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Enhanced Detection of Benign and Malignant Breast Cancer Cells via DEA-ELM Hybrid Approach

Yasin Sönmez

Department of Computer Technologies, Vocational School of Technical Sciences, Batman University, Batman 72100, Türkiye

Corresponding Author Email: yasin.sonmez@batman.edu.tr

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ABSTRACT

Breast cancer remains a major global health problem, especially among women over 40. Early detection is critical for curing the disease. For this, recent advances in computer-aided diagnosis are important in improving diagnostic accuracy. This study proposes a new classification model that combines Differential Evolution Algorithms (DEA) with Extreme Learning Machines (ELM) to distinguish between benign and malignant breast cancer cells accurately. The UC Irvine Machine Learning Repository Breast Cancer Wisconsin (Diagnostic) public breast cancer cells image database was used to classify benign and malignant cells in breast cancer. In our architecture, the number of hidden neurons is optimized by DEA to improve the classification performance. The proposed DEA-ELM model achieved the highest overall performance, with an accuracy of 99.72%, precision of 98.15%, recall of 99.72%, and F1-score of 97.65%. This study provides evidence of the efficacy of the DEA-ELM method in diagnosing breast cancer cells. These findings emphasize the possible use of the approach in the early identification of cancer and developing treatment strategies. The suggested approach can be expanded in future research to enhance its performance by using supplementary datasets and optimizing model parameters.

1. INTRODUCTION

Breast cancer is known as the second most common type of cancer among women globally and poses a significant health risk, especially for women over the age of 40 [1, 2]. The statistics for breast cancer in 2020 painted a concerning picture, with approximately 2.3 million new cases reported [3-5]. This staggering number indicates that one out of every eight cancers diagnosed that year was breast cancer. This high incidence rate highlights the extensive scope of the disease and underscores the urgency for effective prevention, diagnosis, and treatment strategies [4, 5]. The mortality rates associated with breast cancer are equally alarming, with an estimated 700.000 deaths occurring due to the disease in the past year. These figures not only reflect the lethality of breast cancer but also demonstrate the challenges faced in combating the disease. Future projections are even more daunting, with an expected nearly 50% increase in breast cancer cases by 2040. This anticipated rise further emphasizes the need for ongoing research efforts, advanced healthcare services, early detection programs, and awareness campaigns to mitigate the impact of breast cancer on a global scale [5, 6].

The most effective defense against breast cancer is ensuring early detection. New and advanced diagnostic technologies, coupled with computer-aided methods, have accelerated and enhanced the diagnostic process. Early detection of breast cancer is associated with a substantial increase in treatment efficacy and a corresponding improvement in patient survival rates. Breast cancer exhibits a heterogeneous disease profile, necessitating a thorough assessment of tumors with diverse biological characteristics to elucidate the clinical trajectory of the disease and the responses to therapeutic interventions. Studies in the literature [1-6] emphasize the importance of a multidisciplinary approach in managing such tumors and determining therapy options. In this context, personalizing the diagnosis and treatment strategies for breast cancer based on the individual characteristics of the tumor plays a critical role in achieving optimal outcomes [7-9].

The diagnosis of breast cancer is typically conducted through a biopsy. A biopsy is a laboratory procedure performed by a pathologist to identify cancer cells. The pathologist collects tissue samples from breast tissue through various techniques, including fine needle aspiration, core needle aspiration, core needle biopsy, vacuum-assisted biopsy, and surgical biopsy [1, 2]. Afterward, these collected cancer tissues are examined under a microscope. The images obtained under the microscope are called histopathology images. The pathologist analyzes these histopathological images and classifies them as cancerous or non-cancerous. However, there are some disadvantages to the pathologist's evaluation. The evaluation and analysis process conducted by pathologists is often time-consuming. This can prolong the waiting time for patients in the diagnostic process and delay the start of treatment. The cost of biopsies and histopathological analysis performed by pathologists is high. This can pose an additional barrier for patients with difficulty accessing healthcare

services. Pathologists may sometimes struggle to detect or interpret cancer cells accurately. This can lead to false negative results for patients and delays in treatment. Pathologist evaluations can sometimes be subjective. There may be differences in interpretation among different pathologists, leading to inconsistency and misleading results. Pathologists may struggle to make an accurate assessment if the tissue samples obtained during the biopsy are insufficient. This can reduce the reliability of the diagnosis. While the significance of pathologist evaluation in breast cancer diagnosis is unequivocal, it is essential to consider the potential disadvantages associated with these methods [1, 2, 4].

Digital pathology is a research field involving the use of digital imaging and artificial intelligence techniques in pathology. Academic studies in this field demonstrate that significant advancements can be made in diagnosing and prognosis diseases by digitally recording and analyzing pathological examinations and utilizing artificial intelligence algorithms [10, 11]. Digital pathology provides pathologists with a work environment independent of time and location, allowing them to conduct routine pathological examinations digitally. Artificial intelligence algorithms play a crucial role in digital pathology. These algorithms assist in the analysis of pathological images and the acquisition of information used in the diagnosis and prognosis of diseases. For example, artificial intelligence systems developed for cancer diagnosis can help pathologists identify cancerous areas and determine diagnostic and prognostic information. Additionally, digital pathology studies supported by artificial intelligence enable faster patient diagnosis processes. For instance, in one study, a system utilizing an artificial intelligence algorithm assisted pathologists in diagnosing prostate cancer, accelerating the diagnosis process and improving patient management [9]. AI-based techniques can be successfully applied to diagnose diseases early [12, 13]. A convolutional neural network (CNN) model was specifically designed for the automated classification of breast cancer utilizing two types of medical imaging: mammography (MG) and ultrasonography (US). Their CNN model included five trainable convolutional blocks, each containing four convolutional layers and a fully connected layer that served as a classifier. Notably, their model effectively extracted important features from the input images while using fewer adjustable parameters. This suggests that their model efficiently captured relevant information for breast cancer classification. The researchers performed extensive simulations with various datasets. They employed the MIAS, DDSM, and INbreast datasets for mammography, whereas for ultrasonography, they utilized the BUS-1 and BUS-2 datasets. Their CNN model demonstrated superior performance to recent state-of-the-art approaches on these datasets. Additionally, Muduli et al. applied data augmentation techniques—methods designed to enhance the diversity and quantity of training data—to mitigate the problem of overfitting. By augmenting the data, they successfully reduced overfitting and enhanced the model's generalization ability. The reported results indicated high accuracy rates for the classification task. On the MIAS dataset, the CNN model achieved an accuracy of 96.55%. For the DDSM dataset, the accuracy was 90.68%, while on the INbreast dataset, it reached 91.28%. The model demonstrated exceptional performance on the BUS-1 dataset, achieving an accuracy of 100%, and recorded an accuracy of 89.73% on theBUS-2dataset [14].

The study by Tsai et al. [15] focused on BI-RADS (Breast Imaging Reporting and Data System) classification using a database from the E-Da hospital in Taiwan. The researchers used images from the database and relied on labels assigned by physicians to perform the classification. Their approach determined the classification based on the proportion of lesion areas within a specific location. They divided the images into blocks of size 224 × 224 pixels with a 36-pixel pitch. These blocks served as the basis for assessing the presence and characteristics of lesions in the breast images. Tsai employed the EfficientNET deep learning architecture, a state-of-the-art model for image classification tasks to perform the classification task. This architecture extracted relevant features from the breast images and made predictions about the BI-RADS category. The results of their classification experiments showed promising performance. The reported metrics included a precision (PRE) of 94.22%, a sensitivity (SEN) of 95.31%, and a specificity (SPE) of 99.15%. These metrics indicate the model's ability to accurately identify and classify breast lesions based on the BI-RADS system. Overall, Tsai's study demonstrated the successful application of the EfficientNET architecture for BI-RADS classification, achieving high accuracy and sensitivity in detecting breast lesions. These findings suggest the potential of deep learning methods in aiding physicians in diagnosing and assessing breast cancer. Raza et al. [16] proposed a convolutional neural network (CNN) architecture comprising 24 convolutional blocks, which include six convolutional filters, nine Inception modules, and a fully connected layer. In their study, Raza et al. incorporated Batch Normalization alongside activation functions such as ReLU, Leaky ReLU, and ReLU-clipped. The designed architecture achieved impressive results, with an accuracy (ACC) of 99.35%, precision (PRE) of 99.6%, sensitivity (SEN) of 99.66%, and an F1-Score of 99.6%. Raza et al. [16] proposed a CNN architecture for a specific task. The CNN architecture designed by the researchers consisted of 24 convolutional blocks. Each block comprised six convolutional filters, nine Inception modules, and one fully connected layer. These components were carefully structured to extract relevant features from the input data and make accurate predictions. In their work, Raza et al. [16] experimented with different activation functions, including RELU, Leaky-RELU, and RELU-clipped, to introduce non-linearity and enhance the model's learning capabilities. They also utilized batch normalization, a technique that helps stabilize the learning process and improve the model's generalization ability. The performance of their designed CNN architecture was evaluated using various metrics. The reported results demonstrated a high ACC of 99.35%, PRE of 99.6%, SEN of 99.66%, and F1-Score of 99.6%. These metrics indicate the effectiveness of Raza et al.'s CNN architecture in achieving accurate and reliable predictions for the specific task they were addressing. The elevated values of accuracy, precision, sensitivity, and F1-Score suggest that their model demonstrated exceptional performance in classifying and predicting the target variable. Overall, Raza et al.'s study showcased the successful design and implementation of a CNN architecture with multiple convolutional blocks and Inception modules. A study was conducted using digital image analysis and machine learning techniques to classify and predict the diagnosis of breast masses based on fine needle aspiration (FNA). Researchers utilized a machine learning model on digital images obtained from FNA samples. The model was trained to analyze the features in the images and classify and predict the diagnosis of breast masses. The results

showed a diagnostic accuracy of 97% for the predicted outcomes. A real diagnostic accuracy of 100% was reported for 118 new samples [17]. Kowal and colleagues introduced a method for the automatic classification of images. This approach focuses on identifying nuclear regions within the images and utilizing these regions for classification by classifiers [18]. In their methodology, a two-stage segmentation process was applied to the images. The initial stage focused on segmenting the foreground from the background using an adaptive threshold. This approach facilitates the extraction of critical regions, including nuclei, red blood cells, and other salient features within the images. In the second stage, the regions corresponding to nuclei are distinguished from blood cells and other components. Ultimately, the nuclear regions are characterized by various features, which are then utilized as input for the classifiers. Kowal and colleagues assessed the classification accuracy on 500 sample images utilizing three different classifiers: K-nearest neighbor, Naive Bayes, and decision trees. The results indicated a classification accuracy ranging from 96% to 100%.

As seen in the literature review, artificial neural networks (ANN) show acceptable results. But, one of the most important issues in ANN is determining the optimal network structure, which includes both number of neurons in the hidden layer and the employed transfer (activation) function. These values are generally determined by tuning based on trials. Therefore, a practical model is required to distinguish between benign and malignant cells in breast cancer and to address the problems above. The following are this work's main contributions. The primary objective of this study was to enhance classification efficiency and mitigate the challenges associated with ELM to enable the reliable differentiation between benign and malignant cells in breast cancer using Differential Evaluation Algorithm (DEA). Optimizing an ANN may require too much time. Therefore, generally some specialized values/transfer functions are tested in trials. Therefore, manually tuning does not grantee to achieve best ANN model.

On the other hand, ELM has its extremely fast training stage, which may be take 1% of traditional backpropagation based learned ANN. And addition to ELM, DEA is also a fast optimizing method. In place of conventional ELM, a technique with the following benefits was suggested in this study: Because of the enhanced NHN, the DEA-ELM, which is used to separate benign and malignant samples, has better classification accuracy than the ELM. Furthermore, this DEA-based process is used to optimize the efficiency of separating the samples as benign and malignant.

The study is organized as follows: Section 1 presents the collection of breast cancer cell images. Section 2 outlines the methodologies and strategies employed. Section 3 provides the findings from the ELM and Differential Evaluation Algorithm (DEA) investigations used for classification. Finally, Sections 4 and 5 contain the discussions and conclusions, respectively. This article was written with the principal objective of enhancing the classification efficiency and addressing the limitations of the ELM in accurately differentiating between benign and malignant cells in breast cancer. The study proposes using a method called DEA-ELM, which offers several advantages over traditional ELM approaches. The importance of this study lies in its potential to improve the accuracy of breast cancer cell classification, which is crucial for early detection and effective treatment. By addressing the limitations of ELM, the DEA-ELM method offers a better classification accuracy, leading to more accurate identification of benign and malignant cells. This can significantly impact breast cancer research and contribute to improved diagnostic practices.

The contribution of this study to science is twofold. Firstly, it introduces the DEA-ELM method, which combines the benefits of DEA with ELM to improve classification accuracy. DEA enhances the efficiency of distinguishing between benign and malignant samples, leading to improved classification accuracy. This innovative approach showcases the potential of combining different techniques to achieve better results in medical image classification. Secondly, the study showcases empirical results in Section 3. In summary, this article was written to address the limitations of ELM in breast cancer cell classification and propose a novel method, DEA-ELM, that improves classification accuracy. The importance of accurate classification in breast cancer diagnosis and treatment underscores the significance of this study. The contribution lies in introducing the DEA-ELM method, its empirical evaluation, and the potential it holds for enhancing medical image classification.

2. MATERIAL AND METHOD

2.1 Material

This study aims to assess the effectiveness of an ELM by utilizing features extracted through image segmentation on the Breast Cancer Wisconsin (Diagnostic) image data set from the UCI Machine Learning Repository [19]. Figure 1 shows raw images at different zoom values.

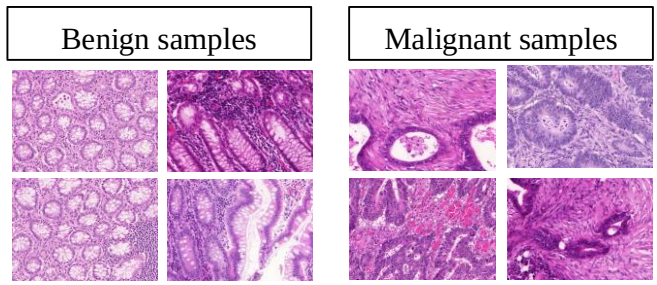

Figure 1. Sample image of the images in the data set

The dataset comprises recorded features for each cell nucleus, including radius, texture, perimeter, area, smoothness, concavity, concave points, symmetry, and fractal dimensions. Each nucleus is labeled based on diagnosis as malignant (M) or benign (B).

The distribution of classes within the dataset is a crucial factor to consider when interpreting the findings and forming conclusions. In this particular dataset, there are 357 malignant cases and 212 benign cases. The imbalance in class distribution, with a higher number of malignant cases than benign cases, can have implications for model performance and evaluation. Imbalanced datasets can introduce challenges in accurately predicting the minority class (benign cases) due to the bias towards the majority class (malignant cases). Figure 2 shows the data distribution in the data set.

In the context of breast cancer classification, a higher number of malignant cases within the dataset indicates the predominance of this condition. However, it is crucial to consider the potential effects of class imbalance on the evaluation metrics and the generalizability of the model's

performance. To tackle the issue of class imbalance, one can utilize effective sampling methods such as oversampling the minority class, undersampling the majority class, or implementing advanced techniques like SMOTE (Synthetic Minority Oversampling Technique). These techniques aim to balance the class distribution and improve the model's performance, particularly in correctly identifying benign cases. Considering the class distribution in the dataset, it is crucial to interpret the results cautiously and consider the potential biases that may arise due to the imbalance. Additionally, further analysis and evaluation of the model should consider the class-specific performance metrics to assess the effectiveness of the classification approach for both malignant and benign cases.

2.2 Method

Figure 3 illustrates the diagram of the proposed classification method. As seen in the figure, the employed method can be divided into four sections. In the first section, procurement and determination of the dataset are attained through the UCI. After the preprocessing steps, training classification models and training regression models. The final phase of the proposed method involves differentiating samples into benign and malignant categories, representing an optimized enhancement of several Hidden Network (NHN) of ELM.

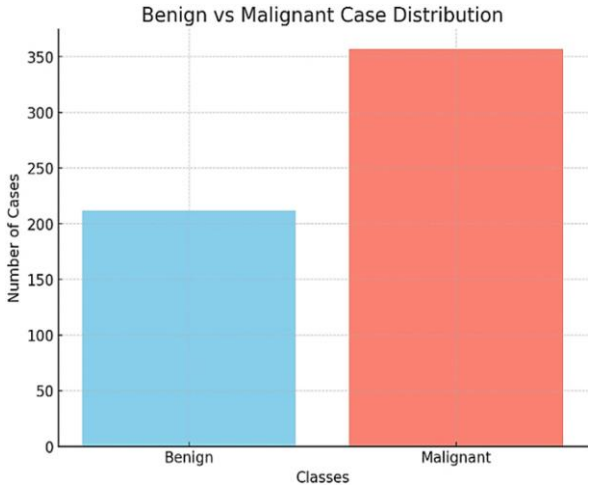

Figure 2. Class distribution in the data set

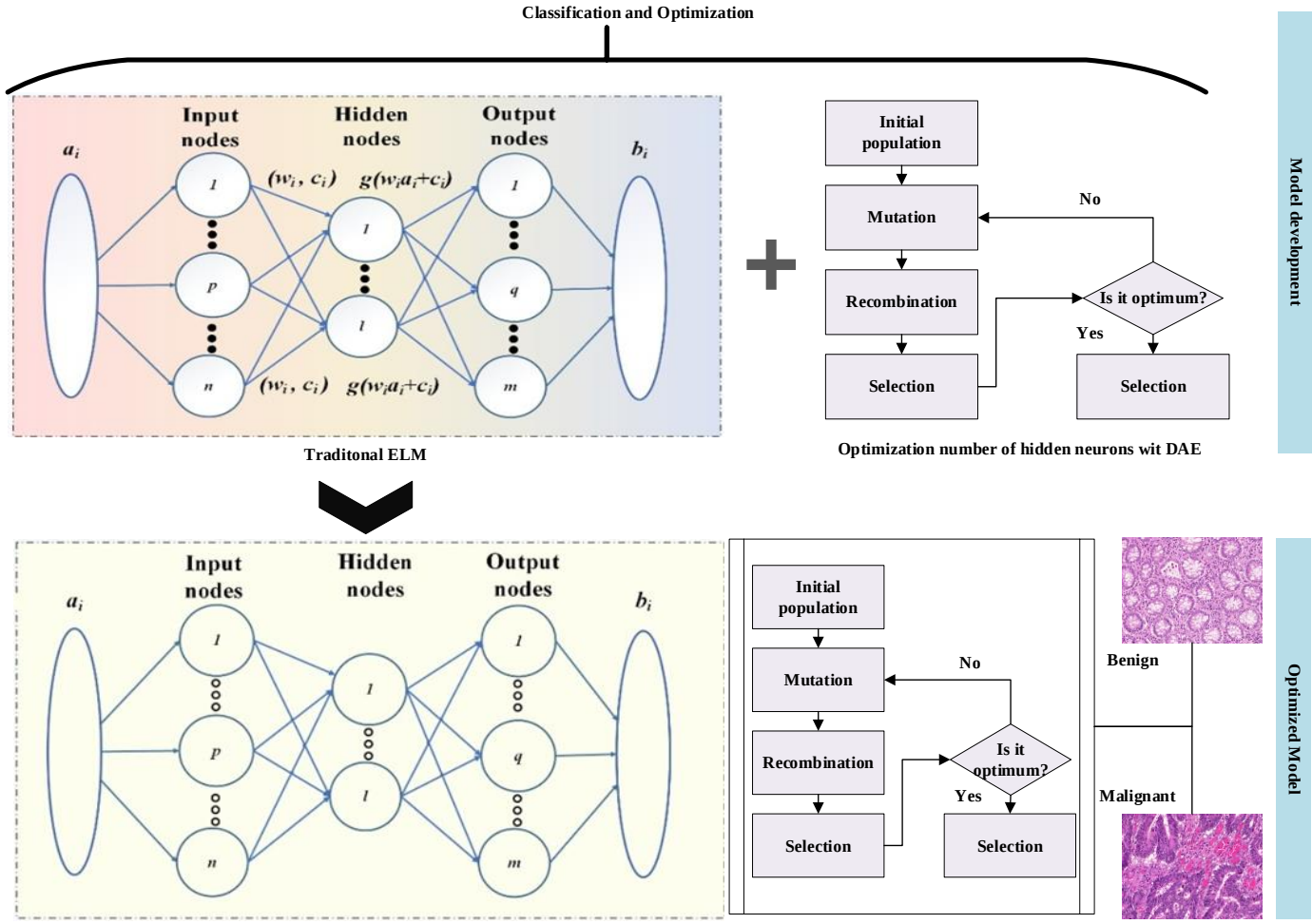

Figure 3. The block schema of the proposed system

2.2.1 ELM

ELM can be defined as a type of single-layer feedforward neural network [20]. This definition underpins a fast and effective learning algorithm [20, 21]. ELM consists of input, hidden, and output layers, similar to feedback ANN structures. The ELM's connection from the input to the hidden layer is defined as Eq. (1) [21]:

$$H = g(XW + b) \quad (1)$$

where, H is the output matrix of the hidden layer, X is the input data matrix, W the is the randomly assigned weight matrix, b

the is the randomly assigned bias vector, and g represents the activation function. In ELM, the link from the hidden layer to the output layer is expressed as Eq. (2) [21]:

$$Y = H\beta \tag{2}$$

where, Y is the output matrix predicted by the model, H is the hidden layer output matrix, and β is the weights matrix in the output layer. Weights in the output layer β are calculated using the least squares method with the Eq. (3) [21]:

$$\beta = H^{\dagger}T \tag{3}$$

where, $H^{\dagger}$ is the Moore-Penrose pseudo-inverse of the matrix and T is the target output matrix.

The key difference from traditional ANNs is that ELM only has a single hidden layer. Using a single hidden layer aims to make the training process faster and more effective [20, 21]. In this layer, the weights are randomly selected and not updated, allowing the operations to proceed with fixed weights. It can be observed that ELM provides a significantly faster training process than traditional ANN methods. Figure 4 presents the ELM architecture.

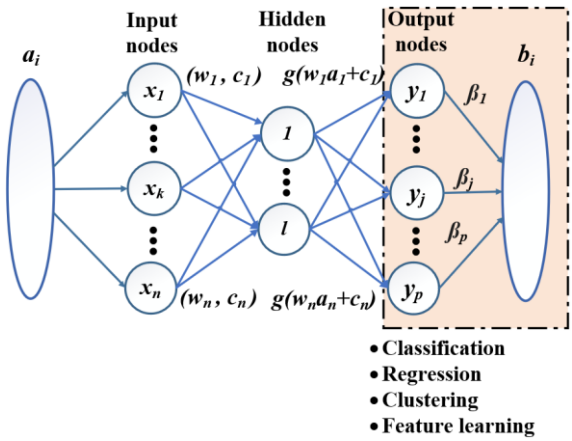

Figure 4. ELM architecture

The operation of an ELM differs from traditional feedforward networks. During training, the input data is directly passed to the hidden layer, where it is multiplied by randomly assigned weights and processed through activation functions. The resulting values are then transmitted to the output layer. Unlike traditional networks, the weights and biases in the hidden layer are not optimized; instead, the output layer weights are computed analytically using the Moore-Penrose generalized inverse. This approach provides a direct solution to approximate the target outputs, avoiding the iterative optimization process typical of conventional neural networks.

ELM operates on a different principle from traditional feedforward ANN networks. During the training process of ELM structures, data is directly transferred from the input layer to the hidden layer. Then, it undergoes multiplication with the weights at each hidden node and passes through the respective activation function [22]. This procedure transmits the obtained values to the output layer. The weights and biases in the hidden layer are randomly selected and are not subjected to any optimization process [20-22]. Instead, different analytical approaches are used to calculate the weights in the output layer. This approach, which eliminates iterative optimization and the need for multiple hidden layers as in traditional neural networks, aims to achieve a much faster solution [23]. The ELM approach can provide practical advantages, particularly in applications requiring real-time processing and handling of large datasets. It has been effectively employed in various domains, including image processing, speech recognition, and text analysis. However, the random weight assignment in ELM can negatively affect the stability and performance of the model, leading to limitations in specific applications. Therefore, when employing ELM, it is essential to carefully evaluate the model's sensitivity and generalization capability, considering these disadvantages [23].

2.2.2 DEA

The DEA, introduced by Price and Storm [24, 25, 29], is an advanced technique that addresses the challenges of constant parameters. DEA is an empirical procedure that relies on genetic algorithm principles and operators. It offers practical solutions to the limitations of continuous data [26-29]. DEA has been widely applied in various areas, where repetitions in the algorithm explore superior outcomes by leveraging the operators.

The core objective of the algorithm is to enhance its efficiency in addressing the limitations associated with constant score coding. This enhancement is achieved by implementing specific modifications to the genetic operators, namely crossing, mutation, and selection, which are fundamental components of Genetic Algorithms (GA). However, in the context of data envelope analysis (DEA), a unique approach is taken, in which individual chromosomes are treated independently. Unlike traditional methods, where all operators are uniformly applied to each individual, DEA adopts a more personalized strategy. Here, creating a new individual involves the random selection of three other chromosomes, introducing a dynamic element to the evolutionary process. This process encompasses both mutation and crossover operations. The compatibility between the newly generated and incumbent chromosome is assessed, with the more favorable chromosome being transitioned to the subsequent population as a fresh individual. The election operator is also used in this selection process. The evaluation of solutions produced by DEA is contingent upon their efficacy in attaining the specified objective function. The fitness function $f(x)$ can be defined as Eq. (4) [27, 28]:

$$f(x) = \sum_{i=1}^{n} w_i x_i \tag{4}$$

where, x represents the genetic characteristics of individuals, and w represents the weights. The cross-over process is defined as Eq. (5) [28, 29]:

$$x_{\text{new}} = (1-\alpha)x_i + \alpha x_j \tag{5}$$

A cross-over is made between two individuals with parameter α. A mutation is a slight change. The following equation can describe it as Eq. (6) [26, 29]:

$$x_{\text{mutated}} = x + \epsilon \tag{6}$$

where, ϵ is a small random change. The DEA process is distinguished by its straightforward design, rapid parameter

optimization, and user-friendly coding, offering significant advantages and key features. A D vector represents the D factor in the algorithm. The initial step of the algorithm involves selecting an individual from the NP inhabitant vector. This particular individual undergoes advanced implementations of mutation, crossover, and selection operators [26]. The primary steps of the DEA algorithm are illustrated in Figure 5.

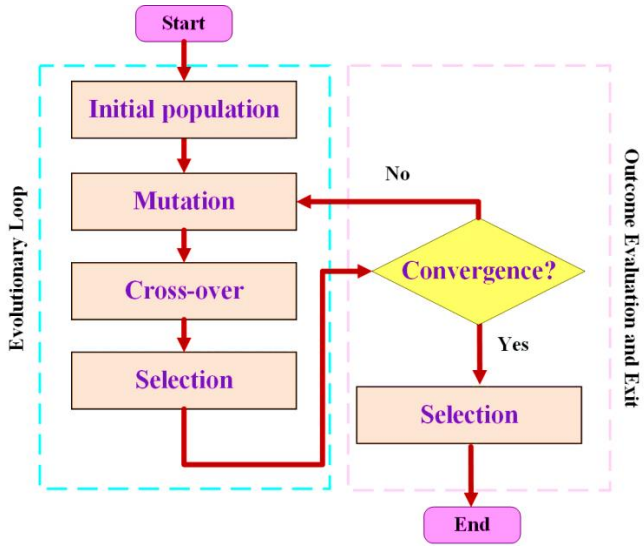

Figure 5. DEA steps

The number of variables in the problem determines the quantity of genes in each chromosome. In the realm of DEA, the population size (i.e., the number of chromosomes) must always exceed three. This requirement arises from utilizing three additional chromosomes, apart from the current one, to facilitate the creation of new chromosomes. In the mutation process, random alterations are introduced to different segments of the genes within the existing chromosome. In the context of DEA, three supplementary chromosomes are chosen for mutation. The variance between the first two selected chromosomes is calculated and multiplied by the scaling parameter.

2.3 Implementation of the DEA and ELM

Before employing the proposed method, each of the features is normalized and transferred in the range of 0-1. The implementation of DEA-ELM is given Figure 6.

In the proposed method TF and NHN are optimized. Each step defines the process of generating ELM individuals, calculating their costs, and regenerating them using DEA. These steps constitute the basic building blocks of the method and ensure that certain goals are achieved in the process:

Step 1: Determining the subsets of TF and NHN.

Step 2: Generating a group of ELM individuals that the TF and NHN assigned randomly based on DEA.

Step 3: Calculating the costs of each individual based on accuracy.

Step 4: Regenerate a new group of ELM individuals based on newly assigned the TF and NHN according to DEA (mutation, crossover).

Step 5: Recalculate costs, regenerate a new population and continue this process until stop criteria is achieved. The other details about implementation are given below:

-The objective of employed DEA-ELM is to maximize test accuracy.

-The range of NHN is 1-500.

-The TF subset consists the following activation functions Radbas, Sin, Sig, Hardlim, and Tribas.

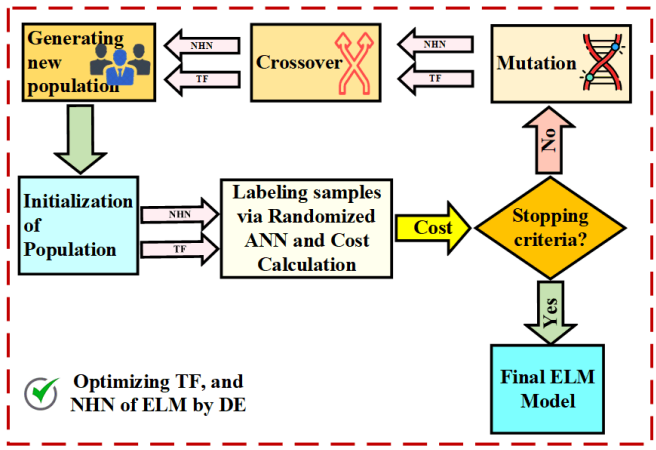

Figure 6. DEA steps

2.4 Employed performance parameters

A diverse range of statistical performance metrics can be employed to assess the effectiveness of a model. Among these, the most commonly used metrics are:

Accuracy: Training the model enables the computation of performance metrics by analyzing the confusion matrix through calculations. One of these metrics is accuracy, which is determined by dividing the number of accurately predicted values by the total test data count. Essentially, it provides an understanding of whether the model is working correctly. Eq. (7) represents the calculation required to determine accuracy [30].

$$ACC = \frac{TP + TN}{TP + FP + TN + FN} \tag{7}$$

Precision: The precision of model predictions is represented by the precision value. It determines the proportion of actual positives among the instances that the model predicts as positive on the test data. Eq. (8) represents the calculation required to determine the precision metric [30-33].

$$PRE = \frac{TP}{TP + FP} \tag{8}$$

Recall: Recall is a commonly used performance evaluation method, especially in classification problems. This parameter is used to calculate the proportion of positive class values that are correctly identified as positive by the model. A high recall value indicates that the model has high sensitivity. Eq. (9) represents the steps required to calculate the recall metric [30-33]:

$$Recall = \frac{TP}{TP + FN} \tag{9}$$

F1-Score: The F1-Score utilizes the harmonic mean of precision and recall as a performance evaluation metric. This method aims to ensure control over extreme cases for the model's success. Eq. (10) represents the steps required to

calculate the F1-Score metric [30-33].

$$F1-Score = 2 * \frac{PRE * Recall}{PRE + Recall} \quad (10)$$

K-Fold Cross-Validation: The K-Fold Cross-validation technique is a reliable and efficient way to assess a machine learning model's performance.

This approach involves randomly dividing the dataset into "k" subsets of equal size and performing operations on these subsets. One of the subsets is selected as the test data, while the remaining subsets serve as the training set. This process is repeated for "k" iterations, with each K subsets used as the test set once. The results are then calculated by averaging the performance measurements from each iteration. The K-Fold Cross-Validation method aims to test the sensitivity of the trained model to different parts of the dataset and obtain more robust generalization performance estimates [34-36]. This study applies the K-Fold Cross-Validation process to the data to overcome overfitting and underfitting issues. This method aims to achieve higher success rates and train a reliable training/test model.

3. RESULTS

The decision tree (DT), random forest (RF), Naive Bayes, support vector machine (SVM), ELM, and DEA-ELM algorithms were tested for performance in this section. The ELM's Radbas, Sin, Sig, Hardlim, and Tribas activation functions were used to create achievement effects within this scope (Table 1).

Table 1. Performance results of the methods

Algorithm	Accuracy (%)	Precision (%)	Recall (%)	F1-score (%)
DEA-ELM	99.72	98.15	99.72	97.65
ELM	96.53	95.34	96.53	95.09
SVM	94.6	95.15	94.6	91.65
Naive Bayes	93.86	94.41	93.86	93.73
RF	92.11	92.99	92.11	91.88
DT	88.6	91.24	88.6	88.77

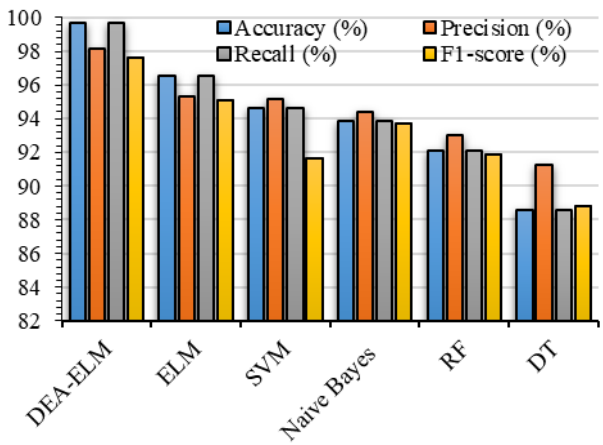

Figure 7. Performance metrics efficiency results of the methods

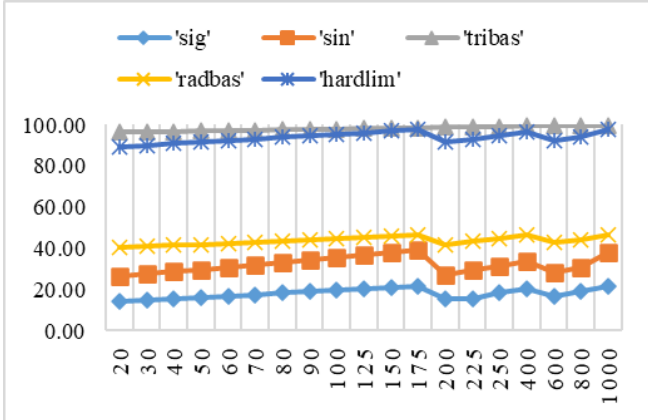

Figure 8. DEA-ELM test ACC comparison with activation functions

Each sample was separated into two groups: test and training sets. Additionally, the samples were examined using a 10-fold cross-validation technique. A graphical comparison of the performance metrics results of the methods is presented in Figure 7.

As shown in Figure 8, classifier outcomes were obtained by adjusting the NHN of ELM to 20, 30, 40, 50, 60, 80, 90, 100, 125, 150, 175, 200, 225, 250, 400, 600, 800, and 1000.

The primary goal of this study was to evaluate the model's performance by enhancing its capabilities. ELM's NHN through DEA. The DEA, a potent meta-heuristic enhancement technique, was used for this. The classification using ELM yielded better results when the DEA was applied.

Differential Evolution Algorithms - Extreme Learning Machine (DEA-ELM) model demonstrates the highest overall performance, with an accuracy of 99.72%, precision of 98.15%, recall of 99.72%, and F1-score of 97.65%. The high values across all metrics indicate this model is highly effective at the given task, with an excellent ability to correctly identify positive instances (PRE) and a low rate of false negatives (high recall). This suggests the DEA-ELM is a robust and reliable classification algorithm for the problem. In summary, the DEA-ELM emerges as the top performer, exhibiting exceptional ACC, PRE, recall, and F1 scores. The ELM and SVM also demonstrate strong classification capabilities, while Naive Bayes, RF, and DT show progressively lower but still viable performance. This comparative analysis provides valuable insights into these algorithms' relative strengths and weaknesses for the given problem. The testing scores for five different activation functions were obtained using DEA-ELM. The enhancement in NHN achieved through DEA-ELM is detailed in Table 2. The table suggests that the 'tribas' and 'hardlim' activation functions, when combined with a sufficiently large number of hidden neurons (around 225 and 175, respectively), can achieve exceptionally high training accuracies. In contrast, the 'sig,' 'sin,' and 'rabbis' activation functions tend to have lower and less consistent training accuracy performance across the range of NHN values provided.

Table 2 displays the test accuracy (ACC) of the DEA-ELM model using different activation functions across various hidden neuron counts (NHN). Overall, accuracy improves with more hidden neurons, indicating enhanced model capacity. The tribes and hardline functions consistently achieve high accuracy, peaking at 99.72% with several configurations, while the sig, sin, and rabbis functions perform

poorly across all counts. The results suggest that optimal neuron selection and activation function choice are crucial for maximizing classification performance in breast cancer diagnosis, with stabilization of high accuracy evident beyond around 200 neurons.

Table 2. Test ACC for DEA-ELM using activation functions

NHN	sig	sin	tribas	radbas	hardlim
20	14.31	26.31	96.31	40.31	89.31
30	14.97	27.47	96.52	40.87	90.07
40	15.63	28.63	96.73	41.43	90.83
50	16.29	29.79	96.94	41.99	91.59
60	16.95	30.95	97.15	42.55	92.35
70	17.61	32.11	97.36	43.11	93.11
80	18.27	33.27	97.57	43.67	93.87
90	18.93	34.43	97.78	44.23	94.63
100	19.59	35.59	97.99	44.79	95.39
125	20.25	36.75	98.20	45.35	96.15
150	20.91	37.91	98.41	45.91	96.91
175	21.57	39.07	98.62	46.47	97.67
200	15.42	27.23	98.83	41.79	91.43
225	15.73	29.39	99.05	43.35	93.19
250	18.72	31.55	99.25	44.91	94.95
400	20.37	33.71	**99.72**	46.47	96.71
600	16.53	28.15	**99.72**	42.67	92.55
800	19.18	30.87	**99.72**	44.23	94.31
1000	21.43	37.83	**99.72**	46.63	97.83

Table 3. A summary of previous studies

Ref.	Proposed Method	ACC (%)
[14]	Deep Convolution Neural Network	96.55
[15]	Deep Neural Network Model	94.22
[16]	Deep Learning	99.63
[37]	Explainable AI	97.58
[38]	Multi-Level fully Convolutional	99.50

The DEA-ELM method was preferred in this study due to its high efficiency and speed. ELM offer rapid training and low computational demands, making them ideal for large medical image datasets. The method achieved an impressive accuracy of 99.72% in distinguishing between benign and malignant breast cancer cells, thanks to DEA's optimization of hidden neurons. This combination leverages the strengths of both approaches, rapid training and refined optimization, enhancing diagnostic accuracy and enabling early cancer detection. Additionally, the approach provides a foundation for future research by allowing for the incorporation of supplementary datasets and parameter optimization.

Table 3 summarizes the accuracy (ACC) of various proposed methods for breast cancer diagnosis. Notably, the highest accuracy reported in this study was 99.72%, which was achieved using the DEA-ELM method. This surpasses Raza's 2023 result of 99.63% with a deep learning approach, demonstrating the effectiveness of the DEA-ELM model. Other methods, such as Muduli's deep convolutional neural network (96.55%) and Tsai's deep neural network model (94.22%), show comparatively lower accuracies. Innovative approaches like Chakravarthy's Explainable AI (97.58%) and Maurya's Multi-Level fully Convolutional (99,50%) highlight significant contributions to model interpretability and efficiency. Overall, this table emphasizes the high performance of the DEA-ELM method in breast cancer diagnosis while illustrating the continuous advancements in the field, indicating a trend toward achieving higher accuracy and improved methodologies. This is crucial for enhancing early detection and treatment outcomes.

4. CONCLUSION

Accurate classification of breast cancer cells into benign and malignant categories is crucial for early diagnosis and effective treatment planning. This study's results highlight the potential of the proposed DEA-ELM approach in improving classification performance for this vital medical task. The key findings of this work highlight several essential aspects. Firstly, the traditional ELM model achieved a reasonably high classification accuracy of 96.53%, indicating the suitability of this machine-learning technique for breast cancer cell classification. However, the further optimization of ELM using the DEA led to a remarkable improvement in the classification performance, reaching an accuracy of 99.72%. This significant improvement can be attributed to the capacity of the DEA to efficiently optimize the number of hidden neurons in an ELM, thereby enhancing the model's generalization capabilities and robustness. The superiority of the DEA-ELM approach over other commonly used machine learning techniques, such as Support Vector Machines (SVM) and decision trees, underscores the benefits of leveraging the strengths of both ELM and DEA algorithms. When combined, ELM's rapid training and generalization capabilities with DEA's optimization prowess yield a highly accurate and efficient classification model for breast cancer cells. One of the fundamental advantages of the DEA-ELM method is its ability to address the complexities and heterogeneity associated with breast cancer. The disease encompasses various genetic, environmental, and lifestyle factors, contributing to its diverse biological manifestations. The DEA-ELM approach is particularly practical in adapting to these intricacies by optimizing the ELM's parameters to identify subtle differences and patterns between benign and malignant cells. This adaptability is crucial for improving classification accuracy and ensuring reliable performance across varied datasets. Moreover, the DEA-ELM method provides a robust framework for medical applications where precision and efficiency are paramount. By automating the classification of breast cancer cells, the DEA-ELM approach reduces the reliance on manual evaluations, which are often time-consuming and prone to variability. The rapid processing capabilities of DEA-ELM enable the analysis of large-scale biopsy samples, streamlining diagnostic workflows and reducing the burden on healthcare professionals. This efficiency accelerates the diagnostic process and ensures consistency and reliability in results, which are critical in clinical decision-making. Various factors, including genetic, environmental, and lifestyle-related elements influence the disease. The DEA-ELM's ability to adaptively optimize the ELM parameters likely enables it to capture the intricate patterns and subtle differences between benign and malignant cells, leading to the observed improvements in classification accuracy.

From a clinical perspective, the high classification performance of the DEA-ELM approach has the potential to enhance the diagnosis and treatment of breast cancer greatly. By automating the cell classification process and achieving consistent and reliable results, this method can alleviate the subjectivity and variability often encountered in manual pathological examinations. Additionally, the rapid processing capabilities of the DEA-ELM model can facilitate the analysis of large-scale biopsy samples, streamlining the diagnostic

workflow and reducing the burden on healthcare professionals. This method can reduce the workload of pathologists in clinical practice, save time, and reduce human errors. It can also increase efficiency in the diagnostic process by enabling faster analysis of large-scale biopsy samples. The successful application of the DEA-ELM approach in breast cancer cell classification suggests the potential for similar optimized models to be extended to other cancer types and medical imaging modalities, further advancing the field of computer-aided diagnosis and personalized healthcare.

In conclusion, the DEA-ELM method presented in this study demonstrates a highly effective and robust approach for classifying benign and malignant breast cancer cells. The optimization of the ELM model through the DEA has led to a significant improvement in classification accuracy, paving the way for more accurate and efficient breast cancer diagnosis and treatment planning. The findings of this work underscore the value of integrating advanced AI and machine learning techniques in medical image analysis and highlight the need for further research in this promising direction. The proposed DEA-ELM method has the potential to be a reliable tool in medical diagnoses with its high-performance classification capabilities. However, testing this method with different datasets and evaluating it in a broader framework would be beneficial in terms of the generalizability and robustness of the model.

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