Egyptian Informatics Journal 24 (2023) 241–255

Contents lists available at ScienceDirect

Egyptian Informatics Journal

journal homepage: www.sciencedirect.com

Full length article

An improvised nature-inspired algorithm enfolded broad learning system for disease classification

Pournamasi Parhi [a,*], Ranjeeta Bisoi [b], Pradipta Kishore Dash [b]

[a] Department of Computer Science Engineering, Siksha 'O' Anusandhan Deemed to be University, Bhubaneswar, Odisha, India
[b] Multidisciplinary Research Cell, Siksha 'O' Anusandhan Deemed to be University, Bhubaneswar, Odisha, India

ARTICLE INFO

Article history:
Received 22 August 2022
Revised 9 March 2023
Accepted 23 March 2023
Available online 31 March 2023

Keywords:
Genomic data
High dimensionality
Notable genes
Feature extraction
Kernel fisher score
Classification
Broad learning system
Sine–cosine
Improvised monarch butterfly optimization

ABSTRACT

Deep analysis of genomic data reveals that many deadly diseases are generated due to genetic mutation. To make the health care system more robust, a machine learning researcher's prime intention is to classify the genomic data more efficiently within less time. As the genomic data suffers from the malediction of excessive dimensionality, the selection of the notable genes is always a big challenge for the researcher. The selection of prominent genomic key attributes by any nature-inspired learning algorithm always remains a non-deterministic polynomial-time (NP-Hard) problem. Therefore, there is always a scope to apply new algorithms. In this projected work, an improvised sine–cosine hybridized Monarch Butterfly Optimization (SC-MBO) algorithm, is embedded with the Broad Learning System (BLS), which is defined as SC-MBO-BLS, for choosing the most significant genes and classifying the genomic data simultaneously. Initially, Kernel-based Fisher Score (K-FS) is applied to select notable genes. Then, the selected genes further undergoes for execution using the SC-MBO-BLS model. To prove the effectiveness of the suggested model, ten cancerous genomic data are considered. Here, several performance evaluators (i.e., precision, MCC, sensitivity, Kappa, F-score, and specificity) are applied for unbiased comparison. This presented model is compared with SC-MBO wrapped Multilayer Perceptron (SC-MBO-MLP), SC-MBO wrapped Extreme Learning Machine (SC-MBO-ELM), and SC-MBO wrapped Kernel Extreme Learning Machine (SC-MBO- KELM) and yields the highest accuracy in ten datasets such as 100%, 98.4%, 99%, 99.6%, 100, 97.2%, 100%, 100%, 98.6%, 99.5% in Leukemia, Colon tumor, Breast cancer, Ovarian cancer, Lymphoma-3, MLL, ALL-AML-3, SRBCT, ALL-AML-4 and Lung cancer respectively. Further, the existing twenty standard models are taken for comparison with the suggested model. Additionally, to assess the presented model, a statistical method i.e., Analysis of variance (ANOVA) is considered. As per the above quantitative and qualitative estimation, it is deduced that the suggested SC-MBO-BLS approach outclasses other considering models.

1. Introduction

Spending a lot of time and money on genetic research, it has been disclosed that genetic mutation is the root cause of all diseases [1]. In this era of machine learning, researchers' main focus is to detect these mutated genes quickly and proficiently. If these genes are detected in their initial stage, then diseases can be treatable easily. To make the health care system more efficient, a robust classification model is required to classify the genetic data accurately with less computational complexity. Now-a-days, with the development of technology, DNA microarray tools provide the facility to monitor the expression levels of various malignant and healthy genes in one experiment. Several genes provide inconsistent and noisy signals throughout the whole samples. Therefore, it is a time taking job to analyze all genes as a whole with a small sample size. As a result, a specific analysis is needed to identify the genes which indicate the patterns of expression interrelated with the disease state. So, an artificial intelligence-based diagnostic system has high significance in this genetic research. In the burgeoning of machine learning in various research areas, researchers take the help of various classification techniques to classify the high dimensional microarray data [1]. Moreover, the gene expression datasets are high dimensional datasets having huge numbers of genes or features but with very fewer numbers of samples. This creates a great drawback in classifying these datasets. Thus, it is always a big challenge for researchers to select the most significant genes in the high

* Corresponding author.

https://doi.org/10.1016/j.eij.2023.03.004
1110-8665/

dimensional microarray data that can help to reduce the computational cost with classificational complexity [2]. Especially two methods are adopted by the researchers to select the significant genes i.e., feature selection and feature extraction. According to the feature extraction technique, the high dimensional feature set is transformed into a reduced lower dimensional feature set by using various linear and nonlinear methods [3]. In the case of the feature selection approach, a subset of the most significant attributes is picked up from the high dimensional microarray data by reducing the irrelevant features which have minimal impact on the performance of the learning model. The drawback of the feature extraction technique is the possibility of losing some useful data due to the total transformation of the actual data. Therefore, in this presented work both feature extraction and feature selection are considered for the betterment of the learning rate.

Additionally, the attribute selection [4], technique is divided of especially three types i.e., Filter, wrapper, and hybrid approach. According to the filter feature selection approach, each feature of the data set is evaluated by applying a statistic measure, then the subset of the most significant feature is selected. But in the wrapper approach, a classifier is used to select the most vital subset of features and here classification accuracy is considered to evaluate the most significant feature subset. Though a learning algorithm is considered to evaluate the best feature subset in the wrapper approach so the effectiveness of the wrapper approach is more than the filter approach but the filter approach is also widely accepted due to its less evaluation cost. In the case of the wrapper feature selection method, the combination of metaheuristic and machine learning approach is used to select the global best feature subset.

Here, some enfolded approaches are elaborated like the genetic algorithm (GA) is wrapped with a support vector machine (SVM) to get the optimal feature subset of the microarray dataset [5].GA is wrapped with an Extreme learning machine (ELM) for cancer data classification [6]. Particle swarm optimization (PSO) is embedded with K-Nearest Neighbor (KNN) to select the most relevant feature subset of cancer biomedical data [7]. Metaheuristic algorithm like Genetic Bee Colony (GBC) and Ant Bee Colony (ABC) is used with an SVM classifier for cancer data feature selection [8,9].GA is wrapped with a Naïve Bayes classifier for gene selection of diabetes data [10]. Breast First Search (BFS) and the very well-known learning algorithm Artificial Neural Network (ANN) are used to select features and classify the colon data [11]. The metaheuristic Bat algorithm (BA) is embedded with the optimum path forest algorithm (OPF) to select the features of medical data [12]. Cat swarm optimization (CSO) is wrapped with a very well-known Kernel extreme learning machine (KELM) for the feature selection of medical data [13]. Adaptive genetic algorithms and mutual information are coupled together for the feature selection of biomedical data [14]. Though in the wrapper approach classification accuracy is considered a key factor for feature selection so it has more possibilities of obtaining better performance than the filter approach but it has some disadvantages over the filter approach as complex computation and data overfitting. So, by taking the advantage of both the wrapper and filter approach a new feature selection hybrid approach is formed. According to the hybrid strategy, the set of significant features is first chosen by using the filter feature selection technique, and then out of these selected features again a set of most significant features are selected by using the wrapper approach. For the last ten years, researchers are using both conventional and metaheuristic machine learning algorithms to classify various high-dimensional microarray data. The main driving force behind the researcher's exploration of numerous innovative strategies for better results is high classification performance and less evaluation time. SVM [15–17], ANN [18], KNN [20], Fuzzy Set Theory [19], multi-Layer perception [23], Functional Link Neural Network [21], Backpropagation [22], Radial Basis Function Neural Network [24], and others have all been introduced as a classifier to solve the problem.

The above-discussed classifiers are well-liked for their capacity to execute a variety of classification tasks. Deep learning is currently very famous among researchers for its efficiency in classification purposes. By increasing the number of layers in a neural network, classification performance is effectively promoted. However, the deep network takes a lot of time due to its intricate deep network. A single-layer feed-forward neural network [SLFNN] is better suited to address the challenges since it can solve regression and classification concerns [25–30]. As a learning algorithm, SLFNN is trained using the traditional gradient descent method [31,32]. However, it has several problems, including overfitting, poor convergence, and trapping in local minimums [33].

As a result, the Random-vector Functional-Link Neural Network (RVFLNN), a non-iterative learning technique, is introduced and shown to improve classification performance [29] and [34]. This technique can also get rid of the disadvantage of deep networks' immense training time. Therefore, RVFLNN requires relatively less training time. However, it has the flaw of not functioning effectively in massive, high-volume data [35]. As a result, a novel approach known as the Broad-learning-system (BLS) is suggested by using the idea of the single-layer feed-forward RVFLNN [36]. To improve classification accuracy, in the BLS concept, the input feature nodes are mapped to extended feature nodes that can form a large network. Though, here the input weights are selected at random. Therefore, the classification performance of the algorithm may be impacted. An optimization technique that improves the algorithm's performance and optimizes the input weight has been offered by researchers as a solution to this problem. Researchers have suggested several *meta*-heuristic algorithms [37,38] such as PSO [39] and [40], GA [44,45], Ant colony optimization (ACO) [39,40], Moth flame optimization (MFO) [42,43] and cuckoo search optimization [41] for optimizing weight and other parameters which can help improve the algorithm performance.

In this research work, the sine–cosine hybridized Monarch Butterfly Optimization algorithm (SC-MBO) is embedded with BLS (SC-MBO-BLS) for the notable gene selection and also for the classification of genomic data simultaneously. The basic MBO algorithm belongs to the swarm intelligence category which is based on the collective behaviors of self-organized and decentralized systems. MBO algorithm solves many complex optimization issues due to its efficiency and effectiveness. According to google scholar citation, the MBO algorithm [46] has been mostly applied in different fields of research. In population-oriented optimization methods, there is no certainty of getting a global optimum outcome in a single run. When the size of iterations (i.e., no. of optimization steps) and the random solutions increase, the possibility of getting a global optimum result also increases. Every stochastic population-oriented optimization algorithm has to follow the exploration and exploitation phases [47]. These two phases should be balanced properly while solving an optimization problem. Here, in the basic MBO algorithm, the position updating equations are modified using the sine–cosine function to get the optimum result.

By considering the specificity, sensitivity, F-score, and Matthews-correlation-coefficient (MCC) as the validation test, the superiority of the above suggested (SC-MBO-BLS) model is compared with that of other established methods such as SC-MBO wrapped multilayer perceptron (SC-MBO-MLP), SC-MBO wrapped Extreme Learning Machine (SC-MBO-ELM), and SC-MBO wrapped Kernel Extreme Learning Machine (SC-MBO-KELM).

This paper's primary objective is:

- To use kernel-based Fisher Score (K-FS) in the first stage of feature extraction.

- To provide a trustworthy classification model, specifically SC-MBO -BLS for classifying the highly dimensional gene expression data.
- To use minimum features to get high accuracy %.
- Other benchmark approaches like SC-MBO-MLP, SC-MBO-ELM, and SC-MBO-KELM are taken into consideration for comparison to demonstrate the superiority of the provided model.
- In the end, a statistical analysis i.e., the ANNOVA test, was conducted to determine the dominance of the proposed method over other common approaches.

The rest of the work has the following alignments in terms of appearance. The provided model is analyzed in section 2. The background approaches are covered in section 3. While the presented method is covered in section 4. Then the experimental setup is described in sections 5 and 6. Which include the experimentation and result validation sections, respectively. Finally, the conclusion is covered in section 7.

2. Overall analysis of the presented method

Fig. 1 shows the overall analysis of the presented method. Initially, normalize the dataset by using min–max normalization, then the 10-fold CV method is applied to separate the datasets into training samples and testing samples. In the first stage, the K-FS approach reduces the features of the datasets to 70%, then the SC-MBO-BLS algorithm is applied to find the global optimum feature subset with high classification accuracy.

3. Background approaches

In this part, all the supported background approaches are elaborated.

3.1. Broad learning system (BLS)

Fig. 2 depicts the existing architecture of BLS [36]. The initial attribute set $X \in R^{P\times Q}$ is mapped arbitrarily to the next feature nodes.

$$Z_n = \varnothing_n(XW_{tn} + \beta_{tn}), n = 1 \cdots\cdots p \tag{1}$$

In Eq. (1), $\varnothing_n$ describes the n^{th} mapping function, $and W_{tn}$ $and \beta_{tn}$ point out the random weight and the bias respectively. $Z_p = [Z_1 \cdots\cdots\cdots .Z_p]$ forms a new set of enhancement nodes i.e.,

$$H_l = \xi_l(Z^p W_{ht} + \beta_{hl}), l = 1 \cdots\cdots .q \tag{2}$$

$$H^q = [H_1 \cdots\cdots\cdots .H_q]$$

The resulted output is estimated as

$$\begin{aligned} Y &= [z_1 \cdots\cdots .z_p | \xi_1(z^p w_{h1} + \beta_{h1}) \cdots\cdots .. \xi_q(z^p w_{hm} + \beta_{hm})] w_p^q \\ &= [z_1 \cdots\cdots\cdots .z_p | H_1 \cdots\cdots .H_q] w_p^q \\ &= [z^p | H_q] w_p^q \end{aligned} \tag{3}$$

Here, the w_p^q is described by

$$w_p^q = [Z^p | H^q]^+ Y \tag{4}$$

Then, $A_p^q = [Z^p | H^q]$ and the connected weight W_p^q is estimated by L2 norm regularized least square problem.

$$W_p^q = argmin W_p^q : \|A_p^q W_p^q - Y\|_z^2 + \lambda \|W_p^q\|_z^2 \tag{5}$$

In Eq. (5), the constraint constant is λ.

$$W_p^q = \left(\lambda I + A_p^q A_p^{qT}\right)^{-1} A_p^{qT} Y \tag{6}$$

Here, A_p^{q+} is considered as the inverse of

$$A_p^q i.e., \lim_{\lambda} \left(\lambda I + A_p^q A_p^{qT}\right)^{-1} A_p^q \tag{7}$$

3.2. Existing MBO algorithm

This algorithm is based on two operators as migration operator and butterfly adjusting operator [46,47]. The entire population size, taken in this algorithm has been divided into two equal parts. In population 1, the best fitness value of half of the population is kept and the other half of the population is stored in population 2. The best outcome is considered the global best in each iteration

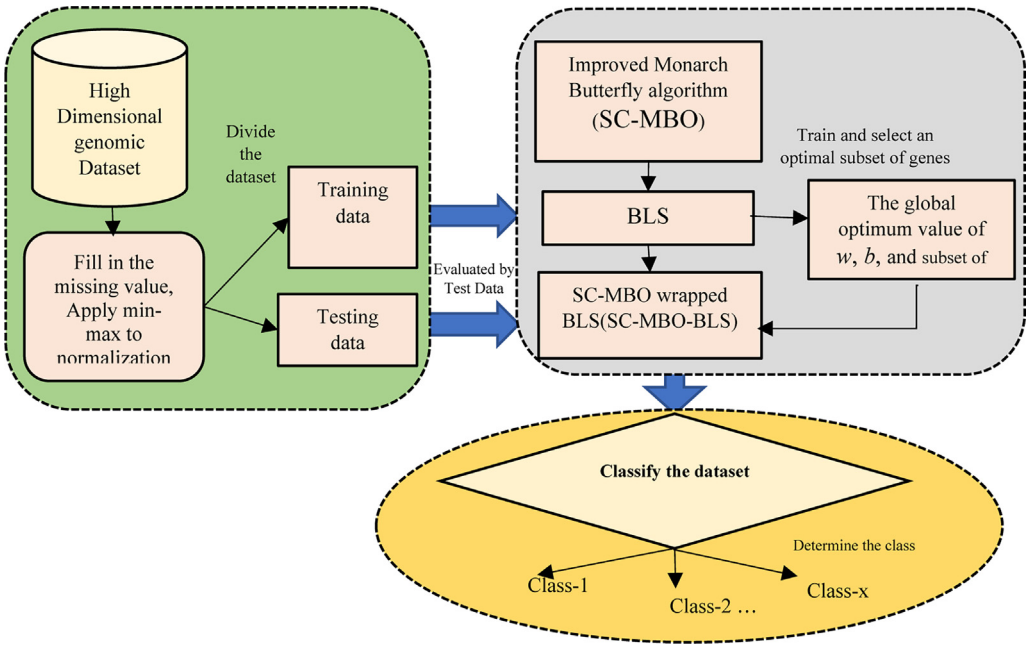


Fig. 1. Basic layout of the presented approach.

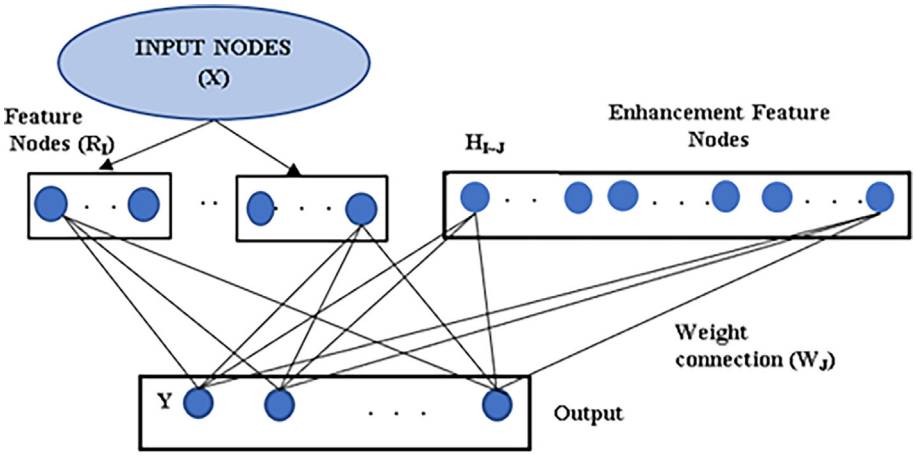


Fig. 2. The basic structure of BLS.

and the updated subpopulation is again mixed with the new population. This newly originated population is again split into 2 subpopulations according to the new fitness function and this procedure is continued till the stopping condition is reached. The pictorial view of the MBO is shown in Fig. 3.

3.2.1. Operator-I (Migration Operator)

By this operator, information is exchanged among both populations. In subpopulation 1, the updation of lth butterfly will be estimated as follows:

$$Y_{l,n}^{t+1} = \begin{cases} Y_{i1,n\,if\ \ r<p}^{t} \\ Y_{i2,n}^{t}\ else \end{cases} \tag{8}$$

In t + 1 generation, $Y_{l,n}^{t+1}$ points out the location of Y_l in lth dimension where l_1 and l_2 are the integer indexes arbitrarily selected among subpopulations 1 and 2. Here, r is considered as the multiplication of random real numbers between (0,1) and migration period.

3.2.2. Operator-II (Adjusting Operator)

The change of position of every butterfly in subpopulation 2 is estimated *based on p* (i.e., adjusting ratio) and *BAR* (i.e., the adjusting rate of butterfly)

$$Y_{l,n}^{t+1} = \begin{cases} Y_{best,n}^{t} if Rand \le p \\ Y_{i3,n}^{t} if Rand > p \Lambda Rand \le BAR \\ Y_{l,n}^{t} + \xi \times (dY_n - 0.5) if Rand > p \Lambda Rand > BAR \end{cases} \tag{9}$$

where $Y_{best,n}^{t}$ is taken as n^{th} element of the global at the current generation t, $Y_{i3,n}^{t}$ is the n^{th} element of the arbitrarily chosen butterfly among subpopulation 2. The weighted factor (ξ) will be estimated as follows:

$$\xi = Z_{max}/t^2 \tag{10}$$

Here, Z_{max} = max no. of walk step of each butterfly in every step and t shows the current generation.

In Eq. (11), dY_n points out the steps of each butterfly and this is estimated by applying Levy flight approach.

$$dx_n = Levy(x_n^t) \tag{11}$$

3.3. Sine-Cosine mechanism

The sine–cosine (SC) algorithm is developed for solving optimization issues by Mirjalili [49]. In this algorithm, the positions of the particles are upgraded by applying the sine and cosine mechanisms. This algorithm follows the below two equations (i.e., Eqs. (12) and (13)) to update the solutions.

$$A_{m,k}^{x+1} = A_{m,k}^{x} + a_1 \times \sin(a_2) \times a_3 \left| B_{m,k}^{x} - z_{m,k}^{x} \right|, a_4 < 0.5 \tag{12}$$

$$A_{m,k}^{x+1} = A_{m,k}^{x} + a_1 \times \cos(a_2) \times a_3 \left| B_{m,k}^{x} - z_{m,k}^{x} \right|, a_4 < 0.5 \tag{13}$$

Here, $A_{m,k}^{x}$ represents the current position at time $\times$, in the whole population, $B_{m,k}^{x}$ represents the location of the best solution,

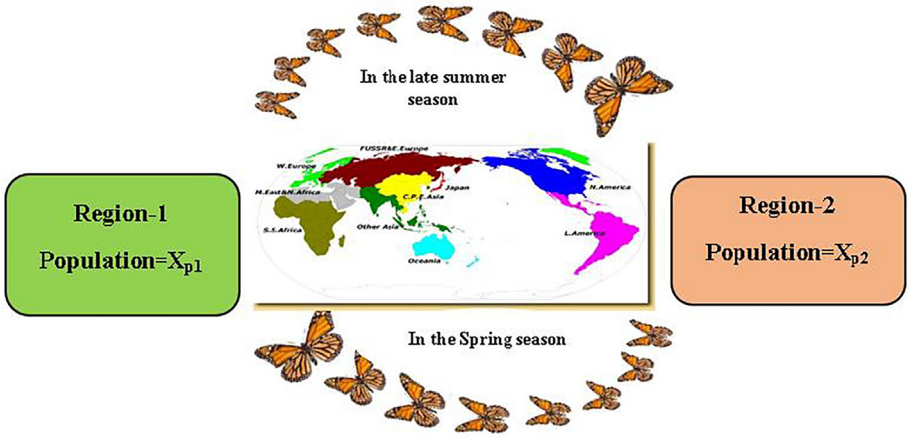


Fig 3. Pictorial view of the Monarch Butterfly.

a_1, a_2, and a_3 denote randomly generated numbers but a_4 is the random number generated between 0 and1.

The solution's next position will be placed among the current solution, then the desired point can be decided by applying a_1 (i.e., $a_1 < 1$, in the *exploitation phase*) or beyond this space (i.e., $a1 > 1$, in the *exploration phase*).

$$a_1 = l(1 - x/x_{max}) \tag{14}$$

In Eq. (14), x represents the current iteration, x_{max} denotes the maximum size of iteration, and in the distance formulation, a random weight is associated with the desired point to learn the impact of that point [49].

3.4. Sine-Cosine hybridized Monarch butterfly optimization (SC-MBO)

The reason behind the merging of MBO and SCA algorithms is described in this section. The prime benefit of SCA is its extraordinary exploration capacity. But in some cases, SCA fails in balancing between the exploitation and exploration phase which creates suboptimal results. In a few cases, SCA skips the global best solution and small exploitation happened. This mechanism reduces the search capability of the algorithm. Meanwhile, at the time of the search process, the MBO algorithm is quite efficient in balancing the exploration and exploitation phase. Further, like other evolutionary algorithms, MBO may be trapped at local optima. Therefore, a hybridization of the two algorithms namely the SC-based MBO (i.e., SC-MBO) algorithm is proposed here to resolve the above issues. The pseudo-codes SC-MBO are described in algorithm 1 and algorithm 2.

Algorithm 1: Migration operator (SC-MBO)

Start
for m = 1 to N1(no. of population (i.e., butterflies in Land1) present)
for k = 1 to j (no. of elements in m^{th} monarch butterfly)
r = rand * S, here, rand ∼ U (0,1)
if r ≤ q **then**
$A_{m,k}^{x+1} = A_{r_1,k}^{x+1}$ Here, $r_1 \sim$ U [1,2,3, …, N1] $A_{m,k}^{x+1} = A_{d_1,k}^{x}$ (15)
elseif rand () < 0.5
$$A_{m,k}^{x+1} = A_{x,k}^{x} + a_1 \times \sin(a_2) \times a_3 \left| B_{m,k}^{x} - A_{m,k}^{x} \right| \text{ (16)}$$
else
$$A_{m,k}^{x+1} = A_{m,k}^{x} + a_1 \times \sin(a_2) \times a_3 \left| B_{m,k}^{x} - A_{m,k}^{x} \right| \text{ (17)}$$
end if
end if
if r > q then
$A_{m,k}^{x+1} = A_{r_2,k}^{x+1}$ Here, $r_2 \sim$ U [1,2, 3, …, N1] (18)
elseif rand () < 0.5
$$A_{m,k}^{x+1} = A_{m,k}^{x} + a_1 \times \sin(a_2) \times a_3 \left| B_{m,k}^{x} - z_{m,k}^{x} \right| \text{ (19)}$$
else
$$A_{m,k}^{x+1} = A_{m,k}^{x} + a_1 \times \cos(a_2) \times a_3 \left| B_{m,k}^{x} - z_{m,k}^{x} \right| \text{ (20) } \textbf{end if}$$
end if
end for k
end for m
End

In the above pseudocode (i.e., Algorithm 1), $A_{m,k}^{x+1}$ shows the k^{th} element of A_m at × + 1 generation and denotes the m position of MB (i.e., monarch butterfly) in Land1. $A_{r_1,k}^{x}$ shows the k^{th} element of A_{r_1} in x$^{\text{th}}$ generation and denotes the currently changed position of r_1 MB. $A_{r_2,k}^{x}$ shows the k^{th} element of A_{r_2} in x$^{\text{th}}$ generation and denotes the currently updated position of r_2 MB.

Algorithm 2: Adjusting operator (SC-MBO)

Start
for n = 1 to N2(no. of population (i.e., butterflies in Land2) present)
for k = 1 to j (no. of elements in n^{th} monarch butterfly)
if r ≤ p **then,**
$A_{n,z}^{x+1} = A_{best,k}^{x}$ here *rand* ∼ *U (01)*(21)
elseif rand () < 0.5
$$A_{n,k}^{x+1} = A_{n,k}^{x} + a_1 \times \sin(a_2) \times a_3 \left| B_{n,k}^{x} - A_{n,k}^{x} \right| \text{(22)}$$
else
$$A_{n,k}^{x+1} = A_{n,k}^{x} + a_1 \times \sin(a_2) \times a_3 \left| B_{n,k}^{x} - A_{n,k}^{x} \right| \text{(23)}$$
end if
end if
if r>p then
$A_{n,k}^{x+1} = A_{r_3,k}^{x+1}$Here, r3 ∼ U [1,2, 3,…, N2](24)
elseif rand () < 0.5
$$A_{n,k}^{x+1} = A_{n,k}^{x} + a_1 \times \sin(a_2) \times a_3 \left| B_{n,k}^{x} - z_{n,k}^{x} \right| \text{(25)}$$
else
$$A_{n,k}^{x+1} = A_{n,k}^{x} + a_1 \times \cos(a_2) \times a_3 \left| B_{n,z}^{x} - z_{n,k}^{x} \right| \text{(26)}$$
end if
end if
if r> R
$A_{n,k}^{x+1} = A_{n,k}^{x} + \beta \times ((dc_k) - 0.5))$(27)
end
end for k
end for n
End

In the above pseudocode (i.e., Algorithm 2), $A_{n,k}^{x+1}$ shows the k^{th} element of A_n in × + 1 generation and denotes the n position of MB in Land2. $A_{r_3,k}^{x}$ shows the k^{th} element of A_{r_3} in x^{th} generation and denotes the currently updated position of r_3 MB. dc_k represents the walk step of n^{th} MB and will be calculated by applying Levy flight mechanism. Here, $\beta = IB_{max}/x$, where IB_{max} = no. of steps of each butterfly in single step.

3.5. Kernel-Fisher score

In the basic Fisher score (FS) feature extraction method, a feature is selected as per its score which is calculated according to Eq. (28). Initially, a M × N input matrix is taken where M point outs the number of genes and N presents the sample size. Then, in Kernel Fisher score (K-FS) [48] of each gene is computed and the mean value (i.e., a threshold value (THV)) is estimated. The gene with a higher score than THV will be kept in the feature space and the gene with a lower score than THV will be discarded.

$$GS(A_j) = \frac{\left(\bar{f}_j^{(+)} - \bar{f}_j\right)^2 + \left(\bar{f}_j^{(-)} - \bar{f}_j\right)^2}{\frac{1}{(n_+ - 1)}\sum_{x=1}^{n_+}\left(f_{x,j}^{(+)} - \bar{f}_j^{(+)}\right)^2 - \frac{1}{(n_- - 1)}\sum_{x=1}^{n_-}\left(f_{x,j}^{(-)} - \bar{f}_j^{(-)}\right)^2} \tag{28}$$

In the above Eq. (28), f_x is taken as the training vector, $\bar{f}_j$ is considered as the j^{th} attribute of the datasets, n_+ and n_- are assumed as the + ve and -ve instances, $\bar{f}_j^{(+)}$ is taken as the j^{th} attribute of the + ve value of the datasets and $\bar{f}_j^{(-)}$ is taken as the j^{th} attribute of the -ve value of the datasets. Likewise, $f_{x,j}^{(+)}$ is assumed as the

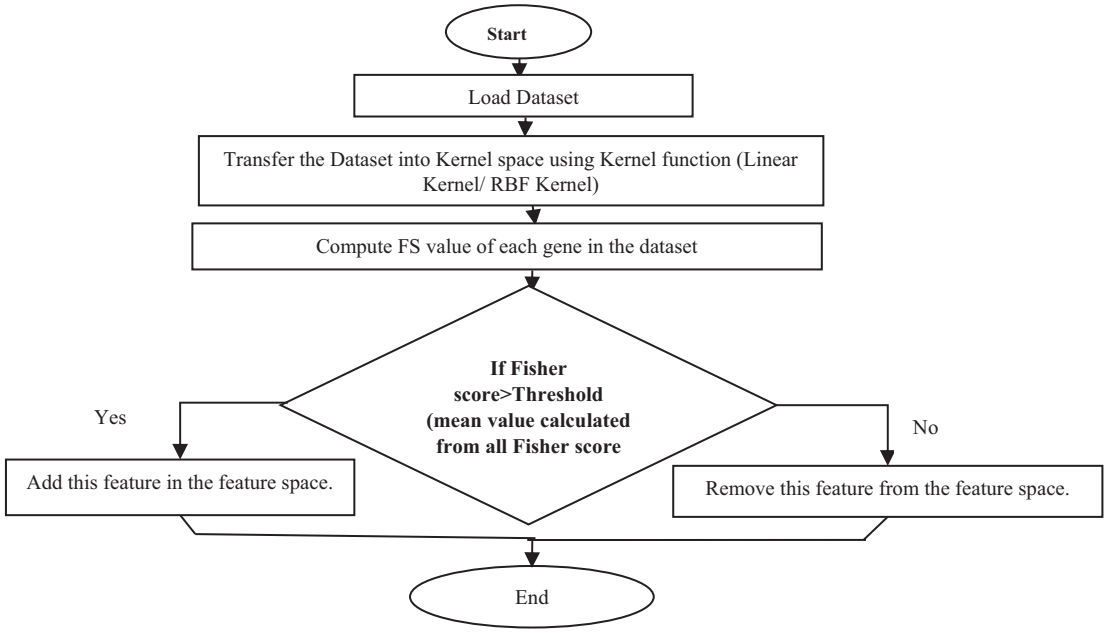


Fig. 4. Flow chart of KFS.

j^{th} attribute of the x^{th} + ve valued instances and $\bar{f}_j^{(-)}$ is assumed as the j^{th} gene or attribute of the x^{th}, -ve valued instances.

The mutual information between genes is not taken in standard FS. To avoid this demerit, K-FS [48] transforms non-linearly separable data into linearly separable data using a kernel function which decreases the computational overhead. The stepwise flow chart of K-FS is depicted in Fig. 4.

4. Suggested methods

4.1. Proposed SC-MBO-BLS algorithm

Initially, K-FS [48,49] approach is used to extract the most significant genes. In this method, each gene is associated with a rank. This technique selects up to 500 genes [50] among thousands of genes in the dataset. These preselected genes are forwarded to SC-MBO-BLS for getting the best gene subset.

In this presented approach, the **SC-MBO-BLS** technique is used to optimize the bias (b) and weight (w) of BLS and to find the optimum gene subset simultaneously. Fig. 5 and algorithm 3 give a complete framework of the presented model.

Let us consider, $X^j = \left\{w, b, X_1^j, X_2^j, X_3^j, \cdots., X_K^j\right\}$ as an individual solution with K dimensional attribute and j=$\{1, 2, 3, \cdots., K\}$. In this set of solutions, the first two bits are reserved for w and b and the other bits are considered as gene subsets. Here, 0 expresses the rejection and 1 expresses the selection of the genomic attribute subset. Therefore, X^j is shown as $X^j = [w, b, 1, 0, 0, \cdots.., 1]$.

By applying a logistic function, the value of every gene is expressed in Eq. (29)-(31)

$$x_p^q = \begin{cases} 1, logsig\left(x_p^q\right) > 0.5 \\ 0, otherwise \end{cases} \tag{29}$$

In Eq. (29),

$$logsig\left(x_p^q\right) = \frac{1}{1 + e^{\left(-y_k^m\right)}} \tag{30}$$

$$fit(value) = Acc(avg) = \frac{\sum_{i=1}^{10} test\_Acc_i}{10} \tag{31}$$

Algorithm:3	**Suggested SC-MBO-BLS**
Input:	Set size of population (P), ratio of migration RM, Peri (i.e., migration period), Adjusting Rate of Butterfly (AR), max step of walk of Levy flight Z_{max} and iteration size (IS), Fitness (f), Upper and Lower bound (i.e., UpB and LoB)
Output:	Classification accuracy percentage and the length of the subset of genes.
S1:	for each independent solution repeat step 2 and 3
S2:	By applying logistic function, the value of every gene is converted into 0 and 1. Here, 1 is considered as selection and 0 is considered as rejection of that particular gene.
S3.	Find out the fitness by applying w, b, and gene subsets
S4:	end for
5:	Keep aside the fitness values in descending order and select the best value and worst value.
6:	According to fitness value, set the population size (P).
7:	Identify the location of the best solution.
8:	Equate the mean of the fitness values.
9:	while X< IS do
10:	if X == 1 then
11:	for Y=1: P do
12:	Update w, b by using Eqs. (15) -(27).
13:	end for
14:	else if (meanFit_ curr_ solution – meanFit_prev_solution) / meanFit_ curr_ solution > .001
15:	Then
	Replicate steps 11 to step14
16:	Else
17:	break.
18:	end if
19:	end if
20:	for each single improved solution do
21:	Mark the LoB and UpB of the solution place, bias(b), and weight (w).
22:	Repeat steps 1 to 4 for getting the new values of fitness.
23:	if fit_current_sol > fit_previous_sol, then
24:	Upgrade the fitness value of the sol and its place, bias(b), and weight (w).
26:	Else
27:	Set out the prev_sol_ fit.
28:	Store the solution place, bias(b), and weight (w)..
29:	end if
30:	Replicate the step 5 to step8
31:	end for
32:	end while
33:	Get the concluding result as CA (classification accuracy) % with the feature subset length.

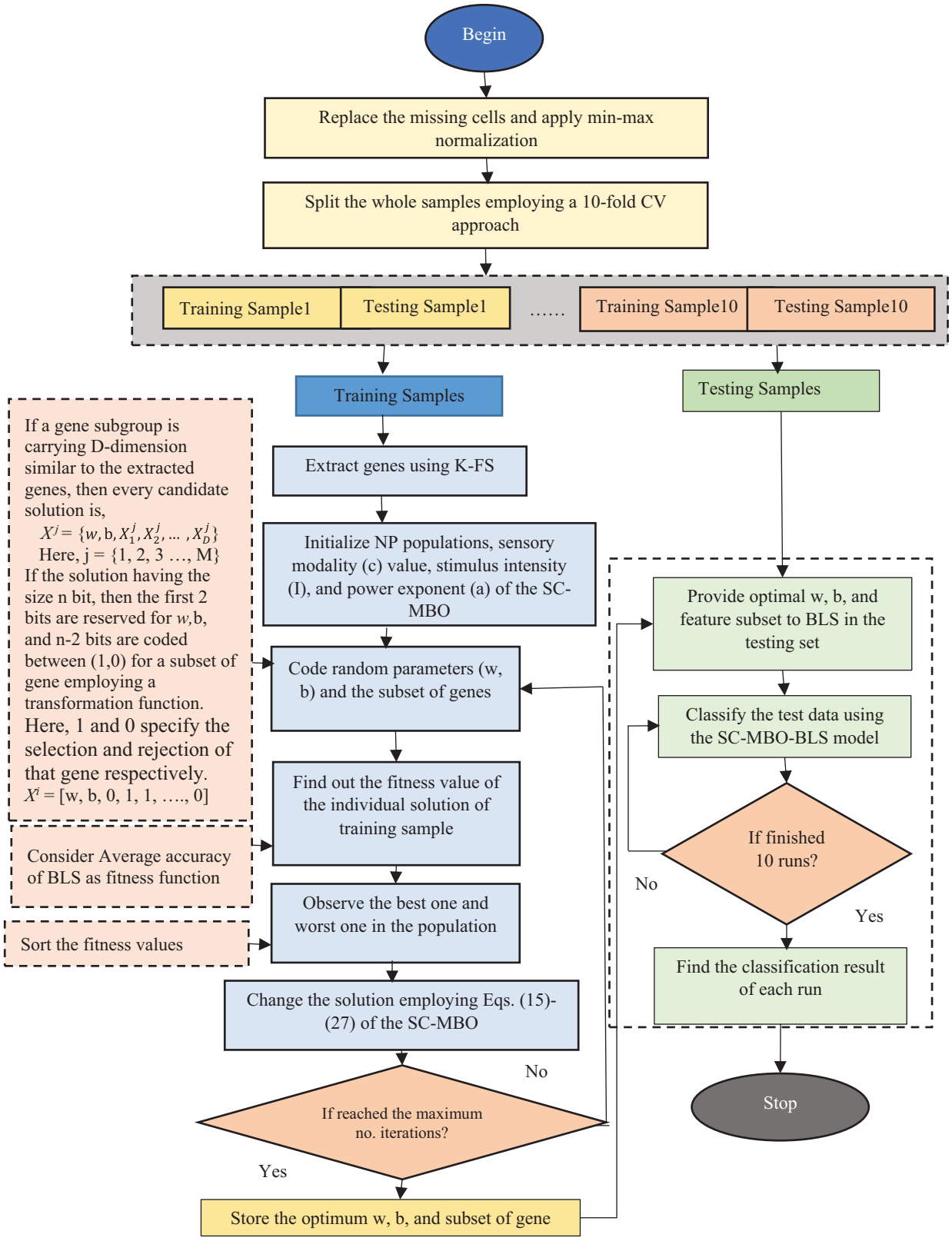


Fig. 5. Pictorial representation of the SC-MBO-BLS model.

Table 1
Explanation of 10 standard datasets.

Datasets	Dimensions	Sample size	No. of Genes	Classes
Leukemia [51]	72 × 7129	72	7129	2
Colon tumor [52]	62 × 2000	62	2000	2
Breast cancer [53]	97 × 24482	97	24,482	2
Ovarian cancer [54]	253 × 15154	253	15,154	2
MLL [53]	72 × 12582	72	12,582	3
Lymphoma-3[55]	62 × 4026	62	4026	3
SRBCT [56]	88 × 2308	88	2308	4
ALL-AML-3 [57]	72 × 7129	72	7129	3
ALL-AML-4 [53]	72 × 7129	72	7129	4
Lung cancer [55]	203 × 12600	203	12,600	5

Table 2
Default Parameter value taken in all the algorithms.

MLP	ELM	KELM	BLS	Sine-Cosine	MBO
No. of Iterations (Max) = 100Number of HL (Hidden Layers) = 3Number of HN (Hidden Nodes) in every layer = 5	Default size of population = 100 Default size of max iterations = 100 w =rand (0,1) b = rand (0,1)	Default size of max iterations = 100 C and γ value = [2–7, 2–8, . . ., 27, 28]	No. of iterations (Max) = 100We (coefficients of feature nodes) =rand (0,1) W_h (coefficients of enhancement nodes) = rand (0,1) b = rand (0,1) Enhancement Nodes = 100N1 (number of feature nodes per window) = 100N2 (number of windows of feature nodes) = 100	Default size of population = 100 Default size of max iterations = 100Constant (l) = 3.0 a_1 = 20 a_2 = rand(0,2π) a_3 = 20 a_4 = rand (0,1)	Population size = 100 Default size of max iterations = 100 Default period of migration = 1.2 Default ratio of migration = 5/12AR (Default Adjusting rate) = 5/12 Default size of max generation = 100 Default size of max step walk = 1

5. Experimental details

5.1. Execution environment

The whole work is carried out under the following execution environment:

CPU: Intel(R) Core (TM), Processing speed of CPU is 2 GHz, OS used: Windows 10, Language: MATLAB, version- R2020A and Random Access Memory: 8 GB DDR2 RAM.

5.2. Detailed description of used dataset

The detailed elaboration of the used datasets is shown in Table 1.

5.3. Default parameters

The default values of the all models parameters are described in Table 2.

5.4. Model evaluation parameters

$$Sensitivity(Sn) = \text{True Positive (TP)} / (\text{True Positive (TP)} + \text{False Negative(FN)}) \quad (32)$$

$$Specificity(Sp) = \text{True Nagative(TN)} / (\text{True Nagative(TN)} + \text{False Positive}(FP)) \quad (33)$$

- Precision (Pr):

$$Pr = TP/(TP + FP) \quad (34)$$

- **F-Score (Fs)**:

$$Fs = \frac{2 \times Pr \times Sn}{Pr + Sn} \quad (35)$$

Table 3
K-FS extracted eminent genomic attributes and its accuracy percentage in three binary datasets.

Dataset	# Eminent Genes	ACC percentage
Leukemia	5	75.76
	10	83.19
	50	94.62
	100	97.32
	200	**98.82**
	500	98.57
Colon tumor	5	73.62
	10	78.58
	50	86.26
	100	88.7
	200	**89.72**
	500	87.82
Breast Cancer	5	85.62
	10	90.12
	50	93
	100	96.72
	200	**97.62**
	500	96.8
Ovarian cancer	5	82.63
	10	92.82
	50	96.75
	100	**98.85**
	200	97.7
	500	97.85

Table 4
K-FS extracted eminent genomic attributes and its accuracy percentage in three multi-class datasets.

Datasets	# Eminent Genes	ACC percentage
Lymphoma-3	5	80.82
	10	96.15
	50	96.74
	100	98.2
	200	**100**
	500	99.82
MLL	5	79.96
	10	85.21
	50	88.9
	100	94.77
	200	**97.85**
	500	97.65
ALL-AML-3	5	52.86
	10	51.2
	50	89.8
	100	94.46
	200	93.78
	500	**94.86**
SRBCT	5	59.97
	10	66.83
	50	89.53
	100	98.48
	200	**100**
	500	100
ALL-AML-4	5	64.83
	10	68.36
	50	88.98
	100	92.64
	200	93.82
	500	**94.9**
Lung cancer	5	86.56
	10	91.5
	50	92.45
	100	94.3
	200	95.07
	500	95.62
	1000	**95.86**
	1200	95.2
	1500	95

- **Matthews correlation coefficient (MCC):**

$$MCC = \frac{(TP \times TN) - (FP \times FN)}{\sqrt{(TP + FP)(TP + FN)(TN + FP)(TN + FN)}} \tag{36}$$

- **Kappa (Kpa)**:

$$Kappa(Kpa) = \frac{(Observed\_Acc - Expected\_Acc)}{(1 - Expected\_Acc)} \tag{37}$$

$$Observed\_Acc = \frac{TP + TN}{TP + FP + TN + FN} \tag{38}$$

$$Expected\_Acc = \frac{\frac{(TP+FN)\times(TP+FP)}{TP+FP+TN+FN} + \frac{(FP+TN)\times(FN+TN)}{TP+FP+TN+FN}}{TP + FP + TN + FN} \tag{39}$$

6. Result discussion

6.1. Pre-extraction of notable genes

Initially, K-FS approach is used to pre-extract the notable genes. The most prominent *N* number of genes (i.e., upto1500 genes) are extracted from the thousand's genes of the entire dataset. Tables 3 and 4 illustrate topmost extracted genes and its accuracy % of all the datasets.

6.2. Results obtained from SC-MBO-BLS

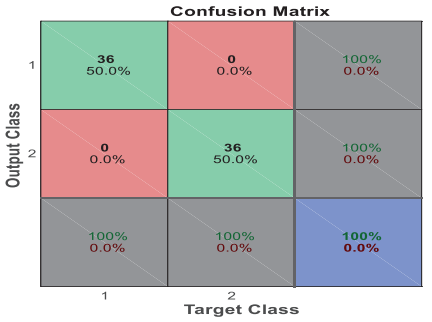
By using K-FS pre-extraction approach, 100 prominent attributes of Ovarian, 200 prominent attributes of Leukemia, colon tumor, breast cancer, Lymphoma, MLL, and SRBCT, 500 prominent attributes of ALL-MLL3, ALL-MLL4 and 1000 prominent attributes of Lung cancer are extracted. These extracted genes are then forwarded to SC-MBO-BLS model.

In Table 5, all performance evaluators of ten microarray datasets like acc%, sensitivity, precision, F-Score, MCC, specificity, and Kappa are noted. According to Table 5, it is observed that Leukemia, Lymphoma-3, SRBCT, and ALL-AML-3 datasets outperform the others by resulting 100% accuracy. Here, negative samples of Leukemia, Colon, Breast cancer, and Lymphoma-3 are very well classified by giving a specificity rate 100%. Similarly, positive samples of Leukemia, Ovarian, SRBCT, and ALL-AML-4 are very well classified by giving a sensitivity rate 100%. The confusion matrix of all ten datasets is illustrated in Fig. 6(a)-4(j).

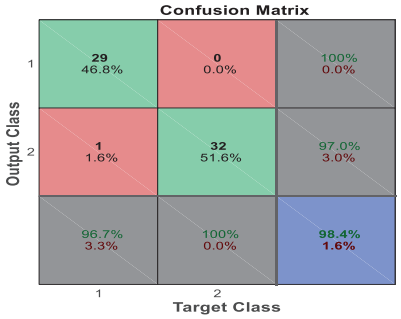
Here, the convergence graph of SC-MBO-MLP, SC-MBO-ELM, SC-MBO-KELM, and SC-MBO-BLS approaches in ten-microarray datasets are depicted in Fig. 7(a)-4(j). It is noted that the accuracy percentages of ten datasets are incremented continuously up to 100 iterations. In the case of Leukemia, the accuracy is converging after the 50^{th}, 55^{th}, 84^{th}, and 89^{th} iterations in SC-MBO-BLS, SC-MBO-KELM, SC-MBO-ELM, and SC-MBO-MLP models respectively. In Colon, the accuracy is converging after 44^{th}, 66^{th}, 78^{th}, and 84^{th} iterations in SC-MBO-BLS, SC-MBO-KELM, SC-MBO-ELM, and SC-MBO-MLP models respectively. In Breast cancer data, the accuracy is converged after 44^{th}, 65^{th}, 73^{th}, and 80^{th} iterations in SC-MBO-BLS, SC-MBO-KELM, SC-MBO-ELM, and SC-MBO-MLP models respectively. In Ovarian cancer data, the accuracy is converged after 54^{th}, 70^{th}, 74^{th}, and 80^{th} iterations in SC-MBO-BLS, SC-MBO-

Table 5
Noted performance evaluating parameter's value (in %) of the SC-MBO-BLS.

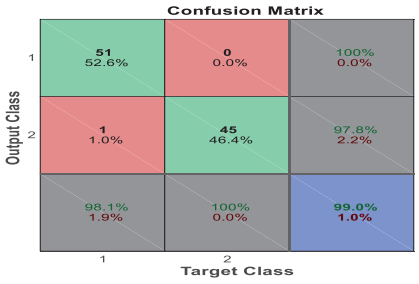
Types of Datasets	Dataset	Acc	Sen	Spe	MCC	F-measure	Kappa
Binary class	Leukemia	100	100	100	100	98.83	94.32
	Colon tumor	98.4	96.67	100	96.82	98.31	96.77
	Breast cancer	99	98.08	100	97.95	99.03	97.93
	Ovarian cancer	99.6	100	99.16	99.21	99.63	99.21
Multi-class	Lymphoma-3	100	99.97	100	99.98	100	100
	MLL	97.2	96.43	97.73	94.16	96.43	94.16
	ALL-AML-3	100	99.98	100	100	100	100
	SRBCT	100	100	100	100	100	100
	ALL-AML-4	98.6	100	97.22	97.26	98.63	97.22
	Lung cancer	99.5	99.09	100	99.02	99.54	99.01



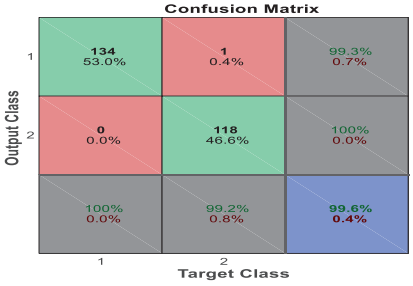
(a) Leukemia



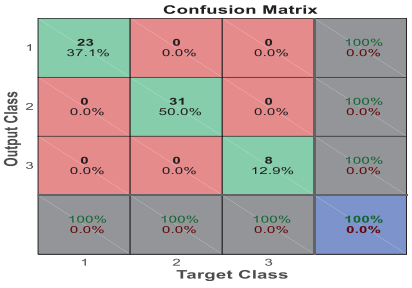
(b) Colon



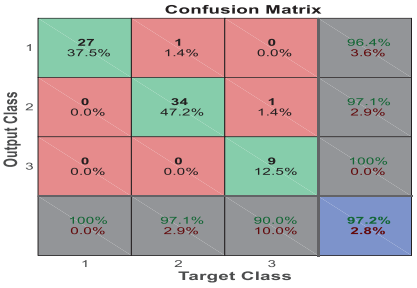
(c) Breast cancer



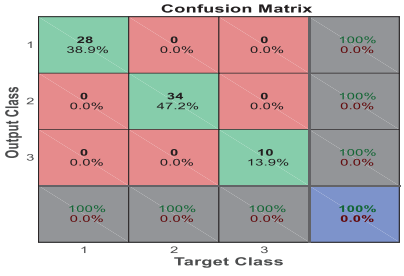
(d) Ovarian



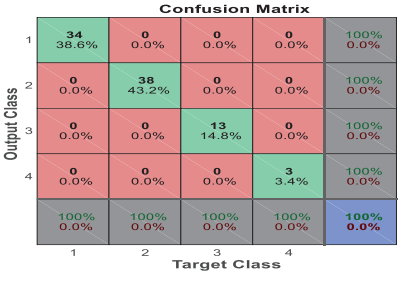
(e) Lymphoma



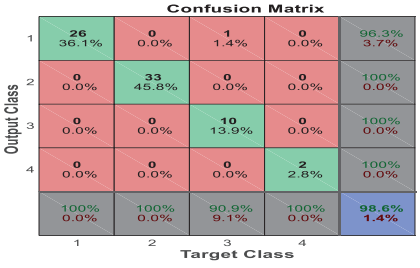
(f) MLL



(g) ALL-MLL-3



(h) SRBCT



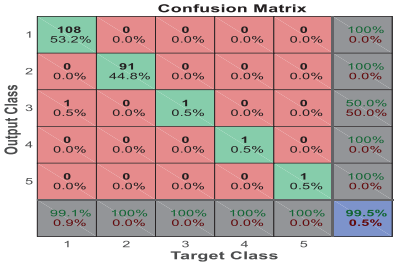
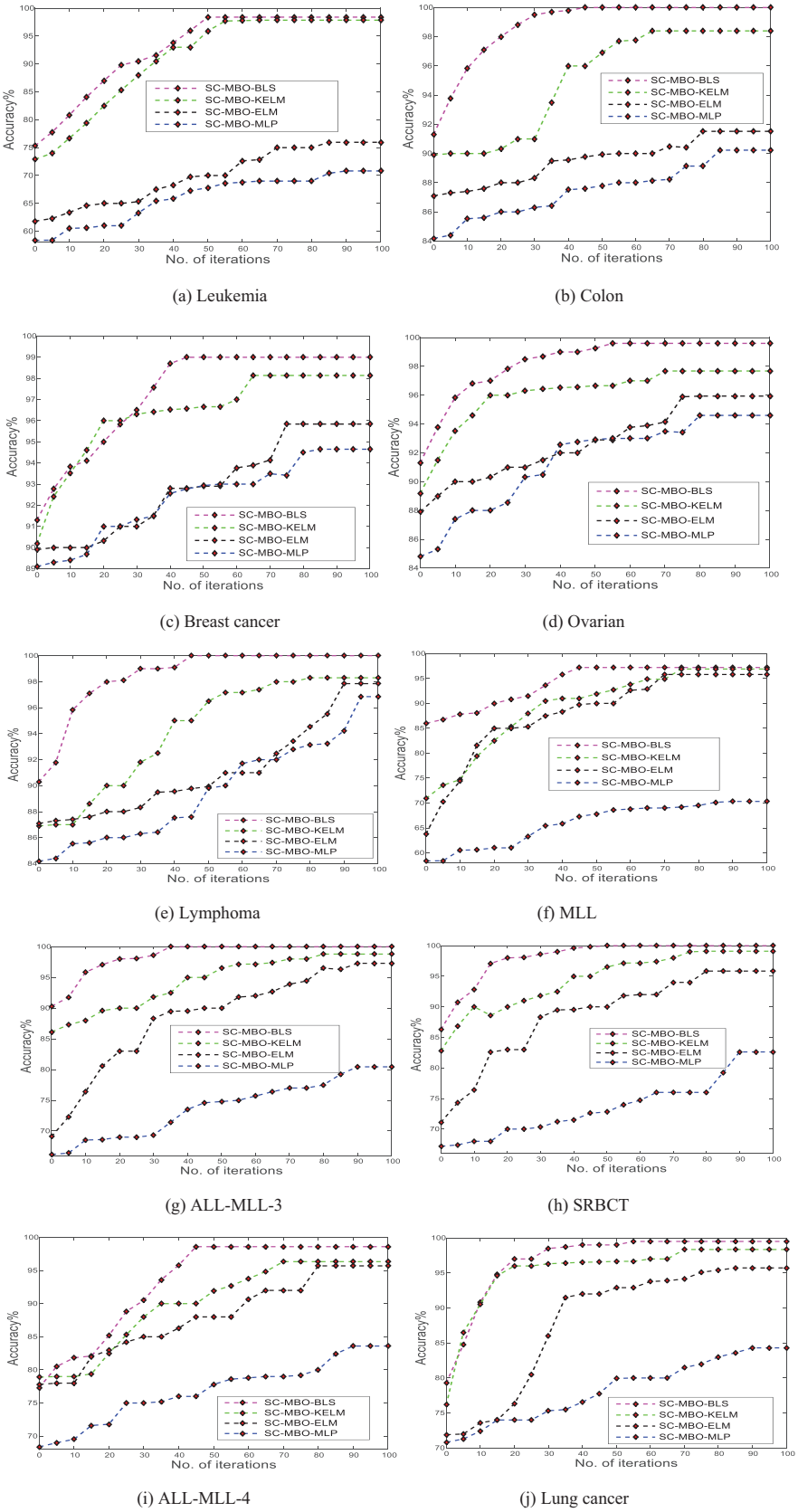


Fig. 6. Confusion matrix of ten microarray dataset.



(a) Leukemia (b) Colon

(c) Breast cancer (d) Ovarian

(e) Lymphoma (f) MLL

(g) ALL-MLL-3 (h) SRBCT

(i) ALL-MLL-4 (j) Lung cancer

Fig. 7. Convergence graphs of ten microarray datasets.

Table 6
ACC% comparison between all the approaches.

Datasets	SC-MBO-MLP	SC-MBO-ELM	SC-MBO-KELM	SC-MBO-BLS
Leukemia	90.23	91.52	98.4	100
Colon tumor	70.82	75.96	97.85	98.4
Breast cancer	94.65	95.89	98.12	99
Ovarian cancer	95.94	97.68	98	99.6
Lymphoma-3	96.98	97.85	98.3	100
MLL	70.32	95.8	96.9	97.2
ALL-AML-3	80.45	97.3	98.8	100
SRBCT	82.62	95.85	99.1	100
ALL-AML-4	83.6	95.7	96.34	98.6
Lung	84.3	95.72	98.35	99.5

Table 7
Notable genetic features selected bySC-MBO-BLS technique in four binary class microarray datasets.

Dataset	Name of the Gene	# Genes selected
Leukemia	Y00787_s_at X95735_at M23197_at	3
Colon tumor	M63391 H08393 Z50753 M26383	4
Breast cancer	Contig48393_RC Contig25534_RC N65982 AI830996	4
Ovarian cancer	MZ244.95245 MZ245.24466 MZ246.41524	3

KELM, SC-MBO-ELM, and SC-MBO-MLP models respectively. In Lymphoma-3 cancer data, the accuracy is being converged after 45^{th}, 75^{th}, 86^{th}, and 93^{rd} iterations in SC-MBO-BLS, SC-MBO-KELM, SC-MBO-ELM, and SC-MBO-MLP models respectively. In MLL cancer data, the accuracy is converged after 45^{th}, 70^{th}, 73^{th}, and 84^{th} iterations in SC-MBO-BLS, SC-MBO-KELM, SC-MBO-ELM, and SC-MBO-MLP models respectively. In ALL-AML-3 data, the accuracy is converged after 35^{th}, 74^{th}, 84^{th}, and 90^{th} iterations in SC-MBO-BLS, SC-MBO-KELM, SC-MBO-ELM, and SC-MBO-MLP models respectively. In SRBCT cancer data, the accuracy is being converged after 44^{th}, 76^{th}, 80^{th}, and 90^{th} iterations in SC-MBO-BLS, SC-MBO-KELM, SC-MBO-ELM, and SC-MBO-MLP models respectively. In ALL-AML-4 cancer data, the accuracy is being converged after 45^{th}, 70^{th}, 79^{th}, and 90^{th} iterations in SC-MBO-BLS, SC-MBO-KELM, SC-MBO-ELM, and SC-MBO-MLP models respectively. In Lung cancer, the accuracy is converging after 53^{th}, 64^{th}, 83^{th}, and 88^{th} iterations in SC-MBO-BLS, SC-MBO-KELM, SC-MBO-ELM, and SC-MBO-MLP models respectively.

Here, the suggested (SC-MBO-BLS) algorithm is compared with the other approaches like SC-MBO hybridized KELM, SC-MBO hybridized ELM, and SC-MBO hybridized MLP, to show a neutral comparison. This comparison is shown in Table 6. In the SC-MBO-BLS model, the discussed microarray dataset like Leukemia, Colon tumor, Breast cancer, Ovarian cancer, Lymphoma-3, MLL, ALL-AML-3, SRBCT, ALL-AML-4 and Lung cancer have performed 90.23%, 70.82%, 94.65%, 95.94%, 96.98%, 70.32%, 80.45%, 82.62%, 83.6%, and 84.3% accuracy respectively.

Table 8
Notable genetic features selected by the SC-MBO-BLS technique in six multi-class microarray datasets.

Multi-Class Dataset	Name of the Gene	# Genes selected
Lymphoma-3	GENE1622X GENE2403X GENE2152X	3
MLL	32847_ at 1389_ at 37539_ at 39931_ at	4
ALL-AML-3	X76223_s_at X59871_at M21624_at	3
SRBCT	gene 714 gene 1003 gene 2 gene 554	4
ALL-AML-4	M23197_at M92287_at M31303_rna1_at 37210_at	4
Lung cancer	36149_at 37478_at 36924_r_at 37210_at	4

6.3. Selected eminent genomic features by SC-MBO-BLS

In Tables 7 and 8, the highly influenced genes are noted which are selected by the SC-MBO-BLS algorithm. From Leukemia, 3 notable genes are selected. From colon, 4 notable genes are selected. From Ovarian, 3 notable genes are selected. Likewise, 4 key genes (i.e., Contig48393_RC, Contig25534_RC, N65982, AI830996) are chosen from Breast cancer, 3 key genetic features (i.e., GENE1622X, GENE2403X, GENE2152X) are chosen from Lymphoma-3, 4 key genetic features (i.e., 32847_ at, 1389_ at, 37539_ at, 39931_ at) are chosen from MLL, 3 key genetic features (i.e., M21624_at, X76223_s_at, X59871_at) are chosen from ALL-AML-3, 4 key genetic features (i.e., gene 2, gene 554, gene 714, gene 1003) are chosen from SRBCT, 4 key genetic features (i.e., M23197_at, M92287_at, M31303_rna1_at, 37210_at) are chosen from ALL-MLL-4, and 4 key genetic features (i.e., 36149_at, 37478_at, 36924_r_at, 37210_at) are chosen from Lung cancer.

6.4. Execution period of the SC-MBO-BLS

In Table 9, the execution time of both the K-FS part and SC-MBO-BLS part are noted down. The execution time of the presented model relies on the population size, size of iterations, size of samples, and fitness function cost. In Table 9, the execution time of both parts in Leukemia, Colon tumor, Breast cancer, Ovarian cancer, Lymphoma-3, MLL, SRBCT, ALL-AML-3, ALL-AML-4, and Lung

Table 9
Noted Execution Time (ET) of both K-FS part and SC-MBO-BLS part.

Dataset	ET of K-FS	ET of SC-MBO-BLS	Complete ET
Leukemia	0.192	168.125	168.317
Colon cancer	0.712	156.62	157.332
Breast Cancer	0.718	142.62	143.338
Ovarian	0.75	58.625	59.375
Lymphoma-3	0.625	60.312	60.937
MLL	0.625	143.62	144.245
SRBCT	0.165	172.283	172.448
ALL-AML-3	0.562	142.845	143.407
ALL-AML-4	0.714	190.82	191.534
Lung cancer	3.025	242.74	245.765

Table 10
A qualitative ndard models.

Existing approaches	Leukemia	Colon	Breast	Ovarian	Lymphoma-3	MLL	ALL-AML-3	SRBCT	ALL-AML-4	Lung
PSO-AKNN [7]	–	–	–	–	–		90.66 (3.3)	94(8.5)	–	–
IWSS-MB-NB [55]	97.1 (6.4)	86 (5.2)	–	–	–		–	–	–	–
DRFO-CFS [56]	91.18 (13)	90 (10)		100 (16)	–		–	–	–	–
mRMR-ABC [9]	–	–		–	96.96 (5)		96.12 (20)	96.30 (10)	–	–
CC-PSO[58]	–	–		–	96.8(306)		93.7(63)	–	–	–
8-SPMSO [59]	98.1(20)	94.2 (20)		–	–		–	–	–	–
GBC [8]	–	–	–	–	98.48(5)		95.83(8)	96.38(6)		
MCSO [13]	–	–		–	–		–	71.04(100)	–	–
FRQR [60]	97.22 (7)		–	99.60 (9)	–	–	–	–	–	99.45 (6)
GEM [5]	91.5 (3)	91.2 (8)		–	–		–	–		
BDE-XRankf [61]	82.4(6)	75(4)		95(3)	–		–	–	–	–
WCSSA-KELM [62]	99.0 (3)	95.5 (5)	94.3	100 (4)	99.71 (3)	–	99.38 (4)	100 (7)	–	98.90 (5)
CBFS-ISVM [63]	98.75 (3)	–	–	–	–	90.53 (3)	–	98.89 (5)	–	–
NB-ERGS [64]		82.86 (10) -		99.49 (2.8)		88.89 (10)	93.06 (10)	–	–	98.34 (10)
KNN-IGIS [65]	–	77.47 (5.3)	–	99.49 (2.8)	94.37 (3)	84.12 (7)	89.05 (4.7)	91.35 (8.3)	81.9 (6.1)	92.06 (12.4)
RMA-SVM [66]	91.67 (4)	–	–	–	–	95.83 (6)	–	97.59 (5)	–	–
DR-FS-MFMR [67]	31.94[10]	88.06 [40]	–	–	61.71[90]	–	–	–	–	
FS-DANI [68]	93.74 ± 3.21	–	62.49 ± 4.31	91.68 ± 3.55	–	–	–	–	–	
RFODL-MGEC [69]	–	94.74	–	98.68	–	–	–	–	–	
CDNC-ELM [70]	90.18	88.73	–	–	–	–	–	82.82	–	
FLAE-OFSP [71]	96.09	81.83	–	99.6	89.35	92.75	–	–	–	
SC-MBO-MLP	90.23 (14)	70.82 (15)	94.65 (17)	95.94 (12)	96.98 (14)	70.32 (18)	80.45 (13)	82.62 (11)	83.6 (18)	84.3 (15)
SC-MBO-ELM	91.52 (11)	75.96 (14)	95.89 (13)	97.68 (16)	97.85 (11)	95.8 (15)	97.3 (16)	95.85 (9)	95.7 (12)	95.72 (17)
SC-MBO-KELM	98.4 (12)	97.85 (10)	98.12 (10)	98 (9)	98.3 (8)	96.9 (7)	98.8 (13)	99.1 (10)	96.34 (10)	98.35 (16)
SC-MBO-BLS	100 (3)	98.4 (4)	99 (4)	99.6 (3)	100 (3)	97.2 (4)	100 (3)	100 (4)	98.6 (4)	99.5 (4)

Table 11
ANOVA Test comparison in terms of Acc%.

Dataset	SC-MBO-MLP	SC-MBO-ELM	SC-MBO-KELM	SC-MBO-BLS	Total
Number of datasets	10	10	10	10	40
∑X	849.91	939.27	980.16	992.3	2314.84
Mean	84.991	93.927	98.016	99.23	57.871
∑X2	89627.8639	92510.6243	96203.9338	98473.77	223434.3422
Standard deviation	0.303242317	0.8578973	0.886303184	0.933392855	0.745208914

Table 12
P-value estimation using anova test.

Source	SS	Df	MS	
Between-treatments	1246.41842	3	415.4728067	*f* value = 12.09611
Within-treatments	1236.515184	36	34.347644	*p* value = 0.030957
Total	2482.934	39		

cancer are 168.317, 157.332, 143.338, 59.375, 60.937, 144.245, 172.448, 143.407, 191.534, and 245.765 respectively.

6.5. Qualitative analysis

A qualitative based analysis has been made to show a neutral comparison. In Table 10, 16 standard models have been compared with K-FS based SC-MBO-BLS technique by its classification accuracy and selected genetic features.

From the above table, it is revealed that K-FS based SC-MBO-BLS performs better than others. Some model like DRFO-CFS and WCSSA-KELM [62] achieve 100% accuracy in Ovarian and SRBCT respectively but these models select a greater number of gene as compared to the proposed method.

6.6. A Statistic-based comparison in terms of classification accuracy

To find the mean value of the definite groups, a widely approved statistical evaluator i.e., ANOVA (Analysis of variance)

has been taken in this research experiment. ANOVA performs a statistical evaluation of the presented method. Usually, ANOVA is based on a null hypothesis. In this evaluating approach, initially, the F-value is computed, then the p-value is observed as per F-value. According to the p-value, it is finalized whether to observe or discard the alternative hypothesis. If the p-value is less than or equal to 0.05 (considering the significance level to 5%) then the null hypothesis is rejected, and the accuracies of all the techniques are dissimilar. Eventually, the statistical evaluation of the model through the ANOVA test is given in Tables 11 and 12. Here, the p-value is found as 0.0309. this value is smaller than the formerly taken p-value. So, the alternative hypothesis is dismissed and the presented method is more statistically significant than others.

7. Conclusion

In this presented research study, an optimization algorithm Sine-Cosine hybridized MBO is merged with an eminent classifier, viz., BLS to choose the most notable genetic features with enhanced classification results. In this study, to estimate the presented algorithm, ten microarray datasets are considered in which 4 datasets are binary and the other six are multiclass. In the first stage, a pre-extraction technique (Kernel-based FS) is applied to choose subsets of genes and then these extracted genetic feature subsets have to go through the SC-MBO-BLS model for further evaluation. Here, other performance evaluators like sensitivity, precision, specificity, F-score, Kappa, and MCC are taken for a neutral comparison. Moreover, to show the dominance of the suggested technique, some standard approaches like SC-MBO-MLP, SC_MBO-ELM, SC_MBO-KELM, and 16 standard models have been compared with K-FS based SC-MBO-BLS technique by its classification accuracy and selected genetic features. Eventually, to compute the mean value of the definite groups, a widely approved statistical evaluator i.e., ANOVA (Analysis of variance) has been taken in this research experiment. From the above statistical and quantitative study, it is concluded that the presented SC-MBO-BLS technique will be a trustworthy support for the detection of numerous diseases.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

References

[1] Aydadenta H, Adiwijaya A. A clustering approach for feature selection in microarray data classification using random forest. J Inf Process Syst 2018;14(5):1167–75.

[2] Wang H, Jing X, Niu B. A discrete bacterial algorithm for feature selection in classification of microarray gene expression cancer data. Knowl-Based Syst 2017;126:8–19.

[3] Bicciato S, Luchini A, Di Bello C. PCA disjoint models for multiclass cancer analysis using gene expression data. Bioinformatics 2003;19(5):571–8.

[4] Ang JC, Mirzal A, Haron H, Hamed HNA. Supervised, unsupervised, and semi-supervised feature selection: a review on gene selection. IEEE/ACM Trans Comput Biol Bioinform (TCBB) 2016;13(5):971–89.

[5] Hernandez JCH, Duval B, Hao JK. A genetic embedded approach for gene selection and classification of microarray data. In: European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics. Springer; 2007. p. 90–101.

[6] Shukla AK, Singh P, Vardhan M. A two-stage gene selection method for biomarker discovery from microarray data for cancer classification. Chemom Intel Lab Syst 2018;183:47–58.

[7] Kar S, Sharma KD, Maitra M. Gene selection from microarray gene expression data for classification of cancer subgroups employing PSO and adaptive K-nearest neighborhood technique. Expert Syst Appl 2015;42(1):612–27.

[8] Alshamlan HM, Badr GH, Alohali YA. Genetic bee colony (GBC) algorithm: a new gene selection method for microarray cancer classification. Comput Biol Chem 2015;56:49–60.

[9] H. Alshamlan, G. Badr, Y. Alohali, mRMR-ABC: A hybrid gene selection algorithm for cancer classification using microarray gene expression profiling, BioMedRes.Int.2015(2015)604910–604910.

[10] Choubey, Dilip Kumar, et al. "Classification of Pima indian diabetes dataset using naive bayes with genetic algorithm as an attribute selection." *Communication and computing systems: proceedings of the international conference on communication and computing system (ICCCS 2016)*. 2017.

[11] Akizur RM, Muniyandi RC. Feature selection from colon cancer dataset for cancer classification using artificial neural network. Int J Adv Sci Eng Inform Technol 2018;8(4-2):1387–93.

[12] Rodrigues D et al. A wrapper approach for feature selection based on bat algorithm and optimum-path forest. Expert Syst Appl 2014;41(5):2250–8.

[13] Mohapatra P, Chakravarty S, Dash PK. Microarray medical data classification using kernel ridge regression and modified cat swarm optimization-based gene selection system. Swarm Evol Comput 2016;28:144–60.

[14] Rani MJ, Devaraj D. Two-stage hybrid gene selection using mutual information and genetic algorithm for cancer data classification. J Med Syst 2019;43(8):1–11.

[15] Cristianini N, Shawe-Taylor J. An introduction to support vector machines and other kernel-based learning methods. Cambridge University Press; 2000.

[16] Ibrahim HT et al. A grasshopper optimizer approach for feature selection and optimizing SVM parameters utilizing real biomedical data sets. Neural Comput & Applic 2019;31(10):5965–74.

[17] Malathi V, Marimuthu NS, Baskar S. Intelligent approaches using support vector machine and extreme learning machine for transmission line protection. Neurocomputing 2010;73(10-12):2160–7.

[18] Zurada JM. Introduction to artificial neural systems, Vol. 8. St. Paul: West; 1992.

[19] Aydogan EK, Karaoglan I, Pardalos PM. HGA: hybrid genetic algorithm in fuzzy rule-based classification s high-dimensional problems. Appl Soft Comput 2012;12(2):800–6.

[20] Anagaw A, Chang Y-L. A new complement naïve Bayesian approach for biomedical data classification. J Ambient Intell Hum Comput 2019;10(10):3889–97.

[21] Naik B et al. A harmony search based gradient descent learning-FLANN (HS-GDL-FLANN) for classification. In: Computational Intelligence in Data Mining-Volume 2. New Delhi: Springer; 2015. p. 525–39.

[22] Heermann PD, Khazenie N. Classification of multispectral remote sensing data using a back-propagation neural network. IEEE Trans Geosci Remote Sens 1992;30(1):81–8.

[23] Al-Shargabi, Bassam, Feda Alshami, and Rami Alkhawaldeh. "Enhancing multi-layer perception for breast cancer prediction."*International Journal of Advanced Science and Technology*(2019).

[24] Fernández-Navarro F et al. Evolutionary generalized radial basis function neural networks for improving prediction accuracy in gene classification using feature selection. Appl Soft Comput 2012;12(6):1787–800.

[25] Guliyev NJ, Ismailov VE. A single hidden layer feedforward network with only one neuron in the hidden layer can approximate any univariate function. Neural Comput 2016;28(7):1289–304.

[26] Arulampalam G, Bouzerdoum A. A generalized feedforward neural network architecture for classification and regression. Neural Netw 2003;16(5-6):561–8.

[27] Pao Y-H, Takefuji Y. Functional-link net computing: theory, system architecture, and functionalities. Computer 1992;25(5):76–9.

[28] Samanta, Sourav, et al. "Haralick features based automated glaucoma classification using back propagation neural network."*Proceedings of the 3rd International Conference on Frontiers of Intelligent Computing: Theory and Applications (FICTA) 2014*. Springer, Cham, 2015.

[29] Igelnik B, Pao Y-H. Stochastic choice of basis functions in adaptive function approximation and the functional-link net. IEEE Trans Neural Netw 1995;6(6):1320–9.

[30] Huang G-B, Chen Y-Q, Babri HA. Classification ability of single hidden layer feedforward neural networks. IEEE Trans Neural Netw 2000;11(3):799–801.

[31] LeCun, Yann, et al. "Handwritten digit recognition with a back-propagation network."*Advances in neural information processing systems2* (1989).

[32] Denker, John S., et al. "Neural network recognizer for hand-written zip code digits."*Advances in neural information processing systems*. 1989.

[33] Shen Lu et al. Multiple empirical kernel mapping based broad learning system for classification of Parkinson's disease with transcranial sonography. 2018 40th Annual International Conference of the IEEE Engineering in Medicine and Biology Society (EMBC). IEEE; 2018.

[34] Pao Y-H, Park G-H, Sobajic DJ. Learning and generalization characteristics of the random vector functional-link net. Neurocomputing 1994;6(2):163–80.

[35] Chen CLP, Zhang C-Y. Data-intensive applications, challenges, techniques and technologies: a survey on Big Data. Inf Sci 2014;275:314–47.

[36] Chen CLP, Liu Z. Broad learning system: An effective and efficient incremental learning system without the need for deep architecture. IEEE Trans Neural Networks Learn Syst 2017;29(1):10–24.

[37] Lu H et al. A kernel extreme learning machine algorithm based on improved particle swam optimization. Memetic Comput 2017;9(2):121–8.

[38] Sayyad H, Manshad AK, Rostami H. Application of hybrid neural particle swarm optimization algorithm for prediction of MMP. Fuel 2014;116:625–33.
[39] Mansour IB, Alaya I, Tagina M. A gradual weight-based ant colony approach for solving the multiobjective multidimensional knapsack problem. Evol Intel 2019;12(2):253–72.
[40] Zhang H et al. Developing a novel artificial intelligence model to estimate the capital cost of mining projects using deep neural network-based ant colony optimization algorithm. Resour Policy 2020;66:101604.
[41] Mohapatra P, Chakravarty S, Dash PK. An improved cuckoo search based extreme learning machine for medical data classification. Swarm Evol Comput 2015;24:25–49.
[42] Yamany W et al. Moth-flame optimization for training multi-layer perceptrons. 2015 11th International computer engineering Conference (ICENCO). IEEE; 2015.
[43] Majhi SK. How effective is the moth-flame optimization in diabetes data classification. In: Recent Developments in Machine Learning and Data Analytics. Singapore: Springer; 2019. p. 79–87.
[44] Chang Y-T et al. Optimization the initial weights of artificial neural networks via genetic algorithm applied to hip bone fracture prediction. Adv Fuzzy Syst 2012;2012.
[45] Li H et al. Genetic algorithm for the optimization of features and neural networks in ECG signals classification. Sci Rep 2017;7(1):1–12.
[46] Wang G-G, Deb S, Cui Z. Monarch butterfly optimization. Neural Comput & Applic 2019;31(7):1995–2014.
[47] Mirjalili S. SCA: a sine cosine algorithm for solving optimization problems. Knowl- Based Syst 2016;96:120–33.
[48] Polat K, Güneş S. A new feature selection method on classification of medical datasets: Kernel F-score feature selection. Expert Syst Appl 2009;36 (7):10367–73.
[49] Kira K, Rendell LA. A practical approach to feature selection. In: Machine learning proceedings 1992. Morgan Kaufmann; 1992. p. 249–56.
[50] Cai H et al. Feature weight estimation for gene selection: a local hyperlinear learning approach. BMC Bioinf 2014;15(1):1–13.
[51] Golub TR, Slonim DK, Tamayo P, Huard C, Gaasenbeek M, Mesirov JP, et al. Molecular classification of cancer: class discovery and class prediction by gene expression monitoring. Science 1999;286(5439):531–7.
[52] Alon U, Barkai N, Notterman DA, Gish K, Ybarra S, Mack D, et al. Broad patterns of gene expression revealed by clustering analysis of tumor and normal colon tissues probed by oligonucleotide arrays. Proc Natl Acad Sci 1999;96 (12):6745–50.
[53] http://csse.szu.edu.cn/staff/zhuzx/Datasets.html.
[54] Petricoin III EF, Ardekani AM, Hitt BA, Levine PJ, Fusaro VA, Steinberg SM, et al. Use of proteomic patterns in serum to identify ovarian cancer. Lancet 2002;359(9306):572–7.
[55] Zhu Z, Ong Y-S, Dash M. Markov blanket-embedded genetic algorithm for gene selection. PatternRecognit 2007;40(11):3236–48.
[56] Wang A et al. Incremental wrapper based gene selection with Markov blanket. 2014 IEEE International Conference on Bioinformatics and Biomedicine (BIBM). IEEE; 2014.
[57] Bolón-Canedo V, Sánchez-Maroño N, Alonso-Betanzos A. Distributed feature selection: An application to microarray data classification. Appl SoftComput 2015;30:136–50.
[58] Chinnaswamy, Arunkumar, and Ramakrishnan Srinivasan. "Hybrid feature selection using correlation coefficient and particle swarm optimization on microarray gene expression data."*Innovations in bio-inspired computing and applications*. Springer, Cham, 2016. 229-239.
[59] García-Nieto J, Alba E. Parallel multi-swarm optimizer for gene selection in DNA microarrays. Appl Intell 2012;37(2):255–66.
[60] Arunkumar C, Ramakrishnan S. Attribute selection using fuzzy roughset based customized similarity measure for lung cancer microarray gene expression data. Future Comput Inf J 2018;3(1):131–42.
[61] Apolloni J, Leguizamón G, Alba E. Two hybrid wrapper-filter feature selection algorithms applied to high-dimensional microarray experiments. Appl Soft Comput 2016;38:922–32.
[62] Baliarsingh SK et al. Analysis of high-dimensional genomic data employing a novel bio-inspired algorithm. Appl Soft Comput 2019;77:520–32.
[63] Maulik U, Chakraborty D. Fuzzy preference based feature selection and semisupervised SVM for cancer classification. IEEE Trans NanoBiosci 2014;13 (2):152–60.
[64] Chandra B, Gupta M. An efficient statistical feature selection approach for classification of gene expression data. J Biomed Inform 2011;44(4):529–35.
[65] Nakariyakul S. A hybrid gene selection algorithm based on interaction information for microarray-based cancer classification. PLoS One 2019;14(2): e0212333.
[66] Ghosh M et al. Recursive memetic algorithm for gene selection in microarray data. Expert Syst Appl 2019;116:172–85.
[67] Saberi-Movahed F et al. Dual regularized unsupervised feature selection based on matrix factorization and minimum redundancy with application in gene selection. Knowl-Based Syst 2022;256:109884.
[68] Qi Y et al. A new feature selection method based on feature distinguishing ability and network influence. J Biomed Inform 2022;128:104048.
[69] Vaiyapuri T et al. Red fox optimizer with data-science-enabled microarray gene expression classification model. Appl Sci 2022;12(9):4172.
[70] Rostami M et al. Gene selection for microarray data classification via multi-objective graph theoretic-based method. Artif Intell Med 2022;123:102228.
[71] Nosrati V, Rahmani M. An ensemble framework for microarray data classification based on feature subspace partitioning. Comput Biol Med 2022;148:105820.