Optimising Deep Neural Networks for Tumour Diagnosis Algorithms Based on Improved MRFO Algorithm

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Abstract

INTRODUCTION: Cancer has become one of the most prevalent diseases with the highest mortality rate in the world, and timely detection and early acceptance of medical therapeutic interventions are effective means of controlling the progression of cancer patients and improving their post-intervention outcomes.

OBJECTIVES: To make the defects of incomplete features, low accuracy and low real-time performance of current tumour diagnosis methods.

METHODS: This paper proposes a tumour diagnosis method based on the improved MRFO algorithm to improve the optimization process of DBN network parameters. Firstly, the diagnostic features are extracted by analysing the tumour diagnosis identification problem; then, the manta ray foraging optimization algorithm is improved by combining the good point set initialization strategy, the adaptive control parameter strategy and the distribution estimation strategy, and the tumour diagnostic model based on the improved manta ray foraging optimization algorithm to optimize the parameters of the depth confidence network is constructed; finally, the high accuracy and real-time performance of the proposed method are verified by the analysis of simulation experiments.

RESULTS: The results show that the proposed method improves the accuracy of the diagnostic model.

CONCLUSION: Addresses the problem of poor accuracy and real-time availability of tumour diagnostic methods.

Keywords: tumour diagnosis algorithms, adaptive control parameter strategy, distribution estimation strategy, manta ray foraging optimisation algorithm, deep confidence networks

Received on 20 February 2024, accepted on 26 March 2024, published on 08 April 2024

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doi: 10.4108/eetphlt.10.5147

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1. Introduction

Oncology and cancer have become the major causes of death worldwide, and have become a major public health problem, seriously affecting the quality of life and health of human beings [1]. Although the global mortality rate of oncology cancer has shown a decreasing trend due to early screening and the continuous improvement of comprehensive treatment, the incidence of oncology cancer has been increasing year by year, and there is a trend of rejuvenation, and the epidemiological situation is not optimistic [2]. Oncology cancer has become one of the highest prevalence and mortality rates in the world, and timely detection and early acceptance of medical therapeutic interventions are effective means of controlling the progression of oncology cancer patients and improving their post-intervention [3]. Therefore, exploring effective ways to improve oncology cancer census and exploring effective ways to improve early diagnosis rate are of great significance to improve the survival rate and mortality rate of oncology cancer patients [4]. At the same time, accurate diagnosis of tumour cancers is a particularly important advance in curing tumour cancers, and being able to accurately diagnose tumour cancers has an extremely important significance in prolonging the survival time of patients and improving their quality of life [5].

Tumour cancer diagnosis is essentially a classification and recognition problem [6], by taking X-ray photographs of the tumour cancer, acquiring ware medical images, then
extracting features from the region of interest, and finally using certain algorithms to classify the extracted features, so as to differentiate whether the tumour is benign or malignant, and thus determine whether it is suffering from tumour cancer [7]. Currently, tumour cancer diagnosis and recognition methods include region-based methods, contour evolution-based methods, machine learning-based methods, statistical-based methods, and methods based on multi-resolution analysis [8]. Machine learning based methods are mainly divided into generative model based methods and discriminative model based methods [9]. Generative model-based methods include Markov Random Fields, Gaussian Mixture Models [10]; discriminative model-based methods include Support Vector Machines, Random Forests, Deep Neural Networks [11]. Literature [12] used traditional statistical clustering methods to cluster patient case data to solve the problem of classification prediction of diseases; Literature [13] used correlation analysis to explore the relationship between disease recurrence and basic patient indicators; Literature [14] proposed an incremental decision tree algorithm based on the fast decision tree algorithm to deal with a large amount of routine medical data; Literature [15] used KNN, neural network, decision tree and Bayesian classification methods to explore the heart disease data and conducted a method comparison test; Literature [16] applied the association rules and neural network classification methods in data mining to the prediction problem of breast tumour, and the experimental analysis yielded a good prediction result; Literature [17] proposed a medical data clustering classification based on the combination of neural network, genetic algorithm and fuzzy classification algorithm algorithm, and analysed the characteristic data structure and features of medical data; Literature [18] used the LSSVM method to solve the classification problem of tumour diagnosis and identification in medical data; Literature [19] proposed a method combining SVM with autoregressive integrative sliding average model for predicting the patient's blood glucose value; Literature [20] applied the support vector machine algorithm, random forest algorithm, CatBoost algorithm to the breast tumour diagnosis and identification, through analysis and comparison of the results of different algorithms, CatBoost algorithm has the best performance.

In response to the above literature analysis, the existing oncology cancer diagnostic methods have the following shortcomings:

1) the traditional expert system diagnostic methods are subjective, and the diagnostic results are unscientific [21];
2) the existing oncology cancer diagnostic methods based on machine learning algorithms are unable to reflect the non-linear relationship between pathological features and whether or not one has breast cancer, and are unable to establish an accurate diagnostic model [22];
3) the existing diagnostic models have robustness is poor and lacks generalisation [23].

Deep Belief Networks (DBN)[23] DBN algorithm is a type of neural network for machine learning, which can be used for both unsupervised and supervised learning. DBN is a probabilistic generative model as opposed to the traditional discriminative model of neural networks, where the generative model creates a joint distribution between observations and labels. By training the weights between its neurons, the whole neural network can be made to generate training data according to the maximum probability. The group intelligent optimization algorithm mainly simulates the group behaviours of insects, beasts, birds and fish, which search for food according to a certain cooperative way, and each member of the group constantly changes the direction of the search by learning from its own experience and the experience of the other members, which achieves the effect of obtaining the global optimal results [24]. The combination of deep confidence network and intelligent optimization algorithm makes the tumour cancer recognition effective, which makes the research of tumour cancer recognition model based on intelligent optimization algorithm optimization to improve the deep confidence network become the hotspot of experts' research.

Aiming at the problems existing in the current tumour cancer recognition method, this paper proposes a tumour cancer recognition method based on intelligent optimization algorithm optimizing the improved deep confidence network. The main contributions of this paper are:

1) extracting the features of tumour cancer diagnosis and recognition by describing the problem of tumour cancer diagnosis and recognition, and constructing the feature system of tumour cancer diagnosis and recognition;
2) constructing the tumour cancer diagnosis and recognition model by combining the improved intelligent optimization algorithm and the deep confidence network;
3) verifying the method of this paper through simulation, which has a higher recognition accuracy and recognition real-time performance.

2. Analysis of the problem of diagnostic identification of tumours

2.1. Data sources

This paper carries out research on tumour diagnosis recognition methods for breast tumour diagnosis problems. Breast tumour diagnostic data comes from the UCI machine learning library, with a total of 569 samples, of which the benign breast tumour data samples are 357 cases and the malignant breast tumour data samples are 212 cases. Each diagnostic sample data contains 30 feature data and 1 diagnostic result of benign and malignant classification, which are associated with the benign and malignant classification of breast tumour tumours. The examination method applied for this diagnosis is cell sectioning of the lesion area of breast tumour patients in order to obtain microscopic images of the nuclei of multiple cells in the section of the lesion part [25].
2.2. Diagnostic Characterisation Data

In this paper, firstly, the nuclear microscopic images of multiple lines of eight sections of the same lesion site were processed separately to obtain the radius of the nucleus, texture of the nucleus, perimeter of the nucleus, area of the nucleus, smoothness of the nucleus, compactness of the nucleus, convexity of the nucleus, number of points of the nucleus, symmetry of the nucleus, and the degree of nuclear fracture of the nucleus in the nuclear microscopic image of each cell [26]. Then the nuclear micrographic image data of multiple cells belonging to the same lesion site section were averaged, standard deviation and worst value [27], i.e., the required 30 feature data. The 30 feature data include mean value of nucleus radius X1, mean value of nucleus texture X2, mean value of nucleus circumference X3, mean value of nucleus area X4, mean value of nucleus smoothness X5, mean value of nucleus compactness mean value X6, nucleus concavity mean value X7, nucleus depression point mean value X8, nucleus symmetry mean value X9, nucleus fracture mean value X10, nucleus radius standard deviation X11, nucleus texture standard deviation X12, nucleus perimeter standard deviation X13, nucleus area standard deviation X14, nucleus smoothness standard deviation X15, nucleus compactness standard deviation X16, standard deviation of nucleus concavity X17, standard deviation of nucleus concavity point X18, standard deviation of nucleus symmetry X19, standard deviation of nucleus fracture X20, worst value of nucleus radius X21, worst value of nucleus texture X22, worst value of nucleus perimeter X23, worst value of nucleus area X24, worst value of nucleus smoothness X25, worst value of nucleus compactness X26, worst value of nucleus concavity X27, worst value of nucleus concavity point X28, worst value of nucleus symmetry X29, worst value of nucleus breakage X30. The principle of influencing factors selection is shown in Figure 1.

<table>
<thead>
<tr>
<th>Var</th>
<th>Definition</th>
<th>Value range</th>
<th>Var</th>
<th>Definition</th>
<th>Value range</th>
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<tbody>
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<td>Radius average</td>
<td>6.98–27.42</td>
<td>X16</td>
<td>Compactness SD</td>
<td>0.019–0.245</td>
</tr>
<tr>
<td>X2</td>
<td>Texture average</td>
<td>9.71–30.72</td>
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<td>Depression SD</td>
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</tr>
<tr>
<td>X3</td>
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<td>Dent points SD</td>
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<tr>
<td>X4</td>
<td>Area average</td>
<td>143.5–2501</td>
<td>X19</td>
<td>Symmetry SD</td>
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</tr>
<tr>
<td>X5</td>
<td>Smoothness average</td>
<td>0.053–0.16</td>
<td>X20</td>
<td>Crack SD</td>
<td>0.0078–0.0789</td>
</tr>
<tr>
<td>X6</td>
<td>Compactness average</td>
<td>0.019–0.245</td>
<td>X21</td>
<td>Worst radius</td>
<td>7.93–36.04</td>
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<td>X7</td>
<td>Depression average</td>
<td>0–0.427</td>
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<td>X8</td>
<td>Dent points average</td>
<td>0–0.2</td>
<td>X23</td>
<td>Worst circumference</td>
<td>50.41–251.2</td>
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<tr>
<td>X9</td>
<td>Symmetry average</td>
<td>0.106–0.304</td>
<td>X24</td>
<td>Worst area</td>
<td>185.2–4254</td>
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<td>X10</td>
<td>Crack average</td>
<td>0.05–0.097</td>
<td>X25</td>
<td>Worst smoothness</td>
<td>0.071–0.2229</td>
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<tr>
<td>X11</td>
<td>Radius SD</td>
<td>0.1115–2.873</td>
<td>X26</td>
<td>Worst compactness</td>
<td>0.027–1.058</td>
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<tr>
<td>X12</td>
<td>Texture SD</td>
<td>0.3902–4.885</td>
<td>X27</td>
<td>Worst depression</td>
<td>0–1.252</td>
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<tr>
<td>X13</td>
<td>Circumference SD</td>
<td>0.757–21.98</td>
<td>X28</td>
<td>Worst dent points</td>
<td>0–0.291</td>
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<tr>
<td>X14</td>
<td>Area SD</td>
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<td>X29</td>
<td>Worst symmetry</td>
<td>0.156–0.6638</td>
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<tr>
<td>X15</td>
<td>Smoothness SD</td>
<td>0.0022–0.1354</td>
<td>X30</td>
<td>Worst crack</td>
<td>0.055–0.2075</td>
</tr>
</tbody>
</table>

Figure 1. Diagnostic features of breast cancer

3. Deep confidence network (D CN)

Deep Belief Networks (DBN) [28] consist of multiple Restricted Boltzmann Machines (RBM) layers, a typical type of neural network is shown in Figure These networks are restricted to a visible layer and a hidden layer with connections between the layers but not between the units within the layers. The hidden layer units are trained to capture the correlation of higher order data exhibited in the visible layer, the exact structure of which is shown in Figure 2. As can be seen from Figure 2, the input layer \( v \) and the hidden layer \( h^1 \) constitute the first layer of the RBM, and the input data is mapped through the activation function to the hidden layer \( h_1 \), which is input to the second layer of the RBM (the hidden layer \( h_2 \) and the hidden layer \( h_3 \)), and the data is passed through the hidden layer sequentially to reach the output layer.
(1) Calculate the RBM energy function. Assuming that \( \theta = (\omega, a, b) \) is the DBN network parameter, the energy function of RBM is expressed as:

\[
E(v, h|\theta) = -\sum_{i=1}^{n} a_i v_i - \sum_{j=1}^{m} b_j h_j - \sum_{i=1}^{n} \sum_{j=1}^{m} v_i \omega_{ij} h_j
\]  

(1)

Where, \((v, h)\) is the state value of DBN, \(\omega\) is the connection weight of the visible and hidden layers, \(a\) and \(b\) are the bias of the visible and hidden layers respectively, and the hidden and visible layer states are binary states, i.e. \(v \in \{0,1\}\) and \(h \in \{0,1\}\).

(2) The stochastic gradient method is used to solve the DBN network parameters \(\theta\). The corresponding parameters \(\theta^*\) are obtained by solving the maximum of the log-likelihood function:

\[
\theta^* = \arg_{\theta} \max L(\theta) = \arg_{\theta} \max \sum_{k=1}^{K} \ln p(v^k|\theta)
\]  

(2)

where \(K\) is the number of training samples.

(3) The joint probability distribution function can be determined from the energy function:

\[
p(v, h|\theta) = e^{-E(v, h|\theta)} / Z(\theta)
\]  

(3)

\[
Z(\theta) = \sum_{v} \sum_{h} e^{-E(v, h|\theta)}
\]  

(4)

(4) Determine the state of the visible layer. The activation probability of the jth network node of the hidden layer is

\[
p(h_j = 1|v, \theta) = \text{sigmoid}(b_j + \sum_{i=1}^{n} v_i \omega_{ij})
\]  

(5)

(5) Determine the hidden layer state. The activation probability of the ith network node of the visual layer is

\[
p(v_i = 1|h, \theta) = \text{sigmoid}(a_i + \sum_{j=1}^{m} h_j \omega_{ij})
\]  

(6)

(6) According to Gibbs sampling theorem, the RBM parameter \(\theta\) is updated with the following formula:

\[
\Delta \omega_{ij} = \frac{\partial \log p(v)}{\partial \omega_{ij}} = \varepsilon \left(\langle v_i h_j \rangle_{\text{data}} - \langle v_i h_j \rangle_{\text{predict}}\right)
\]  

(7)

\[
\Delta a_i = \frac{\partial \log p(v)}{\partial a_i} = \varepsilon \left(\langle v_i \rangle_{\text{data}} - \langle v_i \rangle_{\text{predict}}\right)
\]  

(8)

\[
\Delta b_j = \frac{\partial \log p(v)}{\partial b_j} = \varepsilon \left(\langle h_j \rangle_{\text{data}} - \langle h_j \rangle_{\text{predict}}\right)
\]  

(9)

where \(\varepsilon\) denotes the learning rate, \(\langle v_i \rangle_{\text{data}}\) is the expectation of training after input data, and \(\langle v_i \rangle_{\text{predict}}\) is the expectation of the model itself.

4. Improvement of the MRFP algorithm

4.1. Standard MRFP algorithm

Manta Ray Foraging Optimization (MRFO) [29] is a population-based meta-heuristic optimization algorithm that solves the optimization problem by modelling three foraging behaviours of manta rays. These three foraging behaviours are: chain foraging, spiral foraging and somersault foraging. Similar to other population-based algorithms, MRFO also generates individuals randomly in the search space to form an initial population. The mathematical models for each of the three foraging behaviours are presented next.

Chain foraging

Manta rays form a foraging chain by connecting their heads and tails in a line. While the first individual moves only towards the food, the rest of the individuals move not only towards the food, but also towards the individuals in the foraging chain located in front of them. The mathematical model of chain foraging is described as follows:
Spiral foraging

When manta rays find plankton in deep water, they form long foraging chains and then move in a spiral towards the food. This behaviour is similar to the whale optimisation algorithm, but in addition to spiralling closer to the food, they also follow the individual in front of them. The mathematical model of spiral foraging can be given by the following equation:

\[ X_{i}^{t+1} = \begin{cases} X_{\text{best}}^{t} + r_5 \cdot (X_{\text{best}}^{t} - X_i^{t}) + \alpha \cdot (X_{\text{best}}^{t} - X_i^{t}) & i = 1 \\ X_i^{t} + r_2 \cdot (X_{\text{best}}^{t} - X_i^{t}) + \alpha \cdot (X_{\text{best}}^{t} - X_i^{t}) & i = 2, 3, \ldots, NP \end{cases} \]

\[ \alpha = 2 \cdot r_3 \cdot \sqrt{\log(r_i)} \]

\[ \beta = 2e^{-\frac{(iter_{\text{max}} - iter)}{iter_{\text{max}}}} \cdot \sin(2\pi r_7) \]

where \( r_2, r_3, r_4 \) are uniformly distributed random vectors with values ranging from 0 to 1. \( X_{\text{best}}^{t} \) is a uniformly distributed random number. \( \beta \) is a weight factor. \( \text{iter}_{\text{max}} \) and \( \text{iter} \) are the maximum number of iterations and the current number of iterations, respectively.

Food sources (optimal individuals) were mainly used as reference points for spiral foraging, which helped to fully exploit the space around the optimal individuals. In addition, randomly generated locations in the search space were used as reference locations for spiral foraging in order to extend the search range. This allowed all individuals to search areas away from their current optimal position. The stochastic spiral foraging mechanism focuses primarily on exploration, allowing MRFOs to perform extensive global searches. The specific mathematical model is described below:

\[ X_{\text{rand}}^{t} = lb + r_8 \cdot (ub - lb) \]

where \( X_{\text{rand}}^{t} \) is the randomly generated reference position in the search space. \( r_8, r_9, r_{10} \) are uniformly distributed random vectors with values ranging from 0 to 1. \( ub \) and \( lb \) are the upper and lower boundaries of the search space, respectively.
Somersault foraging

In this stage, the food position is considered to be a fulcrum. Each individual flips around the pivot point, thus finding a new location. The mathematical model of this stage is represented as follows:

$$F \text{igure 5. Somersault type foraging}$$

$$X_i^{new} = X_i^{current} + S \cdot (r_{11} \cdot X_{best}^{current} - r_{12} \cdot X_i^{current}), i = 1, 2, \ldots, NP$$

(7)

Among them, $S$ is the coefficient affecting the rollover range of manta ray, which usually takes the value of 2. $r_{11}$ and $r_{12}$ are uniformly distributed random vectors, which take the value of 0–1.

The MRFO algorithm regulates the exploration and exploitation behaviour by controlling the variation of $\frac{iter}{\text{iter}_{\text{max}}}$. When $\frac{iter}{\text{iter}_{\text{max}}} < \text{rand}$, MRFO mainly performs the exploration behaviour, generating random food sources as reference points in the search space. When $\frac{iter}{\text{iter}_{\text{max}}} \geq \text{rand}$, the MRFO algorithm utilises the optimal individual as a reference point, which facilitates the exploitation of the algorithm. In addition, a random number is used to select either chain foraging or spiral foraging. After that, somersault foraging is performed.

4.2. Improvement strategies

In order to enhance the full-domain exploration capability of the MRFO algorithm and avoid the algorithm from falling into a local optimum, this paper adopts a good point set initialisation strategy [30], an adaptive control parameter strategy [31] and a distribution estimation strategy [32] to improve the manta ray foraging optimisation algorithm.

**Good point set initialisation strategy**

The quality of the initialised population of MRFO algorithm affects the solution optimisation speed of the algorithm, and an excellent population initialisation strategy can make the individuals of the population traverse the whole search space more evenly, increase the population diversity and improve the convergence speed of the algorithm. In order to improve the population search diversity and make the population uniformly distributed in the search space, this paper proposes a good point set initialisation strategy to improve the initialisation method of MRFO algorithm. Suppose $G_s$ is a unit cube in $s$-dimensional Euclidean space, if $r \in G_s$, for:

$$P_a(k) = \left[\left(r_1^{(a)} \cdot k\right), \left(r_2^{(a)} \cdot k\right), \ldots, \left(r_s^{(a)} \cdot k\right)\right], 1 \leq k \leq n$$

(8)

Its deviation is satisfied:

$$\phi(n) = C(r, \varepsilon) n^{\varepsilon^{-1}}$$

(9)

Then $P_a(k)$ is called the set of good points and $r$ is the good point. $\left(r_i^{(a)} \cdot k\right)$ represents the fractional part, $\varepsilon$ is any positive number, $C(r, \varepsilon)$ is a constant related only to $r, \varepsilon, n$ denotes the number of points, and $r$ is:

$$r = \left\{2 \cos \left(\frac{2\pi k}{p}\right), 1 \leq k \leq s\right\}$$

(10)

where $p$ is the smallest prime number satisfying $(p - 3)/2 \geq s$. The initialised population distribution graph using the set of good points is shown in Figure 3.

**Adaptive control parameter strategy**

The MRFO algorithm regulates exploration and exploitation behaviour by controlling changes in $\frac{iter}{\text{iter}_{\text{max}}}$. The change of $\frac{iter}{\text{iter}_{\text{max}}}$ is a linearly
increasing variable that does not accurately reflect and adapt to the complex nonlinear search process. Nonlinear parameter control strategy style is an effective measure to prevent the algorithm from maturing prematurely. In this paper, an adaptive control parameter strategy with a mixture of sine and cosine functions is proposed, as shown in Figure 7, and the specific mathematical model is as follows:

\[ Coef = \sin\left(\frac{\pi \cdot \text{iter}}{2 \cdot \text{iter}_{\text{max}}^\text{max}}\right)^{2.5 \cdot \text{cos}(\text{iter}/\text{iter}_{\text{max}}^\text{max})} \]  \hspace{1cm} (11) 

\[ S = (S_{\text{min}} - S_{\text{max}}) \cdot \frac{\text{iter}}{\text{iter}_{\text{max}}} + S_{\text{max}} \]  \hspace{1cm} (12)

Where \( S_{\text{min}} \) and \( S_{\text{max}} \) are the minimum and maximum values of the parameter \( S \).

**Distribution estimation strategy**

The chained foraging strategy of the standard MRFO algorithm uses the optimal individual and neighbouring individuals for position updating, which can easily lead to premature convergence of the algorithm. If the optimal individual has already fallen into the local optimum, the chaining rule will cause all subsequent individuals to approach the local optimal individual. In order to improve the performance of the algorithm, this paper proposes a distribution estimation strategy with the following mathematical model:

\[ X_{i+1} = \text{mean} + y \cdot y \cdot N(0, \text{Cov}) \]  \hspace{1cm} (13)

\[ \text{mean} = \left(X_{\text{exp}} + X_{\text{mean}} + X_i^i\right)/3 \]  \hspace{1cm} (14)

\[ \text{Cov}(i) = \frac{1}{NP/2} \sum_{i=0}^{NP/2} (X_{i+1}^i - X_{\text{mean}}^i) \times (X_i^i - X_{\text{mean}}^i)^T \]  \hspace{1cm} (15)

\[ X_{\text{mean}}^i = \sum_{i=0}^{NP/2} \omega_i \times X_i^i \]  \hspace{1cm} (16)

\[ \omega_i = \frac{\ln\left(NP/2 + 0.5\right) - \ln(i)}{\sum_{i=1}^{NP/2} \ln\left(NP/2 + 0.5\right) - \ln(i)} \]  \hspace{1cm} (17)

where \( X_{\text{mean}}^i \) denotes the weighted position of the dominant population, \( \omega \) denotes the weighting coefficients in the dominant population in descending order of fitness values, and \( \text{Cov} \) denotes the weighted covariance matrix of the dominant population. The distribution estimation strategy with chained foraging measurement class was randomly selected for execution.

**4.3. Improvement of MRFP algorithm step by step process**

Based on the improvement strategy and optimisation process, the GoodADMRF algorithm (MRFO based on Good point set, Adaptive control parameter strategy and Distribution estimation strategy) pseudo-code is shown in Figure 8 with the following steps.
5. Ideas for tumour diagnosis methods based on the GoodADMRFO algorithm for optimising deep confidence networks

Combining GoodADMRFO and deep confidence network, this section proposes a tumour diagnosis method based on GoodADMRFO algorithm to improve DBN network.

5.1. Decision variables and objective functions

The traditional iterative approach to DBN network optimisation can easily cause the optimisation of DBN network parameters to fall into local optimum. In order to overcome the above problems, this paper adopts the GoodADMRFO algorithm to optimise the DBN network parameters. The optimisation decision variable of the GoodADMRFO algorithm is $\theta = (\omega, a, b)$.

In order to overcome the DBN training accuracy, the Error, F-score, and FPR functions are used as the objective functions.
functions of the GoodADMRFO-DBN algorithm and are calculated as follows:

$$\text{Fitness}(X) = \alpha \cdot \text{Error} + \beta \cdot \frac{1}{F\text{-score}} + \gamma \cdot \text{FPR}$$

\(18\)

$$\text{Error} = 1 - \text{Accuracy}$$

\(19\)

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

\(20\)

$$\text{FPR} = \frac{FP}{TN + FP}$$

\(21\)

$$\text{Precision} = \frac{TP}{TP + FP}$$

\(22\)

Among them, \(\alpha + \beta + \gamma = 1\) ; \(\alpha = 0.4\) , \(\beta = 0.4\) , \(\gamma = 0.2\) .

5.2. Steps and processes

The tumour diagnosis model based on GoodADMRFO algorithm optimized DBN network is mainly based on the mapping relationship between features and recognition types with tumour diagnostic features as input and diagnostic recognition types as output. The flowchart of the tumour diagnosis method based on GoodADMRFO-DBN algorithm is shown in Figure 9. The specific steps are as follows:

Step 1: According to the state of the tumour, the tumour diagnostic features are extracted; the features are dimensionality reduced using principal component analysis; the dataset is divided into a training set, a validation set and a test set;

Step 2: The GoodADMRFO algorithm is used to encode the initial DBN parameters, and also initialise the algorithm parameters such as the population parameters and the number of iterations; the population is initialised and the objective function value is calculated;

Step 3: Update the mean and Cov of the distribution estimation strategy; if rand<0.5 and Coef<0.5, use the spiral foraging strategy based on the optimal individual; if rand<0.5 and Coef<0.5, use the spiral foraging strategy based on the random individual; if rand>=0.5, use the chain foraging strategy based on the distribution estimation strategy of chain foraging strategy; calculate the fitness value and update the optimal solution;

Step 4: Based on the somersault foraging strategy, the position is updated; the fitness value is calculated and the optimal solution is updated;

Step 5: Determine whether the termination condition is satisfied, if so, exit the iteration, output the optimal DBN network parameters, and execute step 3, otherwise continue to execute step 6;

Step 6: Decode the GoodADMRFO-based optimised DBN parameters, obtain the optimal DBN parameters, and construct the GoodADMRFO-DBN-based tumour diagnosis model;

Step 7: Diagnose and identify the current test set using the trained tumour diagnostic model, and output the corresponding diagnostic results.

Figure 9. Flowchart of GoodADMRFO-DBN based tumour diagnosis approach
6. Experiments and analysis of results

In order to verify the accuracy and timeliness of the tumour diagnostic model proposed in this paper, five diagnostic algorithms were selected for comparison, and the specific parameter settings of each algorithm are shown in Table 1. The data were mainly obtained from the sample data of breast tumour diagnostic cases in the UCI Machine Learning Library. The experimental simulation environment is Windows 10, CPU is 2.80GHz, 8GB memory, programming language Matlab2017b.

<table>
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<th>Arithmetic</th>
<th>Parameterisation</th>
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</thead>
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<td>DBN</td>
<td>Three hidden layers with 100, 100, 100 nodes in each layer</td>
</tr>
<tr>
<td>MRFO-DBN</td>
<td>Three hidden layers, with the number of nodes being determined by Section 6.1 and the number of populations being determined by Section 6.1</td>
</tr>
<tr>
<td>MRFO-3-DBN</td>
<td>Three hidden layers, the number of nodes is determined by Section 6.1, and MRFO does not use a good point set initialisation strategy</td>
</tr>
<tr>
<td>MRFO-2-DBN</td>
<td>Three hidden layers, the number of nodes is determined by Section 6.1, and MRFO does not use an adaptive control parameter strategy</td>
</tr>
<tr>
<td>MRFO-1-DBN</td>
<td>Three hidden layers, the number of nodes is determined by Section 6.1, and MRFO does not use a distribution estimation strategy</td>
</tr>
<tr>
<td>GoodADMRFO-1-DBN</td>
<td>Three hidden layers, the number of nodes is determined by Section 6.1, and MRFO does not use a good point set initialisation strategy</td>
</tr>
</tbody>
</table>

6.1. Parameter setting analysis

In order to analyse the impact of the population size of MRFO algorithm and the number of hidden layer nodes of DBN network on the tumour diagnosis method, this paper compares and analyses the performance of the tumour diagnosis method under the conditions of different population sizes and different numbers of hidden layer nodes of the network, respectively. Figure 10 gives a graph of the impact of different population sizes and different numbers of network hidden layer nodes on diagnosis accuracy, and Figure 11 gives a graph of the impact of different population sizes and different numbers of network hidden layer nodes on diagnosis time.

As can be seen from Figure 10, as the number of populations of the optimization algorithm increases, the accuracy of tumour diagnosis also gradually increases; as the number of DBN hidden layer nodes increases, the accuracy of tumour diagnosis also gradually increases; when the number of populations increases to 70, the increase in the accuracy of tumour diagnosis becomes slow, and even the performance decreases; when the number of hidden nodes of the DBN network increases to 80, the effect of the increase in the accuracy of tumour diagnosis is not obvious. As can be seen from Figure 11, with the increase in the number of populations of the optimization algorithm, the tumour diagnosis time also increases gradually; with the increase in the number of hidden nodes of DBN, the tumour diagnosis time also increases gradually; when the number of populations is increased to 90, the tumour diagnosis time change no longer increases and tends to be stable; when the number of hidden nodes of DBN network is increased to 80, the tumour diagnosis time increases more quickly. In summary, the intelligent optimisation algorithm selected in this paper has a population size of 80 and the number of hidden nodes of DBN network is 90.

Figure 10 gives the results of tumour cancer diagnosis based on each algorithm. As can be seen from Figure 10, comparing the GoodADMRFO-DBN and DBN algorithms shows that the optimisation and improvement strategy improves the diagnostic accuracy of the DBN and MRFO-DBN algorithms; comparing the MRFO-DBN and MRFO-1-DBN algorithms shows that the good point set initialisation strategy improves the MRFO-DBN diagnostic accuracy; comparing MRFO-DBN and MRFO-2-DBN shows that the adaptive control parameter strategy improves the MRFO-DBN diagnostic accuracy; comparing MRFO-DBN with MRFO-3-DBN shows that the distribution estimation strategy improves the MRFO-DBN diagnostic accuracy. Meanwhile, GoodAD-based MRFO-DBN has the highest diagnostic identification accuracy.
6.2. Experimental prediction performance analysis

In order to verify the effectiveness and superiority of the tumour cancer diagnosis method based on the GoodADMRFO-DBN algorithm, GoodADMRFO-DBN is compared with five other models such as DBN, MRFO-DBN, MRFO-1-DBN, MRFO-2-DBN, MRFO-3-DBN, and the performance results of each model are shown in Figure 12, Figure 13 and Figure 14.

Figure 10. Effect of different population sizes and number of hidden nodes on diagnostic accuracy

Figure 11. Effect of different population sizes and number of hidden nodes on diagnosis time
Figure 12. Tumour cancer diagnosis results based on each algorithm

In order to further verify the superiority of the tumour diagnosis method based on the GoodADMRFO-DBN algorithm, the results of the diagnostic performance of each algorithm are statistically given in this section, as shown in
Figure 13 and Figure 14. From Figure 13, it can be seen that the diagnostic accuracy mean value of GoodADMRF-DBN algorithm based on GoodADMRF-DBN algorithm is larger than other algorithms, and the accuracy standard deviation is smaller than other algorithms, and the diagnostic effect is better than other algorithms; the diagnostic time mean value of GoodADMRF-DBN algorithm based on GoodADMRF-DBN algorithm is smaller than DBN and MRFO algorithms, but larger than MRFO-1-DBN and MRFO-2-DBN, MRFO-3-DBN algorithms, and the standard deviation of time is better than the other algorithms, which shows that the stacking of the three strategies may increase the computational burden, but the robustness becomes better. In conclusion, the tumour diagnosis method based on GoodADMRF-DBN algorithm works better than other algorithms and meets the real-time requirements.

<table>
<thead>
<tr>
<th>Algorithm</th>
<th>Accuracy mean</th>
<th>Accuracy SD</th>
<th>Time mean</th>
<th>Time SD</th>
</tr>
</thead>
<tbody>
<tr>
<td>DBN</td>
<td>89.10%</td>
<td>1.77</td>
<td>0.0244</td>
<td>0.0019</td>
</tr>
<tr>
<td>MRFO-DBN</td>
<td>92.32%</td>
<td>1.99</td>
<td>0.0092</td>
<td>0.0017</td>
</tr>
<tr>
<td>MRFO-1-DBN</td>
<td>93.32%</td>
<td>1.23</td>
<td>0.0041</td>
<td>0.0008</td>
</tr>
<tr>
<td>MRFO-2-DBN</td>
<td>93.76%</td>
<td>1.19</td>
<td>0.0033</td>
<td>0.0016</td>
</tr>
<tr>
<td>MRFO-3-DBN</td>
<td>94.11%</td>
<td>0.67</td>
<td>0.0032</td>
<td>0.0002</td>
</tr>
<tr>
<td>GoodADMRF-DBN</td>
<td>95.57%</td>
<td>0.38</td>
<td>0.0052</td>
<td>0.0001</td>
</tr>
</tbody>
</table>

**Figure 13.** Comparison of tumour diagnosis accuracy and time analysis based on each algorithm

As can be seen from Figure 14, the diagnostic optimisation process based on the GoodADMRF-DBN algorithm is better than MRFO-DBN, MRFO-1-DBN, MRFO-2-DBN, MRFO-3-DBN, with a faster convergence speed and better convergence accuracy than the other algorithms. In conclusion, the optimisation of tumour diagnosis based on GoodADMRF-DBN algorithm has faster convergence speed and better convergence accuracy.

**Figure 14.** Convergence curve analysis of tumour diagnosis accuracy based on each optimisation algorithm
7. Conclusion

Aiming at the defects of incomplete features, low accuracy and low real-time performance of tumour diagnosis methods, this paper proposes a tumour diagnosis method based on the improved MRFO algorithm to improve the optimization process of DBN network parameters. The method extracts diagnostic data features by analysing the tumour diagnosis identification problem. The manta ray foraging optimisation algorithm is improved by combining the good point set initialisation strategy, adaptive control parameter strategy and distribution estimation strategy, and the parameters of the depth confidence network are optimised using the improved manta ray foraging optimisation algorithm to construct a tumour diagnosis model. Simulation experiments are carried out using breast tumour diagnostic feature data, and the following conclusions are drawn:

(1) By comparing the diagnostic performance of the MRFO-DBN and DBN algorithms, the MRFO algorithm can improve the diagnostic accuracy of DBN;
(2) By comparing the diagnostic performance of GoodADMRFO-DBN with MRFO-DBN, MRFO-1-DBN, MRFO-2-DBN, and MRFO-3-DBN algorithms, and optimising the improvement strategies to further improve the diagnostic model accuracy;
(3) GoodADMRFO-DBN diagnostic time meets real-time requirements.

The time performance of the diagnostic model proposed in this paper is not good, and further improvement of GoodADMRFO-DBN diagnostic time is the next research focus.

References

[22] Bibikova M , Fan J. Liquid biopsy for early detection of lung


