the network, a signal is transmitted to other neurons by every single neuron via the connection betwixt them. A number of input nodes, hidden nodes, and '1' or more output nodes are required to organize these neurons. Initially, the input is received by the input node; then, obtained data is forwarded to the hidden node in which to alter the input's strength, the input is multiplied with separate weight values along with activation functions. In general, the weight values are assigned randomly; then, in the hidden node, to learn the complex patterns, the Sigmoid Activation Function (SAF) is employed. The classification accuracy is affected along with the processing time is elevated owing to such random weight assignment. Furthermore, the vanishing gradient problem is a drawback in the SAF. Therefore, in the proposed model, the optimized weight values are assigned to the NN to overcome the aforementioned complications. Thus, the SCJF optimization algorithm is utilized here. Furthermore, to prevent the vanishing gradient, the Soft Swish activation is utilized rather than the SAF. Consequently, the modified version of ANN is mentioned as SCJFSANN. The following figure shows the ANN's general structure.

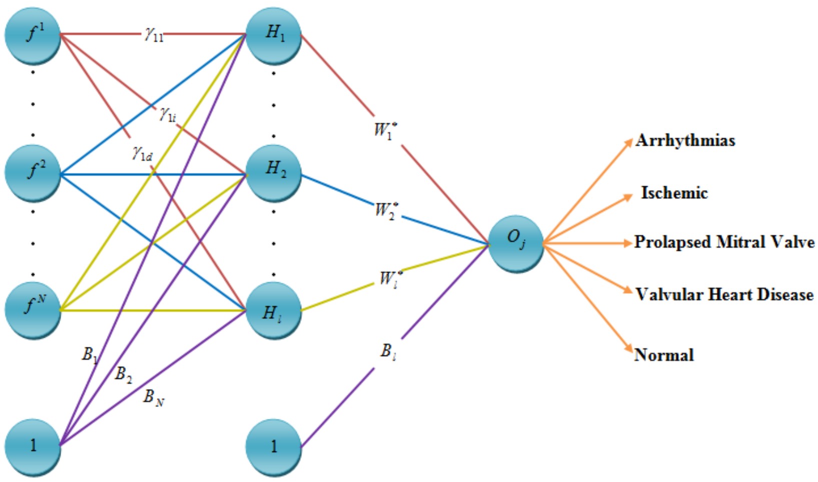

Fig 5: Neural structure of ANN

The following are the processes subsumed in the SCJFSANN model.

- The reduced features $\left(f^{i}=f^{1},f^{2},\ldots\ldots,f^{N}\right)$ are inputted to the NNs' input node; then, the information is forwarded to the first hidden layer in which the data is processed by a set of associated weights $\left(W_l^*\right)$ and biases $\left(B_l\right)$. Every single hidden layer $\left(H_l\right)$ measures the output as,

$$H_l=\sum_{l=1}^{L} f^{i}W_l^{*}+B_l \tag{21}$$

Where, the number of hidden layers in SCJFSANN is specified as $l=1,2,\ldots L$, the l^{th} hidden layer's optimized weight value is symbolized as W_l^* and the l^{th} hidden layer's bias parameter is notated as B_l.

- Next, to learn the input data's complex patterns, the soft swish activation function (γ) is utilized, which is represented as,

$$\gamma(H_l)=H_l*\exp(H_l)\Big/\sum_{l=1}^{L}\left(e^{H_l}+e^{-H_l}\right) \tag{22}$$

- Lastly, to predict the heart disease type, the hidden layer output is inputted to the output layer $\left(O_l\right)$. Then, to analyze the training process, Mean square error (E) is wielded. It is formulated as,

$$E=\frac{1}{N}\sum_{p=1}^{n}\left(y_p-a_p\right)^2 \tag{23}$$

Here, the desired output is denoted as y_p and the actual output for the input samples is indicated as a_p. Afterward, to mitigate the error value, the weight values are optimized by employing the SCJF optimization model. Finally, the output is produced by the classifier as a normal ECG signal in which Prolapsed mitral valve, Arrhythmias, Ischemic, and Valvular heart disease are the sorts of diseases detected.

3.6.1 Weight Optimization by SCJF

From the movement along with the food searching behaviour of jellyfish, JellyFish (JF) optimization model, a nature-inspired strategy, is developed. JF are free-swimming marine animals; they are found worldwide as of surface waters to the deep sea. '3' policies are subsumed in the JF algorithm: (i) the movement of ocean current is followed by the JF or it will move within the swarm along with it includes a time control mechanism; (ii) They will travel towards the direction where the food is more, and (iii) the objective function determines the amount of food found. The amount of food varies at varied locations that are searched for by JF. The position containing a larger quantity of food is regarded as the best position (optimal solution) whilst analogizing the food sizes. Nevertheless, the general JF algorithm contains certain drawbacks concerning its solution search equation; they are: the convergence speed is affected by the JF population's random initialization, and owing to lower population diversity, it tends to be trapped at local optima. However, when running with constrained problems, composite functions, along with certain non-separable functions, the algorithm's convergence rate obtained will be of inferior quality. Consequently, the initial population is generated by the Sinusoidal Chaotic (SC) maps in such a manner that the search space information can be extracted to ameliorate the population diversity; thus, making the initialization process highly effectual. Regarding the modifications made in the conventional JF, the proposed JF is named SCJF. The following are the steps subsumed in the SCJF.

Step 1: Primarily, by utilizing the SC mapping function, the initial JF population (Weight values of NN) is engendered. The population initialization is mathematically formulated as,

$$W^{j+1} = -\alpha \sin(W); \;\; W^{j} \in (0,1) \tag{24}$$

Where, the j^{th} jellyfish SC value is signified as $W^{j}\left(j = 1,2,\ldots,F\right)$, the initial population is defined as $W^{j} \in (0,1)$, and the constant parameter is notated as α.

Step 2: To recognize the best solution $\left(W^{best}\right)$, the fitness of every single JF $f\left(W^{j}\right)$ is gauged following population initialization. Regarding the classifier accuracy, the fitness is measured in the proposed weight optimization. The JF's positions are updated regarding their movement after determining the best JF.

Step 3: The movement of the ocean current is followed by the JF; in addition, it comprises a time control mechanism. The time control mechanism subsumes the time control function $\left(\delta_t\right)$, which is modelled as,

$$\delta_t = \left| \left(1 - \frac{t}{\max(t)}\right) * \left(2 * \beta(0,1) - 1\right) \right| \tag{25}$$

Here, the current iteration and the maximum number of iterations are specified as $t, \max(t)$, respectively, and the random number in the interval (0, 1) is represented as $\beta(0,1)$. The value of δ_t oscillates betwixt 0 and 1; subsequently, it is analogized with the constant $\delta^{0} = 0.5$.

Step 4: The JF moves towards the ocean current if $\delta_t > \delta^{0}$. Thus, the JF's position $\left(W_{t+1}^{j}\right)$ at $t+1$ is updated as,

$$W_{t+1}^{j} = \chi * \left(W^{best} - 3\chi m\right) + W_t^{j} \tag{26}$$

$$m = \frac{1}{F} \sum_{i=1}^{F} W_t^{i} \tag{27}$$

Here, the JF's current best position is exhibited as W^{best}, the mean value of all jellyfish positions is depicted as m, the current position is notated as W_t^{j} and a random number within [0, 1] is symbolized as χ.

Step 5: The jellyfish move towards the swarm if $\delta_t < \delta^{0}$. Passive and active are the 2 sorts of movements followed within the swarm. Mostly, the JF follows the passive movement, which is updated as,

$$W_{t+1}^{j} = W_t^{i} + 0.1 * \chi * (U - L) \tag{28}$$

Where, the upper and lower bounds in the search space are demonstrated as U and L. Regarding the fitness function $f\left(W^{j}\right)$, the location is updated in the active movement. It is expressed as,

$$W_{t+1}^{j} = \begin{cases} W_t^{j} + \chi\left(W_t^{k} - W_t^{j}\right) & if \;\; f\left(W^{j}\right) \geq f\left(W^{k}\right) \\ W_t^{j} + \chi\left(W_t^{j} - W_t^{k}\right) & if \;\; f\left(W^{j}\right) < f\left(W^{k}\right) \end{cases} \tag{29}$$

Here, the k^{th} JF (position of previous best JF) is depicted as W_t^{k}, and the fitness of k^{th} JF is modelled as $f\left(W^{k}\right)$. Additionally, the JF movements are chosen regarding δ_t. Until reaching the maximum number of iterations, the process is repeated. At last, the best solution attained at the end of every single iteration is considered as the optimal solution (optimized weight values), which is signified as W^*. Figure 6 demonstrates the proposed SCJFSANN classifier's pseudo-code.

Pseudocode for proposed SCJFSANN model

Input: Reduced features (f^t)

Output: Detected diseases (y_σ)

Begin

Input f^t to the input layer

For each (l)

  Initialize associated weights (W^j), and biases (B_l)

  Optimize (W^j)

  While $j \le F$ **do**

    Generate jellyfish population using sinusoidal chaotic map

    Compute $f(W^j)$ to recognize W^{best}

    Evaluate time control function (δ_t)

    If $\delta_t > \delta^0$

      Renew the position of jellyfish (W^j_{t+1})

      Estimate $m = \frac{1}{F}\sum_{t=1}^{F} W^j_t$

    Else if $\delta_t < \delta^0$

      Keep informed the position by $W^j_{t+1} = W^j_t + 0.1 * \chi * (U - L)$

      If $f(W^j) \ge f(W^k)$

        Execute position update

      Else

        Carry out $W^j_t + \chi(W^j_t - W^k_t)$

      End if

    End if

    Update the best solution

    Attain optimized weights W^*

  End while

  Estimate the hidden layer output (H_l)

  Assess soft swish activation (γ)

  Obtain the types of diseases y_σ

  Determine $E = \frac{1}{N}\sum_{\sigma=1}^{n}(y_\sigma - a_\sigma)^2$

End for

End

Fig 6: Pseudocode of the proposed classification technique

4. Results And Discussion

Here, the obtained outcomes were evaluated with the prevailing methodologies to prove the proposed model's efficacy regarding certain performance metrics. The model is executed in MATLAB; in addition, it utilizes the openly accessible dataset for training.

4.1 Performance assessment of proposed SCJFSANN

ANN, Adaptive Neuro-Fuzzy Interference System (ANFIS), Support Vector Machine (SVM), and Decision Tree (DT) are the prevailing methodologies with which the proposed model is analogized regarding the accuracy, precision, recall, f-measure, sensitivity, specificity, False Negative rate (FNR), along with False Positive Ratio (FPR). Figure 7 exhibits the graphical representation of accuracy, precision, together with recall.

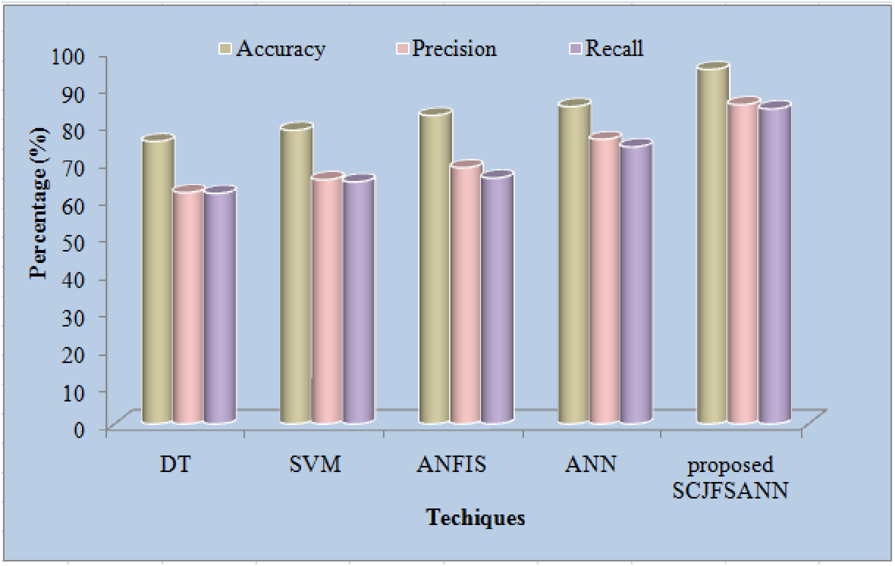

Fig 7: Graphical representation of accuracy, precision, and recall of the proposed and existing techniques.

The measurement's closeness to the true or accepted value is shown by the accuracy. The system's best performance was revealed by a higher accuracy. The proposed SCJFSANN classifier attained an accuracy of 94.93%. The accuracy attained by the prevailing ANN, ANFIS, SVM, and DT models are 85.04%, 82.61%, 78.71%, and 75.64%, respectively. Thus, the proposed model detects heart diseases more accurately by attaining a higher accuracy than the existing models. Similarly, the proposed model attained a precision of 85.55% whereas the precision values of 76.21%, 68.63%, 65.45%, and 61.93% were attained by the prevailing ANN, ANFIS, SVM, and DT methodologies respectively. Furthermore, the proposed one attained a recall of 84.43%. Conversely, a lower recall was attained by the prevailing methodologies. For example, a recall value of 74.21% was obtained by the existent ANN model. Therefore, it is evident that a higher performance was attained by the proposed system than the prevailing models. Table 1 shows the sensitivity, specificity, and f-measure of the proposed along with existing classifiers.

Table 1: Superiority measure of the proposed classification model

Techniques/ Performance metrics	Sensitivity	Specificity	F-measure
Proposed SCJFSANN	84.12	93.23	83.99
ANN	80.09	89.81	79.63
ANFIS	74.74	82.04	75.27
SVM	71.98	76.36	72.85
DT	67.49	74.16	68.54

The SCJFSANN classifier attained a sensitivity, specificity, and f-measure of 84.12%, 93.23%, and 83.99% correspondingly. These values are much higher than that of the previous systems. Sensitivity attained by the conventional ANN, ANFIS, SVM, and DT models are 80.09%, 74.74%, 71.98%, and 67.49%. Likewise, the specificity along with f-measure of the existent ANN, ANFIS, SVM, and DT are also lower when analogized to that of the proposed model. For instance, the traditional DT attained a specificity and f-measure of 74.16% and 68.54%, correspondingly. Thus, the proposed model detects heart diseases with higher sensitivity, specificity, and f-measure and tends to be highly accurate than the prevailing methodologies. Figure 8 demonstrates the outcome analysis regarding FPR.

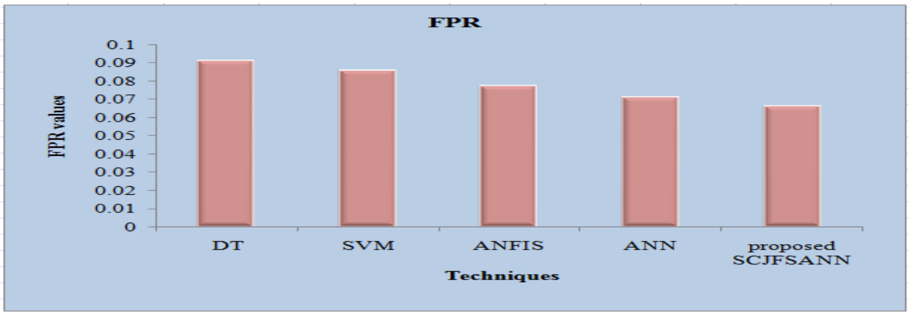

Fig 8: FPR assessment of SCJFSANN and existing ANN, ANFIS, SVM, and DT

The proposed classifier obtained a lower FPR of 0.06613. Meanwhile, the higher FPR attained by the prevailing classifiers are ANN (0.07082), ANFIS (0.07703), SVM (0.08543), and DT (0.09093). In comparison with the prevailing methodologies, the SCJFSANN classifier acquired a lower FPR value. The test's false rejection is measured as FPR. Therefore, the best performance is attained with a lower FPR. Thus, it is confirmed that heart diseases were detected by the proposed model with lower FPR than the conventional methodologies. Table 2 shows the FNR analysis for better measurement.

Table 2: FNR value of proposed and existing methods

Techniques/ Performance metrics	FNR
Proposed SCJFSANN	0.21368
ANN	0.38921
ANFIS	0.46782
SVM	0.54969
DT	0.60913

In table 2, to prove the proposed system's efficacy, the proposed along with prevailing methodologies' FNR values are analogized. The inaccurate detection of the hypothesis (test) is termed FNR. For example, a person actually undergoes the disease but the test result specifies that the person does not hold any disease; here, the test outcome is false, which is mentioned as FNR. Thus, the model shows better performance with lower FNR. Consequently, the FNR attained by the SCJFSANN classifier is 0.21368 whereas the conventional ANN attained an FNR of 0.38921, which is higher than that of the proposed one. Likewise, the FNR obtained by other prevailing systems also varies. Thus, it is clear that heart diseases were classified more effectually by the proposed mechanism than by the prevailing methodologies.

4.2 Superiority measurement of proposed CSHT

HT, Discrete Wavelet Transform (DWT), and Short Time Fourier Transform (STFT) are the prevailing methodologies with which the proposed CSHT's superiority in detecting the ECG signal's peak values is evaluated regarding the accuracy of detection. The figure below shows the graphical representation of the aforementioned validation.

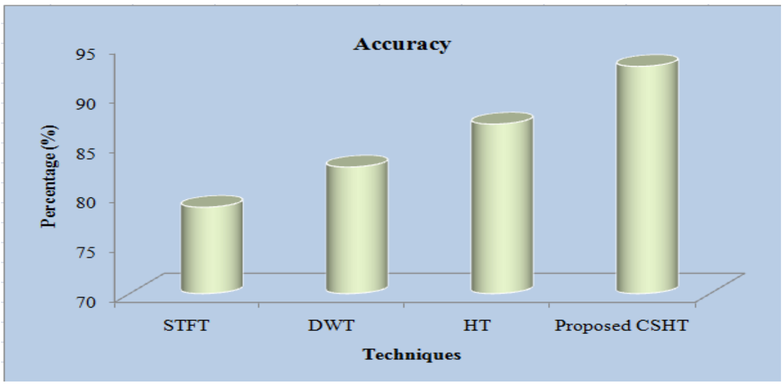

Fig 9: Graphical assessment of CSHT based on the accuracy

As per figure 9, the signal's peak values were detected more accurately by the CSHT model than by the traditional systems. The detection accuracy values attained by the CSHT and prevailing HT are 92.85% and 87.05%, in that order. Similarly, the accuracy values obtained by the existent DWT and STFT are 82.73% and 78.69%, correspondingly. Thus, it is evident that better performance was achieved by the proposed system that the prevailing methodologies.

5. Conclusion

Regarding ECG signals, an effective HDPS is proposed here by employing the PLT-SegNet together with SCJFSANN methodologies. To detect along with to classify heart diseases, several processes were undergone by the proposed methodology by utilizing the ECG signals. Lastly, for assessing the proposed model's efficiency, the performance, as well as comparative evaluation, is conducted for the proposed and the existing methodologies. For the evaluation, the openly accessible dataset is utilized in this research methodology. The performance evaluation demonstrated that the ECG signal peaks are detected by the proposed model with an accuracy of 92.85%; in addition, it also classifies various sorts of heart diseases with higher accuracy and precision of 94.93% and 85.55%, respectively, and with lower FPR and FNR of 0.06613 and 0.21368, in that order. On the whole, the proposed methodology outshined the prevailing methodologies by obtaining effectual outcomes. In the upcoming future, the work will be advanced by utilizing the Phonocardiogram (PCG) signals with highly enhance ML strategies to detect heart diseases.

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