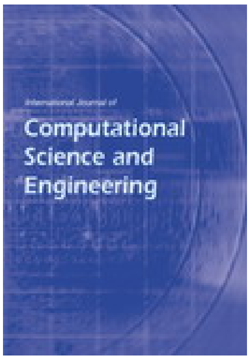

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Yibin Xiong, Jun Wu, Qian Wang, Dandan Wei

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SAPNN: self-adaptive probabilistic neural network for medical diagnosis

Yibin Xiong

School of Information Science and Technology,
Hunan Institute of Science and Technology,
Yueyang, China
Email: xyb2020@foxmail.com

Jun Wu, Qian Wang* and Dandan Wei

School of Information Engineering,
Zunyi Normal University,
Zunyi, China
Email: wujun.myway@gmail.com
Email: wwgowithwind@gmail.com
Email: 2470911470@qq.com
*Corresponding author

Abstract: A self-adaptive probabilistic neural network (SAPNN) is proposed in this paper. Firstly, a hybrid cuckoo search (HCS) algorithm is proposed. Secondly, HCS is used in probabilistic neural networks for adapting the smoothing factor parameters. In order to accurately evaluate SAPNN proposed in this paper, the disease datasets of breast cancer, diabetes and Parkinson's disease were used for testing. Finally, comparison with several other methods shows that the accuracy of SAPNN is the best in all cases. The results of various evaluation indexes show that the proposed SAPNN in this paper is a novel method that can be applied to medical diagnosis.

Keywords: ancillary diagnosis of disease; cuckoo search; information sharing; mutation strategy; probabilistic neural network.

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Biographical notes: Yibin Xiong received his BS in Information and Computing Sciences from Zunyi Normal University in 2021. He is currently pursuing his MS in Information and Communication Engineering at Hunan Institute of Science and Technology. His research interests include pattern recognition and intelligence computing.

Jun Wu received his BS and MS in Software Engineering from Dalian University of Technology in 2013 and 2016, respectively. He is currently working at Zunyi Normal University. His research interests include data mining and bioinformatics.

Qian Wang received his PhD in Pattern Recognition from the Institute of Automation, Chinese Academy of Sciences, China in 2007. His research interests include computer vision, image processing and artificial intelligence. He has published ten research papers in international conferences and journals on pattern recognition.

Dandan Wei is currently working at Zunyi Normal University. Her research interests include digital signal processing and database technology.

1 Introduction

With the continuous improvement of 5G technology and smart medical tools, it is no longer a problem to conduct regular medical checkups, remote rapid pre-diagnoses, etc. (Jadhav et al., 2022). Nowadays, the country is strongly advocating the practice strategy of 'AI+' to encourage the use of artificial intelligence (AI) technology combined with medicine to achieve assisted diagnosis. It can improve diagnostic accuracy and reduce the burden of doctors. Therefore, the use of AI for disease diagnosis has become a major trend (Zhu et al., 2019), we only need to compile a large database of information obtained from previous diagnosis of patients and indicators of high probability of disease, and only need a few important indicators of disease that can be used to pre-diagnose the health of the entire body. This greatly reduces the possibility of making wrong decisions due to doctor fatigue or inexperience. Based on the above, medical diagnosis models combined with machine learning have become a hot research topic.

The development of medical diagnosis is often closely related to the advantages and disadvantages of machine learning (ML) methods. The ML methods can gain experience through self-learning of past historical information, and realise accurate judgement of new information. Thus, medical models incorporating AI were applied in medical image assisted diagnosis (Sun et al., 2020), drug development (Urban et al., 2019), medical robotics (Di Lallo et al., 2021), and disease risk prediction (Romaszko et al., 2021), respectively. In each of these specific applications, ML methods involve a large number of training parameters, and different parameter settings often yield very different results. However, swarm intelligence optimisation (SIO) algorithms have the characteristics of simplicity, flexibility and iterative optimisation search, many scholars gradually began to focus on their optimisation methods for ML parameters. In SIO, particle swarm optimisation (PSO) (Lu et al., 2020), cuckoo search (CS) (Chitara et al., 2018), genetic algorithm (GA) (Ouyang et al., 2021), differential evolution (DE) (Li et al., 2021), invasive weed optimisation (IWO) (Ouyang et al., 2018), artificial bee colony (ABC) (Liu et al., 2019), etc are commonly used. The goal of these algorithms is to obtain the maximum prediction accuracy. In view of the high misdiagnosis rate and time-consuming of traditional medical diagnosis, the main purpose of this paper is to propose a hybrid cuckoo search (HCS) algorithm to optimise probabilistic neural network (PNN) (Specht, 1990). Thus, a self-adaptive PNN (SAPNN) is formed. The main contributions of this paper are as follows:

- add mutation operation to the original CS, which makes the search space more diversified
- by sharing and exchanging information among populations, the ability of population search is enhanced
- a self-adaptive PNN combining PNN and HCS is proposed.

The rest of the paper is structured as follows. Section 2 is about work related to CS and PNN. Section 3 will introduce the medical diagnosis model based on HCS and PNN algorithm, and give the execution steps of the problem solution. Section 4 mainly shows the experimental results of SAPNN and discusses the solution performance of the proposed algorithm in detail. Section 5 will summarise the whole research work and the future outlook.

2 Related work

Abeaham and Nair (2021) proposed a new integration method to detect COVID-19 from computed tomography (CT) scans. The method they proposed is mainly based on five different CNN (MobilenetV2, Shufflenet, Xception, Darknet53 and EfficientnetBo) and kernel support vector machine (KSVM). Dolatabadi et al. (2017) optimised the performance of SVM classifier through principal component analysis (PCA) to enhance the diagnosis of coronary artery disease (CAD). In their methods, PCA is used to reduce the dimension of extracted features, and SVM is used for classification and recognition. El-Sappagh et al. (2022) proposed a new two-stage deep learning model. In the first stage, multiple classifiers are used to predict whether the patient is normal cognition, mild cognitive impairment (MCI) or Alzheimer's disease (AD); in the second stage, long short-term memory (LSTM) model were used for regression analysis. So far, researchers only rely on various methods to detect medical diseases, but seldom use SIO algorithm.

The advantages of the SIO algorithm are its simple implementation operation, high feasibility of the algorithm, and few parameters, which can be good for solving various optimisation class problems. Various classifiers and ML methods have the disadvantage of low accuracy due to poor parameter settings. Thus, Rajammal et al. (2022) proposed a wrapper-based binary improved grey wolf optimiser (BIGWO) for feature selection in the diagnosis of Parkinson's disease. In BIGWO, mutation strategy and adaptive k-nearest neighbour (AkNN) are adopted. Gunnasundari et al. (2018) proposed a new multi swarm heterogeneous binary PSO algorithm (MHBPSO) for feature selection in the diagnosis of liver and kidney diseases. MHBPSO consists of four variants of PSO. The four variants algorithms share their global optimal location with each other, and eventually choose the best one among the four algorithms. The results show that the proposed MHBPSO can effectively select elite features to minimise disease diagnosis. These two examples illustrate the ability of the SIO algorithm to achieve improved accuracy in disease diagnosis.

Cuckoo search (CS), a novel SIO algorithm, benefits from the imitation of the parasitic brooding behaviour of cuckoos (Yang and Deb, 2009). The algorithm uses the Lévy flight mechanism and random wandering to update the current location during the iterative process, so the CS variant has been used extensively for optimisation related to engineering applications. For example, Gude and Jana (2022) proposed a photovoltaic (PV) cell parameter identification method based on optimisation algorithm, which can effectively estimate the parameters of PV cells and modules. Firstly, combined with multi-agent system (MAS) and CS, the MASCSO algorithm is proposed, and then the MASCSO algorithm is used to estimate the parameters of PV cells and modules. Yousri et al. (2021) proposed an enhanced cuckoo search algorithm for COVID-19 image classification to enhance the ability to accurately identify type of patients when processing

COVID-19 classification tasks. Fractional-order calculus (FO) is added to the proposed method, and four different heavy tail distributions are used to replace Lévy flight. Rahaman and Sing (2021) proposed a more efficient satellite image segmentation method using adaptive cuckoo search (ACS) for the presence of randomness and fuzzy regions in the segmentation of satellite images. In addition, Chakraborty and Mali (2022) also proposed a fuzzy modified CS algorithm (FMCS) for biomedical images. FMCS algorithm hopes to find the best clustering centre by combining the idea of fuzzy set and MCS strategy. Such a fuzzy system can achieve efficient image segmentation.

PNN is a feedforward neural network based on Bayesian minimum risk criterion first proposed in 1990, and this network model is well suited for pattern classification tasks due to its simple learning process and fast training speed. Particularly in face recognition, Ouyang et al. (2020) proposed an efficient hybrid face recognition method, which uses improved kernel linear discriminant analysis (IKLDA) to reduce the dimension of samples, so as to reduce the difficulty of solving. Then the face image is classified by PNN classifier. Comparing this method with other classification algorithms on three face databases (ORL, Yale, and AR), the results show that the classifier with IKLDA method has higher recognition accuracy. Guan et al. (2021) used the optimised PNN for greenhouse environmental monitoring. Among them, the improved k-means clustering algorithm(K-means-α) is used to cluster the samples as training samples. Then add PSO to PNN to optimise its smoothing factor parameters, and finally get the optimised PNN (α-PSO-M-PNN). Naik et al. (2019) firstly used symmetric Laplace distribution to replace Gaussian distribution to solve the problems of PNN. Then a weight coefficient estimation method is introduced between the mode layer and the summation layer. Eventually, the bat algorithm is added to obtain the optimal smoothing parameter vector. The PNN designed above is integrated to obtain high-performance results.

3 The proposed SAPNN algorithm

3.1 Traditional cuckoo search

Cuckoo search is largely abstracted from the cuckoo's lazy egg-laying behaviour, which eliminates the need for the cuckoo to incubate its own eggs, thus drastically reducing brood rearing time. However, there is a certain probability that the host will find alien eggs, so the host will attack the cuckoo's eggs or even abandon the entire nest. Because of this risk, cuckoos begin to mimic their host species, for example by changing the colour and pattern of their eggs, or by making similar calls when they first hatch. Consequently, in order to model the breeding behaviour of cuckoos, the following three ideal rules must be followed:

- cuckoos randomly select the nest of a host species to lay eggs, and lay only one egg at a time.
- the number of nests is fixed and the best positioned nests are passed on to the next generation.
- the probability of a host finding a cuckoo egg is $Pa \in [0,1]$, where each egg represents a solution.

Based on the above three ideal rules, we can learn that a host nest represents a candidate solution. In addition, Lévy flight belongs to Markov process, which refers to the random walking path with heavy tail distribution on the step probability. Each step is completely random and has a heavy tail distribution in the same direction, and there is a large step with a high probability in random walking, so it is widely used in the measurement and simulation of random natural phenomena. The search methods for Lévy flight to update the bird's nest location are local search and global search. The local search formula is defined as follows:

$$x_i^{t+1} = x_i^t + H\left(Pa - \varepsilon\right) \otimes \alpha s \otimes \left(x_j^t - x_k^t\right) \tag{1}$$

In equation (1), x_j^t and x_k^t are randomly selected solutions in the t^{th} generation. $\otimes$ refers to entry-wise multiplications. $H(\mu)$ is the Heaviside function. p_a is used to balance the global and local switching probabilities. s is the step size. ε is a uniformly distributed pseudo-random number. The global search mechanism is realised by the principle of Lévy flight mechanism. See formula (2).

$$x_i^{t+1} = x_i^t + \alpha \otimes L\left(\lambda\right) \tag{2}$$

In equation (2), α is the step scaling factor. $L(\lambda)$ is the path generated by the Lévy flight. Based on the candidate solutions generated by the random tour of Lévy flight, assume that the m^{th} candidate solution of the CS at the evolution to generation t is x_m^t, where $x_m^t = \left(x_{m,1}^t, x_{m,2}^t, \cdots, x_{m,j}^t, \cdots, x_{m,D}^t\right)$, $j \in [1, D]$. Thus, the expression for the new individual (candidate solution) x_m^{t+1} resulting from the random wandering using Lévy flight is shown in formula (3).

$$x_m^{t+1} = x_m^t + \left(x_m^t - x_{gb}^t\right) \cdot \left(\gamma_0 \otimes L\left(\lambda\right)\right) \tag{3}$$

In equation (3), x_{gb}^t is denoted as the global optimal solution. γ_0 is the initial search step size.

Let t be the flight time, $L(\lambda) \sim u = t^{-\lambda}$, $1 < \lambda \leqslant 3$. By mathematical substitution, this can be equated to formula (4).

$$L\left(\lambda\right) \sim \frac{u}{|v|^{1/\lambda}} \tag{4}$$

In equation (4), both u and v obey normal distribution, $u \sim N(0, \sigma_u^2)$ and $v \sim N(0,1)$. Where σ_u^2 is provided by formula (5).

$$\sigma^2 = \left(\frac{\Gamma\left(1+\lambda\right)}{\Gamma\left(\left(1+\lambda\right)/2\right)\lambda} \cdot \frac{\sin\left(\pi\lambda/2\right)}{2^{(\lambda-1)/2}}\right)^{1/\lambda} \tag{5}$$

where $\Gamma\left(\cdot\right)$ is the standard gamma function.

In CS, the partial solution is discarded randomly by discovery probability Pa ,that is, when $rand > Pa$, random walks are used to generate the same number of new solutions. See formula (6).

$$x_m^{t+1} = x_m^t + r \cdot \left(x_k^t - x_s^t\right) \tag{6}$$

Table 1 Detailed information about the dataset

Dataset	*No. of sample*	*No. of features*	*Classes*	*No. of healthy*	*No. of diseases*
WBC-1992	699	10	2	458	241
WBC-1995	569	32	2	212	357
PID	768	8	2	500	268
PDD	195	23	2	48	147

Table 2 Evaluation results of the four methods on the WBC-1992 dataset

Indicators	*PNN*	*PCCS-PNN*	*CSAPC-PNN*	*SAPNN*
Accuracy	0.9314 ± 0.0095	0.9677 ± 0.0119	0.9578 ± 0.0128	*0.9751 ± 0.0049*
Recall	0.9512 ± 0.0101	0.9819 ± 0.0162	*0.9836 ± 0.0024*	0.9760 ± 0.0094
Specificity	0.9012 ± 0.0232	0.9426 ± 0.0322	0.9116 ± 0.0313	*0.9615 ± 0.0176*
Precision	0.9360 ± 0.0133	0.9687 ± 0.0184	0.9528 ± 0.0221	*0.9785 ± 0.0123*
F1_score	0.9436 ± 0.0075	0.9751 ± 0.0093	0.9678 ± 0.0111	*0.9771 ± 0.0034*

Table 3 Evaluation results of the four methods on the WBC-1995 dataset

Indicators	*PNN*	*PCCS-PNN*	*CSAPC-PNN*	*SAPNN*
Accuracy	0.9177 ± 0.0231	0.9638 ± 0.0178	0.9577 ± 0.0168	*0.9653 ± 0.0134*
Recall	0.8807 ± 0.0364	0.9781 ± 0.0173	0.9764 ± 0.0214	*0.9912 ± 0.0196*
Specificity	0.9836 ± 0.0691	*0.9453 ± 0.0595*	0.9261 ± 0.0340	0.8888 ± 0.0443
Precision	0.9897 ± 0.0407	*0.9695 ± 0.0314*	0.9584 ± 0.01956	0.9432 ± 0.0185
F1_score	0.9320 ± 0.0167	0.9734 ± 0.0136	0.9671 ± 0.0122	*0.9765 ± 0.0083*

In equation (6), r is the control scaling factor, which satisfies $r \in U(0,1)$. x_k^t and x_s^t are two different solutions chosen randomly in the t^{th} generation, respectively.

3.2 Probabilistic neural network

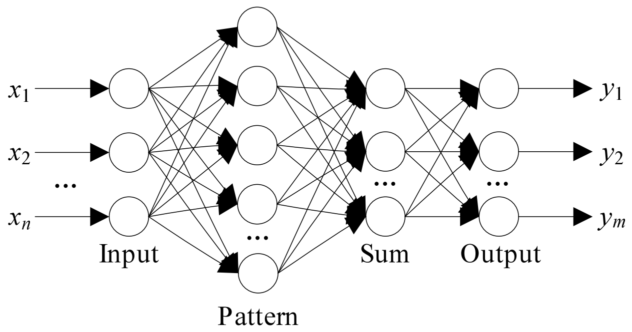
PNN is mainly contains input layer, pattern layer, summation layer and output layer. It can quickly and effectively solve classification problems of arbitrary dimensions, and the specific network structure is shown in Figure 1. The most important one is the pattern layer, which can get the corresponding matching relationship by calculating the distance between the input vector and each pattern in the training set. Each neural node of the summation layer is only connected to its corresponding class of sample nodes, and the probability accumulation of the same class is calculated to obtain the corresponding estimated probability density function (PDF). For the probability density function, there are the following three assumptions (Chen and Chu, 2009):

- the classification of PDF is consistent
- the PDF follows a Gaussian normal distribution
- the covariance matrix of the PDF is the diagonal matrix.

The neuron nodes of the pattern layer can be computed output according to formula (7).

$$P_{ij}(X) = \frac{1}{(2\pi)^{\frac{p}{2}}\sigma^p} \times \sum_{i=1}^{N} \exp\left(\frac{-(X - Y_{ij})^t (X - Y_{ij})}{2\sigma^2}\right) \tag{7}$$

Figure 1 Network structure diagram of PNN



In equation (7), p is the dimension of the feature vector X. σ is the smoothing factor. Y_{ij} is the output feature of the mode layer to the summation layer. Thus, the summation layer averages the outputs of all neurons of the same class to obtain the maximum likelihood function for calculating the classification of feature vector X as C_i:

$$F_i(X) = \frac{1}{(2\pi)^{\frac{p}{2}}\sigma^p}\left(\frac{1}{N_i}\right) \times \sum_{i=1}^{N} \exp\left(\frac{-(X - Y_{ij})^t (X - Y_{ij})}{2\sigma^2}\right) \tag{8}$$

In equation (8), N_i is the total number of samples in category C_i. Finally, the sample X is classified in the output layer according to the Bayesian decision criterion, as shown in formula (9)

$$C(X) = \arg\max F_i(X), \; i = 1, 2, \ldots, m \tag{9}$$

In equation (9), $C(X)$ is denoted as the prediction category of sample X. m is the total number of categories in the training sample.

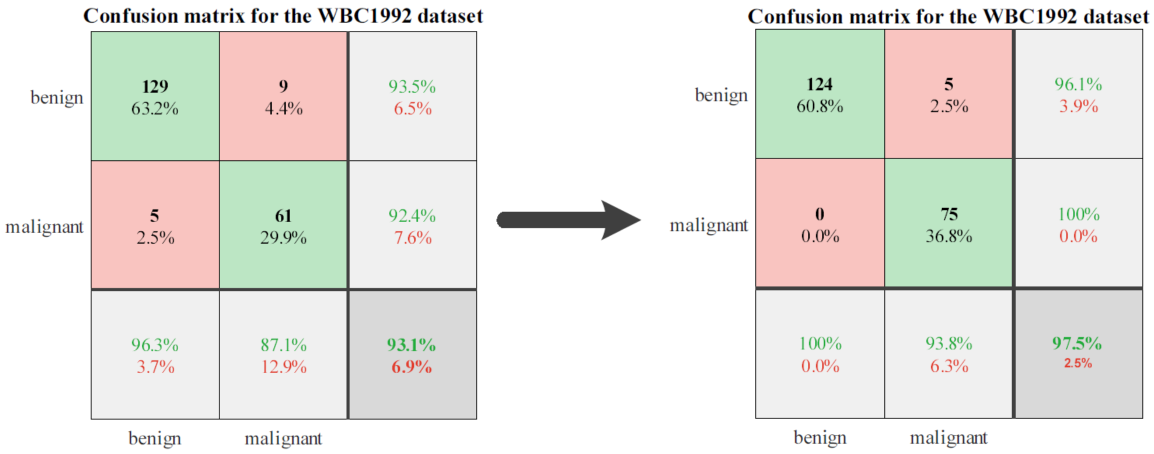
Table 4 Evaluation results of the four methods on the PID dataset

Indicators	*PNN*	*PCCS-PNN*	*CSAPC-PNN*	*SAPNN*
Accuracy	0.6778 ± 0.0156	0.6799 ± 0.0514	0.6844 ± 0.0372	*0.7574 ± 0.0282*
Recall	0.7793 ± 0.0602	*0.8905 ± 0.1040*	0.7781 ± 0.0257	0.7974 ± 0.0305
Specificity	0.5076 ± 0.0834	0.3022 ± 0.2772	0.5257 ± 0.0957	*0.5903 ± 0.0823*
Precision	0.7306 ± 0.0459	0.6973 ± 0.0738	0.7404 ± 0.0623	*0.8012 ± 0.0341*
F1_score	0.7514 ± 0.0124	0.7756 ± 0.0309	0.7575 ± 0.0337	*0.7957 ± 0.0209*

Table 5 Evaluation results of the four methods on the PDD dataset

Indicators	*PNN*	*PCCS-PNN*	*CSAPC-PNN*	*SAPNN*
Accuracy	0.9138 ± 0.0172	0.9576 ± 0.0523	0.9614 ± 0.0313	*0.9661 ± 0.0544*
Recall	0.7647 ± 0.0517	0.7665 ± 0.2334	*0.8833 ± 0.1014*	0.8824 ± 0.1340
Specificity	0.9756 ± 0.0227	*0.9758 ± 0.0412*	0.9738 ± 0.0301	0.9531 ± 0.0663
Precision	0.9286 ± 0.0715	*0.9468 ± 0.0912*	0.9157 ± 0.1178	0.8500 ± 0.2121
F1_score	0.8387 ± 0.0334	0.8226 ± 0.1537	0.8888 ± 0.0543	*0.9118 ± 0.1248*

Figure 2 Confusion matrix of PNN and SAPNN on the WBC-1992 dataset, (a) PNN (b) SAPNN (see online version for colours)



Confusion matrix for the WBC1992 dataset

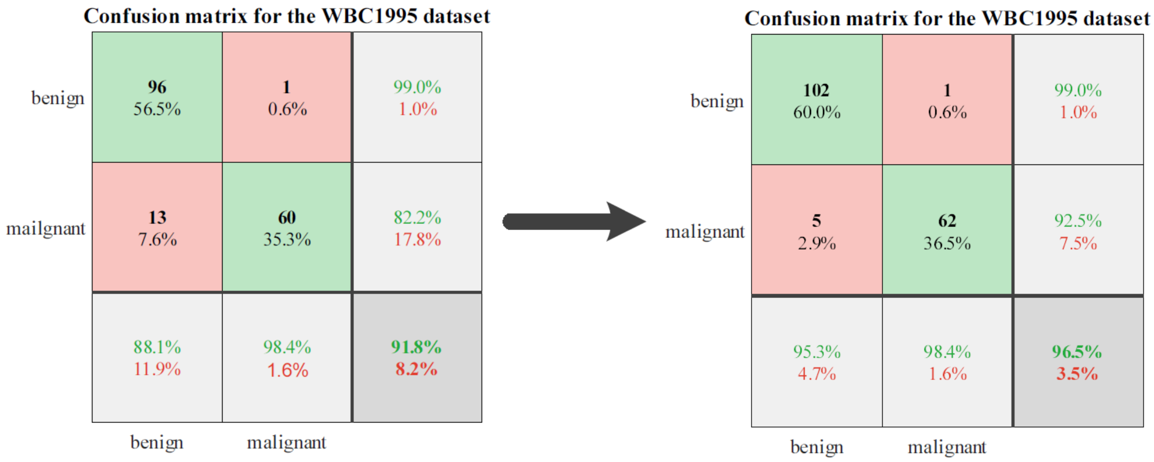
	benign	malignant	
benign	129 63.2%	9 4.4%	93.5% 6.5%
malignant	5 2.5%	61 29.9%	92.4% 7.6%
	96.3% 3.7%	87.1% 12.9%	93.1% 6.9%

Confusion matrix for the WBC1992 dataset

	benign	malignant	
benign	124 60.8%	5 2.5%	96.1% 3.9%
malignant	0 0.0%	75 36.8%	100% 0.0%
	100% 0.0%	93.8% 6.3%	97.5% 2.5%

(a) (b)

Figure 3 Confusion matrix of PNN and SAPNN on the WBC-1995 dataset, (a) PNN (b) SAPNN (see online version for colours)



Confusion matrix for the WBC1995 dataset

	benign	malignant	
benign	96 56.5%	1 0.6%	99.0% 1.0%
mailgnant	13 7.6%	60 35.3%	82.2% 17.8%
	88.1% 11.9%	98.4% 1.6%	91.8% 8.2%

Confusion matrix for the WBC1995 dataset

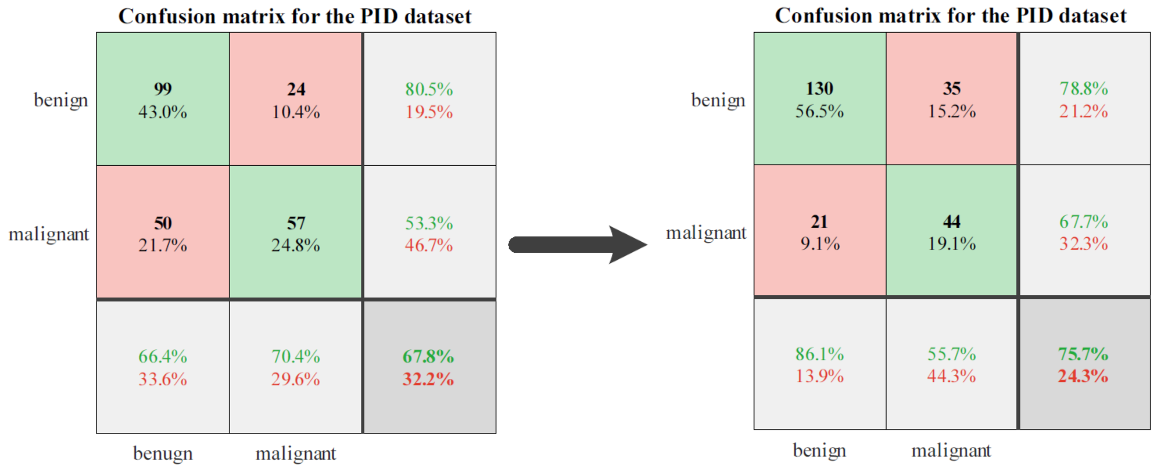
	benign	malignant	
benign	102 60.0%	1 0.6%	99.0% 1.0%
malignant	5 2.9%	62 36.5%	92.5% 7.5%
	95.3% 4.7%	98.4% 1.6%	96.5% 3.5%

(a) (b)

3.3 SAPNN

We know from Subsection 3.1 that the basic cuckoo search algorithm suffers from slow convergence and insufficient exploitation capability in the late evolutionary stage, so we added the following strategy to improve it in a hybrid way to form the hybrid cuckoo search algorithm (HCS). Then, a self-adaptive PNN (SAPNN) combining HCS and PNN was proposed.

Figure 4 Confusion matrix of PNN and SAPNN on the PID dataset, (a) PNN (b) SAPNN (see online version for colours)



Confusion matrix for the PID dataset

	benugn	malignant	
benign	**99** 43.0%	**24** 10.4%	80.5% 19.5%
malignant	**50** 21.7%	**57** 24.8%	53.3% 46.7%
	66.4% 33.6%	70.4% 29.6%	**67.8%** **32.2%**

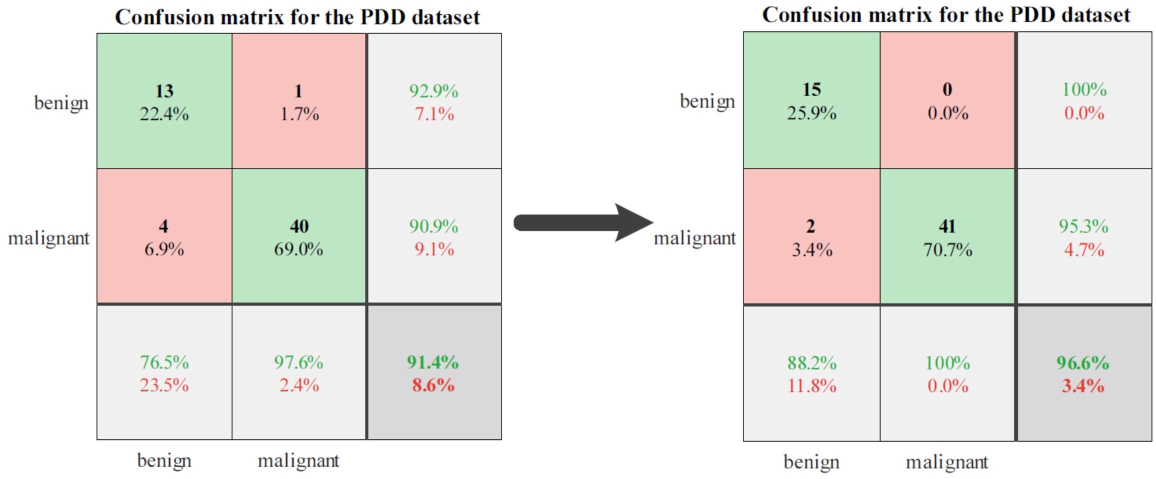
(a)

Confusion matrix for the PID dataset

	benign	malignant	
benign	**130** 56.5%	**35** 15.2%	78.8% 21.2%
malignant	**21** 9.1%	**44** 19.1%	67.7% 32.3%
	86.1% 13.9%	55.7% 44.3%	**75.7%** **24.3%**

(b)

Figure 5 Confusion matrix of PNN and SAPNN on the PDD dataset, (a) PNN (b) SAPNN (see online version for colours)



Confusion matrix for the PDD dataset

	benign	malignant	
benign	**13** 22.4%	**1** 1.7%	92.9% 7.1%
malignant	**4** 6.9%	**40** 69.0%	90.9% 9.1%
	76.5% 23.5%	97.6% 2.4%	**91.4%** **8.6%**

(a)

Confusion matrix for the PDD dataset

	benign	malignant	
benign	**15** 25.9%	**0** 0.0%	100% 0.0%
malignant	**2** 3.4%	**41** 70.7%	95.3% 4.7%
	88.2% 11.8%	100% 0.0%	**96.6%** **3.4%**

(b)

3.3.1 *Mutation strategy*

DE is an intelligent optimisation algorithm with high efficiency and accuracy, and researchers have proposed a variety of differential strategies since its introduction. For example DE/rand/1, DE/best/1, DE/rand-to-best/1, DE/rand/2, DE/best/2, DE/current-to-best/1, DE/current-to-rand/1, etc, where DE/current-to-best/1 is more optimised than the other differential strategies (Deng et al., 2022). Therefore, the DE/current-to-best/1 differential strategy is selected for hybrid improvement in this paper. Its mathematical expression is as follows:

$$x_m^{t+1} = x_m^t + F \cdot \left(x_{best}^t - x_m^t\right) + F \cdot \left(x_{r1}^t - x_{r2}^t\right) \tag{10}$$

In equation (10), F is the scaling step factor, which generally takes the value of a pseudo-random number between $[0, 1]$. r_1 and r_2 are random integers that are not identical to each other between $[1, N]$. x_{best}^t is the optimal individual in the t^{th} generation. In order to make the mutation of each generation more diverse and the distribution of individuals richer, we improved the scaling step factor by the following operation.

$$F_i = Cauchy\,(0, 1) \tag{11}$$

where $Cauchy$ indicates that the step factor F follows a Cauchy distribution and that each population has a different value of F.

3.3.2 *Information sharing*

The search behaviour of SIO algorithm may lead to the loss of the diversity of search space, which makes it difficult to search forward. This requires us to improve the exploration and development ability of the algorithm to escape the dilemma of local optimisation. Inspired by the existing research (Rakhshani and Rahati, 2017), Through the mutual information exchange between populations, the search ability and diversity of populations can be greatly improved. According to the literature, firstly, the population is divided into three randomly generated groups and recombined after each iteration. Then the population will be updated according to the current way of reorganisation, which makes the population after each reorganisation can make full use of its domain information. This will help the population to show a variety of random behaviours in the whole optimisation stage, and better avoid local optimisation. The specific calculation method is shown in formula (12).

$$x_m^{t+1} = \begin{cases} x_m^t + H\left(Pa - \varepsilon\right) \\ \otimes \left(x_j^t \otimes r - x_m^t\right), if\ q < SP \\ x_m^t + H\left(Pa - \varepsilon\right) \\ \otimes \left(x_j^t - x_m^t \otimes r\right), if\ q < 1 - SP \\ x_m^t + H\left(Pa - \varepsilon\right) \\ \otimes \left(x_j^t - x_m^t\right) \otimes r, if\ q \geq 1 - SP \end{cases} \tag{12}$$

In equation (12), r, ε and q are uniformly distributed random numbers. The SP is calculated as follows:

$$SP = \frac{1}{1 + e^{1 - (G_{\max}/G+1\ )^{\tau}}} \tag{13}$$

where G and $maxG$ denote the number of current generations and maximum iterations, respectively. In the literature (Wang et al., 2019), the optimal range of τ is [1.5, 2.2], and this paper sets $\tau = 2$.

Algorithm 1 Pseudo-code of HCS algorithm

```
Input: population size $N$, conversion probability $Pa$,
       maximum number of iterations $maxG$;
Output: global optimal nest $\boldsymbol{x}_{gb}$, global optimal fitness
        value $f\left(\boldsymbol{x}_{gb}\right)$;
Generate initial nests $\boldsymbol{x} = \left(x_1, x_2, \cdots, x_N\right)^T$;
Evaluate the fitness $f(\boldsymbol{x}_i)$ of each nest $\boldsymbol{x}_i$;
Get the initial global optimal nest $\boldsymbol{x}_{gb}$;
$G = 0$;
while $G < maxG$ do
    for $i = 1; i \leq N; i++$ do
        Update $\boldsymbol{x}_i$ with equation (2);
        Continue to update $\boldsymbol{x}_i$ with equation (10);
    end
    Evaluate the quality $f(\boldsymbol{x}_i)$ of new nest $\boldsymbol{x}_i$;
    Get the current global optimal nest $\boldsymbol{x}_{gb}$;
    if $rand > Pa$ then
        Generate a nest $\boldsymbol{x}_i'$ randomly by equation (12);
        Evaluate the fitness $f\left(\boldsymbol{x}_i'\right)$ of $\boldsymbol{x}_i'$;
    end
    if $f\left(\boldsymbol{x}_i'\right) < f\left(\boldsymbol{x}_i\right)$ then
        Replace nest $\boldsymbol{x}_i$ with $\boldsymbol{x}_i'$;
        Replace nest $f\left(\boldsymbol{x}_i\right)$ with $f\left(\boldsymbol{x}_i'\right)$;
    end
    G = G+1;
    Get the current global optimal nest $\boldsymbol{x}_{gb}$;
    Get the current global optimal fitness value $f\left(\boldsymbol{x}_{gb}\right)$;
end
return $\boldsymbol{x}_{gb}, f\left(\boldsymbol{x}_{gb}\right)$;
```

3.3.3 *Design of SAPNN*

Subsection 3.2 shows that the smoothing factor σ of the conventional PNN is only a constant value, which does not correctly reflect the classification results corresponding to each input variable for the actual working problem. Therefore, building an self-adaptive PNN helps to solve this problem, and the key for a particular classification problem is to enable the network to pick different pattern classes according to σ. The SIO algorithm is just able to adapt to the PNN and select the optimal σ value, so we use the HCS algorithm (see Algorithm 1) for optimising the smoothing factor of the PNN network, where the parameters of HCS are set as shown in Table 6. Its fitness function will be designed in this paper as the classification error rate of the training set and the test set, which is calculated in formula (14).

$$f(x) = \arg\min\left(TrainError + PredictError\right) \tag{14}$$

From equation (14), it follows that the aim of $f\left(x\right)$ is to solve for minimisation of the classification error rate, and so it can be translated to use HCS to solve the minimisation problem.

Table 6 Parameter setting for the HCS algorithm

Name of parameter	*Value*
Size of population	30
Problem dimensions	1
Iterations	50
Discovery probability	0.25
Mutation factor F	0.5

4 Results and discussion

We intend to introduce the classification performance of SAPNN method in medical diagnosis tasks, The configuration used for all experiments is a Windows 10_64-bit system running with 8 GB of RAM; the software used is MATLAB R2018b; and the core processor is an Intel(R) Core(TM) i5-7500. Finally, we selected four medical disease datasets through UCI (https://archive.ics.uci.edu/ml/index.php). And the detailed descriptions of the specific datasets can be found in Subsection 4.1.

4.1 *Description of the dataset*

Diagnostic data for breast cancer were obtained from two versions of the Wisconsin Breast Cancer (WBC) dataset, WBC-1992 (Wolberg et al., 1990) and WBC-1995 (Street et al., 1993). The WBC-1992 dataset contains 699 samples, and each sample has ten attribute values. The WBC-1995 dataset contains 569 samples and each sample has 32 attribute values. Compared to WBC-1992 is more detailed, but both datasets are from the donation of Dr. Wolberg. Pima Diabetes Disease (PID) dataset (Eggermont et al., 2004), which consists of 768 samples represented by eight attributes. Diagnostic data for Parkinson's disease were obtained from the Parkinson's disease dataset (PDD) (Little et al., 2008), which has a total of 195 samples and 23 attributes. All of the above datasets belong to the dichotomous problem, and the purpose of all of them is to distinguish between healthy and diseased populations, and the information of the four datasets can be seen in Table 1.

4.2 Evaluation criteria

In order to validate the SAPNN method used in this paper for medical diagnosis, five different assessment criteria were adopted for evaluation (Priya and Sivakumar, 2022), including the following: accuracy, recall, specificity, precision, and F1_score. Where accuracy is the percentage of the number of correctly identified samples among all samples, as shown in formula (15). Recall is used to measure the number of positive cases that are correctly identified, as shown in formula (16). Specificity is the percentage of all negative cases that are scored correctly, as shown in formula (17). Precision is the percentage of the number of correctly identified samples among all samples judged to be correct, as shown in formula (18). And F1_score is the combined assessment factor of precision and sensitivity, as shown in formula (19).

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \tag{15}$$

$$Recall = \frac{TP}{TP + FN} \tag{16}$$

$$Specificity = \frac{TP}{FP + TN} \tag{17}$$

$$Presision = \frac{TP}{TP + FP} \tag{18}$$

$$F1\_score = 2 \times \frac{Precision \times Recall}{Precision + Recall} \tag{19}$$

where TP is the number of positive examples correctly divided. TN is the number of correctly divided negative cases. FP is the number of positive instances incorrectly classified. FN is the number of erroneously classified negative instances.

4.3 Experimental results and analysis

All experimental results in this paper are obtained by averaging the results after 20 independent runs, and in addition, because the SAPNN proposed in this paper mainly combines optimisation algorithms, we compare SAPNN with basic PNN and two newly proposed improved optimisation algorithms, in order to investigate the optimisation performance between optimisation algorithms. Two latest optimisation methods include PCCS (Cheng and Xiong, 2022) and CSAPC (Wei and Yu, 2020). Firstly, we randomly selected 70% of the total sample as the training dataset and the remaining 30% as the test dataset, and then compared them with other methods by the mean and standard deviation of the statistics. Tables 2 to 5 show the results of the four diagnostic methods evaluated on each dataset and the best results are marked in italic. Overall, the SAPNN model achieved the best classification results on all four disease diagnosis datasets. It can be seen that: in solving the problem of breast cancer diagnosis, SSAPNN has the highest accuracy, specificity and precision on the WBC-1992 dataset with 97.54%,96.15% and 97.85%, which indicates that the SAPNN model is able to identify the normal population and sick population more accurately, but has slightly lower recall than the CSAPC-PNN model, this indicates that SAPNN model is inferior to CSAPC-PNN model in correctly identifying positive cases. The F1_score shows that SAPNN is doing well in terms of overall performance, with values as high as 0.9771. And SAPNN obtained the best accuracy and recall on WBC-1995 dataset, which were 96.53% and 99.12% respectively. But it is not as good as PCCS-PNN model in specificity and precision. This means that SAPNN model can accurately identify positive medical records without missing real patients. In addition, from the F1_score of 0.9765, SAPNN model is still better than the other three diagnostic models on the whole.

In solving the problem of diabetes diagnosis, SAPNN obtained the best results on the PID dataset except the recall index. However, SAPNN still has the highest F1_score with a value of 0.7957. Finally, in solving the problem of Parkinson's disease, SAPNN only obtained the best accuracy on the PDD dataset, which was 96.61%. The PCCS-PNN model obtained the best specificity with 97.58% and precision with 94.68%, and the CSAPC-PNN model obtained the best recall. Despite this, SAPNN still achieved the best F1_score with 0.9118 in terms of overall effect.

In addition to the five evaluation criteria mentioned above, the confusion matrix is a performance metric that provides more insight into the testing accuracy of the proposed model. The comparison of the confusion matrix of the traditional PNN on the four datasets after HCS optimisation is represented from Figures 2 to 5. The results show that the HCS optimised PNN model is able to correctly classify most of the samples, achieving 97.5%, 96.5%, 75.7%, 96.6% on WBC-1992, WBC-1995, PID, PDD respectively correct rates, an improvement of 4.4%, 4.7%, 7.9% and 5.2% respectively compared to PNN.

5 Conclusions

In this work, we mainly address the problems of traditional CS by adding two strategies to form HCS, and then the method not only compensates for the high misdiagnosis rate of traditional PNNs due to the fixed smoothing factor, but also organically integrates SIO algorithms with neural networks. Experimental simulation results show that SAPNN outperforms other algorithms in terms of accuracy and F1_score when applied to four standard medical disease datasets. In the process of diagnosing the disease, the number of features often leads to misdiagnosis, which is not studied in this paper, but in future we will select important features before diagnosing the disease, which may further improve the accuracy of the diagnosis.

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