
Modified bio-inspired algorithms for diagnosis of breast cancer using aggregation

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Abstract: The most widely detectable of all cancers found in women is breast cancer. The mortality rate is also the second-highest among women with a 12% growth rate. It is very pertinent to diagnose breast cancer in the nascent stages so that the survival of the patient is ensured with the help of proper medication. Several algorithms have been proposed in this regard. However, they have failed to achieve the desired level of accuracy. An improved version of the particle swarm optimisation and firefly algorithm is presented in this paper to overcome the drawbacks of the existing algorithm. The two algorithms are further aggregated to improve the accuracy of the results. The aggregated algorithm is used on the Breast Cancer Wisconsin (Diagnostic) Data Set (real-valued dataset), and results are calculated for different classifiers. An accuracy of 92%–96% is shown by improved particle swarm optimisation and 1%–2% overall hike in the accuracy by improved firefly algorithm, respectively. Finally, the aggregated algorithm shows an accuracy of 93%–97%. Further, random forest classifier has displayed the best accuracy of 97%.

Keywords: breast cancer; bio-inspired algorithms; aggregation; particle swarm optimisation; PSO; firefly algorithm; feature selection; linear support vector machine; SVM; decision tree; K-nearest neighbour; KNN; random forest classifiers; RFCs.

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1 Introduction

Breast cancer originates due to the mutation of DNA genes of breast tissue, which form tumours if present in groups. It may be inherited or developed due to exposure to any radiation of any kind. It is recommended to detect breast cancer at its early stages so that it does not spread to other regions of the body. There are various algorithms used for the early diagnosis of breast cancer. One set of algorithms is evolutionary computation. These algorithms have fascinated a lot of great minds for optimising tasks in the present time. These algorithms include the general bio-inspired optimisation algorithm based on a living organism's population, which mimics growth processes such as mutation, reproduction, and selection to resolve the optimisation tasks (Sharma et al., 2019a, 2019b). The bio-inspired optimisation algorithms are designed to tackle complex problems in science and engineering and help in finding optimal solutions. Generally, these algorithms are used when problems are nonlinear and bound to nonlinear constraints, which suggest many difficulties such as high dimensionality and time requirements to find the optimal solution (Darwish, 2018). The efficiency of bio-inspired algorithms depends on balancing two main objectives, exploration (exploring the search space for promising solutions) and exploitation (exploiting the best solutions found so far) (Kumar et al., 2013). However, a single algorithm cannot provide efficiency to a certain level. Therefore, combining two algorithms can help in achieving better accuracy. Aggregation is the process of combining two or more algorithms to get optimal accuracy by considering the desired aspects from each algorithm. Aggregation is widespread among various computer science fields, mainly to find optimised results in real-world implementations.

In this paper, a sequential aggregation of improved particle swarm optimisation (IPSO) and improved firefly algorithm (IFA) is performed. To achieve optimal accuracy, features are input to one algorithm, and the resultant subset is passed to the second algorithm. After aggregation, the number of features is reduced, and there is a significant increase in the result. The use of aggregation is beneficial in the diagnosis of breast cancer as it provides a more accurate classification of findings into benign and malignant. Initially, the performance of four popular bio-inspired optimisation algorithms, i.e., firefly algorithm (FA), artificial bee colony (ABC) optimisation, particle swarm optimisation (PSO), and ant colony optimisation (ACO) are compared. Out of these best two among them are selected for aggregation. It increases the effectiveness of search, which can be achieved when both algorithms get combined in a cooperative way or else the resultant may produce negative results.

Feature selection is a method of selecting a subset of features from a full dataset such that subset analyses the target with an accuracy relatable to the efficiency of the original features set and with less computational cost (Sharma et al., 2019a; Ojala et al., 1996). It is an essential process in machine learning in modern times. Due to an increase in data concerning features and instances, the quality of data can result in an inconsistent form, which may lead to inaccurate results and a waste of memory. Hence feature selection is necessary to remove this inconsistency to get optimal accuracy. Feature selection is divided into wrapper-based and filter-based algorithm. The statistical approach is used in the filter-based algorithm for scoring each feature, and the wrapper-based algorithm is costlier than the filter method concerning computational time, which uses a machine-learning algorithm for evaluation.

The paper is lined up as: the related work corresponding to aggregation and the bio-inspired algorithm is described in Section 2. The proposed algorithm, followed by the experiment, is described in Section 3. Experimental results produced through the execution of the proposed algorithm on the Breast Cancer Wisconsin (Diagnostic) Data Set are described and discussed in Section 4. Finally, Section 5 consists of conclusions and future scope.

2 Literature review

Evolutionary algorithms are processing algorithms that are inspired by and the biological processes to answer complex real-life problems. Many bio-inspired algorithms are in use, but they all follow a common belief, which is to initialise a population of individuals, select the fittest among them, which creates a path in the fitness of the population (Nayyar et al., 2018). Besides this, every algorithm shows distinctive characteristics that can be studied further deeply into each technique. As per the unified approach suggested by De Jong, the evolutionary algorithm must have these components, i.e., fitness function, representation, parent's selection, population, mutation operator, crossover operator, survivor selection and termination condition (De Jong, 1975). These components describe the working of the algorithm and may differ from algorithm to algorithm. One of the algorithms is ABC, in which a new candidate solution is generated based on the current solution and a randomly selected one. However, the random selection method is unstable. To speed up the search, a new neighbourhood selection is proposed. For each current solution, some solutions from the current population are selected randomly. Then, the best one is chosen among those solutions as the neighbourhood solution to generate new solutions (Xiong and Tang, 2019).

Another algorithm is PSO, which is based on mutual group nature of the living being such as fish schooling, birds, insect swarming, where the cumulative objective is met based on feedback from all other units of the group (Shi and Eberhart, 2005; Shi and Eberhart, 1999). Optimising functions with discontinuous, non-differential with several nonlinearly related parameters is the primary purpose of this optimisation (Floreano and Mattiussi, 2008). The algorithm works in a few continuous stages based on the behaviour of the creature it mimics. Each member of the swarm seeks a possible result at every position during the process. Each member communicates by broadcasting a signal comparable to the fitness of likely results to different members of the group. When a member tries to find a more suitable result from currently obtained solutions, a new path is found with inertial fitness to direct the particles to an ideal solution regularly.

FA works far well than any other swarm optimisation. It works on the multi-modal objective to solve the NP-hard dilemma with non-convex target functions. Population-based exploration is the basis on which the FA can be formed to get the required accuracy. This algorithm is based on the bio-luminescence signalling of fireflies, which they use to communicate and avoid danger. Bioluminescence signalling is used for food searching and breeding purposes among fireflies. Illumination of tail light tells about the fitness of firefly (Gandomi et al., 2011; Yang, 2009; Yang et al., 2012). In the general process, the magnitude of light shows the appeal of a firefly, which implies the fitness of likely result. An initial population is generated in the first stage of the process. In further steps, fitness is altered and calculated for each firefly of the population. After sorting fireflies according to fitness, best k fireflies are chosen for the next evaluation stage. FA is also useful as it can be used alongside other algorithms in hybrid approaches to improve accuracy (Rahmani and MirHassani, 2014; Ahammed et al., 2018).

The other evolutionary algorithms are crow search algorithm, which performs better in optimising the results of mathematical functions or feature extractions. The algorithm creates a search space in which crow's moves toward the continuous-valued position. The sigmoid function is used to convert the position of crows to binary (Gupta et al., 2018a, 2018a).

3 Proposed work/methodology

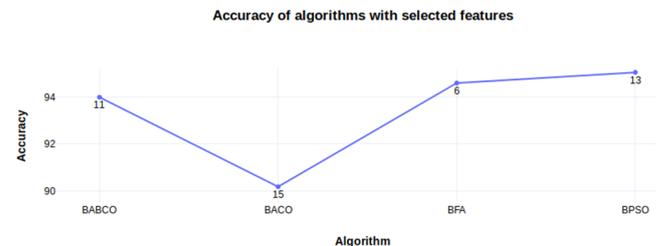
This section discusses the improvements done in the algorithms selected for aggregation and methodology used.

3.1 Selection of algorithms

The methodology starts with selecting the best two algorithms for aggregation out of the existing algorithms. This is done by performing feature selection on four

existing algorithms namely binary ant colony optimisation (BACO), binary artificial bee colony optimisation (BABCO), binary particle swarm optimisation (BPSO), and binary firefly algorithm (BFA). The dataset is executed on the four algorithms, and the number of features along with accuracy reduced by different algorithms is noted, as shown in Figure 1. It shows that features reduced by BABCO, BACO, BFA and BPSO are 11, 15, 6, and 13 respectively with an accuracy of 94%, 90.2%, 94.4% and 94.7%. Since BPSO and BFA have achieved the highest accuracy. Therefore, BPSO and BFA are chosen for aggregation. Aggregation is the process of combining two or more algorithms to get better results than that which can be obtained by algorithms separately. It is done in such a way that one algorithm is executed and the following algorithm is executed on the result of the previous algorithm. The numbers in the figure represent the features reduced by algorithm, as in the Breast Cancer Wisconsin (Diagnostic) Data Set, the number of features is 32.

Figure 1 Accuracy of four algorithms with selected attributes (see online version for colours)

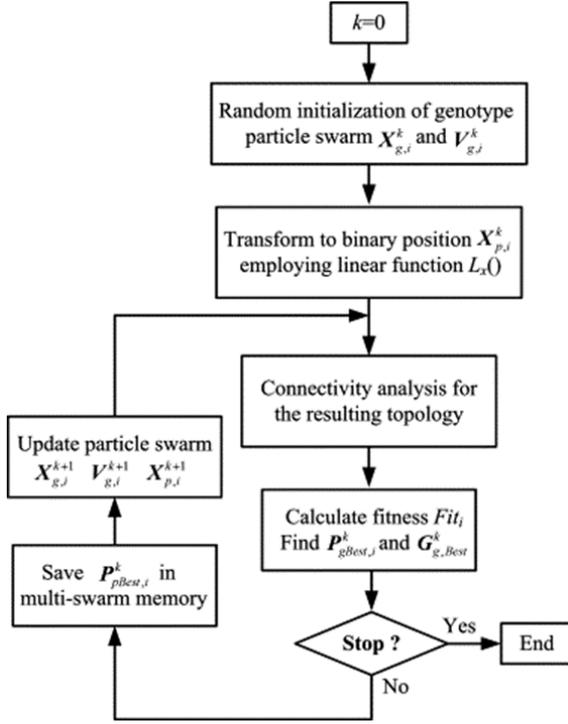


In Figure 1, it can be seen that the number of features selected in the BFA is lesser than BPSO. Hence BPSO is executed first, and then the result is fed to firefly optimisation. It is done to ensure that both algorithms work efficiently. If the sequence will be reversed, there is a possibility that the BFA may reject features that might be selected by BPSO, thereby tampering the result.

3.2 Improved particle swarm optimisation

This algorithm operates as a basic algorithm but with minor modification. For feature selection, each feature is represented as a binary number where '1' represents as the feature is selected, and '0' represents that feature is not possible. Each particle in the swarm works on separate feature string of 1 s and 0 s where features are randomly selected initially, and then particle selects local best solution. The improved version of the algorithm consists of an additional step of calculating fitness which increases randomness and improves efficiency. This step is executed in the calculate fit fitness step in the flow chart shown in Figure 2. If the solution is best among all, it is selected as the global best solution. This process repeats for each particle for a particular number of iteration or until the optimal result is achieved.

Figure 2 IPSO flowchart



Algorithm 1 Improved particle swarm optimisation

```

start
  Initialise particles population equal to features present
  while termination criterion is not satisfied
    for every particle p at xp do
      evaluate fitness value f(xp)
      if f(xp) is better than pbestp then
        pbestp ← xp
      end if
    end for
    Define gbestp as best position found by any of p's
    neighbours so far
    for every particle p do
      vp ← compute_velocity(xp, pbestp,
      gbestp)
      S(vp) = 1/1 + e - v
      if rand() < S(vp(t + 1)) then
        xp(t + 1) = 1
      else
        xp(t + 1) = 0
      end if
    end for
  end while
end

```

A general pseudo-algorithm for the IPSO algorithm is shown as Algorithm 1, and the flowchart is shown in Figure 2.

3.3 Improved firefly algorithm

Similar to IPSO, feature selection in IFA is performed in the binary method and with an additional constraint. In the algorithm process, the resultant subset of features of IPSO is taken as a constraint, and all features further processed in the algorithm must belong to the resultant subset. Initially, when each firefly randomly selects a subset of features, it is compared with the sequential subset, and if the feature is not present, it is rejected, another feature may or may not be selected in place of it. To improve its efficiency, the variable affecting the working of an algorithm, α and γ is changed iteratively to introduce the real-time effect in the process. An additional constraint comparison of global best is made with particle swarm accuracy, which is then compared with the accuracy provided by particle swarm. The termination constraint in firefly is also changed from iteration to get an optimal result better than IPSO. A general pseudo-algorithm for IFA is shown in Algorithm 2, and the flowchart is shown in Figure 3.

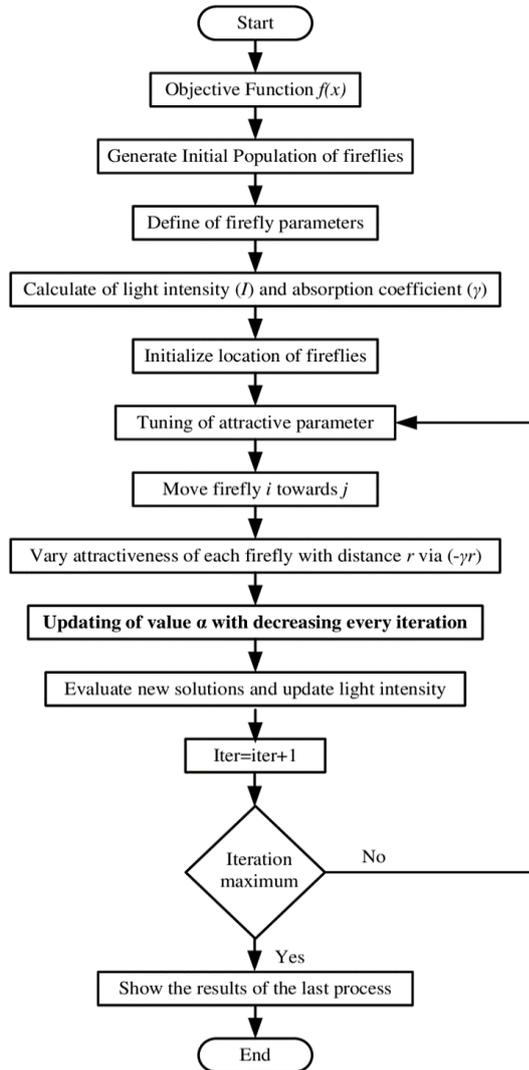
Algorithm 2 Improved firefly algorithm

```

start
  initialise population while checking with pso_results
  initialise  $\alpha$ ,  $\beta$ ,  $\gamma$  and max_iter
  determine objective function f(x)
  for each firefly calculate Intensity(I) at cost(x)
    while gbest > pso_best
      while t < max_iteration
        for x = 1 to n
          for y = 1 to n
            if (Iy > Ix)
              in kth dimension move firefly y to
              firefly x
            end if
            vary attractiveness with distance  $r = e^{-\gamma r^2} + \alpha e$ 
            find new results and update light
            intensity
          end for y
        end for x
        find best fireflies after sorting according to
        fitness
      end while
    end while
  end for
  post transform results and visualisation
end

```

Figure 3 IFA flowchart



3.4 Proposed methodology

The proposed method is an aggregation of IPSO and IFA. The algorithm works by first selecting the features using IPSO. The selected features are fed as input to the IFA algorithm. The steps are shown in Figure 4. The proposed algorithm is better than the existing algorithm in the following ways:

- 1 In general cases of PSO, when calculating velocity or position of a particle, the velocity depends on the previous velocity and the personal best and globally best position, while position depends on the previous position and current velocity. As an improvement, while calculating velocity and location for the next iteration, additional ϵ is added, which is a normal distribution to introduce real-world randomness. This way, it will lead to more mutation and will cover more search zone for efficiency. This will improve accuracy by adding another step of calculating fitness.

- 2 In general cases of FA, the search zone for fireflies is in the form of uniform distribution, α and γ , and the bioluminescence variable is treated as constant throughout the process. To improve the FA's efficiency, the variable α and γ are changed iteratively to introduce the real-time effect in the model. It helps in increasing efficiency. A normal distribution is used in place of uniform distribution to match real-world scenarios. And a threshold value is used, which is the efficiency given by IPSO, all fitness values less than the threshold will be rejected for optimal efficiency. Additionally, a mask is used so that features selected in IPSO are not repeated in IFA.

Figure 4 Proposed algorithm



4 Implementation and results

In this section, the proposed algorithm is implemented, and results are compared with the existing algorithms. The algorithms are run multiple times with four classifiers, namely decision tree, K-nearest neighbours (KNN), linear support vector machine (SVM), and random forest classifier (RFC). The experiment has been executed 20 times, and then the mean has been calculated.

4.1 Input parameters

For data prediction, it is necessary to make a data model classifier. Classification is a method of predicting class or label of provided data points. Any data type can be computed accordingly on classifiers. This subsection describes the classifiers used during the experimentation.

1 Decision tree classifier (DTC)

The DTC generates a set of questions that are used to classify data together with its classes. Decision tree is simple to visualise and more comfortable to understand. Both categorical and numerical data can be classified using it, and it takes comparatively low data preparation. The main problem comes when a small variation is done, which can change the whole tree and may lead to a wholly separate tree, which leads to high computational cost.

2 K-nearest neighbour

KNN falls under lazy learning as no model is formed instead of checks directly from training data. In this classification, k neighbours are selected from test data and result from those neighbours is computed. This classification is useful in a big dataset and is not effective for noisy data. It has high computational cost as multiple comparisons are made during prediction.

3 Random forest classifier

As the name suggests, the RFC is a collection of multiple decision trees made on a separate subset of data. The result is calculated by taking the mean of all trees. The training sub-sample size is constant all over, but they are randomly replaced at each iteration. It is time-consuming and has a high computational cost but shows better accuracy than decision trees.

4 Support vector machine

SVM is a method of training dataset in a hyperplane. In this, data is pointed in a hyperplane, and test data points are then compared with hyperplane points, after which class is predicted by the closeness of clusters formed in the hyperplane. It is recommended for data with high dimensionality. The algorithm is memory efficient and has a nominal computational cost.

Table 1 shows the parameters for each classifier used in this experiment.

Table 1 Input parameters for classifiers

Classifier	Parameter
Decision tree	Minimum depth = 30
	Minimum sample split = 20
	Maximum sample leaf = 1
K-nearest neighbours	Neighbours = 3
	Leaf size = 30
Random forest	Estimators = 25
Linear support vector machine	Minimum sample split = 2
	Maximum iteration = 10

Parameters essential for the execution of IPSO and IFA are shown in Table 2 and Table 3, respectively.

Table 2 Input parameters for IPSO

Parameters	Value
Number of populations	50
Maximum iteration	200
Move rate	0.5
Limit search range	4

Table 3 Input parameters for IFA

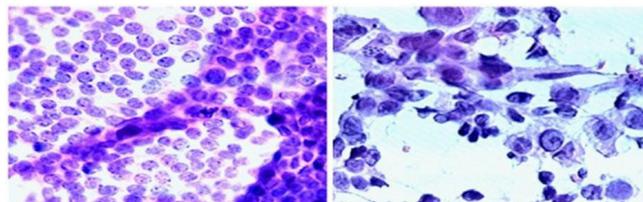
Parameters	Value
Number of populations	50
Maximum iteration	200
Alpha	0.25
Beta	0.5
Gamma	0.2

4.2 Dataset

Breast Cancer Wisconsin (Diagnostic) Data Set developed in November 1995 is used as the dataset in this paper.

Digital Image of breast mass fine needle aspirate biopsies are used for calculation of features. Cell nucleus characteristics of breast mass are the main illustration of the image. Five hundred sixty-nine records are presented in the dataset with 32 attributes, out of which two are unnecessary for feature selection (ID and diagnosis). Each instance is diagnosed into either malignant (cancerous) or benign (not cancerous). Out of 569 instances, 357 are not cancerous, and rest 212 is cancerous. The method used in it is a curve-fitting algorithm that computes ten features from each one of the cells in the sample, then it calculates the mean value, extreme value, and standard error of each feature for the image, returning a 30 real-valuated vector. Figure 5, shows the fine needle aspirate biopsy cell image for benign and malignant types, respectively.

Figure 5 FNAB cells of benign and malignant type (see online version for colours)



The ten real-valued features which are calculated for every cell nucleus of breast mass are shown in Table 4.

Table 4 Real-valued features for every cell nucleus

Real-valued features	Meaning
Radius	Mean of the distance between points on perimeter and centre
Texture	The standard deviation of greyscale values
Perimeter	The perimeter of the nucleus
Area	The area covered by the perimeter
Smoothness	local variation in radius
Compactness	The perimeter square/area
Concavity	The severity of concave portions of the contour
Concave points	Number of concave portions of the contour
Symmetry	The symmetry of the nucleus
Fractal dimension	The coastline approximation of nucleus

The mean, worst or largest, and standard error of these features are calculated for every cell, resulting in 30 features. For training and testing, the purpose dataset is grouped in ratio 4:1, i.e., training data = 80% and testing data = 20%.

Figure 6 PCA of dataset (see online version for colours)

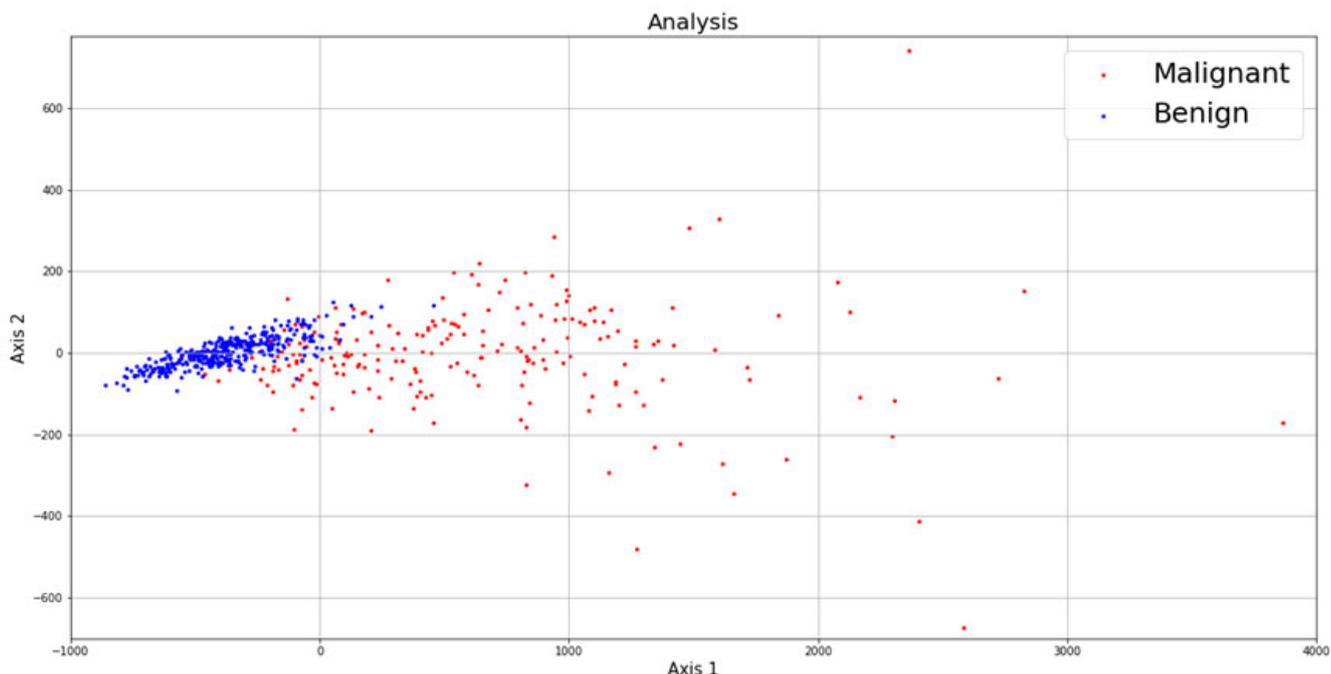
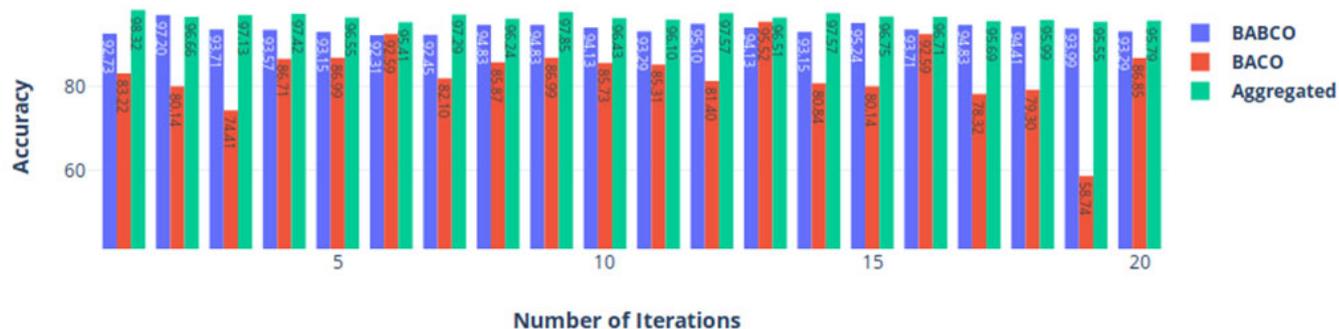


Figure 7 Accuracy comparisons of 20 runs in aggregated algorithm, BACO and BABCO, (a) accuracy graph using decision tree (b) accuracy graph using SVM (c) accuracy graph using KNN (d) accuracy graph using random forest (see online version for colours)

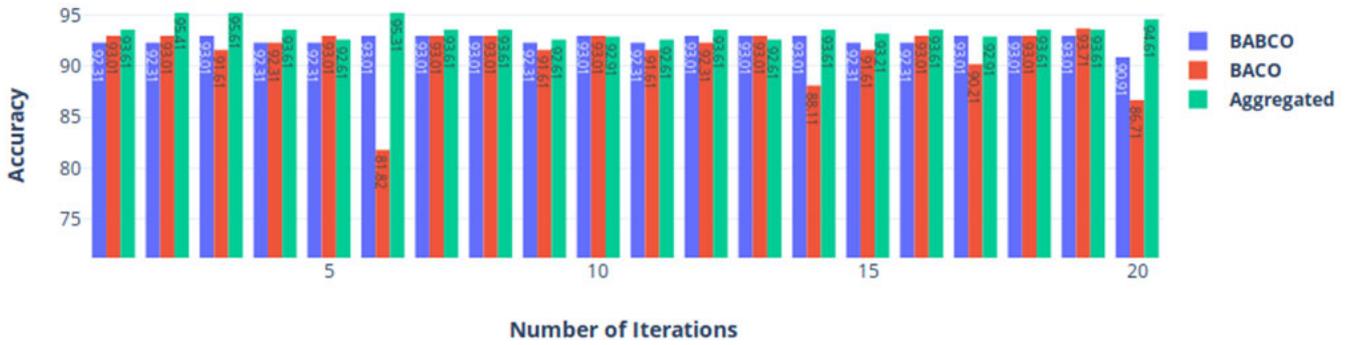


(a)

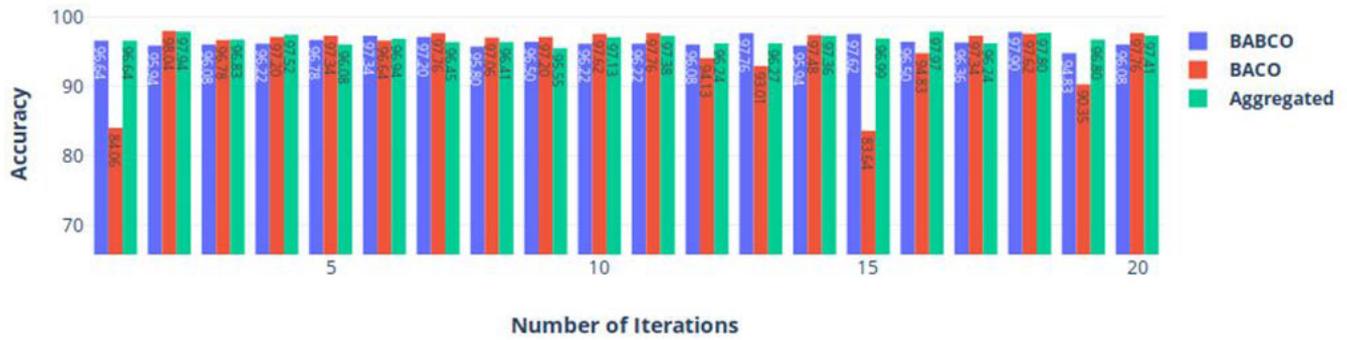


(b)

Figure 7 Accuracy comparisons of 20 runs in aggregated algorithm, BACO and BABCO, (a) accuracy graph using decision tree (b) accuracy graph using SVM (c) accuracy graph using KNN (d) accuracy graph using random forest (continued) (see online version for colours)



(c)



(d)

In Figure 6, principal component analysis (PCA) of the dataset is displayed as a scatter plot graph showing the distribution of a dataset. In Figure 6, red dots represent the malignant, and blue dots represent the benign instances of the dataset. It helps in understanding the diverse range of the dataset.

4.3 Results

During the experiment, the termination condition has been set by maximum iteration as it can predict the utmost accuracy. During the initial iteration, it is seen that the IFA has shown almost equal accuracy to IPSO. Hence as an additional condition is added to find better accuracy. In IFA, the statement is introduced that if the global best solution at the end of the program is less than that of IPSO, then IFA executes again. The finish condition is not set by the accuracy required, as it may lead to an infinite loop if the algorithm is not capable of reaching that accuracy. And it is difficult to guess the accuracy limit as accuracy varies with the classifier used.

Figure 7 shows the results when the existing and proposed algorithms are executed on the dataset using the four classifiers. The results shown in the graph are a mean of 20 runs. As can be seen in Figure 7(a), the DTC has shown a significant increase in accuracy between IPSO and IFA at every run and a maximum of 1.95% overall from 94.67% in IPSO to 96.62% in IFA. The other three classifiers have shown good accuracy, i.e., SVM has shown

an increase of 1.89%, KNN have shown a 1.25% increase, and RFC has shown a minimum increase of 0.85%.

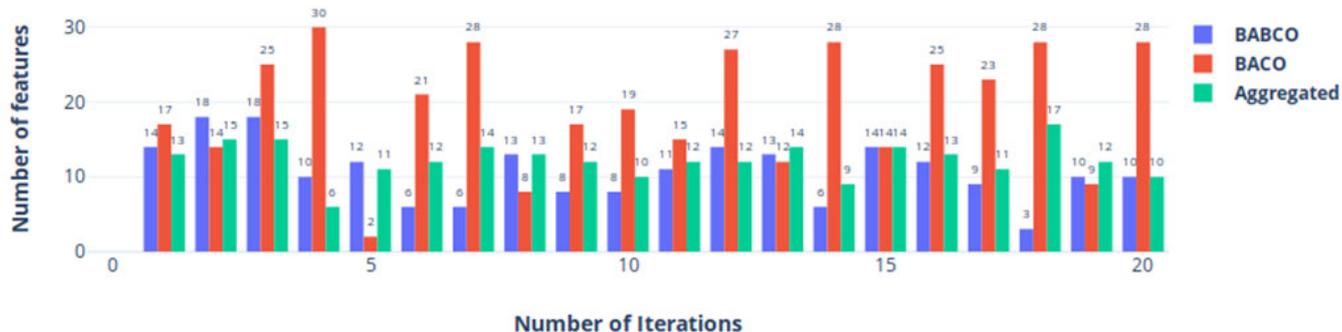
Figure 8 shows a comparison of proposed and existing algorithms in terms of features reduced in each classifier. SVM has a reduced maximum of five features from 13 to 8 features overall. It has shown minimum feature selection also. Other classifiers have shown a further reduction of 3 and 4 features. Decision tree has reduced three features the same as KNN, and Random Forest has shown a decrease of four features.

In Figure 9, complexity time taken by proposed algorithms with each classifier is shown. Complexity time is calculated by taking the mean of the total time taken for 20 runs of the process. Decision tree and KNN have minimum complexity time and almost equal time of 65.5 seconds. SVM has shown the time of 458 secs. Random forest has taken a maximum of 1,121 seconds of complexity time.

A tabular comparison of the improved algorithm with the existing algorithms is shown in Table 5. The improved algorithm is an aggregation of IPSO and IFA. In this, the output of IPSO is used as an input to IFA for better optimal results.

As seen in Table 5, the proposed algorithm shows better results than the existing algorithm in terms of accuracy and features selected. This is because of the introduction of an additional step for calculating fitness and normal distribution of variables α and γ . This is true for all the qualifiers selected for comparisons.

Figure 8 Feature reduction by aggregated algorithm, BACO and BABCO, (a) feature selection using decision tree (b) feature selection using SVM (c) feature selection using KNN (d) feature selection using random forest (see online version for colours)



(a)

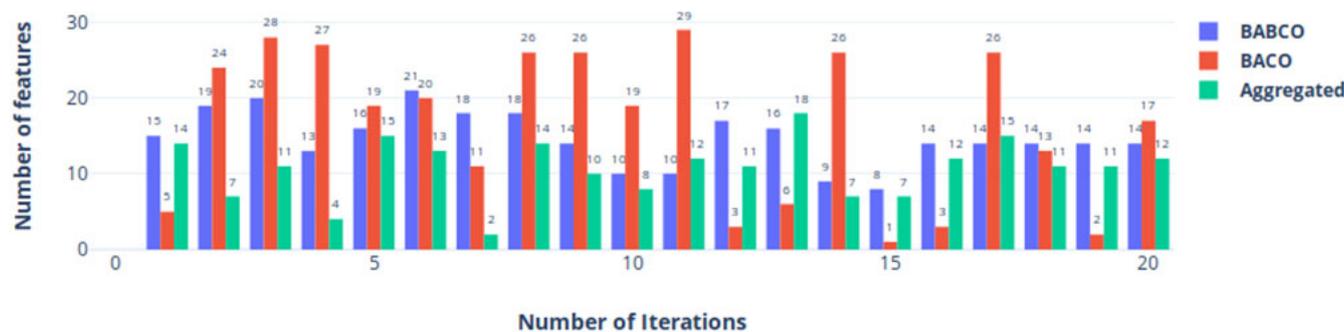
Feature Selection using Support Vector Machine



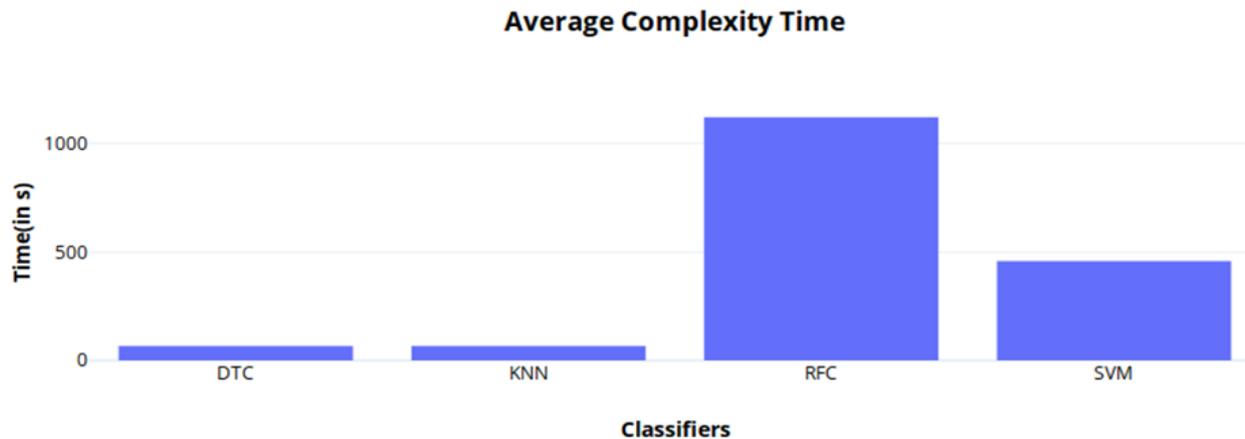
(b)



(c)



(d)

Figure 9 Complexity time comparison (see online version for colours)**Table 5** Comparison of results

Algorithm	Classifier	Accuracy (in %)	Features selected
Binary ant colony optimisation (BACO) (Sharma et al., 2019a)	DTC	90.91	19
	KNN	91.43	17
	SVM	83.2	9
	RFC	95.18	16
Binary artificial bee colony optimisation (BABCO) (Sharma et al., 2019a)	DTC	92.82	10
	KNN	92.62	10
	SVM	94	11
	RFC	96.5	14
Aggregated algorithm	DTC	96.6	12
	KNN	93.6	11
	SVM	96.6	8
	RFC	97	10

5 Conclusions and future scope

The early and accurate detection of breast cancer can save the lives of many women across the globe. The existing algorithms fail to detect cancer accurately. This paper has proposed a novel methodology for the accurate diagnosis of breast cancer. The algorithm is an aggregation of IPSO and IFA. The algorithm is executed on four classifiers, namely decision tree, KNN, linear SVMs, and RFCs. The results, when compared with the existing algorithm, show a significant increase in accuracy. An accuracy of 96.6%, 93.6%, 96.6%, 97% is observed for the four classifiers decision tree, KNN, linear SVMs, and RFCs, respectively. Moreover, the number of features is reduced 12, 11, 8, 10 for DTC, KNN, SVM and RFC respectively.

A keen study, along with comparative analysis, reflects that a few features repeat themselves in every result (texture mean, smoothness mean, texture_worst, concave points_worst). These features ought to be carefully considered as they are crucial in the process of diagnosing the cancer. It is also noticed that aggregation results have

increased overall accuracy significantly. In the future, aggregation of algorithms or hybridisation can be employed for the prediction of more diseases as they deliver results with a higher level of accuracy in significantly less computational time.

References

- Ahmed, M.J., Swathi, A., Sanku, D., Vedula, C. and Ramesh, H. (2018) 'Performance of firefly algorithm for null positioning in linear arrays', *Proceedings of 2nd International Conference on Micro-Electronics, Electromagnetics and Telecommunications*, pp.383–391, DOI: 10.1007/978-981-10-4280-5_40.
- Darwish, A. (2018) 'Bio-inspired computing: algorithms review, deep analysis, and the scope of applications', in *Future Computing and Informatics Journal*, Vol. 3, No. 2, pp.231–246 [online] <https://doi.org/10.1016/j.fcij.2018.06.001>.
- De Jong, K.A. (1975) *An Analysis of the Behavior of a Class of Genetic Adaptive Systems*, Doctoral dissertation, University of Michigan, Dissertation Abstracts International, Vol. 36, No. 10, 5140B (University Microfilms No. 76-9381).
- Floreano, D. and Mattiussi, C. (2008) *Bio-Inspired Artificial Intelligence: Theories, Methods, and Technologies*, MIT Press, Cambridge, ISBN: 9780262062718674.
- Gandomi, A.H., Yang, X.S. and Alavi, A.H. (2011) 'Mixed variable structural optimization using firefly algorithm', in *Computers & Structure Journal*, Vol. 89, Nos. 23–24, pp.2325–2336 [online] <https://doi.org/10.1016/j.compstruc.2011.08.002>.
- Gupta, D., Rodrigues, J.J.P.C., Sundaram, S., Khanna, A., Korotayev, V. and de Albuquerque, V.H.C. (2018a) 'Usability feature extraction using modified crow search algorithm: a novel approach', in *Neural Computing and Applications Journal*, SCIE [online] <https://doi.org/10.1007/s00521-018-3688-6>.
- Gupta, D., Sundaram, S., Khanna, A., Hassanien, A.E. and de Albuquerque, V.H.C. (2018b) 'Improved diagnosis of Parkinson's disease based on optimized crow search algorithm', *Computer and Electrical Engineering Journal*, Vol. 68, pp.412–424, SCIE [online] <https://doi.org/10.1016/j.compeleceng.2018.04.014>.

- Kumar, R., Girdhar, G. and Kumar, R. (2013) 'Hybridization in genetic algorithms', in *International Journal of Advanced Research in Computer Science and Software Engineering*, Vol. 3, No. 4, pp.403–409.
- Nayyar, A., Garg, S., Gupta, D. and Khanna, A. (2018) 'Evolutionary computation-theory and algorithms', Chapter 1, of *Advances in Swarm Intelligence for Optimizing Problems in Computer Science*, CRC Press, Taylor & Francis Group, ISBN: 9781138482517 – CAT# K349007.
- Ojala, T., Pietikäinen, M. and Harwood, D. (1996) 'A comparative study of texture measures with classification based on featured distributions', in *Pattern Recognition*, Vol. 29, No. 1, pp.51–59 [online] [https://doi.org/10.1016/0031-3203\(95\)00067-4](https://doi.org/10.1016/0031-3203(95)00067-4).
- Rahmani, A. and MirHassani, S.A. (2014). 'A hybrid firefly-genetic algorithm for the capacitated facility location problem', in *Information Sciences Journal*, Vol. 283, pp.70–78 [online] <https://doi.org/10.1016/j.ins.2014.06.002>.
- Sharma, M., Gupta, S., Sharma, P. and Gupta, D. (2019a) 'Bio-inspired algorithms for diagnosis of breast cancer', in *International Journal of Innovative Computing and Applications*, Vol. 10 Nos. 3/4, pp.164–174, DOI: 10.1504/IJICA.2019.103380.
- Sharma, P., Jain, R., Sharma, M. and Gupta, D. (2019b) 'Parkinson's diagnosis using ant-lion optimization algorithm', in *International Journal of Innovative Computing and Applications*, Vol. 10 Nos. 3/4, pp.138–146, DOI: 10.1504/IJICA.2019.103370.
- Shi, Y. and Eberhart, R.C. (1999) 'Empirical study of particle swarm optimization', *Proceedings of the 1999 IEEE Congress on Evolutionary Computation*, DOI: 10.1109/CEC.1999.785511.
- Shi, Y. and Eberhart, R.C. (2005) 'Parameter selection in particle swarm optimization', in *International Conference on Evolutionary Programming VII*, pp.591–600 [online] <https://doi.org/10.1007/BFb0040810>.
- Xiong, X. and Tang, J. (2019) 'A new artificial bee colony based on neighborhood selection', in *International Journal of Innovative Computing and Applications*, Vol. 10, No. 1, pp.12–17, DOI: 10.1504/IJICA.2019.100526.
- Yang, X.S. (2009) 'Firefly algorithms for multimodal optimization', in *International Symposium on Stochastic Algorithms, SAGA 2009: Stochastic Algorithms: Foundations and Applications*, pp.169–178, Springer Berlin Heidelberg [online] https://doi.org/10.1007/978-3-642-04944-6_14.
- Yang, X.S., Hosseini, S.S.S. and Gandomi, A.H. (2012) 'Firefly algorithm for solving nonconvex economic dispatch problems with valve loading effect', in *Applied Soft Computing Journal*, Vol. 12, No. 3, pp.1180–1186 [online] <https://doi.org/10.1016/j.asoc.2011.09.017>.