Enhancing Breast Cancer Diagnosis using a Modified Elman Neural Network with Optimized Algorithm Integration

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***Abstract*—Breast cancer is a class of cancer that starts in the cells of the breast. It happens once the cells of the breast divide and amplify abnormally and uncontrollably. Other parts of the body, including lymph nodes, bones, lungs, and liver, can be affected by breast cancer. Early diagnosis and treatment are critical in helping to lessen the risk of death from breast cancer. Machine learning is a type of artificial intelligence that can be used to diagnose breast cancer. It uses algorithms to analyze data and assess patterns associated with breast cancer. Machine learning models can help improve diagnostic accuracy, reduce false-positive results, and improve the efficiency of diagnosis. Elman Neural Networks (ENNs) are machine learning algorithms that can be used to diagnose breast cancer. ENNs use medical data to detect patterns that are associated with the presence of cancer. The accuracy of ENNs in diagnosing breast cancer is still being researched, but they have the potential to help improve diagnostic accuracy and reduce false-positive results. In the existing study, a new modified version of ENN founded on a combination of an upgraded version of the imperialist competitive algorithm is proposed for this objective. Likewise, the results of the model compared with some other methods illustrated the proposed method's higher efficiency.**

***Keywords*—Breast cancer model; Elman Neural Network; upgraded imperialist competitive algorithm**

I. Introduction

A class of cancer that begins in the cells of the breast is called breast cancer. It occurs once the cells in the breast start to expand abnormally and uncontrolled. It can affect both men and women, although women are more likely to be diagnosed with it than men [1]. The advantage of recognizing breast cancer in the initial steps is that it can significantly increase a person's chances of survival and decrease the risk of complications from surgery and other treatments [2]. Early treatment is also more likely to be successful, as tumors are generally smaller when detected in their earliest stages. Furthermore, early detection can reduce the risk of cancer spreading to other organs in the body.

The use of AI, machine learning, and computer-aided detection (CAD) technologies can help with early breast cancer diagnosis [3]. The CAD utilizes algorithms to pinpoint potentially harmful areas in mammography images and compare them with existing patterns [4]. Moreover, AI-based automatic identification of tumors is becoming more precise and is allowing doctors to detect smaller, possibly more aggressive cancers sooner. Additionally, AI is the wing of computer science focused on developing machines able to execute duties that usually demand human wit. ML (Machine learning) is a type of AI which involves algorithms and models that can "learn" from data to make decisions on their own [5].

An ANN (artificial neural network) is a type of ML algorithm inspired by how neurons work in the human brain to process information. It uses a large number of connected "neurons" to form an interconnected web of nodes [6]. Each node can take in data, process it, and pass it along to another node, eventually forming a prediction or classification.

Vijayakumar et al. suggested a technique based on DNN (deep Feed-forward Neural Network) with four Activation Functions (AFs) for the category of breast cancer [7]. Its purpose was twofold: increase understanding of how different AFs can be used in different layers of a DNN and develop a predictive model with improved accuracy. The model performance was evaluated using a 10-fold Cross Validation (CV) method and various metrics. Results showed that the proposed solution performed better than other AFs-based DNNs, making it a viable expert-level system for breast cancer dataset classification [6]. Also, the method provided better results than the other validated techniques.

Al-Haija et al. introduced a precise and comprehensive computational model for diagnosing breast cancer with the help of ResNet-50 CNN [8]. The given framework used the ResNet-50 CNN as a pre-trained neural network on ImageNet for the purpose of transferring learning to classify the BreakHis dataset into benign or malignant. The evaluation results demonstrated that their method attained outstanding classification accuracy, exceeding the performance of other models trained on a similar dataset.

Ahila et al. presented a bio-inspired algorithm to optimize variables of a neural network for computer-aided diagnosis of breast ultrasound images [9]. The preprocessing of the images involves sigmoid filtering, despeckling, and anisotropic diffusion, followed by extraction of the location of concern from which weave and morphological features are tallied. The classification task is achieved using a wavelet neural network tuned with grey wolf optimization, culminating in evaluating the model's performance against 346 images via the receiver operating and confusion matrix characteristic. Analysis shows this method produces higher accuracy than existing methods, thus proving its application in accurate tumor detection and classification. Among different kinds of artificial neural

networks, Elman Neural Network (ENN) is an artificial Recurrent Neural Network (RNN) type of Artificial Intelligence (AI) that can be used to analyze and identify patterns in data. It has a recurrent connection between its input and output layers, allowing it to remember the previous output when computing its current output. This memory enables the algorithm to learn from past experiences and apply them to future decisions. In this study, a modified form of ENN (Elman Neural Network) founded on a modified metaheuristic has been used in order to Model Breast Cancer. The method is a variation of the Elman Neural Network specifically adapted for breast cancer modelling. The modifications are designed to enable the algorithm to analyze hundreds of different features of the breast tissue in order to identify cancerous cells accurately. In this process, the modified Elman Neural Network can model the data.

In summary, this paper delves into the pivotal role of AI, machine learning, and neural networks in revolutionizing the early detection and accurate classification of breast cancer. Through an exploration of various models, including Elman Neural Networks, ResNet-50 CNNs, and optimized algorithms, we aim to illuminate the strides being made towards enhancing diagnostic accuracy and ultimately improving patient outcomes. The subsequent sections delve deeper into these methodologies, their applications, and the promising results they yield. By harnessing the power of technology and innovative approaches, we aim to contribute to the ongoing efforts in combating breast cancer and transforming the landscape of medical diagnosis.

II. Elman Neural Networks

ENNs are a Recurrent Neural Network developed by Ronald J. Elman in the late 1980s [10]. Unlike traditional feed-forward neural networks, Elman Neural Networks can retain and use information from previous inputs, allowing them to understand context and patterns over time better. This makes them particularly well-suited for processing time series data [11]. They have been used in various applications, such as predicting stock market prices and recognizing speech patterns.

The core components of the network are analogous to those in a feed-forward neural network [12]; the junctions between the input layer (W_h^i), the hidden layer (W_h^h), and the output layer (W_h^o) are similar to what's found in a multi-layer neural network. As seen in Fig. 1, this is an overall representation of an Elman Neural Network.

Furthermore, Elman Neural Networks includes an extra layer known as the context layer (W_h^c), which takes input from the hidden layer's outputs in order to store the values of the hidden layer from the prior step [11]. This is visible in Fig. 1.

It is assumed that the dimensions of both the output and input layers are n, such that:

$$x^1(t) = [x_1^1(t), x_2^1(t), \dots, x_n^1(t)]^T \quad (1)$$

$$y(t) = [y_1(t), y_2(t), \dots, y_n(t)]^T \quad (2)$$

While the context layer dimension is m.

The l^{th} input layer and the k^{th} hidden layers are undeniably essential for optimal functionality.

$$u_i(l) = e_i(l), \quad (3)$$

$$v_k(l) = \sum_{j=1}^{N} \omega_{kj}^1(l) x_j^c(l) + \sum_{i=1}^{n} \omega_{ki}^2(l) u_i(l) \quad (4)$$

where, $i = 1,2,\dots,n$ and $k = 1,2,\dots,N$.

The $\omega_{kj}^l(l)$ describes the hidden layers' weights from the o^{th} node and $x_j^c(l)$ signals converted from the k^{th} the node of the context layer powerfully demonstrates that there should be. Therefore, the weight of the hidden layer k for the input layer i can be determined by $\omega_{kj}^2(l)$.

Therefore, the following approach can determine the last output of the hidden layer presented to the context layer.

$$W_k(l) = f_o\left(\bar{v}_k(l)\right) \quad (5)$$

where,

$$\bar{v}_k(l) = \frac{1}{\max(v_k(l))} \times v_k(l) \quad (6)$$

where, $\bar{v}_k(l)$ specifies the hidden layer's normal value.

As a result, the context layer produces its output in the following way.

$$C_k(l) = \beta \times C_k(l-1) + W_k(l-1), \quad (7)$$

Such that $W_{k|k=1,2,\dots,N}$ defines the self-connected feedback between [0, 1].

As a result, the Elman Neural Network's output layer has been gained as follows:

$$y_o(l) = \sum_{k=1}^{N} \omega_{ok}^3(l) W_k(l), \quad (8)$$

Such that, $\omega_{zk}^3(l)$ specifies the connection weight from the k^{th} layer into the z^{th} layer, where, $z = 1,2,\dots,n$.

Utilizing Ren et al.'s method [13], the structure of the ENN has been enhanced. This approach is executed according to the pseudocode provided in Table I.

Such that c is a constant, t specifies the recent iteration, μ signifies the learning rate.

To maximize the effectiveness of the upgraded Elman Neural Network, it is essential to incorporate it with a metaheuristic algorithm. In this study, an upgraded version of the imperialist competitive algorithm has been utilized for this purpose.

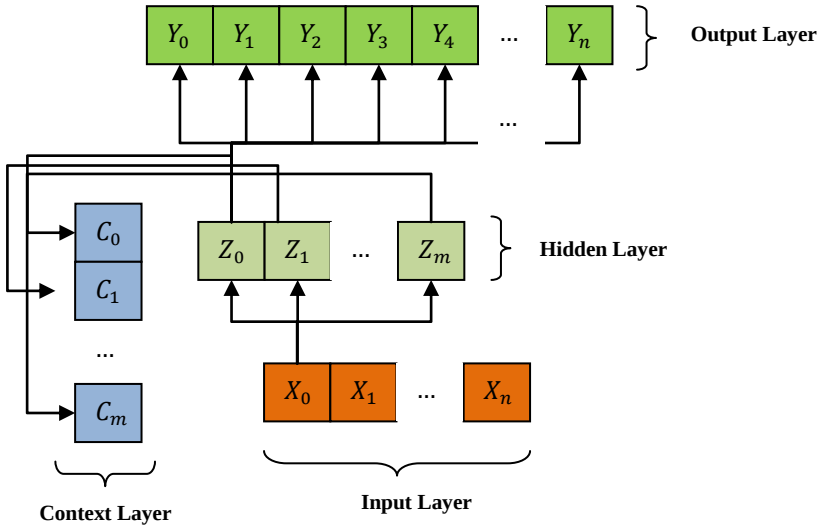

Fig. 1. Configuration of the Elman Neural Networks.

TABLE I. PSEUDOCODE OF THE IMPROVED ENN ON THE BASIS OF REN ET AL.'S METHOD [13]

Learning rate value initialization $\mu = \varepsilon$

In the lth iteration:
if l ≤ 2 :
$\mu = defaultvalue$;
end if $t \geq 3$&& e(l)<1.02e(l - 1):
$\mu = \frac{c(1+\frac{1}{l})^l}{exp(1)}$
else
$\mu = defaultvalue$
end
end
Improve weights;
compute e(t);
If stop criteria have been earned:
stop;
else
carry on

III. UPGADED IMPERIALIST COMPETITIVE ALGORITHM

A. The Conception of the Imperialist Competition Algorithm

As a population-based optimization approach, the Imperialist competition algorithm is introduced to solve optimization problems that take inspiration from human societal and cultural processes [14]. It begins with an initial population of random values and progresses toward an optimal solution by exploring the problem space, much like other population-based optimization methods.

This algorithm uses principles of assimilation, imperialistic competition, and revolution to solve complex optimization issues [15]. It takes the form of countries and gradually optimizes the solutions through an iterative process until it finds the best solution. As with other heuristic-based algorithms, it initiates with a haphazard initial population named “countries”. A few of the highest-performing elements, akin to the GA elites, are then picked as "imperialists," while the remainder is considered colonies [16]. These colonies were drawn to the imperialist based on their strength via a specific process. Any empire's power is determined by its imperialist country (as the central core) and its colonies.

The initial stage of the algorithm includes setting up the conditions for displaying the solution, generating the first group of entities, and forming the original colonies. The response will be shown as a vector with n components, where n is the quantity of orders and g is the number of pieces per order. Any piece must be manufactured n times, meaning it is repeated in each part number of the string [17]. Assembling begins by taking all parts that were created in the preliminary phase of production. The starting population of the ICA (the quantity of countries) is randomly generated. The algorithm stops when the set processing time elapses.

In order to ensure that a solution is always possible in the permutation display method for this problem, it is essential to observe the entire permutation and keep any operators from disrupting its completion [18]. To figure out the costs of each

country, their cost function is measured. From the number of empires, the participants in the candidates with the less cost function value are chosen as the remaining colonizers. The "Roulette wheel selection" technique is employed to split the colonies among the colonizers. This entails taking the cost of all colonists and computing their normalized cost with Eq. (9).

$$C_n = \exp(-c_n / \max c_i) \quad (9)$$

where, c_i describes the n^{th} imperialist cost value, and C_n signifies the n^{th} colonizer and n specify the normalized cost i of the maximum cost among all colonizers. n_E describes the number of empires. With $\max c_i$ having a normalized cost, the normalized relative power of any colonizer is computed according to Eq. (10) and is the basis for dividing the colonized countries among the colonizers.

$$p_n = \left| \frac{C_n}{\sum_{i=1}^{N_E} c_i} \right| \quad (10)$$

And

$$\sum_{i=1}^{N_E} P_i = 1 \quad (11)$$

The roulette cycle technique is one of the most well-known selection approaches. Initially, the selection chance figures are organized nearby one another, and afterwards, a haphazard number in the scope of zero to one is made. This scope is chosen on the grounds that the aggregate of the determinations in likelihood will dependably be equivalent to one. The random number is compared to the roulette wheel interval to determine the colonizer that corresponds to it. Since the probability of each colonizer taking up a section of the roulette wheel, higher quality colonizers (with lower cost functions) are more likely to be picked. After assigning all countries to their respective colonizers, the process moves into a loop with the colonial competition algorithm, continuing until a set stopping condition is reached.

In every empire, the colonizing country tries to increase the number of its colonies in order to increase its influence; therefore, in each empire, the colonized countries move towards the respective colonizer. In the presented algorithm, the attraction policy is defined as follows: to change the colony based on the emperor, two points in the colony are selected and before and after these two points are removed; then the removed components are added to the solution based on their relative order in the colonizer.

The revolution brings about an abrupt alteration to a nation's social and political qualities. In the imperialist competition algorithm, revolution is simulated by moving an imperial country to a separate random position. From a computational standpoint, the revolution halts the evolutionary moves from getting stuck in a nearby optimum snare, potentially enhancing the spot of a nation and carrying it towards areas with a more desirable situation. In the presented algorithm, each colony within a respective empire may revolt with a designated likelihood.

In this Algorithm, 2 positions are randomly chosen and swapped. As a result of the migration to a colonizing nation and the implementation of policies of revolution, some of these countries might potentially move up in comparison to the colonizer. This means that the colonizer and the colonized will exchange places with one another, and the algorithm will continue with the newly appointed ruling nation. This country can then begin to enforce assimilation policies on its colonies.

The might of the colonizing country as well as a ratio of the entire might of its colonies, is the entire power of an empire; Hence, the whole cost of an empire is calculated through Eq. (12):

$$TC_n = c_n + \zeta[mean\ (c_n^i)] \quad (12)$$

where, TC_n describes the whole cost of the n^{th} empire and $mean\ (c_n^i)$ signifies the mean amount of the cost of the colonizer n, ζ is a positive integer. Any empire that cannot improve its power and lose its competitive power during the colonizer's competition will be eliminated. For modelling this fact, it is supposed that the empire being deleted is the feeble-existent empire. Therefore, in each iteration of the algorithm, one or a number of the weakest colonies are removed from the weakest empire, and a rivalry is created among every empire to take over these colonies. Noteworthy colonies will not necessarily be taken over by the strongest emperor. Rather, stronger empires are more likely to take over. For simulating the rivalry between empires to take over this colony, first of all, its normalized total cost is determined from the entire cost of the empire via Eq. (13):

$$NTC_n = \exp(-Tc_n / \max Tc_i) \quad (13)$$

NTC_n describes the normalized total cost of the n^{th} empire, TC_n is the n^{th} empire, and $\max Tc_i$ is the total cost of the weakest empire.

With the normalized total cost, the probability of taking over the competing colony by each empire is calculated through Eq. (14):

$$Pemp_n = \frac{\mathrm{NTC_n}}{\sum_{\mathrm{i=1}}^{\mathrm{n_E}} NTC_i} \quad (14)$$

With the possibility of taking over any empire, the said colony belongs to the empire that wins the Roulette wheel. In the proposed algorithm, when an empire having no colonies is added as a colony to another empire. Selection Empire is made through the roulette cycle.

This research introduces a modified version of the imperialist competitive algorithm (ICA) called the upgraded imperialist competition (UIC) algorithm that hopes to address the issues of being prone to local minima and slow convergence speeds. Despite its successes, the original algorithm still poses a challenge.

B. Upgraded Imperialist Competition Algorithm

To avoid becoming stuck in a local optimum, population-based evolutionary algorithms can apply the concept of revolution (colonial competition) or mutation (genetic algorithm). This research specifically investigates the use of the Quad Countries Algorithm and its “rejection policy” in order to help populations escape from such traps.

The algorithm of the Quad Countries Algorithm is based on the ICA, and in addition to colonial and colonizing countries, two new types of countries with the names of independent

countries and countries seeking independence have been added to its set of countries [19]. Independent countries search the solution space randomly, and countries seeking independence distance themselves from colonizing countries according to a targeted policy called exclusionary policy.

In the basic Imperialist competitive algorithm, when the revolution operator is applied, firstly, the position of a number of colonial countries changes randomly, and secondly, it changes in the form of divergence (moving away from the colonizer).

While in the ICA, inspired by the policy of repelling the algorithm of the Quad Countries Algorithm, at the time of the revolution, firstly, the position of some colonial countries changed in a purposeful way, and secondly, it changes in the form of convergence (getting closer to the colonizer).

The purposeful calculation of the new position of the colonial countries when the revolution is applied is that the total distance between the colonizer and the target country is first calculated in all dimensions.

Then by multiplying the current position of the desired colony country by the resulting vector (Center), the desired country moves to a new position. This causes when the revolution operator is applied, the position of a percentage of the population elements is purposefully moved in the direction of the best element (the colonizer) to change.

$$Center = \sum(Col_i - Imp_j) \quad (15)$$

Eq. (15) shows how to calculate the Center vector. In this regard, first, the sum of the distances of all colony countries (Col) with the colonizing empires (Imp) is calculated. Then the product of this vector with a coefficient of 0.1 in the vector of the current position of the colony gives the new position of the colony country.

$$Col_i^{new} = Col_i^{old} \times (0.01 \times Center) \quad (16)$$

In the basic colonial competition algorithm, when a revolution occurs, the colonies move randomly in space and away from the colonizer, the best element of the empire, hoping to gain a better position in the problem space. While the colonies in the improved colonial competition algorithm avoid random movements while analyzing the movement of the best element of the group, they follow its movement and in order to reach a better position, not only do they not move away from the colonizer, but also according to their distance from the emperor. The leader's movement is inspired, and they step in that direction. This method makes all the colonies participating in the revolution process guess the optimal global location in the same number of algorithm iterations and converge around the global optimal point.

IV. Optimal Modified ENN using UIC Algorithm

In the given section, the procedure for refining the ENN has been outlined. To refine the suggested ENN, the aim is to determine its best possible weights. This study implements a two-layered neural network for modelling purposes, as shown below:

$$\sum_{i=1}^{H} w_i \sigma\left(\sum_{j=1}^{d} w_j \times x_j + b\right) \quad (17)$$

Where H describes the hidden layer neurons' quantity, w signifies the network's weightings, the bias is defined by b, and the activation function for the neurons is defined by σ. The main steps for the developed ENN optimization can be outlined as follows:

1) Set the starting positions of the population.

2) Compute the error function value for all of the locations. The error function is achieved as follows:

$$Error = 0.5 \times \sum_{k=1}^{g} \sum_{j=1}^{m} \left(Y_j(k) - E_j(k)\right)^2 \quad (18)$$

Where m is the output nodes quantity, g stands for the training set quantity, and the output of the real and the expected output value are defined, In turn, by $Y_j(k)$ and $E_j(k)$.

3) Save the finest place of the population.

4) Adjust the locations of the population by moving closer (or away from) the neighbors founded on local attractive and repulsive forces.

5) Introduce the random solutions movement.

6) Analyze the termination criteria to determine if the network has achieved the desired error rate.

7) Should the termination criteria be met, proceed to step 9. Otherwise:

8) Utilize chaos dynamics to develop chaotic positions and go to phase 2.

9) Stop the process

V. Simulation Results

This insightful study utilizes input variables to ascertain whether breast cancer is benign or malignant accurately.

A. Dataset Description

The objective of this study is to leverage input variables for predicting the classification of breast cancer as either malignant or benign. To achieve this, the researchers analyzed a dataset sourced from a Wisconsin Hospital's breast cancer patient records, which was accessible via the UCI machine learning repository [20]. This dataset comprises a total of 699 examples, each characterized by nine distinct features. It's noteworthy that among these samples, sixteen instances lack complete attribute information. Collectively, these data points are represented in the form of a 683x9 matrix, where each row corresponds to a patient's data entry.

Within the dataset, a fundamental division exists between two primary categories of breast tumors: benign and malignant. The analysis reveals that out of the entire dataset, 444 patients (approximately 65%) are diagnosed with benign tumors, while the remaining 239 patients (about 35%) are diagnosed with malignant tumors. This distribution of tumor types forms a critical foundation for the subsequent analysis and model development.

The essence of the dataset lies in its nine features, which play a pivotal role in determining the classification of breast cancer. These features encompass a diverse range of parameters, including clump thickness, uniformity of cell size, and uniformity of cell shape, marginal adhesion, single epithelial cell size, bare nuclei, bland chromatin, normal

nucleoli, and mitoses. Each of these attributes holds significance in differentiating between benign and malignant tumors.

By delving into these specifics, the study provides a more comprehensive context regarding the dataset's origin, its composition, the distribution of tumor types, and the significance of the individual features that contribute to the accurate classification of breast cancer.

Table II provides the descriptive statistics of the disease and its varying range [21]. The number of network inputs is nine parameters, as in similar studies in Table II. A confusion matrix is generally used to check the success and efficiency of disease classification and diagnosis systems. The analysis of this matrix in the classification and diagnosis of patients leads to four classes of TP, TN, FN, and FP (True Positive, True Negative, False Negative, and False Positive).

From the results of the confusion matrix, three indicators of sensitivity (accuracy of the system in detecting the malignant type), specificity (accuracy of the system in detecting the benign type) and precision (the proportion of all cases that were correctly classified) are obtained, which are used to analyse the performance of the classification systems. The algorithm used in this research is presented in Fig. 2.

As the algorithm shows, in this research, after separating the test and test samples and dividing them into two benign and malignant, cancer was modelled with the help of two different types of neural networks, including the Bayesian network [22] and the standard improved ENN to demonstrate its efficiency and the outcomes were compared with each other. During the simulations, 80% of the data are employed for training, and 20% are used for testing the dataset.

B. Results and Discussions

This research examined 685 patients with breast cancer whose data was derived from the Wisconsin hospital in the UCI machine learning database. The number of clinical variables in each patient equalled nine risk factors. In order to train the network, 80% of the patients (548 samples) were used. The remained 10% (137) were used to test the system. As the range for each of the nine disease risk factors ranged from one to ten, Tables III to IV illustrate their frequency distributions.

Several strategies have been presented in various studies to discover the relationships between breast cancer factors. The use of artificial neural networks to diagnose the type of cancer has been investigated in various studies. In this research, we tried to use the proposed modified ENN/UIC network to improve disease diagnosis.

The confusion matrix of the proposed modified ENN/UIC network compared with the Bayesian network (BN) [22] and the standard improved ENN is shown in Fig. 3.

Fig. 3 makes it abundantly evident that, as shown by the numerous metric indicators, the proposed modified ENN/UIC model beats the modified ENN model and BN model with regard to predictive ability. Remarkably, the improved ENN/UIC model offers a breast cancer model that is more accurate. Figure 4 indicates the comparison between the three types of networks used in this research [22].

In Fig. 4, using the suggested modified ENN/UIC model with 98.54% accuracy yield the best results when compared to the other approaches, including the ENN/UIC model with 96.78% and BN model with 97.95% accuracy. The simulation results show that applying the proposed strategy yields superior outcomes when compared. The results indicated that all three types of neural networks have the ability to predict breast cancer disease with high ability.

TABLE II. INPUT VARIABLES AS MATRIX COLUMNS INCLUDING NINE FEATURES TO DETERMINE THE TYPE OF CANCER [21]

Attribute	Domain
Clump Thickness	1-10
Uniformity of Cell Size	1-10
Uniformity of Cell Shape	1-10
Marginal Adhesion	1-10
Single Epithelial Cell Size	1-10
Bare Nuclei	1-10
Bland Chromatin	1-10
Normal Nucleoli	1-10
Mitoses	1-10

TABLE III. DESCRIPTIVE STATISTICS OF THE DISEASE AND ITS VARYING RANGE

feature name	Class	$Means \pm SD$
The thickness of the gland	Benign malignant Total	2.88 ± 1.784 7.28 ± 2.549 4.55 ± 2.932
Cell size uniformity	Benign malignant Total	1.41 ± 0.967 6.69 ± 2.835 3.26 ± 3.76
Uniformity of cell shape	Benign malignant Total	1.52 ± 0.968 6.69 ± 2.678 3.33 ± 2.899
Stickiness of edges	Benign malignant Total	1.46 ± 0.928 5.68 ± 3.288 2.94 ± 2.976
The size of a single mucous cell	Benign malignant Total	2.22 ± 0.988 5.44 ± 2.554 3.34 ± 2.334
Bare nuclei	Benign malignant Total	1.46 ± 1.178 7.74 ± 3.228 3.65 ± 3.755
Light color	Benign malignant Total	2.19 ± 1.173 5.88 ± 2.393 3.56 ± 2.561
Normal nuclei	Benign malignant Total	1.37 ± 0.966 5.97 ± 3.458 2.88 ± 3.164
Cell nucleus division	Benign malignant Total	1.18 ± 0.521 2.71 ± 2.675 1.71 ± 1.844

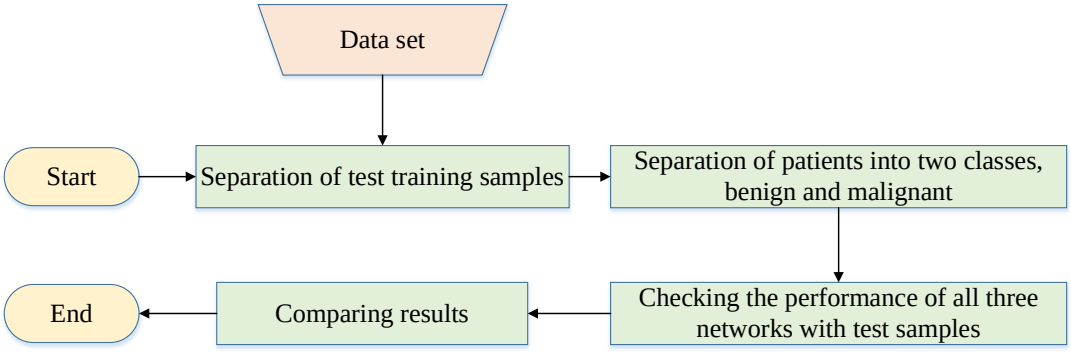

Fig. 2. The flowchart of proposed framwork in this research.

TABLE IV. PREVALENCE OF NINE RISK FACTORS ASSOCIATED WITH BREAST CANCER IN REGARDED CASES

		1	2	3	4	5	6	7	8	9	10	Total
Stickiness of edges	Percent	80.6	6.0	4.8	1.8	0.9	0.5	1.4	1.2	2.1	0.0	99.3
	Abundance	571	36	32	13	5	4	10	9	15	0	695
Normal nuclei	Percent	62.4	5.3	6.1	2.7	2.8	3.2	2.4	3.4	2.2	8.7	99.2
	Abundance	423	37	43	19	20	23	17	22	16	61	681
Light color	Percent	22.6	22.8	23.1	5.7	4.8	1.4	10.3	4.2	1.7	2.8	99.4
	Abundance	151	162	163	40	35	10	72	29	12	21	695
Bare nuclei	Percent	57.6	4.4	4.1	2.8	4.4	0.7	1.2	3.1	1.4	18.8	98.5
	Abundance	403	32	29	20	31	5	9	22	10	133	694
The size of a single mucous cell	Percent	6.4	57.4	10.3	7	5.5	5.8	1.7	0.4	0.4	4	98.9
	Abundance	45	376	72	49	39	41	12	22	3	31	690
Cell nucleus division	Percent	56.3	8.4	8.4	4.8	3.4	3.0	1.8	3.7	0.6	7.8	98.2
	Abundance	394	59	59	33	24	21	12	26	4	54	686
Cell size uniformity	Percent	53.5	6.5	7.5	5.4	4.4	3.7	2.8	4.1	0.9	9.7	98.5
	Abundance	374	46	53	38	31	26	20	29	6	68	691
The thickness of the gland	Percent	19.9	7.3	14.8	11.4	18.4	4.8	3.4	6.4	2.2	9.9	98.5
	Abundance	139	51	103	80	129	34	24	45	15	69	689
Uniformity of cell shape	Percent	49.6	8.4	7.7	6.3	4.7	4.2	4.4	3.9	1.2	8.4	98.8
	Abundance	347	59	54	44	33	30	31	27	8	59	692

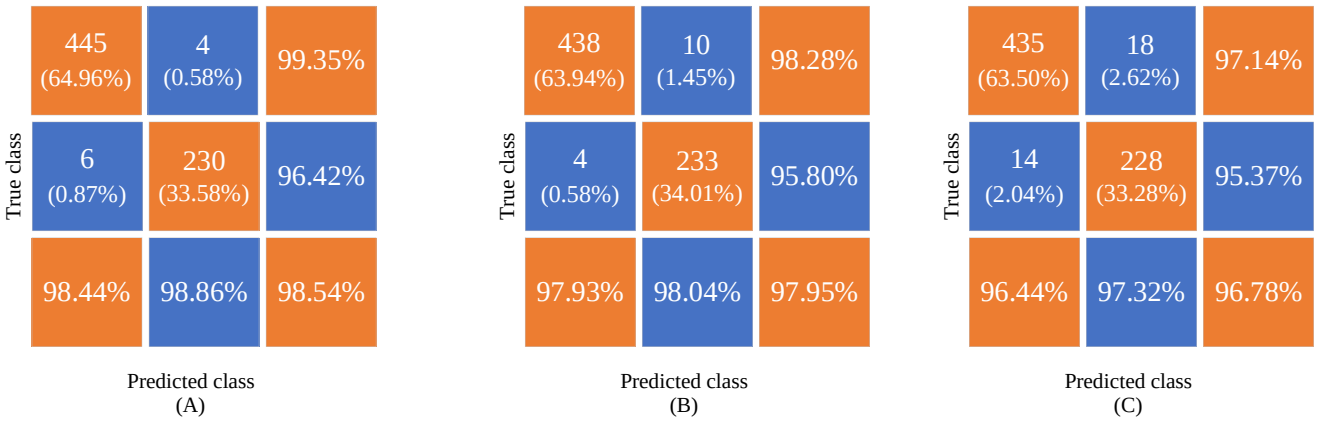

Fig. 3. Confusion matrix of (A) modified ENN/UIC, (B) BN, and (C) modified ENN.

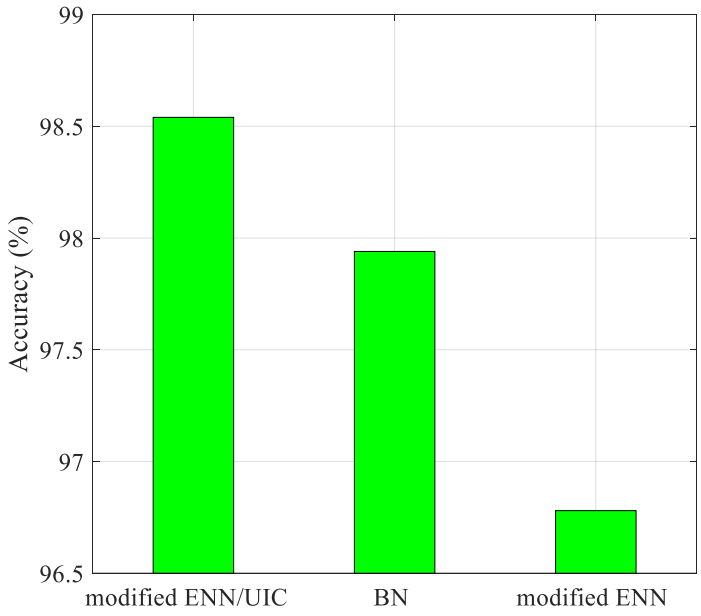

Fig. 4. Comparison between three types of networks used in this research.

VI. Conclusion

Among different cancers, one cancer that starts from breast cells is breast cancer. Both men and women are affected by this disease, but this cancer is more prevalent among women. Symptoms of breast cancer can consist of a mass in the breast, a change in the form or measure of the breast, variations to the skin over the breast, like puckering or dimpling, and a discharge from the tit. Breast cancer treatment can be various, contingent on the sort and phase of the disease, but may comprise chemotherapy, radiation therapy, surgery, hormone therapy, and aimed therapy. Many deep neural networks show excellent results in accurately classifying tumor cells. Therefore, a deep artificial neural network can be used along with other non-invasive diagnostic methods that are usually used (such as mammography and radiography), as a diagnostic support system with high sensitivity and specificity to identify benign and malignant breast tumors. The existing study aimed to diagnose benign and malignant breast cancer using a new method based on deep neural networks and an improved meta-heuristic algorithm. Since artificial neural networks based on deep calculations in the diagnosis of diseases have attracted the attention of many researchers in recent years, therefore, in this research, a novel optimized and improved process was used for classifying the type of breast cancer into two categories, malignant and benign. First, a modified version of the Elman Neural Network was trained with samples. Then, it was optimized on the basis of an upgraded version of the imperialist competitive algorithm.

At last, the model was evaluated with test samples. The model validation was performed based on a breast cancer dataset of the Wisconsin hospital. For a failed comparison, the outcomes of the proposed technique were validated by two other methods, including the Bayesian network and the standard improved ENN without optimization. Outcomes showed that all three methods provide good accuracy for a cancer diagnosis; using the proposed method for this aim achieved higher accuracy.

Looking forward, advancements in nanotechnology hold the potential to revolutionize early detection and monitoring of

breast cancer. Researchers are exploring the development of highly sensitive and specific nanosensors that can detect subtle molecular changes associated with cancer cells. These nanosensors could be integrated into wearable devices, providing continuous monitoring of biomarkers in bodily fluids. This real-time data could offer clinicians valuable insights into disease progression and treatment response, enabling more precise and timely interventions. Moreover, the combination of nanotechnology with AI could enhance the accuracy of data interpretation, leading to earlier and more accurate diagnoses. While this field is still in its infancy, the convergence of nanotechnology and AI could pave the way for groundbreaking advancements in breast cancer management, ultimately improving patient outcomes and quality of life.

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