Optimizing Deep Neuro-Fuzzy Network for ECG Medical Big Data Through Integration of Multiscale Features

Xin Wang, *Member, IEEE*, Jianhui Lv, *Member, IEEE*, Byung-Gyu Kim, *Senior Member, IEEE*, Bidare Divakarachari Parameshachari, *Senior Member, IEEE*, Keqin Li, *Fellow, IEEE*, Dongsheng Yang, *Senior Member, IEEE*, and Achyut Shankar, *Senior Member, IEEE*

***Abstract*—Electrocardiogram (ECG) analysis and diagnosis are important auxiliary means for preventing and detecting cardiovascular diseases. Traditional approaches often face challenges due to the sheer volume of data, difficulty in extracting meaningful features, limitations in model complexity, and the requirement for real-time analysis in clinical settings. This article presents a pioneering approach for automatic ECG diagnosis through the application of a novel multiscale deep neuro-fuzzy network (MDNFN) structure. The MDNFN is designed to address the complexity of arrhythmia classification by incorporating deep learning and fuzzy logic processing across multiscale feature extraction. To optimize the performance of the MDNFN, an innovative model optimization technique based on the particle swarm optimization algorithm is introduced, offering an efficient exploration of the parameter space. Extensive experiments across diverse datasets validate the superior performance of the proposed model compared with existing methods. The MDNFN demonstrates heightened accuracy and robustness, supported by its adaptability to different frequency and time scales inherent in ECG signals. The study establishes the model's efficacy through comprehensive experimentation, providing compelling evidence for its potential application in real-world clinical scenarios.**

***Index Terms*—Deep neuro-fuzzy network, electrocardiogram (ECG) analysis, fuzzy system, medical Big Data, multiscale feature.**

I. Introduction

Electrocardiogram (ECG) analysis, a critical component in cardiac healthcare, has traditionally relied on expert interpretation that is often constrained by human error and inefficiency [1]. The aging of the population and the development of telemedicine equipment have resulted in ECG medical Big Data, which has put tremendous pressure on limited medical resources. Automating the interpretation process with the intelligent approach can reduce the workload on healthcare professionals and minimize the risk of misdiagnosis, ultimately leading to improved patient outcomes [2]. This advancement is particularly crucial given the increasing prevalence of cardiac diseases globally and the need for timely and accurate diagnosis.

ECG signals are complex, exhibiting a range of features at different scales that are indicative of various cardiac conditions. The ability to accurately interpret these signals is crucial for effective diagnosis. ECG signals consist of P waves, QRS complexes, and T waves, each representing different aspects of cardiac activity [3]. Variations in these waveforms can indicate a wide range of cardiac abnormalities, from arrhythmias to myocardial infarction.

Deep learning, a subset of machine learning, excels in handling large datasets and learning complex patterns [4], [5]. It is particularly suited for analyzing the intricate and varied nature of ECG signals. Deep learning algorithms, especially convolutional neural networks (CNNs), are adept at automatically extracting relevant features from raw data, a significant advantage over traditional methods. These algorithms can learn to identify subtle patterns in ECG signals that may be indicative of cardiac conditions, often surpassing the accuracy of manual interpretation. Deep learning's ability to handle large datasets and learn from data makes it ideal for ECG signal analysis. However, the interpretability of deep learning models remains a challenge. This is where fuzzy logic comes into play. Fuzzy logic, with its ability to handle uncertainty and provide interpretable results [6], [7], complements deep learning by offering a framework to make sense of the complex patterns recognized by deep neural networks [8]. The deep neuro-fuzzy network is a hybrid artificial intelligence (AI) model that combines the advanced feature extraction capabilities of deep learning with the interpretability and rule-based reasoning of fuzzy logic [9]. This approach allows for a more nuanced analysis of ECG signals, which addresses the limitations of deep learning models in terms of interpretability. Fuzzy logic introduces an element of

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Xin Wang is with Northeastern University, Shenyang 110819, China, and also with Dongneng (Shenyang) Energy Engineering Technology Company Ltd., Shenyang 110819, China (e-mail: dnsy_heinrich@neueet.com).

Jianhui Lv is with The First Affiliated Hospital of Jinzhou Medical University, Jinzhou 121012, China (e-mail: lvjianhui2012@163.com).

Byung-Gyu Kim is with Sookmyung Women's University, Seoul 04310, Republic of Korea (e-mail: bg.kim@sookmyung.ac.kr).

Bidare Divakarachari Parameshachari is with the NITTE Meenakshi Institute of Technology, Bengaluru 560064, India (e-mail: paramesh@nmit.ac.in).

Keqin Li is with State University of New York, New Paltz, NY 12561 USA (e-mail: lik@newpaltz.edu).

Dongsheng Yang is with Northeastern University, Shenyang 110819, China (e-mail: yangdongsheng@mail.neu.edu.cn).

Achyut Shankar is with the WMG, University of Warwick, CV74AL Coventry, U.K. (e-mail: ashankar2711@gmail.com).

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human-like reasoning to AI and enables the model to handle the ambiguity and imprecision inherent in medical Big Data [10].

The motivation behind the incorporation of fuzzy logic into deep learning for ECG analysis stems from the complementary nature of these two paradigms and the unique benefits they offer individually. Deep learning techniques, characterized by their ability to automatically learn hierarchical representations from data, have demonstrated remarkable success in various domains, including image recognition, natural language processing, and medical diagnostics. However, traditional deep learning models may encounter challenges in handling uncertainty, imprecision, and ambiguity inherent in medical data such as ECG signals. Fuzzy logic, on the other hand, provides a formal framework for reasoning under uncertainty by allowing for the representation of vague or imprecise information using linguistic variables and fuzzy sets. By integrating fuzzy logic with deep learning, we aim to leverage the interpretability and robustness of fuzzy logic while harnessing the representation learning capabilities of deep neural networks. This hybrid approach enables us to develop models that can effectively handle the inherent uncertainties in ECG data and enhance the performance of diagnostic tasks.

The integration of AI into this field marks a transformative shift toward enhanced accuracy and efficiency. This article introduces an innovative approach to ECG diagnosis using a multiscale deep neuro-fuzzy network (MDNFN), which synergizes the strengths of deep learning and fuzzy logic to extract and interpret multiscale features from ECG signals, thereby facilitating more accurate diagnoses.

The proposed MDNFN model is designed to capture multiscale features in ECG signals, which are crucial for identifying various cardiac abnormalities. By integrating multiscale analysis with the robust feature extraction capabilities of deep learning and the interpretability of fuzzy logic, this model aims to provide a comprehensive and accurate tool for automatic ECG diagnosis. This model's ability to analyze ECG signals at multiple scales allows for the detection of a wide range of cardiac conditions, potentially even those that are at a nascent stage or are less pronounced. The integration of deep learning and fuzzy logic not only enhances the model's diagnostic capabilities but also improves its usability and acceptability in clinical settings, where interpretability and reliability are paramount.

We summarize the contributions of this article as follows.

1) We introduce a novel MDNFN structure specifically designed for the automatic identification and classification of arrhythmias in ECG signals. In contrast to traditional approaches, this structure engages in deep learning and fuzzy logic processing across multiple scales, which captures and analyzes ECG features at different scales comprehensively and accurately. The introduction of this multiscale architecture enables the model to better adapt to arrhythmia patterns at various frequencies and time scales, thereby enhancing classification accuracy and robustness.
2) We design an optimization method based on the particle swarm optimization (PSO) algorithm [11] to further enhance the performance of the proposed MDNFN. Leveraging PSO, we effectively explore the parameter space, which identifies optimal parameter combinations to maximize the model's performance.
3) Validations through extensive experiments on the well-known database demonstrate the significant superiority of the proposed MDNFN model compared with existing methods.

The rest of this article is organized as follows. In Section II, we delve into the existing body of knowledge with a thorough exploration of related work and provide context and insights into the evolution of techniques for automated ECG diagnosis. Section III forms the core of our study, which details the methodology employed in our approach, including the data preprocessing and feature selection, the architecture of the proposed MDNFN, and the optimization. Moving forward, Section IV outlines the experiments conducted to validate the efficacy of our model. This encompasses the experimental setup and database details, an in-depth performance analysis against benchmark methods, and an ablation study to dissect the impact of individual components within the MDNFN. Finally, Section V concludes this article.

II. Related Work

The application of AI in ECG Big Data diagnosis is not new, and numerous studies have explored various approaches. We classify existing algorithms into three categories, namely, classification algorithms based on knowledge reasoning, traditional machine learning methods, and neural networks.

The advancement of ECG technology has paralleled the utilization of knowledge reasoning techniques by researchers in arrhythmia identification, as evidenced by studies [12] and [13]. Knowledge reasoning involves the retrieval or alignment of test data within a knowledge base, guided by expert control strategies, to infer new facts. At a broader scale, employing knowledge reasoning for the automatic categorization of arrhythmias entails an amalgamation of individual patient data (such as gender and medical history) with medical knowledge to construct a specialized knowledge base and corresponding reasoning mechanisms. Initial research in this domain primarily focused on employing production rules, and elementary or fuzzy logic to represent ECG signal knowledge and develop relevant knowledge bases. Exarchos et al. [14] introduced an automatic detection technique for ischemic cardiac pulses utilizing association rule mining. Further, Exarchos et al. [15] integrated data mining with fuzzy models extracting dependable rules from representative training sets and formulating a fuzzy decision tree model in conjunction with the C4.5 algorithm, achieving a 96% accuracy rate across four heartbeat categories in the MIT-BIH database. Teijeiro et al. [16], in 2018, developed a classifier model predicated on expert knowledge rules, which demonstrated a 98.7% accuracy in heartbeat recognition within the MIT-BIH database, albeit necessitating manual extraction of ECG features. However, the primary limitation of this approach is its excessive reliance on the medical professional knowledge base. Adjustments to the knowledge base require extensive retraining of the model, rendering the process resource-intensive. The subtlety of certain disease characteristics further complicates knowledge organization, challenging model training and timely modification of the medical knowledge base. Consequently, these models exhibit a relatively simplistic inference structure and lack robust generalization capabilities.

Once features are extracted from the ECG data, algorithms such as machine learning can be used to build models on the data for ECG analysis and classification. Statistics-based machine learning developed rapidly in the early 1990s, resulting in a large number of studies and applications of statistical machine learning methods on arrhythmias. Statistics-based machine learning methods are then widely used to solve the problem of arrhythmia classification. Asl et al. [17] achieved a significant milestone by classifying six types of arrhythmias with an accuracy exceeding 98.3%, utilizing a combination of two algorithms: Support vector machine (SVM) and linear discriminant analysis (LDA). This was accomplished by extracting 17 original input features. In a similar vein, Leutheuser et al. [18] attained a 93.30% accuracy rate in classifying two arrhythmia types. Their methodology involved the application of the Naive Bayes algorithm to extract high-order statistics from segmented ECG data, followed by implementation based on template characteristics. Pan et al. [19] proposed a novel approach for arrhythmia classification, combining discrete wavelet and random forest techniques. While these methods show a high success rate in heartbeat recognition and reduce reliance on expert knowledge, they are not without limitations. These include insufficient generalization capabilities, a heavy dependence on manually-crafted features, and the inherent complexities and limitations of such designs. In addition, these approaches often exhibit poor adaptability when dealing with long ECG signals.

Deep learning models, particularly CNNs, have been widely used for feature extraction in ECG signals. Yang et al. [20] introduced an innovative approach to online heartbeat recognition with the development of a new fuzzy neural network model. This model leverages the Hermite function for feature extraction, exemplifying a novel application in the field. Giler et al. further contributed to this domain by proposing a feedforward neural network (FFNN) as a classifier, coupled with wavelet transform (WT) for feature extraction. The training of this model was conducted using the Lavenberg-labeling algorithm. Expanding upon these methodologies, Ceylan and Özbay [21] also employed FFNN as a classifier, but integrated it with principal component analysis (PCA) and WT for feature extraction, and the fuzzy C-means clustering (FCM) method for feature reduction. Their results highlighted that the combined application of PCA, FCM, and FFNN exhibited the most efficacious outcome among ten different arrhythmias. In another significant advancement, Rahhal et al. [22] introduced a modification to deep neural network structures by adding a reconstruction layer atop the hidden layer. This novel heartbeat classification algorithm demonstrated robustness in comparative experiments, with notable accuracy and high computational efficiency, significantly enhancing heartbeat recognition. Zhang et al. [23] achieved commendable recognition rates in the heartbeat recognition task on the MIT-BIH database. Their approach involved the integration of recurrent neural network (RNN) with density clustering technology, presenting a core innovation in this research area. These diverse methodologies underscore the evolving landscape of heartbeat recognition techniques, highlighting the intersection of neural networks, machine learning, and feature extraction methodologies in advancing cardiac health diagnostics.

These models have shown significant success in identifying cardiac anomalies, such as arrhythmias, myocardial infarction, and heart failure. However, the black-box nature of these models often limits their clinical applicability due to the lack of interpretability. Neuro-fuzzy systems have been employed in ECG analysis to address this issue. These systems use fuzzy rules and membership functions to provide a more interpretable analysis, making them more acceptable in clinical settings. However, traditional fuzzy systems may lack the ability to handle the complexity and variability inherent in ECG signals.

The concept of integrating deep learning with fuzzy logic in ECG analysis is emerging as a promising solution. This hybrid deep neuro-fuzzy approach aims to combine the high-level feature extraction capabilities of deep learning with the interpretability and rule-based reasoning of fuzzy logic. Previous studies have demonstrated the potential of such hybrid systems in improving the accuracy and interpretability of ECG analysis. Our work builds upon these foundations, introducing a multiscale perspective to this hybrid approach. By focusing on multiscale feature extraction, our MDNFN model aims to capture a more comprehensive range of cardiac signals, potentially leading to more accurate and reliable diagnoses.

III. Method

In this section, we describe the main structure and processing steps of the proposed MDNFN method. First, we perform preprocessing and feature extraction on the ECG Big Data to prepare for input to the subsequent model. Second, the overall structure and data flow of the multiscale deep fuzzy neural network are described in detail. Finally, we introduced the optimization method of MDNFN, which uses the improved particle swarm algorithm to optimize the learning of the model. The overall process and model framework are shown in Fig. 1.

A. Data Preprocessing and Feature Selection

The ECG signal is inherently susceptible to interference, both from internal and external sources, such as baseline drift [24]. Such disturbances can lead to varying degrees of distortion in the ECG signal, potentially resulting in diagnostic inaccuracies, including misinterpretations by clinicians or misidentifications of arrhythmias by assistive devices. The complexity of ECG noise, which spans both low- and high-frequency ranges and often overlaps with signal spectra, further complicates signal interpretation. To address these challenges, it is imperative to strike an optimal balance between minimizing information loss and maximizing the effectiveness of noise reduction. This balance is crucial as both noise and informative components coexist within the ECG signal spectrum. In this context, the selection of an appropriate threshold for denoising technology becomes a critical factor. Efficiently denoised ECG signals not only enhance classification results but also substantiate the efficacy of the denoising method itself. Consequently, to preserve the integrity of valuable information in the ECG signal, it is

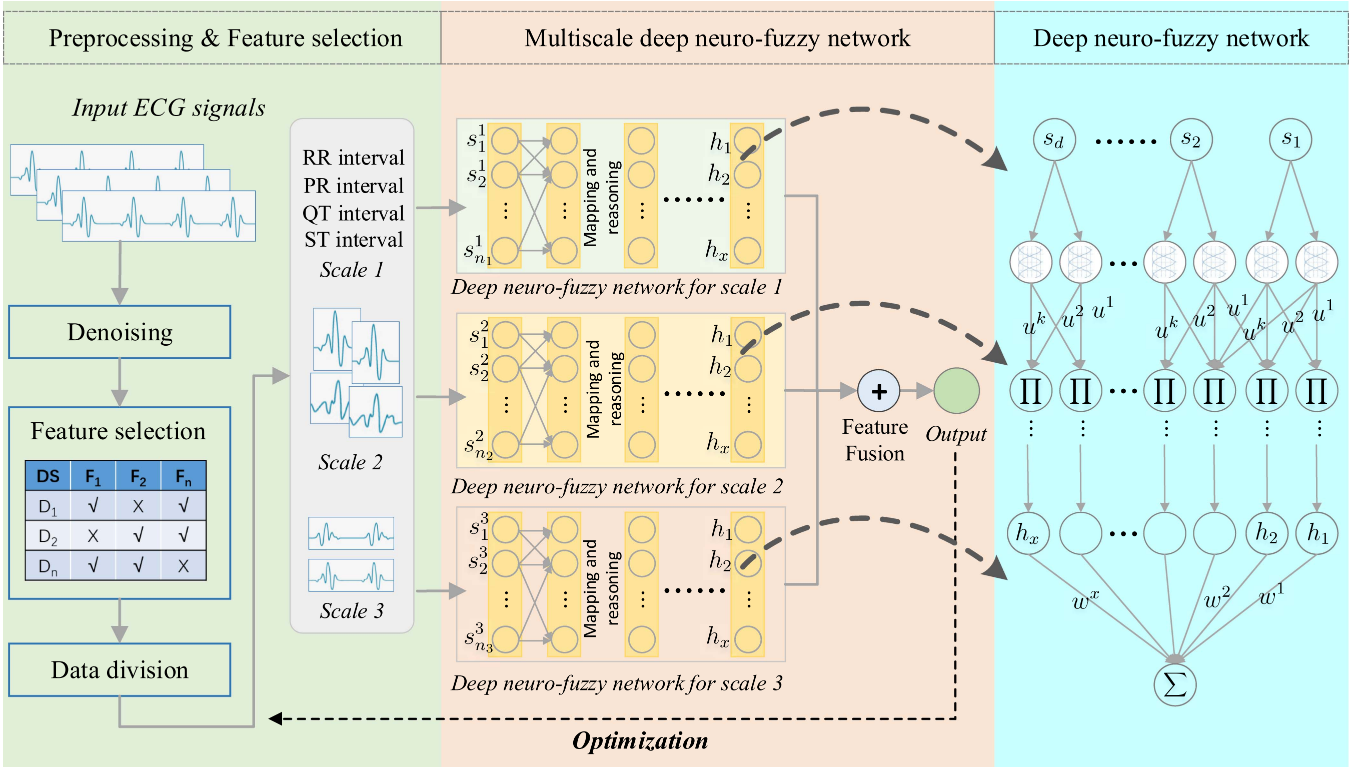

Fig. 1. Overall structure of the proposed MDNFN.

essential to implement noise reduction processes on the original signal. Such processes aim to mitigate the impact of noise while safeguarding the key diagnostic features intrinsic to the ECG signal, thereby facilitating more accurate and reliable cardiac arrhythmia detection and diagnosis.

In our approach, we employ WT as a preprocessing technique for ECG signals. WT is widely recognized for its efficacy in denoising, particularly in engineering applications. The fundamental concept involves manipulating wavelet coefficients based on their characteristics and the mechanisms by which they correspond to noise across various scales. This reduces noise interference in the coefficients, enabling the reconstruction of the signal using the processed coefficients. Our initial step involves analyzing the frequency characteristics of the signal noise. Subsequently, we select an appropriate wavelet function and determine the optimal number of decomposition layers. This selection is based on the frequency passband characteristics of the wavelet function at each scale, which guides the wavelet decomposition of the signal. Following decomposition, we address the wavelet coefficients associated with noise and proceed to their reconstruction. There are typically two prevalent methods for processing these noise-correlated wavelet coefficients. The first involves the outright removal of coefficients associated with noise, a straightforward but potentially signal-compromising method. The second method entails applying threshold closing and modulus maximum techniques to the noise-associated coefficients. This second approach, while simple in its algorithm, effectively retains useful signal components while eliminating noise. The threshold closing method, in particular, processes the noise-corresponding wavelet coefficients using appropriate threshold values. This technique strikes a balance between noise reduction and preservation of vital signal components, making it an effective strategy for enhancing the clarity and utility of ECG signals in clinical diagnostics and research. The selection of threshold is the focus and difficulty of this method. We use the following threshold:

$$\mathrm{Thd} = \delta\sqrt{\frac{2\log(n)}{n}}, \quad \delta = \frac{\mathrm{mid}}{c} \tag{1}$$

where δ is the noise intensity, mid is the absolute value of the normalized wavelet coefficient median, and c is a constant.

Then, we use the soft threshold processing method to set the points whose absolute value is less than the threshold value to zero, and correct the points whose absolute value is greater than the threshold value, as follows:

$$\mathrm{y} = \begin{cases} \mathrm{sign}(x)(\mid x \mid - \mathrm{Thd}), & \text{if } \mid x \mid > \mathrm{Thd} \\ 0, & \text{otherwise.} \end{cases} \tag{2}$$

After denoising is completed, we use wavelets for feature extraction. Specifically, for the ECG signal $s(t)$, we can use the following transformation to calculate the wavelet characteristics of the ECG signal:

$$W = \int_{-\infty}^{\infty} s(t)\Phi(t)dt \tag{3}$$

where $\Phi(t)$ is the wavelet function. Through this transformation, we can calculate the wavelet characteristics in the ECG signal, including the RR interval, PR interval, QT interval, and ST interval.

B. Structure of MDNFN

As mentioned before, we process the multiscale features of the ECG signal. We consider the wavelet features in the ECG signal as fine-grained scale features, namely, RR interval, PR interval, QT interval, and ST interval. A single heartbeat wave can reflect a complete activity process of the heart, so we extracted the features of a single waveform scale. Furthermore, we extracted multiple ECG heartbeat signals over a longer time interval to enable the model to more comprehensively experience the periodic variation characteristics of ECG. In summary, the specific steps of multiscale data processing and feature fusion are as follows. First, we regard ECG signals of different time lengths as different scales, because different time lengths contain different information. That is, wavelets, single heartbeats, and multiple heartbeats are viewed as different scales. Second, ECG signal data of different scales are input into the deep network to extract feature information of different scales. Third, the extracted multiscale features are combined and calculated to obtain the final result. For each scale, we use a deep neuro-fuzzy network to extract corresponding features, and finally perform feature fusion on the extracted features at different scales, as shown in Fig. 1.

Specifically, we employ the Takagi–Sugeno–Kang (TSK) model as the main framework for fuzzy networks [25]. The TSK model, a prominent methodology in fuzzy logic systems, offers a nuanced approach to modeling complex, nonlinear systems. Developed initially by Takagi and Sugeno, and later refined by Kang, this model stands as a pivotal advancement in the domain of fuzzy control and modeling. Distinct from traditional fuzzy models that employ fuzzy sets in both premises and conclusions of rules, the TSK model utilizes fuzzy sets only in the rule premises, with the conclusions consisting of linear functions or constants. The structural framework of a typical TSK rule might be articulated as follows: "If x is A and y is B, then $z = ax + by + c$," where x and y are input variables, A and B are fuzzy sets, and z is the output defined linearly in terms of the inputs. This configuration facilitates a piecewise linear approximation of nonlinear systems, a significant departure from conventional fuzzy logic systems. One of the most salient features of the TSK model is its interpolative capability between linear functions of different rules. This attribute allows the TSK model to adeptly handle complex scenarios where a global nonlinear model is challenging to establish or ineffective. Consequently, the TSK model finds extensive application in diverse fields such as control systems, pattern recognition, system identification, and time-series prediction. The TSK model's primary advantage lies in its efficient modeling of nonlinear systems. It is capable of approximating any real continuous function with a desired level of accuracy, provided a sufficient number of rules and appropriate parameter selection are employed. Furthermore, the parameters within the TSK model, notably the coefficients in its linear functions, are often optimized through various techniques such as gradient descent, genetic algorithms (GAs), or other advanced optimization methods. This optimization is pivotal in fitting the model precisely to a specific set of data. The TSK model represents a sophisticated fusion of fuzzy logic and traditional mathematical modeling. Its ability to handle nonlinear complexities with linear computational simplicity makes it an invaluable tool in the arsenal of modern control systems and data analysis methodologies. The model's flexibility, efficiency, and accuracy in approximation render it indispensable in the realm of complex system analysis and control.

The structure of the deep fuzzy network in the model mainly includes the input layer, mapping layer, rule layer, inference layer, and output layer. The first three layers reflect antecedent learning. $s_1, s_2, \ldots, s_d$ indicates a set of d-dimensional inputs, and the membership degree u^i is obtained through the Gaussian membership function $u^1(s), u^2(s), \ldots, u^k(s)$. $w^1, w^2, \ldots, w^H$ is the weight of the hidden layer and is also the consequent parameter that needs to be solved by the TSK fuzzy neural network. H represents the number of nodes in the hidden layer. In this article, the algorithm we use is the FCM fuzzy clustering algorithm introduced in [26]. It uses an iterative method to find the best fuzzy clustering center and compares the membership degree of the corresponding sample with the distance between the sample and each cluster center. The sum of the products is used as the target parameter J.

Suppose the ECG training dataset is $\{S, Y\}, s_i \in S, y_i \in Y$. Then, the target parameters of the data input process are as follows:

$$\begin{aligned} \min J &= \sum_{i=1}^{K} \sum_{j=1}^{H} U_{ij} \parallel s_j - \boldsymbol{C}_i \parallel^2 \\ \text{s.t.} &\sum_{i=1}^{K} U_{ij} = 1, j = 1, 2, \ldots, H \end{aligned} \tag{4}$$

where U_{ij} is the membership matrix, its iterative calculation is as follows:

$$U_{ij} = \frac{1}{\sum_{k=1}^{K} (\parallel \boldsymbol{s}_j - C_i \parallel / \parallel \boldsymbol{s}_j - C_k \parallel)^{\frac{2}{m-1}}} \tag{5}$$

where C means the fuzzy class center matrix and the calculation is as follows:

$$C_i = \sum_{j=1}^{H} (U_{ij} \times \boldsymbol{s}_j) \Big/ \sum_{i=1}^{H} U_{ij}, i \in [1, K]. \tag{6}$$

In the update process of U and C, we first randomly give a U value, then a new matrix can be obtained between U and C through (5) and (6), and iterate repeatedly until convergence. The fuzzy inference and defuzzification output in the last two layers are mainly learned by RBF from the training dataset through the self-learning method. The least mean square rule is used as the standard to obtain fuzzy consequent parameters.

The output result can be calculated as follows:

$$y = f(\boldsymbol{x}) = \sum_{i=0}^{H} w^i \exp\left(-\frac{\parallel \boldsymbol{h} - \boldsymbol{s}_i \parallel^2}{\delta}\right) \tag{7}$$

where s_i represents the hidden layer node, w^i is the weight of the hidden layer node and is also the parameter of the fuzzy consequent, and the minimum mean square error Er can be calculated as follows:

$$\mathrm{Er} = \sqrt{\frac{1}{H}\sum\nolimits_{i=1}^{H}\left[y_i - F(s_i)\right]^2}. \tag{8}$$

We can use the minimum gradient algorithm to find the minimum Er.

C. Model Optimization With PSO

The final determination of the center and width of the Gaussian membership function of the fuzzy neural network and the connection weights between each layer of the neural network need to be obtained through network training. Therefore, we need to choose an appropriate intelligent algorithm to determine the final value of each variable. In this article, we adopt the PSO algorithm to optimize the network model and combine the shortcomings of the standard PSO with the genetic mutation function in the GA to jump out of the local optimum, thereby establishing a neural network prediction model more quickly and accurately [27].

PSO iteratively updates a population of candidate solutions (particles) by adjusting their positions in the search space based on their individual and collective experiences. To optimize the deep neuro-fuzzy network, we employ PSO to tune the parameters of the model effectively. Specifically, PSO is utilized to optimize the neural network parameters simultaneously. The optimization process aims to minimize a predefined objective function, typically related to the model's performance on a validation dataset. During optimization, each particle in the PSO algorithm represents a potential solution, which consists of a set of parameters defining the structure and configuration of the deep neuro-fuzzy network. These parameters include the number of layers and neurons in each layer, learning rates, and other relevant hyperparameters. The PSO algorithm iteratively updates the positions of particles based on their individual and neighborhood best positions, as well as a global best position discovered by the entire population. This iterative process continues until a termination condition is met, such as reaching a maximum number of iterations or achieving satisfactory convergence. By employing PSO for optimization, our proposed model benefits from its ability to efficiently explore the search space and converge to high-quality solutions. In addition, PSO offers advantages, such as simplicity of implementation, robustness to parameter settings, and scalability to high-dimensional optimization problems.

Specifically, according to the standard PSO algorithm, we can first get the calculation for updating the velocity and position of the particles as follows:

$$\begin{cases} v_r(e+1) = uv_r(e) + c_1 r_1\left[p_r - x_r(e)\right] \\ \qquad\qquad +c_2 r_2\left[p_g - x_r(e)\right] \\ x_r(e+1) = x_r(e) + v_r(e+1) \\ \qquad\qquad 1 \le r \le N, 1 \le d \le D \end{cases} \tag{9}$$

where v_r and x_r represent the searching speed and position of the particle, respectively, p_r represents the optimal solution during the running process of a single particle, p_g represents the optimal solution during the running process of all particles, e represents the number of iterations, N represents the total number of particles, D represents the dimension of the search space, c_1 and c_2 represent two positive learning factors, r_1 and r_2 represent random numbers between 0 and 1, and w represents the inertia weight. In order to prevent the particle from falling into the local optimal point during the position update process, when the particle iterates to each step, it is necessary to calculate the fitness function value $\mathrm{fit}(e)$ of the particle at that step. The specific calculation is as follows:

$$\mathrm{fit}(e) = \mid M_{\mathrm{out}}(e) - M_{\exp} \mid \tag{10}$$

where $M_{\mathrm{out}}(e)$ represents the network output value when the fuzzy neural network is trained to the eth step, and $M_{\exp}$ represents the expected output value when the fuzzy neural network is trained to the eth step.

At the same time, in order to ensure the vitality of the particles, $N/4$ particles with the highest fitness function value $\mathrm{fit}(k)$ in the population were selected to form a variant species group during the iteration process, and the selective variant operation was carried out. The specific variation is as follows:

$$\begin{cases} \hat{\upsilon}_i = \eta\theta\upsilon_i \mathrm{rand} \\ \hat{x}_i = x_i + \hat{\upsilon}_i \end{cases} \tag{11}$$

where the movement direction of the particle takes the value -1 or 1, rand represents a random number between 0 and 1, θ is the variation parameter, usually selected as $0 \le \theta \le 0.2$, $1 \le i \le N/4$, $\hat{\upsilon}_i$ and υ_i, respectively, represent the speed of the ith particle after mutation and before mutation in the dth dimension, $\hat{x}_i$ and x_i, respectively, represent the d-dimensional position of the ith particle after mutation and before mutation. The mutated $N/4$ particles and the original $3N/4$ particles that have not changed form a population containing N particles again. After continuous iteration, the appropriate network weight is finally found.

IV. Experiments

This section is dedicated to thoroughly evaluating the effectiveness and performance of the proposed method. To ensure the accuracy and reproducibility of the experimental results, we begin with a detailed description of the experimental environment. This encompasses the specific configuration of the hardware used, software versions, and any other environmental variables that might influence the outcomes of the experiments. In addition, the dataset used in the experiments is a key element. Therefore, a comprehensive description of the dataset, including its source, scale, feature description, and preprocessing steps, is provided. Special emphasis is placed on the representativeness and diversity of the dataset to ensure the wide applicability of the experimental results. Subsequently, the article delves into a detailed comparison of the performance with other existing methods. This includes the criteria for selecting methods for comparison, performance evaluation metrics (such as accuracy, recall, F1 score, etc.), and the methodology of the comparison. The aim of this section is to demonstrate the advantages and potential shortcomings of the proposed method in various aspects, such as efficiency, accuracy, and robustness. Finally, ablation experiments on various components are conducted to ascertain each part's contribution to the overall performance. By systematically removing or replacing specific parts of the model, a better understanding of the role and importance of each component is achieved. The results of the ablation studies will provide deeper insights into how the model functions and reveal potential areas for improvement.

A. Experimental Setup and Database

In our research, the experimental environment is meticulously configured to ensure high performance and reliability, essential for the computational demands of our study. The hardware setup included an Intel Core i9-10900 K processor with 10 cores at a base frequency of 3.7 GHz. The system is equipped with 32 GB DDR4 RAM at 3200 MHz, ensuring efficient handling of large datasets and complex algorithms. Graphics processing is managed by an NVIDIA GeForce RTX 3080 with 10 GB GDDR6X VRAM. The primary storage is a 1 TB SSD for additional storage needs. On the software front, our platform operated on Windows 10 Pro 64-bit, with all the latest updates. The primary programming language is Python 3.8, supported by libraries such as NumPy, Pandas, TensorFlow, and PyTorch for algorithm development and data processing. In addition, for development and debugging, PyCharm Professional 2021.1 is the chosen IDE for Python. The machine learning framework used is PyTorch 1.7. This comprehensive setup provided a robust and flexible environment, enabling us to efficiently handle the extensive computational demands of our research, ranging from machine learning model training to in-depth data analysis and algorithm development. The important parameters selected in the proposed MDNFN are shown in Table III.

In our experiments, we utilize the MIT-BIH Arrhythmia Database to train and evaluate our method [38]. The MIT-BIH Arrhythmia Database is a seminal dataset in the field of cardiovascular research, widely recognized for its pivotal role in advancing the understanding of cardiac arrhythmias. Developed by the Massachusetts Institute of Technology (MIT) and Beth Israel Hospital, this database has been instrumental in fostering scientific exploration, algorithm development, and diagnostic advancements in the realm of cardiac arrhythmias. The MIT-BIH Arrhythmia Database comprises 48 half-hour excerpts of two-channel ambulatory ECG recordings, acquired from 47 subjects. These recordings are sampled at 360 Hz, providing a rich dataset capturing a diverse range of cardiac arrhythmias. The subjects encompass a variety of clinical conditions, such as congestive heart failure and arrhythmias. This diversity allows researchers to investigate arrhythmias in different pathological contexts. Each record in the database is meticulously annotated by expert cardiologists, offering precise labeling of the onset and offset points of various arrhythmias, such as atrial fibrillation, ventricular tachycardia, and premature contractions. This annotated ground truth facilitates the development and evaluation of algorithms for arrhythmia detection and classification. The dataset's real-world recordings capture the complexity and nuances of arrhythmias in an ambulatory setting, providing a more authentic representation of clinical scenarios compared with simulated data. The continuous nature of the recordings allows for the exploration of long-term trends in arrhythmia occurrences, aiding in the study of intermittent and chronic arrhythmic conditions. The MIT-BIH Arrhythmia Database has become a benchmark for evaluating the performance of arrhythmia detection algorithms. Its widespread use ensures the comparability of results across different studies.

TABLE I
NUMBER OF SAMPLES DIVIDED IN THE RECORDING-BASED METHOD

Types	N	LBBB	RBBB	PVC	P	AP
All	74887	8060	7240	7120	7008	2539
Train data	40420	3944	3773	3862	3560	842
Test data	34467	4116	3467	3258	3448	1697

Among them, the training sample recordings include 101, 102, 106, 108, 109, 112, 114, 115, 116, 118, 119, 122, 124, 201, 202, 203, 205, 207, 208, 209, 215, 217, 220, 223, and 230. The testing sample recordings include 100, 103, 104, 105, 107, 111, 113, 117, 121, 123, 200, 210, 212, 213, 214, 219, 221, 222, 228, 231, 232, 233, and 234.

Before conducting experiments, a rigorous preprocessing pipeline is applied to enhance the quality and usability of the dataset. The steps involved noise reduction, normalization, and segmentation based on the R wave positions. Specifically, following noise reduction, we normalize the ECG signal by the min-max method as follows:

$$s_i' = \frac{s_i - S_{\text{min}}}{S_{\text{max}} - S_{\text{min}}}, \quad i = 1, \ldots, d \tag{12}$$

where S_{min} and S_{max} represent the minimum and the maximum value of the ECG signal. This step standardized the amplitude of the ECG waveforms, ensuring that variations in signal magnitude did not introduce bias during subsequent analysis. Normalization is a crucial step for promoting consistency and comparability across different records. We take the R wave as the center point, move 150 data points to the left and 150 data points to the right to obtain a data sample with a length of 300. Similarly, multiscale data samples are also signals intercepted with the R wave as the center.

Two distinct partitioning methods, recording-based and beat-based, are employed to ensure a fair and comprehensive evaluation in comparison with other methodologies [30]. In the recording-based partitioning strategy, the dataset is divided into distinct segments based on entire ECG recordings. This approach allowed for the evaluation of the model's performance on different overall cardiac patterns present in a single recording. At the same time, we select the top six types of arrhythmias based on their sample numbers as the experimental dataset, including normal beat (N), left bundle branch block beat (LBBB), right BBB (RBBB), premature ventricular contraction beat (PVC), paced beat (P), and atrial premature beat (AP). Table I depicts the number of samples per category for this data partitioning method. At the same time, in order to avoid the impact of data imbalance, we also adopted the beat-based partitioning method. We randomly select 80% as training data and the remaining 20% as test data. Table II depicts the number of samples per category for this data partitioning method.

TABLE II
NUMBER OF SAMPLES DIVIDED IN THE BEAT-BASED METHOD

Types	N	LBBB	RBBB	PVC	P	AP
All	74887	8060	7240	7120	7008	2539
Train data	2000	2000	2000	2000	2000	2000
Test data	500	500	500	500	500	500

TABLE III
SELECTED PARAMETERS IN THE PROPOSED METHOD

Parameters	Values
The number of hidden layers	3
Neurons in each hidden layer	100
Learning rate	0.001
Activation functions	ReLU

In assessing the performance of the proposed methodology, four key evaluation metrics were employed to provide a comprehensive understanding of its effectiveness. These metrics, namely, accuracy (ACC), sensitivity (SEN), specificity (SPEC), and precision (PREC), offer nuanced insights into the model's ability to correctly classify and differentiate between various cardiac conditions.

B. Performance Analysis

In order to gauge the effectiveness of the proposed method MDNFN, we conduct a rigorous performance comparison against several well-established benchmark methods widely used in the domain of arrhythmia detection, including the LDA [28], WT-LDA [29], SVM [32], SVM-RBF [33]), DBN [34], CNN [35], [36], RNN [37], [39], autoencoder (AE) [30], and deep neuro-fuzzy classifier (DNFC).

Table IV depicts the comparison results with existing methods based on heartbeat division (see Table I). From the results presented in Table IV, we can see that our proposed MDNFN method achieves the best performance on three metrics, i.e., ACC (86.83%), SPEC (96.25%), and PREC (60.24%). Specificity results indicate the proposed method's ability to accurately differentiate negative instances, highlighting its effectiveness in minimizing false positives. Precision analysis underscores the accuracy of positive predictions made by the proposed method, showcasing its reliability in correctly identifying instances of cardiac arrhythmias.

Table V depicts the comparison results with existing methods based on heartbeat division (see Table II). We can clearly see that the performance of the proposed MDNFN exceeds all other comparison methods in four indicators. For example, compared with the CNN model, our model exceeds 3.83% in accuracy (95.14% versus 98.97%), which illustrates the effectiveness of the model proposed to fully extract and utilize multiscale features in this article. The proposed method exhibits competitive or superior accuracy compared with the benchmark methods, which signifies its overall effectiveness in correctly classifying instances across all classes.

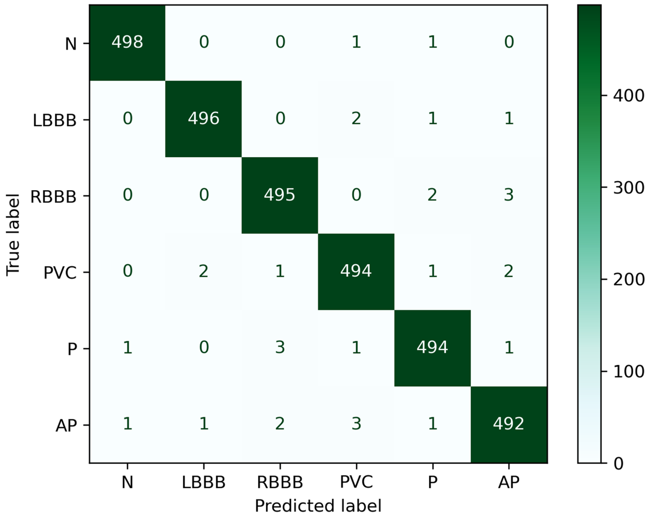

Fig. 2. Confusion matrix of the classification results based on the beat division.

Furthermore, in order to present the classification performance of the model in more detail, we present the confusion matrix of MDNFN classification results for six types of arrhythmias, as shown in Fig. 2. We can see that for each type, the proposed model can correctly identify more than 98% of the accuracy, which is enough to indicate the superior performance of the model. In addition, we can also see that for the three arrhythmia types PVC, P, and AP, their recognition accuracy has declined, which to a certain extent shows that the model has an impact on the recognition accuracy of complex waveforms.

C. Ablation Study

In this section, we systematically deconstruct the proposed MDNFN model to scrutinize the individual contributions of its key components, namely, the multiscale feature structure and the improved PSO-based optimization method employed in this article. This rigorous analysis aims to provide insights into the impact of each element on the overall performance of the model. By isolating and evaluating the role of the multiscale feature structure and the PSO method, we aim to quantify their respective influences on the model's ability to accurately classify ECG signals. This dissection not only affords a nuanced understanding of the model's inner workings but also substantiates the pivotal role played by the multiscale architecture and the PSO optimization in enhancing the overall robustness and performance of the MDNFN model.

Specifically, we conduct a series of controlled experiments wherein we use a single-scale feature network model to compare with the multiscale features, observing the resulting changes in the model's effectiveness. Tables VI and VII, respectively, show the model performance at different scales under two data partitioning conditions. That is, we only utilize a single scale feature extraction model for classification detection of arrhythmia. For example, "Scale 1" indicates the use of wavelet interval scale features, such as RR interval, PR interval, and QT interval, and the corresponding deep neuro-fuzzy network for processing and classification. From the results in the table, we can see that the performance of the feature extraction model at a

TABLE IV
COMPARISON RESULTS WITH EXISTING METHODS BASED ON RECORDING DIVISION

References	Model	Arrhythmia Types	ACC (%)	SEN (%)	SPEC (%)	PREC (%)
Chazal et al. [28]	LDA	5	85.88	66.0	95.57	45.57
Llamedo and Martínez [29]	WT+LDA	4	78.0	**83.08**	93.02	58.25
Wang et al. [30]	AE	5	81.08	54.55	89.42	58.09
Talpur et al. [31]	DNFC	5	83.42	62.74	92.86	51.78
Ours	MDNFN	6	**86.83**	68.72	**96.25**	**60.24**

The bold values indicate the best results.

TABLE V
COMPARISON RESULTS WITH EXISTING METHODS BASED ON HEARTBEAT DIVISION

References	Model	Arrhythmia Types	ACC (%)	SEN (%)	SPEC (%)	PREC (%)
Huang et al. [32]	SVM	5	93.8	94.73	-	76.1
Chen et al. [33]	SVM-RBF	4	97.8	88.83	-	93.76
Meng and Zhang [34]	DBN	6	98.49	97.53	99.66	98.44
Acharya et al. [35]	CNN	5	95.14	66.56	96.94	65.74
Serkan et al. [36]	CNN	5	93.47	96.01	91.64	97.87
Oh et al. [37]	RNN	5	97.88	97.26	98.50	98.48
Wang et al. [30]	AE	5	96.29	96.29	99.24	96.33
Talpur et al. [31]	DNFC	5	96.49	96.84	99.16	96.45
Ours	MDNFN	6	**98.97**	**98.97**	**99.79**	**98.97**

The bold values indicate the best results.

TABLE VI
ABLATION EXPERIMENTS FOR MULTISCALE NETWORK STRUCTURES ON THE RECORDING-BASED DIVISION

Scale	ACC (%)	SEN (%)	SPEC (%)	PREC (%)
Scale 1	79.68	61.76	90.28	55.98
Scale 2	81.03	63.48	92.71	58.64
Scale 3	82.29	59.35	93.45	57.93
ALL	**86.83**	**68.72**	**96.25**	**60.24**

The bold values indicate the best results.

TABLE VII
ABLATION EXPERIMENTS FOR MULTISCALE NETWORK STRUCTURES ON THE BEAT-BASED DIVISION

Scale	ACC (%)	SEN (%)	SPEC (%)	PREC (%)
Scale 1	94.27	94.22	97.56	95.57
Scale 2	96.82	96.81	97.82	96.25
Scale 3	96.19	96.17	98.06	97.14
ALL	**98.97**	**98.97**	**99.79**	**98.97**

The bold values indicate the best results.

single scale has declined. For example, compared with Scale 1, the performance of the multiscale fusion model is improved by about 7% (79.68% versus 86.83%), which fully demonstrates the effectiveness of the multiscale feature fusion structure for arrhythmia classification.

Moreover, we explored different model optimization algorithms to compare the performance of the optimized PSO algorithm used in this article. As mentioned in Section III-C, we adopt the PSO algorithm to optimize the network model and combine the shortcomings of the standard PSO with the genetic mutation function in the GA to jump out of the local optimum, thereby establishing a neural network prediction model more quickly and accurately. We mark the model optimization algorithm used in this article as PSO-pro. In order to verify the effectiveness of this optimization method, we additionally compared and analyzed the state-of-the-art methods and four basic optimization methods, including the improved-AOA [40], GOZDE [41], the ordinary PSO algorithm, GA [42], ant colony optimization (ACO) algorithm [43], and simulated annealing (SA) algorithm [44]. Figs. 3 and 4, respectively, depict the impact of different optimization algorithms on model performance in two cases of data partitioning.

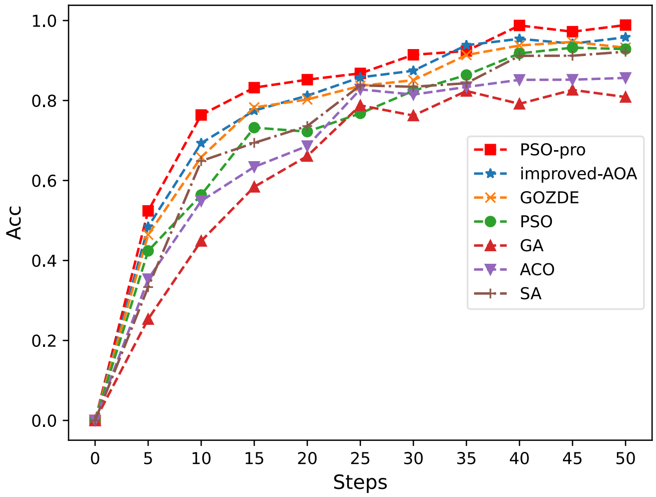

Fig. 3. Impact of different optimization algorithms on model performance based on the beat division.

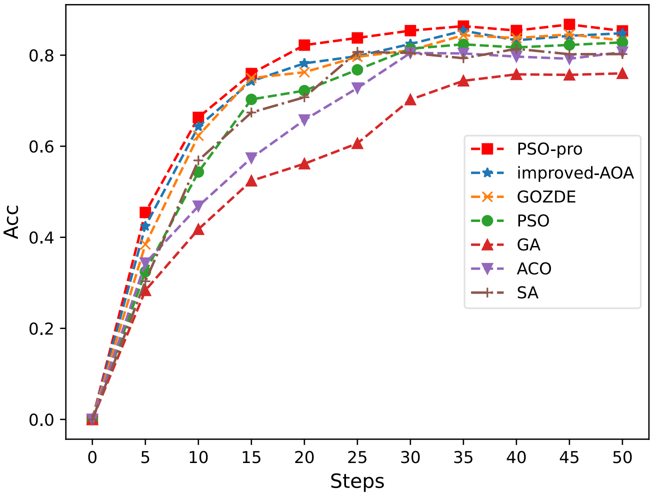

Fig. 4. Impact of different optimization algorithms on model performance based on the recording division.

TABLE VIII
MODEL PERFORMANCE COMPARISON UNDER DIFFERENT LEARNING RATES

Learning rate	ACC (%)	SEN (%)	SPEC (%)	PREC (%)
0.1	83.16	83.79	86.14	84.68
0.01	95.62	95.87	96.82	96.71
0.001	**98.97**	**98.97**	**99.79**	**98.97**
0.0001	96.57	96.74	97.43	96.62

The bold values indicate the best results.

TABLE IX
MODEL PERFORMANCE COMPARISON UNDER DIFFERENT ACTIVATION FUNCTIONS

Activation function	ACC (%)	SEN (%)	SPEC (%)	PREC (%)
sigmoid	93.36	93.58	94.84	93.28
tanh	95.16	95.34	96.42	96.18
Leaky ReLU	97.36	97.41	98.45	97.13
ReLU	**98.97**	**98.97**	**99.79**	**98.97**

The bold values indicate the best results.

The results indicate that the proposed improved PSO algorithm consistently outperforms the other optimization methods in terms of convergence speed and model performance across various data partitioning scenarios. The enhanced PSO algorithm demonstrates its effectiveness in efficiently navigating the parameter space, leading to faster convergence toward optimal solutions. This superior performance can be attributed to the adaptive mechanisms incorporated into the improved PSO, allowing for a more dynamic adjustment of particle trajectories during the optimization process. Compared with the latest methods improved-AOA and GOZDE, our optimization method achieves slightly better performance. Comparatively, while the GA, ACO, and SA algorithms exhibit competitive performances, they demonstrate a relatively slower convergence rate and, in some cases, a tendency to converge to suboptimal solutions. Genetic algorithm, although robust in handling complex optimization problems, can suffer from premature convergence and struggles with fine-tuning parameters. ACO, while effective in certain scenarios, may face challenges in handling continuous optimization tasks due to its discrete nature. SA, although versatile, can be computationally expensive and may require careful tuning of temperature schedules to achieve optimal results. These findings underscore the efficacy of the proposed improved PSO algorithm in the context of model optimization for the proposed multiscale deep neuro-fuzzy model, emphasizing its potential as a preferred optimization technique for enhancing the performance of complex computational models in various applications.

In addition, we conducted a sensitivity analysis to evaluate the impact of two critical parameters, namely, the learning rate and activation functions, on the performance of MDNFN. Table VIII shows the model performance comparison under different learning rates. We observed that varying the learning rate over a range of values influenced both the convergence behavior during training and the final classification performance of the MDNFN. Specifically, lower learning rates resulted in slower convergence but tended to yield more stable training dynamics and better generalization performance. Conversely, higher learning rates led to faster convergence but were prone to overshooting and oscillations in the training loss. Through careful examination of the learning rate sensitivity, we identified an optimal range that balanced convergence speed with classification accuracy, thus providing valuable guidance for parameter selection in the MDNFN architecture. Table IX shows the model performance comparison under different activation functions. We experimented with various activation functions, including ReLU, sigmoid, tanh, and Leaky ReLU, and evaluated their effects on the network's training dynamics and classification performance. Our results indicated that different activation functions exhibited distinct behaviors in terms of convergence speed and final performance metrics. Notably, ReLU and Leaky ReLU activation functions demonstrated superior performance in terms of both convergence speed and classification accuracy, outperforming sigmoid and tanh activations. These findings suggest that the choice of learning rate and activation function play a critical role in shaping the MDNFN's capability to capture complex patterns in ECG signals.

V. Conclusion

In this article, we explore MDNFN to diagnose arrhythmias in ECG signals. We combine the deep neuro-fuzzy network and improved PSO algorithm to propose a novel multiscale feature extraction model, MDNFN. First, we introduce the specific internal details of the model, including the data preprocessing and feature selection, the structure of the multiscale deep neuro-fuzzy model, and the optimization method with PSO. Second, we verify and compare the effectiveness of this method through rigorous and numerous experiments. The development of the MDNFN model represents a significant step forward in the field of cardiac diagnostics. By harnessing the power of AI, specifically deep learning and fuzzy logic, this model offers a novel and effective solution for the automatic analysis of ECG signals. Its ability to provide accurate and efficient results has the potential to greatly benefit both healthcare professionals and patients, contributing to the advancement of cardiac care.

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