# A new model for large dataset dimensionality reduction based on teaching learning-based optimization and logistic regression

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# ABSTRACT

One of the human diseases with a high rate of mortality each year is breast cancer (BC). Among all the forms of cancer, BC is the commonest cause of death among women globally. Some of the effective ways of data classification are data mining and classification methods. These methods are particularly efficient in the medical field due to the presence of irrelevant and redundant attributes in medical datasets. Such redundant attributes are not needed to obtain an accurate estimation of disease diagnosis. Teaching learning-based optimization (TLBO) is a new metaheuristic that has been successfully applied to several intractable optimization problems in recent years. This paper presents the use of a multi-objective TLBO algorithm for the selection of feature subsets in automatic BC diagnosis. For the classification task in this work, the logistic regression (LR) method was deployed. From the results, the projected method produced better BC dataset classification accuracy (classified into malignant and benign). This result showed that the projected TLBO is an efficient features optimization technique for sustaining data-based decision-making systems.

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#### 1. INTRODUCTION

Breast cancer (BC) is the most common cancer among women around the world. About 25% of all new cancer cases are diagnosed as BC in women as stated by the American Cancer Society (ACS). One woman dies from BC every minute and more than 1400 women die every day from BC [1]. Cancer results from the rapid and uncontrollable division of cells which results in the formation of extra tissue mass called tumors in the body [2]. Such tumors are either cancerous or non-cancerous. The spread of the malignant tumors is faster as they spread rapidly to cause harm to the neighboring tissues. Cancer is commonly named based on the affected body part or where it started. Hence, BC is a form of malignant tumor which results from the uncontrolled division of breast cells. Among the major signs of BC are changed and increase in the increase normal size and shape of the breast, pain in the breast, inflammation of the affected or all parts of the breast, varying breast skin colors, presence of a lump beneath the arm area, etc. [2-4].

The World Health Organization (WHO) [5] reported that there are around 1.2 million cases of BC diagnosed in women every year. One out of 8 women in the USA is living with BC. The identification of BC can be done manually by the physician, but it is a difficult task due to the need to remember all the required information for each case, giving rise to low identification accuracy. Breast cancer-related mortality rate can be reduced through disease detection at the early stage [6-9]. Several conventional BC detection methods exist but the higher accuracy of machine learning (ML) classifiers is making them more useful recently. As such, there are several ML methods for early cancer detection and also checking for its relapse. Among these ML methods are artificial neural network (ANN), support vector machine (SVM), Naive Bayes, relevance vector machine, decision trees, K-means, K-nearest neighbor, random forests, etc.

The use of ML-based classification schemes is gaining attention in the medical field as they can help both skilled and unskilled experts in reducing possible errors and accurately providing the required medical data for diagnosis within a short time. However, the high dimensionality of the dataset represents one of the major limitations for effective use of ML classifiers. The important criteria which must be considered for effective ML-based classification are the data quality and a careful feature selection. Feature selection (FS) is the process of extracting a subset of relevant features from the original dataset [10-12]. It involves the use of FS algorithms to filter out irrelevant and redundant data features from the original dataset to prevent over-fitting [6, 13] and improve the classification accuracy of the model. Feature selection also reduces the classification models' complexity in time and space domains [14-18]. The main idea of this paper is to employ the TLBO-based algorithm for features subset selection in BC diagnosis. A recent metaheuristic, teaching-learning-based optimization (TLBO), has been reported to be an efficient optimization tool that is inspired by the knowledge passing mechanisms of teachers and learners in a classroom [19-22]. It has been applied to several well-known combinatorial optimization problems, producing good results [23-26]. The following sections discussed the novel multi-objective TLBO optimization algorithm for attaining better feature selection accuracy.

# 2. RELATED WORKS

Chuang et al. [27] proposed the catfish binary PSO (CatfishBPSO) algorithm. In this algorithm, few features are selected via the introduction of new catfish (particles) into the solution space to achieve 2 major advantages: i) reduced computation time, and ii) higher classification accuracy using the k-NN algorithm. It was applied and compared to 10 classification problems taken from the literature. Experimental results show that CatfishBPSO simplifies the feature selection process effectively, and either obtains higher classification accuracy or uses fewer features than other feature selection methods.

Bahassine et al. [28] proposed a novel feature selection method for Arabic text classification. The method uses an enhanced Chi-square method to improve the classification accuracy. The combination of the proposed Arabic text classification model with SVM classifier significantly enhanced the performance of the model as it achieved the best F-measure value of 90.50% using 900 features.

Sridev and Murugan [29] developed a feature selection technique for medical analysis of BC and compared with several classification algorithms. The objective of the presented algorithm is to select a minimum number of features to provide high classification accuracy. They reduced the feature vectors to 222 for both diagnosis and prognosis BC data sets using rough sets and correlation techniques.

Agrawal et al. [30] proposed a feature selection system for classification of cervical cancer CT images using artificial bee colony algorithm (ABC) and k-NN classifier; and artificial bee colony algorithm with SVM classifier. The result shows that the combination of ABC with SVM gave better performance compared to the combination of ABC with K-NN classifier.

Allam et al. [31] mentioned the importance of automatic medical disease diagnosis to handle the problems efficiently in the early stages. The study also discussed various imaging modalities for capturing the images, feature extraction methods for collecting the required attributes, and feature selection techniques for necessary features like texture, and color.

Chen et al. [32] proposed a coarse-grained parallel genetic algorithm (CGPGA) for optimizing the features in the dataset and constraints for SVM. They also proposed a new fitness function which is composed of classification accuracy, number of selected features, and the number of support vectors to optimize generalization errors. The results showed that the performance was ten times for the accuracy, size of subset features, number of support vectors, and the practice time.

Shahbeig et al. [33] proposed a mutated fuzzy adaptive PSO combined with TLBO algorithm for finding the most relevant and least set of genes in BC microarray data. The need to reduce the number of genes and increase the performance led to the use of a multi-objective for optimization problems. The result showed the model to achieve an accuracy of 91.88% with SVM classifier.

Jung et al. [34] presented a method to obtain additional numerical parameters from BC image data analysis using many neural network algorithms to explains how to get the highest number of numerical

parameters from data of BC image and made a comparison between these algorithms to find the best classification between benign and malignant.

Thein et al. [35] proposed the training of ANN using the island-based model for distinguishing different types of BC with better accuracy and reduced training time on Wisconsin diagnostic and prognostic breast cancer. They proposed 2 different migration topologies with random-random policy and later compared their results. From the results, the torus topology needed more training time compared to the random topology although it presented similar solution performance to the random topology.

Thawkar et al. [36] explored the use of Firefly algorithm to select a subset of features. Artificial neural network and support vector machine classifiers are employed to evaluate fitness of the selected features. Features selected by Firefly algorithm are used to classify masses into benign and malignant, using artificial neural network and support vector machine classifiers. Results show that Firefly algorithm with artificial neural network is superior to Firefly algorithm with support vector machine.

Sasikala et al. [37] proposed a novel shapely value embedded genetic algorithm (SVEGA). The method selects the genes that can maximize the capability to discriminate between different classes. Thus, the dimensionality of data features is reduced and the classification accuracy rate is improved. The number of features reduced from 24,481 to minimum of 6 features.

Sridev and Murugan [29] presented a modified correlation rough set feature selection (MCRSFS). It is composed of two feature reduction algorithms. Rough set quick reduct algorithm is applied at first to obtain the minimal feature subset. Then the second algorithm correlation feature selection (CFS) is used to do further reduction in minimal feature subset. The MCRSFS achieved highest classification accuracy compared to other feature selection methods.

Durgalakshmi and Vijayakumar [38] proposed an efficient method for breast cancer detection based on Wisconsin prognostic breast cancer (WPBC) data set. The correlation matrix method is used for feature selection which remove the insignificant features from the massive amount of dataset, followed with the classification algorithms such as support vector classification, logistic regression and random forest was deployed. The proposed method improves the accuracy [3, 4, 7-12, 15-18, 20-22, 24-26, 39, 40].

# 3. THE PROPOSED ALGORITHM AND MACHINE LEARNING TEQNIQUES

Feature selection is a process of optimizing individuals (records) by extracting the best subset of attributes from such records. During feature selection, fitness is assessed for each record in every generation while new records are generated to establish the population of the subsequent generations. After many generations, the components of the successive generations are better compared to the initial population. The construction of a dataset of optimal features requires a novel algorithm. The technique proposed in this study has two phases. The first phase involves the use of an optimization scheme to select the best set of features for the classification process. Then, in the second phase, the classification models are generated for the evaluation of the proposed intended scheme on BC dataset in terms of its performance. In this study, a multi-objective TLBO optimization algorithm was modeled with two major objectives which are results accuracy maximization and minimization of the number of features such that there will be a set of solutions instead of just one solution. The projected model is comprised of the TLBO and LR for subset feature selection. LR-based classification involves the estimation of an events' occurrence probability based on the similarity of given data points. The LR uses sigmoid function to determine the events' occurrence probability. An event with an occurrence probability of >0.5 is predicted as 'occurred', else, as 'not occurred'. Figure 1 depicts the proposed model while Figure 2 depicts the TLBO algorithm. Three parameters inherit from genetic algorithm to represent and update the set of features, each set of features represented in a chromosome.



Figure 1. The projected feature selection model based on TLBO



Figure 2. The TLBO Algorithm

Each gen in the chromos represent one feature, if the value of the gen 1 the feature is selected and 0 represent unselected feature, as shown in Figure 3. To updates the value of each gen (features) from selected to unselected or Vis versa, crossover between two chromosome and then mutation is used to get new subset of features (chromosome) as shown in Figure 4. The parameters used in this algorithm shown in Table 1.



Chromosome 1	1	1	0	0	0	1	0	1
Chromosome 2	1	1	1	0	0	0	0	1
Crossover								
New	1	1	1	0	0	1	0	1
Chromosome								
	]	Muta	tion					
New	1	1	1	0	1	0	0	1
Chromosome								

f th C+ -1

Figure 4.	Crossover	and	mutation	operations
	010000.01			operations

Table 1. The Parameters of algorithm				
Parameter	Value			
Population size	20			
Number of generation	40			
Croddover type	Half-uniform			
Mutation type	Bit-flip			

#### 4. **RESULTS AND DISCUSSION**

The results of the proposed algorithm are shown in Table 2. The results showed each set of features and the accuracy. Statistical tests were performed on the result to verify the results. Table 3 showed the confusion matrix. Based on the confusion matrix, we can calculate the detection rate using (1).

Detection rate 
$$=$$
  $\frac{TP}{TP+FP}$  (1)  
 $=$   $\frac{444}{444+0} = 1.00$ 

The comparison of the proposed algorithm in this study with PCA and Fine tree built in MATLAB as shown in Table 4 revealed the superiority of the proposed model over the benchmarked schemes.

Table 2. Results for each set of features			
No. Features	Accuracy		
1	0.97		
2	0.99		
3	1.00		

Table 3. Confusion matrix				
	Predicated malignant	Predicated Benign		
Actual malignant	444	0		
Actual Benign	0	239		

Table 4. Comparision table					
No. features	Our Model	PCA+ Fine Tree			
1	0.97	62.1			
2	0.99	95.6			
3	1.00	96.5			

### 5. CONCLUSION

This study presented a multi-objective TLBO algorithm for solving optimal feature selection problems. Accuracy is most important in the field of medical diagnosis to diagnose the patient's disease. The objective of this algorithm is to select minimum number of features providing high classification accuracy. The results from the investigations showed that the proposed TLBO-based feature optimization system can improve the accuracy of classifiers compared to previous methods on BC dataset. The classification model was trained with a reduced number of features. Our future studies will focus on working with a new hybrid algorithm.

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