



Optimal Feature Reduction and Classification Model for Diagnosing Lung Cancer

*V. Sreeprada

Research Scholar, GITAM UNIVERSITY, VIZAG

*sreepradasphd@gmail.com

Dr. K. Vedavathi

HOD, Department of Computer Science, GITAM, Vizag

vkateni@gitam.edu

1995

Abstract:

Of all cancers, the world's prominent cause of death is lung cancer as it is in the beginning asymptomatic and characteristically identified at advanced phases. If lung cancer is identified at a prior stage when it is minor and before it has spread, people have a better option of living longer. Though, identifying lung cancer at the precise time is a perplexing task due to high dimensional database space. The main objective of this paper is to diagnose lung cancer's conditions like Adenocarcinomas (AD), Squamous cell carcinomas (SQ), Carcinoids (COID), and Normal Lung (NL) for given query inputs. This paper proposes an optimal feature reduction and classification model for diagnosing lung cancers. For feature reduction, the various optimization techniques like Genetic Algorithm (GA), Particle Swarm Optimization (PSO), Monarch Butterfly Optimization (MBO) and Modified Monarch Butterfly Optimization (MMBO) are applied. After feature reduction, for classifying the disease, Deep Neural Network (DNN) is utilized. Experimental results have shown that MMBO-DNN method outperforms MBO-DNN, GA-DNN and PSO-DNN in terms of accuracy, sensitivity, specificity and F1-score.

Keywords: OFRCM; Cancer; COID; GA; PSO-DNN; DNN

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1. Introduction

Naturally, lung disease plays a main part in health issue. In any kind of lung disease, primarily the breathing gets disturbed. Here are some general kinds of lung diseases [1]. Lung cancer is the maximum common sort of cancer across genders and the general cause for cancer-related death universally. [2] Lung cancer stands second amongst males and tenth amongst females [3,4] worldwide. Timely recognition of lung cancer could lessen the death rate and intensify the patient's survival rate when the treatment is more probably remedial. Computed tomography (CT) imaging is an effectual medical screening test utilised for lung cancer analysis and recognition. The physician utilises the attained CT images to examine and to identify the lung tissues. On the other hand, in several regular cases, it is problematic for the physician to attain a precise analysis deprived of the aid of extra tool called Computed Aided

Diagnosis (CAD) System.[5] Normally, these methods are joined to progress computer-aided detection (CAD) systems, that offer help to radiologists in the challenging task of classifying irregularities on patients.

Two of the main phases that are requisite to constitute CAD systems are segmentation [6,7] and classification [8,9] into medical images. The classification approach is one sort of prognostic revealing. More particularly, classification is the way toward specifying novel studies predefined classifications or classes. The classification system is utilised to anticipate gathering of collaboration for data samples [10]. Several inquiries described to improve classifiers for recognition or analysis of disease by using machine-learning approaches.[11] Deep learning can outdo conventional image classification procedures.[12] Deep learning is a specific sort of machine learning which contains numerous processing layers to attain high levels of



concept when it comes to learning exemplifications of data.[13]There are some works that use evolutionary and bio inspired procedures to train DNN as an additional indispensable sort of learning [14].

Numerous procedures inspired by the insects and animals performance to unscramble a comprehensive collection of intricate optimization problems [15].The inspiration behind the invention of the suggested Monarch Butterfly Optimization (MBO) procedure system lies in the necessity for effectual feature selection procedure. This inspiration focuses on the development of concealed node size and preliminary weight used at the time of the procedure of feature optimization that features towards enhanced act of the multilayer perceptron network. This scheme meaningfully progresses the amount of divergence by using a worldwide and adaptive butterfly operator with the view to enhance the procedure of universal exploration. From this time, the study uses typical data mining schemes to categorize medical data and also to discover the efficiency of using varied input structures and classifiers for assessing the medical datasets. [16]

1.1 Motivation of the Research and Objectives

Of all cancers, the world's prominent cause of death is lung cancer as it is in the beginning asymptomatic and characteristically identified at advanced phases. If lung cancer is identified at a prior stage when it is minor and before it has spread, people have a better option of living longer. Though, identifying lung cancer at the precise time is a perplexing task due to high dimensional database space.

The research objective is to diagnose lung cancer's conditions like ADenocarcinomas (AD), Squamous cell carcinomas (SQ), Carcinoids (COID), and Normal Lung (NL) for given query inputs. This research focuses on features reduction because the database includes 1000 inputs features and 1-output. Hence an optimal feature reduction and classification model is proposed for diagnosing lung cancers.

2. Related works

Atsushi Teramoto et al. [17] had predicted lung cancer was a principal reason of death universally, and its initial recognition was

generally done with low-dose computed tomography. In that study, they intended to automatize the cataloguing of malevolent lung cells from microscopic images by means of a deep convolutional neural network (DCNN).The cataloguing sensitivity and specificity were 89.3 and 83.3%, correspondingly, attaining an act similar to that of a cytopathologist. By means of the gradient-weighted class activation mapping, they imagined the DCNN recognition act while the network sought for usual benevolent and malevolent cells in images for cataloguing.

N. Balakumar and B. Prabadevi [18] had recommended multi datasets (Liver, Lung, Heart, and Thyroid) are taken into account for the disease prediction analysis. Then, to that, the ideal features are selected by the procedure called Modified Monarch Butterfly Optimization (MMBO). Based on the chosen features, the data are categorized into two types: healthy and non-healthy by the suggested classifier i.e. Deep Neural Network (DNN). The acts of the suggested procedure and classifier are verified on the multi-datasets regarding sensitivity, specificity, and truth. The outcomes validate the MMBO-DNN procedure attains high precision of and less implementation time associated to the prevailing procedures.

WasudeoRahane et al. [19] had intended that lung cancer was one of the substantial causes for death in India. Henceforth, lung cancer recognition system by means of image processing and machine learning was utilised to categorize the existence of lung cancer in a CT- images and blood samples. Classifications are made on structures obtained from the images. The technique is to sense the lung cancer and its stages efficiently and also goal to have more precise outcomes by means of SVM and Image Processing techniques.

H. Mahersiaet *al.* [20] had suggested that lung knobs are possible presences of lung tumor, and their initial recognition reassures early treatment and improves patient's odds for survival. Therefore, CAD frameworks for lung cancer had been suggested in some investigations. Each of these works is encompassed for the best part three stages to differentiate the pulmonary knob: pre-processing, segmentation of the lung and classification of the knob competitors. That



article appraises the contemporary finest class regarding all the procedures and systems that had been investigated in the literature. It similarly offers an analysis of the implementation of the prevailing methods.

Yen Chen *et al.* [21] had done cross-laboratory sanctions for the tumor quiet data from 4 hospitals. In that, they have separated numerous data sets for prognostic applications in lung cancer analysis. Following constructing an enormous amount of diverse

ANN designs using the training data, five survival-time connected genes were identified from 4 microarray gene expression data sets by examining the association amid gene signatures and patient survival time. The experiment confirmed that gene expression data can be used for effective identification of cancer patient's survival classification with a common precision of 83.0% in light of survival time.

3. Proposed Methodology

3.1 Overview

This paper proposes an optimal feature reduction and classification model for diagnosing lung cancers.

For feature reduction, the research includes optimization techniques like GA, PSO, MBO and MMBO. Subsequently, the research used DNN for classification purpose.

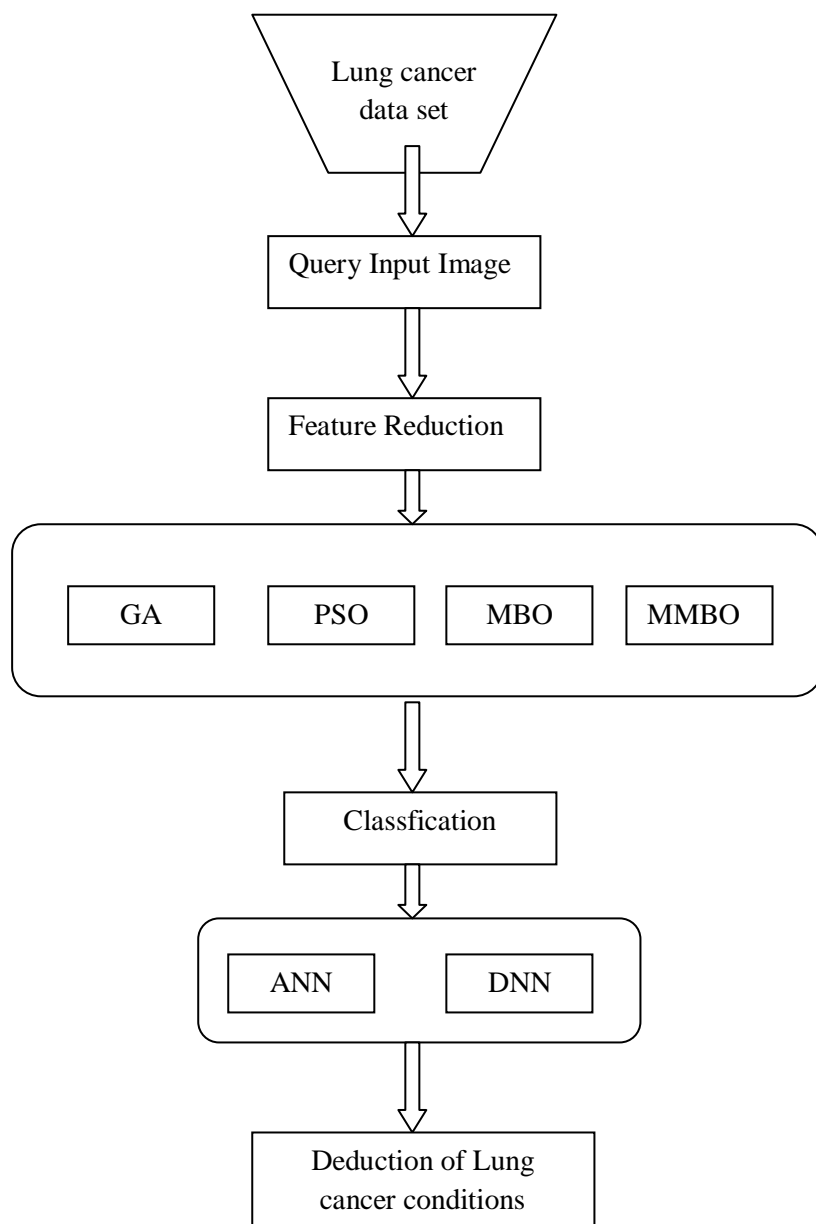


Figure 1 Flow diagram of proposed methodology



3.2 Feature Dimensionality Reduction Method

The sampling survey technique takes a part of the population as samples for investigation. In a usual dimensionality problem, provided a huge number of structures, the last number persist unidentified after dimensionality reduction; hence, by means of listing to examine all samples needs a rigorous workload and may flop. By using the sampling survey technique and some sample scale, this paper examines the structures and number of them after dimensionality reduction. The entire samples must have the similar option of being chosen. To get beneficial data for feature dimensionality reduction, we offer a feature-scoring system and a scoring system for reduced-dimension length.

The feature-scoring system operates as follows:

Step 1 Draw n_1 sets of features with any number of dimensions taken randomly from features with equal probability. Calculate the fitness of each sample based on classification recognition accuracy, data-mining efficiency, or neural network estimation accuracy.

Step 2 Set a threshold value p and select all samples with fitness larger than p ; these samples comprise the set of valid feature scores.

Step 3 Score each feature based on the set of valid feature scores. The score of each feature is composed of the following two parts:

$$F_{feature_score_1} = \frac{\sum_{i=1}^{N_1} (N_1 - R_i) - F_{feature_score_1_min}}{F_{feature_score_1_max} - F_{feature_score_1_min}}$$

Where $F_{feature_score_1}$ is the first part of the score (Score 1) of a feature, N_1 is the number of sets of valid feature scores, R_i is the fitness ranking by the i th set of valid feature scores, $F_{feature_score_1_min}$ is the minimum of all Score 1s, and $F_{feature_score_1_max}$ is the maximum of all Score 1s.

$$F_{feature_score_2} = \frac{\sum_{i=1}^{N_1} (f_{score2}(i)) - F_{feature_score_2_min}}{F_{feature_score_2_max} - F_{feature_score_2_min}}$$

Where $F_{feature_score_2}$ is the second part of the score (Score 2) of a feature; $f_{score2}(i)$ is a piecewise function such that if the i th set of valid feature scores contains the feature, then $f_{score2}(i) = 1$ and $f_{score2}(i) = 0$ otherwise; $F_{feature_score_2_min}$ is the minimum of all Score 2s; and $F_{feature_score_2_max}$ is the maximum of all Score 2s.

The total score of a feature is represented by the following formula:

$$F_{feature_score} = F_{feature_score_1} + F_{feature_score_2}$$

Where $F_{feature_score}$ is the total feature score. According to Formulas (1) and (2), $F_{feature_score_1}$ and $F_{feature_score_2}$, strictly speaking, each belong to the range of [0, 1]. $F_{feature_score_1}$ reflects the degree of contribution of a feature to fitness. $F_{feature_score_2}$ reflects the frequency of a feature in a set of valid feature scores. A feature with a higher $F_{feature_score_1}$ or $F_{feature_score_2}$ can realize a better fitness value.

Step 4 Rank features according to their total scores and choose the first n_2 features for the set of valid features.

3.3 Optimal Feature Selection

Giving out a wide number of structures in databases is a stimulating task for execution process. In the data mining procedure, feature selection is one of the essential tasks and it goals to lessen the



data's dimensionality and their noise in datasets. The purpose of feature selection is to eliminate redundant features from the datasets and to retain the applicable data. Feature selection offers an improved act in both the learning and classification procedures if the probability of over fitting proliferates with the number of features. The succeeding procedures are used for choosing the ideal structures.

3.3.1 Genetic Algorithm

Depending on the evolutionary thoughts of natural selection and genetics, adaptive heuristic search procedure known as Genetic algorithm was suggested. GA is accepted as a fast growing area of artificial intelligence and as a portion of evolutionary computing. Huge, possibly enormous search spaces are considered for navigation purposes in the genetic algorithm. This hunts for ideal amalgamations of things, in which results can be discovered hardly.

On copying the nature, processes such as selection, crosses over, mutation and accepting the problems are used in the genetic algorithms. The mode the organism is made and the programming of the genes of an organism is defined by each organism by means of a set of instructions.

- Chromosomes, which are long strings, connect the genes together.
- Precise trait of the organism is represented by each gene and consists of several different settings.
- Organism's genotype refers the gene and their settings.
- Genes are shared during mating of two organisms. Genes are shared partly by two parents for the resultant offspring which is known as the crossover.
- Then the mutation of the newly created offspring is done. In an organism, the gene is mutated and is articulated as a completely new trait.
- Success of the organism in its lifetime is the basis for the fitness measurement of the organism [30].

3.3.2 Particle Swarm Optimization (PSO)

It is a population-based optimization technique simulated from the social manner of particles. Each particle has a position in source multidimensional search space. The location of a particle is determined based on its specific individual best experiences of a particle (Pbest) and the general best experience (Gbest) amongst a number of swarms. In every single reiteration of PSO, location and velocity for every single particle is rationalized based on simple mechanisms.

3.3.3 Monarch Butterfly Optimization (MBO)

MBO is a metaheuristic algorithm which is inspired by the migration behavior of MBO.

The migration behavior of MBO is explained as follows:

Rule 1: All the monarch butterflies are only located in Land 1 or Land 2.

Rule 2: By using migration operator in Land 1 or in Land 2 monarch butterfly, each child monarch butterfly individual is generated

Rule 3: In MBO algorithm, if the newly generated MBO has better fitness function as compared to its parent, then it will be replaced by its parent. As a result, the population range is remaining unchanged.

Rule 4: By associating the produced with parent one, the butterfly with improved fitness one is allocated for the next generation and they cannot be changed by any other operators. This will not ever denigrate with the increase of generations.



3.3.4 Modified MBO (MMBO)

The general monarch butterfly is modified by the random value selection i.e. the value is selected based on the velocity update of PSO algorithm in the equation (3) and those steps are explained as below.

Initialization

Monarch Butterfly optimizer is initialized with n number of population in land 1 and Land 2; here, each monarch butterflies position representing a given feature set combination and evaluate the fitness according to the position of each MB.

Updating the positions

Updating the position of MBO is performed by two operations namely, migration operator and butterfly adjusting operator.

Migration operator

In consideration, the monarch butterflies in Land 1 and Land 2 are named as Subpopulation 1 and Subpopulation 2 respectively. In the study, the features are initialized as the subpopulation 1 and subpopulation 2. This migration process can be explained as follows,

$$f_{i,t}^{G+1} = f_{r1,t}^G \quad (1)$$

Two criteria in the migration process: (i) When $r \leq p$ the element t in the newly generated monarch butterfly is generated by (2). Here, r can be computed as

$$r = rand * period \dots\dots\dots (2)$$

In equation (2), the random value is chosen based on the velocity update of Particle Swarm Optimization (PSO) algorithm (modified MBO). Its updation process is explained as in equation (3).

Velocity updation using PSO: Based on the behavior of swarm i.e. PSO algorithm, the velocity vector for a particle is updated according to Gbest and Best value. The formulation for updating the velocity of the particles in the PSO is given as:

$$V_i(t+1) = V_i(t) + b_1 rand(pbest(t) - r_i(t)) + b_2 rand(Gbest - r_i(t)) \quad (3)$$

Where, V_i is the particle velocity, r_i is the current particle, rand is a random number between (0, 1), b_1, b_2 are the learning factor, usually $b_1=b_2=2$.

(ii) If $r > p$ then the element t in the newly generated monarch butterfly is generated by

$$f_{i,t}^{G+1} = f_{r2,t}^G$$

Parameter Description: From equation (1), $f_{i,t}^{G+1}$ symbolizes the t^{th} element of i f at generation G+1 that introduces the position of the monarch butterfly i . $f_{r1,t}^G$, Indicates the t^{th} element of r1 f that is the newly generated position of the monarch butterfly r1. G is the current generation process. The term r1 is randomly chosen monarch butterfly from subpopulation 1. From equation (2), the period indicates the migration period, rand is a randomly generated number drawn from the uniform distribution. By altering the value of p, the MMBO algorithm can balance the direction of migration operator. The value of p is set to 5/12 as per migration period.

Butterfly Adjusting Operator

The position of MMBO is also updated by another operator i.e. butterfly adjusting operator. Considering all the MMBO elements (medical data attributes) are in j. If ($rand \leq p$), the position can be updated as,



$$= \begin{cases} f_{j,t}^{G+1} = f_{best,t}^G, & \text{if } rand \leq p \\ f_{j,t}^{G+1} = f_{r3,t}^G, & \text{if } rand > p \end{cases} \quad (5)$$

Under this condition, if $rand > BAR$ (Butterfly Adjusting Rate), it can be further updated as follows:

$$f_{j,t}^{G+1} = f_{j,t}^{G+1} + \alpha * (dx_t - 0.5) \quad (6)$$

Where BAR indicates butterfly aligning rate. The term α indicates the weighting factor that is afforded as $\alpha = \frac{WS_{max}}{G^2}$ where $max\ WS$ max walk step that a monarch butterfly individual can

move in one step at the current generation G . The parameter dx is the walk step of the monarch butterfly j that can be computed by performing Levy flight.

$$dx = Levy(f_j^g) \dots\dots\dots (7)$$

With the use of this MMBO algorithm, the optimal features are selected from the medical dataset which reduces the complexity of the classification process. The healthy and non-healthy data from the considered medical datasets are identified by the presented classification algorithm.

The diagrammatic representation of MMBO procedure is depicted in Figure 2.

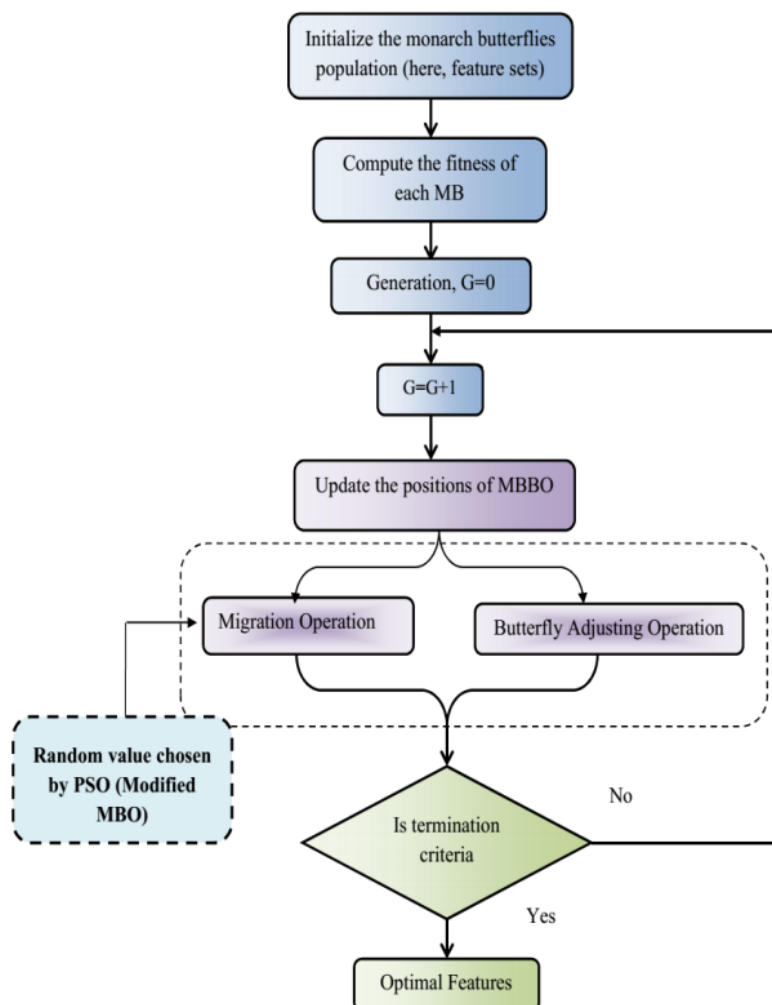


Figure 2 Flowchart of MMBO



3.4 DNN based Classification

In the arena of classification study, DNN model is utilised to categorize the data as two sorts: healthy and non-healthy. The ideal feature set is nursed into the classification method; the achieved data with optimum features advance the exactness of the classification task in association of using the classification task on the actual datasets.

An artificial neural network model with the multiple layers of the hidden units and outputs is termed as DNNs. In its parameter learning, DNN consists of pre-training (using generative deep belief network or DBN) and fine-tuning stages.

3.4.1 Pre-training stage

In the training stage, we use a Deep Belief Network (DBN) that is a deep architecture and typical feedforward network (FFN) in which the input flows from the input layer to the output layer through a number of hidden layers which are in excess of two layers. The DBN model permits the network to produce visible activations on the basis of its hidden units' states, which characterizes the network belief. Here, we implemented the Restricted Boltzmann Machine (RBM) to work out the above problem.

Restricted Boltzmann Machine (RBM) is an exclusive type of Markov random field that has one layer of (typically Bernoulli) stochastic hidden units and one layer of (typically Bernoulli or Gaussian) stochastic visible or observable units.

Initialization: Primarily we initialize the visible units' V to the training vector.

$$F(v, h) = \sum_{i=1}^I \sum_{j=1}^J Opt_{ij} v_i h_j - \sum_{i=1}^I \alpha_i v_i - \sum_{j=1}^J \beta_j h_j \quad (8)$$

Where Opt_{ij} (optimal features selected from MMB algorithm) represents the symmetric interaction term between the visible unit i v and the hidden unit h_j is the bias term, α, β is the number of visible and hidden units. Between hidden units in an RBM, there are no direct influences; it is enormously easy to get an impartial sample of $(v_i, h_j)_{data}$

$$\rho(h_j = 1 | v) = \delta\left(\sum_{j=1}^J Opt_{ij} v_i h_j - \alpha_j\right) \quad (9)$$

Updating process: We update the hidden and visible units are parallel in the provided visible and hidden units. For executing the stochastic steepest ascent in the log probability of the training data, this shows the way to a much-uncomplicated learning rule as

$$\Delta Opt_{ij} = \theta(v_i, h_j)_{data} - (v_i, h_j)_{reconstruction} \quad (10)$$

During the training process of every iteration, dissimilar RBM is stacked on top of it and it forms a multilayer model. The values attained for the units in RBM layers are apportioned by means of network current weight and biases. The output layer of the already-trained layers is engaged as input to the novel RBM. The accomplished deep network weights are engaged in priming a fine-tuning phase.

3.4.2 Fine Tuning Phase

The operational norm of this stage is depended on the normal backpropagation procedure. To classify the data from the actual datasets, an output layer is envisioned in the top of the DNN. Likewise, there is N number of input neurons (depending upon the features), and three concealed layers used in our DNN. The optimized weight is proposed through the training stage with the aid of



the training data set, where back propagation initiates the weights achieved in the pre-training stage.

4. Experimental Results

The proposed model is implemented in Matlab 2019. During the experiment, 100 lung images are trained for 120 iterations. During testing phase, for each query image, the lung cancer is accurately classified and detected.

4.1 Input and Output

Figure 3 shows some of the lung images used for training. Figure 4 shows the input query image and Figure 5 shows the preprocessed , normalized image. The corresponding output images after iterations are shown in Figure 6 and 7. The detected image is shown in Figure 8.

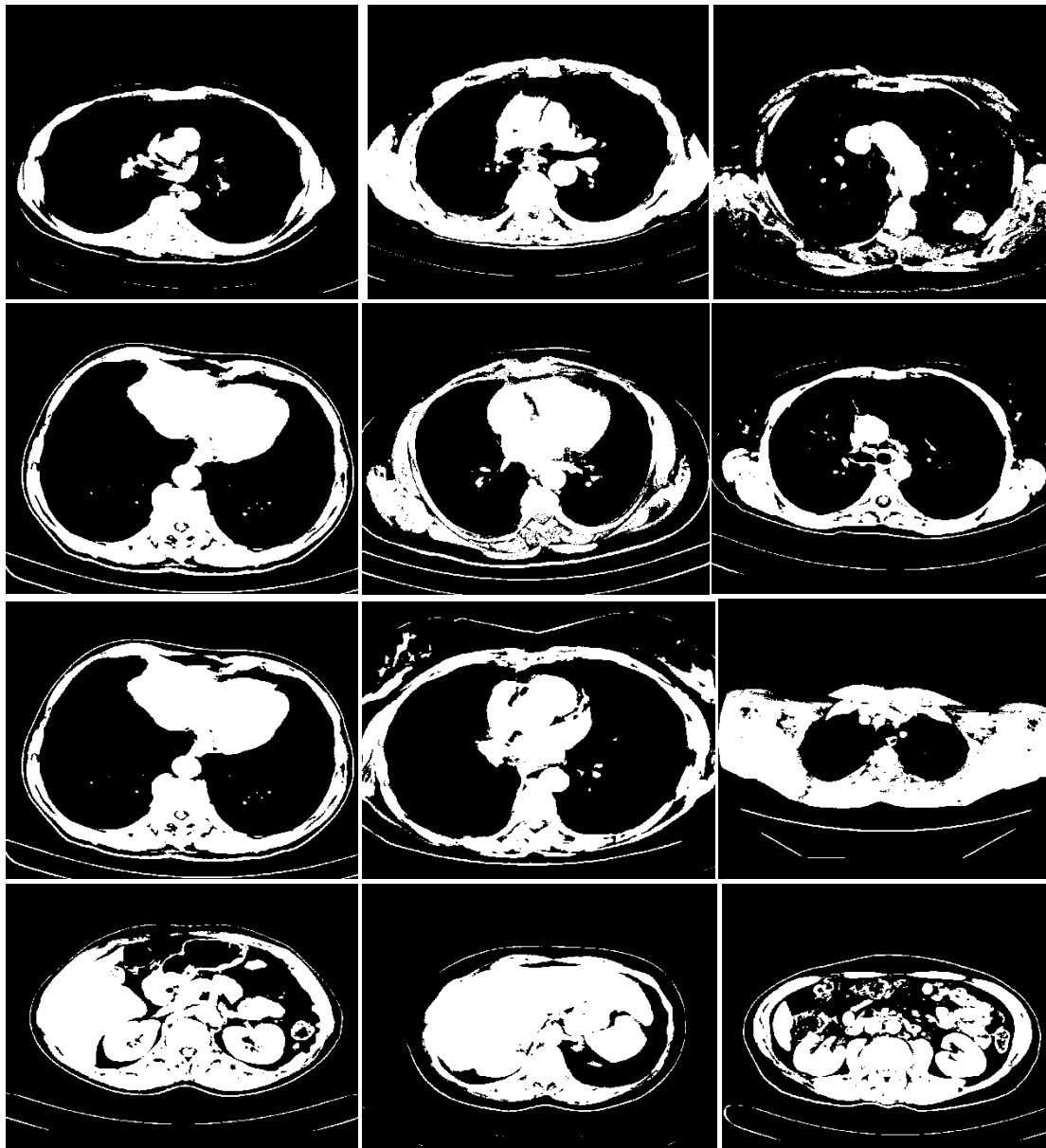
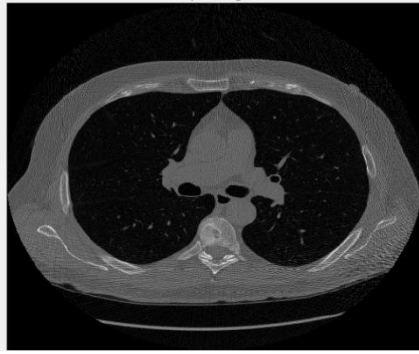


Figure 3 Lung Cancer Input Dataset

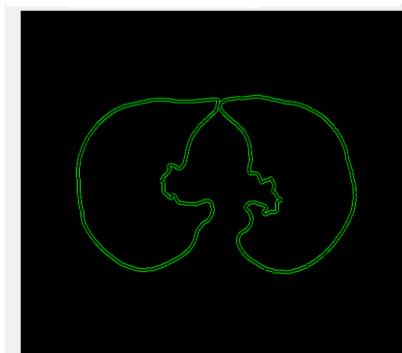




Figur4 Query Image



Figure 5 Normalized Image



Image

Figure 7 Output Image

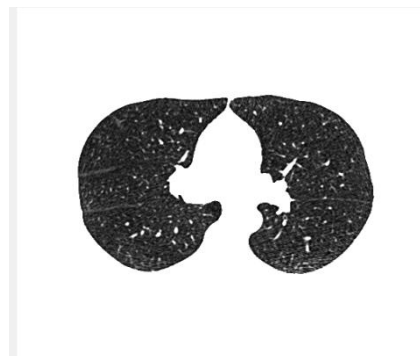


Figure 6
after 120
Iterations

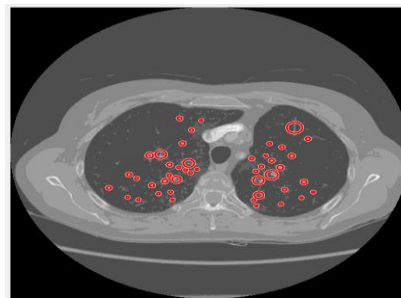


Figure 8 Lung cancer detected output Image

4.2 Performance Results

In this section, the results of MMBO-DNN are compared with MBO-DNN, PSO-DNN and GA-DNN algorithms.

The classification results are evaluated in terms of different parameters which are defined by the following formulae

$$Sensitivity = \frac{No. of TP}{No. of TP + No. of FN} \quad (11)$$

$$Specificity = \frac{No. of TN}{No. of TN + No. of FP} \quad (12)$$



$$Accuracy = \frac{(TP + TN)}{TP + TN + FP + FN} \tag{13}$$

$$MCC = \frac{TP.TN - FP.FN}{\sqrt{(TP + FP)(TP + FN)(TN + FP)(TN + FN)}} \tag{14}$$

$$F1-Score = 2 \cdot \left(\frac{precision * recall}{precision + recall} \right) \tag{15}$$

Where,

$$Precision = \frac{TP}{(TP + FP)} \tag{16}$$

$$Recall = \frac{TP}{(TP + FN)} \tag{17}$$

Here TP - True Positive, TN - True Negative, FP- False Positive, FN-False Negative

Metrics	MMBO-DNN (%)	MBO-DNN (%)	PSO-DNN (%)	GA-DNN (%)
Sensitivity	75.4	71.0	67.0	60.3
Specificity	93.4	90.2	85.0	75.1
Accuracy	96.4	93.1	87.0	82.7
MCC	74.8	70.3	65.1	62.6
F1-Score	77.4	71.5	66.2	64.5

Table 1 Performance comparison of algorithms

Table 1 shows that MMBO-DNN achieves higher accuracy and performance in comparison of other algorithms. The accuracy score of MMBO-DNN is 96%, whereas the accuracy of MBO-DNN is 93%, accuracy of PSO-DNN is 87% and accuracy GA-DNN is 82%.

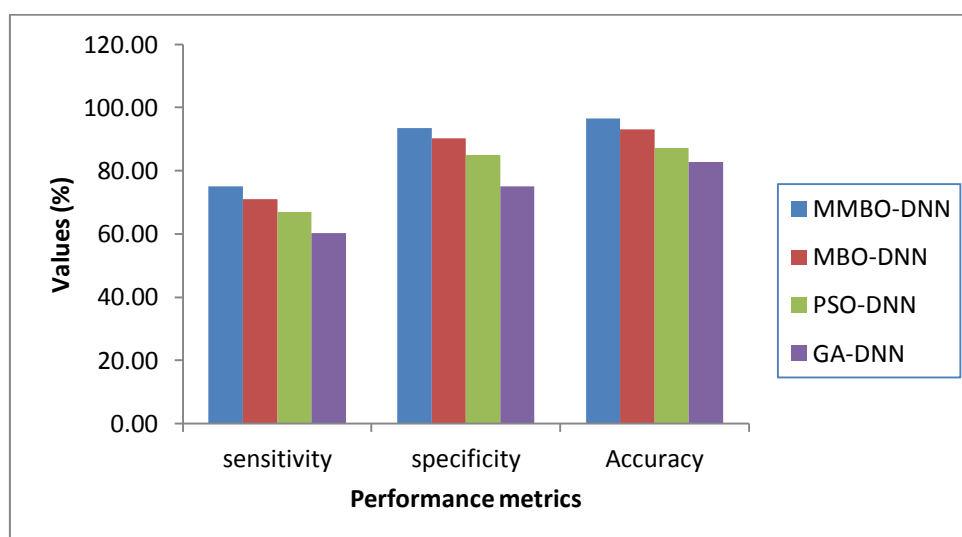


Figure 9 Performance comparison of Accuracy, sensitivity and specificity



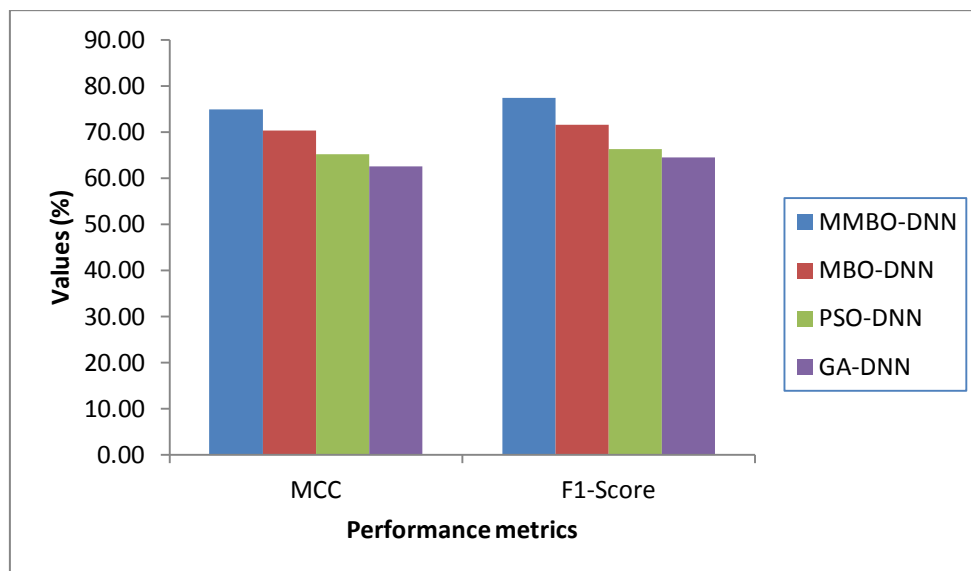


Figure 10 Performance comparison of MCC and F1-Score

Figure 9 and 10 shows the classification accuracy of all the algorithms.

Figure 9 states that MMBO-DNN attains the highest Sensitivity around 75%, MBO-DNN attains around 71%, PSO-DNN attains around 67% and GA-DNN attains around 60%. The Specificity of MMBO-DNN is about 93%, Specificity of MBO-DNN is about 90%, Specificity of PSO-DNN is about 85% and Specificity of GA-DNN is about 75%.

It can be seen from Figure 10 that MMBO-DNN attains the highest MCC score around 74% whereas the MCC of MBO-DNN is around 70%, MCC of PSO-DNN is around 65% and MCC of GA-DNN is around 62%. Similarly, MMBO-DNN attains highest F1-score around 77%, F1-score of MBO-DNN is around 71%, F1-score of PSO-DNN is around 66% and F1-score of GA-DNN is around 64%.

5. Conclusion

This paper proposes an optimal feature reduction and classification model for diagnosing lung cancers. For feature reduction, the various optimization techniques like Genetic Algorithm (GA), Particle Swarm Optimization (PSO), Monarch Butterfly Optimization (MBO) and Modified Monarch Butterfly Optimization (MMBO) are applied. After feature reduction, for classifying the disease, Deep Neural Network

(DNN) is utilized. Experimental results have shown that MMBO-DNN method outperforms MBO-DNN, GA-DNN and PSO-DNN in terms of accuracy, sensitivity, specificity and F1-score

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