

Identification and Diagnosis of Breast Cancer using a Composite Machine Learning Techniques

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Abstract

Throughout the world, cancer is the top cause of mortality in women. Whatever improvement in cancer ailment identification and prognosis is vital to living a healthy life. As a consequence, excellent cancer prediction accuracy is crucial for maintaining treatment and survival criteria current for patients. Machine learning techniques, which have been found to have a major impact on the identification and early treatment of breast cancer, have emerged as a hotspot for study and have been demonstrated to be a potent methodology. We used five machine learning algorithms in this research. There have been various empirical investigations employing machine learning and soft computing techniques to treat breast cancer. This article provides an overview of the available technologies for advanced treatment of breast cancer, as well as an introduction to the concepts and current achievements in personalised medicine that depend on technology. The many kinds of breast cancer are addressed, as well as their worldwide occurrence. It is discussed the importance of recognising irregularities and distinguishing between benign and malignant breast cancer. Levenberg-Marquardt (LM) and Sparse Representation (SR) have been combined to model a new approach for diagnosing breast cancer. With LM's training accuracy and SR's robustness in identifying small deformations, an impressive performance was achieved in terms of accuracy and mean square error. Data has been acquired from the Wisconsin Dataset (WD). This model proves the combination of several classification algorithms could enhance the model in a significant manner and can be used for pre-clinical diagnosis.

Keywords: Breast cancer, Machine learning, Levenberg-Marquardt, Sparse Representation, SR, WBCD, Regularization

INTRODUCTION

Despite the fact that cancer is one of the most dangerous illnesses that humans confront, there is no clear cure. Breast cancer is among the most frequent malignancies. According to the National Breast Cancer Foundation, around 276,000 new instances of aggressive breast cancer will be identified in the United States in 2020, with 48,000 cases of non-invasive breast cancer. Breast cancer is one of the top causes of death in women around the world. According to the American Cancer Society, breast cancer has taken the lives of 41,760 women and more than 500 men in the United States recently. Early detection, diagnostics, surgeries, radiation therapy, and medication therapy are all basic therapies that can be incorporated and organised within conventional healthcare plans in LMCs [1].

New LMC-focused disseminating and implementation studies should help determine the best guideline compliance approaches. Especially younger women, fertility following treatment is a big significant concern. It is essential to connect and teach younger patients about reproductive concerns at the time of diagnosis, as well as continued studies aimed at maintaining fertility in young breast cancer survivors [2]. There is limited evidence known about women's thoughts toward fertility regarding this diagnosis and therapy. Machine learning and artificial intelligence have been used to efficiently identify and treat a variety of serious diseases, aiding in prompt treatment and diagnosis and thereby improving the patient's odds of survival. [3].

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This article has been structured in the following manner: Section II talks about the previous works carried out regarding breast cancer and the machine learning techniques used; Section III discusses the proposed work and its operating functionality; Section IV explains the outcomes obtained using the proposed model and their subsequent discussion; Section V draws a conclusion to this paper.

BACKGROUND

A DNNs model is described in detail in the article [4]. Unlike existing approaches, this model was focused on the Support value of a deep neural network. To improve the functionality, efficacy, and data quality, a normalization method was applied.

In [5], the technique and parameter selection in the pre-processing and classification stages is done automatically. The objectives of this work are to use a variety of strategies to simplify the building of machine learning methods. Breast MRI scans are used to construct a novel Back Propagation Boosting Recurrent Wienmed model (BPBRW) with a Hybrid

Krill Herd African Buffalo Optimization (HKH-ABO) mechanism for diagnosing breast cancer at an early phase, as shown in [6]. The system is primarily used to work with MRI breast images, and a unique Wienmed filter to pre-processing the MRI noisy image data has been built. Bewal et al. used Artificial Neural Network for diagnosing breast cancer [7]. Various scholars in the neural network literature have examined Wisconsin Breast Cancer Data (WBCD) for clinical diagnosis of breast cancer. The effectiveness of multi-layered perceptron networks for breast cancer detection utilizing various back propagation methods is compared. [8] discussed and illustrated a number of approaches for doctors to better comprehend neural network models of key patient metrics and outcomes. Almost any form of clinical outcome model will be suitable for one or more of the strategies shown. [9] incorporated the Wisconsin Dataset for breast cancer. The neural network in [10] has a multi-layered feed forward neural network as its basic structure. The quantity of input units is based on the characteristics of the examples provided. An accuracy of 92% and a sensitivity rate of 98% was observed while this using ANN and LM models [11]. The research carried out in [12] offers a genetic approach for concurrent feature extraction and optimizing parameters of a Multi Layer Perceptron (MLP) neural network for autonomous breast cancer diagnosis. It is extremely important to categorize inconsistencies in breast cancer and to compile pertinent data sets. It was made thanks to a combined effort by IT and oncology professionals [13]. For determining classification accuracy, [14] employed the K closest neighbor (KNN) technique, which is integrated in the R tool. They looked at the Wisconsin dataset (original) from the UCI machine learning library.

Wu et al. proposed a Levenberg-Marquardt parameter that could be employed for numerical experiments for non-linear equations. This convergence is super-linear, and simulation studies depict that LM could efficiently solve non-linear equations [15]. [16] compares two prominent training algorithms for Multilayer Perceptron (MLP) detection of breast cancer tissues (LM and Scaled Conjugate Gradient (SCG)). They used characteristics collected from the Wisconsin Database, a standard dataset for checking the functionality of multiple classifying methods, to test the efficiency of training approaches. [17] uses a shallow modular design to assess the influence of Sparse Representation on recognition rate, employing both regular filter banks and unsupervised filter banks. SR has also been used in medical imaging applications, such as for decomposing linearly correlated images [18]. A dataset for phishing detection has been used in [19]. Gamma correction [20] is a nonlinear mathematical operation that is used to alter the values of individual pixels in an image. A dataset for phishing detection has been used in this work makes use identifying breast cancer among young women using big data by combining LM and SR approaches to form an efficient classification approach. The Wisconsin dataset has been employed in this work.

OVERVIEW OF THE PROPOSED WORK

In the proposed hybrid classification algorithm, an LM and an SR classifier were combined. The SR is employed as a classifier and a LM for optimizing the concealed layer's features extracted, size, and weights in LM. The diagnosis of breast cancer is divided into two stages. In the starting section, there are three distinct classification algorithms, that optimises the chosen features, size, and weights of the LM training units using an evolutionary method. On the learning dataset, the first part's classifiers are concurrently trained.

Pre-processing:

The idea that bad data equals lousy search results, and poor input equals improper output, makes pre-processing data important. As a result, the first phase in establishing any strategy relying on machine learning approaches is usually pre-processing data. Preparation and normalising are included in the pre-processing section of this study.

Regularization

The dataset's feature values are put in the same domain while they are in distinct ranges or domains. It's a regularizing approach that usually leads to improved classifier results. The Z-score approach for regularization process in this study. This method normalises the values of all samples for every feature and is performed to each feature separately. The following equation shows the functioning of the F-score approach.

$$a_{i,j}^{z\text{-score}} = \frac{a_{i,j} - \mu_j}{\sigma_j} \quad (1)$$

Here $a_{ij}^{z-score}$ and a_{ij} are the regularized and actual values of j th characteristics. σ_j and μ_j would be the standard deviation and average values.

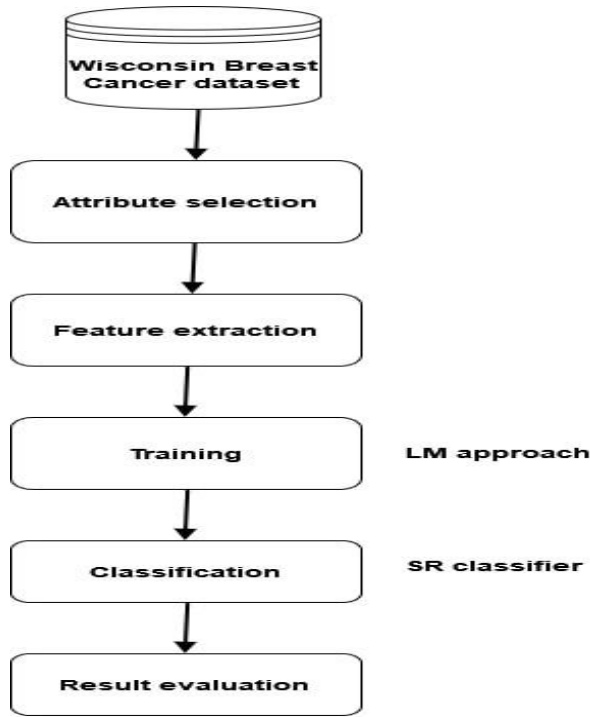


Fig. 1: Internal section of the overall Proposed method using BPNN and SR classifiers.

Classification process

A combined model based on the LM approach is used in this article. LM is among the methods for combining multi-classifiers and creating groups classifiers that seeks to understand each classifier's error and improve overall system performance suitably. Every classification approach outputs are utilised as inputs for higher-level learning in subsequent classifications, affecting how they've been merged in this manner.

Levenberg-Marquart algorithm

LM approach [16] seeks to overcome the following nonlinear least square minimization issue:

$$f(a) = \frac{1}{2} \|p(a)\|^2 \tag{2}$$

Here p is the residual vector. The LM accomplishes this by using two update rules, the Vanilla Gradient Descent (VGD) and the Gauss-Newton (GN) algorithm, to combine curvature and gradient data. The rule for Levenberg-Marquardt is given by:

$$a_{i+1} = a_i - (H - \mu \text{diag}(H))^{-1} \nabla f(a_i) \tag{3}$$

H will be the Hessian matrix, the error function gradient is given by $\nabla f(a_i)$, the median factor among the GN and VGD is given by μ . Big movements in low-curvature area are made to fast skip by plateaus, while modest steps in the area of high curvature are undertaken to progressively approach on minima.

Sparse representation: Screening

The fundamental goal of SR is to combine input signals linearly using an SR vector and a large vocabulary. In SR, the main issues are how to create and solve vectors using a large dictionary.

The x measurement, the predefined label vector B , and the training data matrix A .

Find the value for Ω :

$$\Omega = \{x_1^T x, x_2^T x, \dots, x_n^T x\} \tag{4}$$

Here T will be the transpose of the elements, which are arranged in decreasing fashion.

$$\hat{X} = \{x_1, x_2, \dots, x_n\} \tag{5}$$

here

$$z = \min \left\{ \frac{n}{\log(n)}, m \right\} \tag{6}$$

Regression using SR

Solve the least squares problem between \hat{X} and x ; i.e. Evaluate the value for Y , that is $\hat{X}^{-1}x$

Here \hat{X}^{-1} is the inverse of Moore-Penrose.

Classification using SR

Assign the corresponding testing point with the help of

$$h_n^{scr}(x) = \arg \min_{s \in [S]} \theta(a, \hat{X}_s, \hat{Y}_s) \tag{7}$$

Here θ is the principal angle.

The result of this operation's sparse representation will be denoted by $h_n^{scr}(x)$. The sparse representation technique is carried out in this manner. d^j is used to obtain the representation process with sparse features. The objective function is minimised to obtain a sparse relation.

$$\min_{\{d^j\}} \left\| a - \sum_j e^j * d^j \right\|_2^2 + R \sum_j \|d^j\|_1 \tag{8}$$

e^j is the filters, R is the regularization parameter. Sparse representation can be efficiently applied for practical problems like and guarantees a recovery in convex relaxation also [18].

The pseudo code and functionality for the proposed DSLI technique are shown in Algorithm 1.

Algorithm 1 Proposed Composite LM-SR algorithm:

Input: $p(a)$, $p'(a)$, μ , α , β , $BG(i)$, $TM(i)$, I ;

Output: OPvalue;

Initialize $p(a)$, μ , diffp;

for $i = 0$ to I , do

$p(a) = p'(a)$;

diffp = diff($p'(a) - p(a)$);

if diffp ≥ 1

then

$\mu = \mu + \alpha$;

end

if diffp ≤ 1

then

$\mu = \mu - \beta$;

end

if OPvalue ≤ 0.5 then

result = 0;

else

result = 1;

end

for $i=0$ to I , do

if diffp ≤ 0.2 then

OPvalue = MG(i);

else

Opvalue = BG(i);

end

end

end

Here MG(i) high score and BG(i) low score are datasets corresponding to Malignant stage and Benign stage respectively. The absolute difference between the densities is evaluated and assigned in the form of OPvalue (i). For a TM value between 0.4 to 0.6, the final value resides in either of the two samples depending on the magnitude of the difference value.

RESULTS AND DISCUSSION

Dataset

We employed the LM technique to estimate breast cancer hazards in this study. The SR machine learning method was used to analyse the breast cancer Wisconsin (original) dataset. The dataset contains 733 instances, 12 attributes, as well as incomplete ones (?) that are substituted by the characteristic mean values. 512 (69.85%) occurrences will belong to the benign class, while 221 (30.15%) cases will correspond to the malignant class.

Description

Table I: Wisconsin dataset for breast cancer

Attribute	Domain
Code number of a case	ID number
Clump thickness	Between 1 and 10
Consistency of Cell size	Between 1 and 10
Consistency of Cell shape	Between 1 and 10
Marginal adhesion	Between 1 and 10
Size of one Epithelial cell	Between 1 and 10
Bare nuclei	Between 1 and 10
Bland chromatin	Between 1 and 10
Normal nuclei	Between 1 and 10
Mitoses	Between 1 and 10
Class	Benign: 2, Malignant: 2.

The information was separated into two groups: training and testing. The testing set was not seen by any neural networks during training phase. Its main purpose is to see how effectively neural network groupings generalise after training. 80% were in the training set, whereas 20% of the examples were in the testing set. The back propagation network is made up of three layers: a nine-unit input layer, a six-unit concealed layer, and a single-unit output layer. The output layer's unit value indicates whether the input is a normal cell or not. All link weights in the network are adjusted to random values at the start of training. The maximum and minimum values of all input vectors are set to 0 and 1, respectively. MATLAB 2013a is used to carry out all of the calculations. Fig. 2 represents the count of occurrences each diagnosis in a Wisconsin Breast Cancer dataset possess.

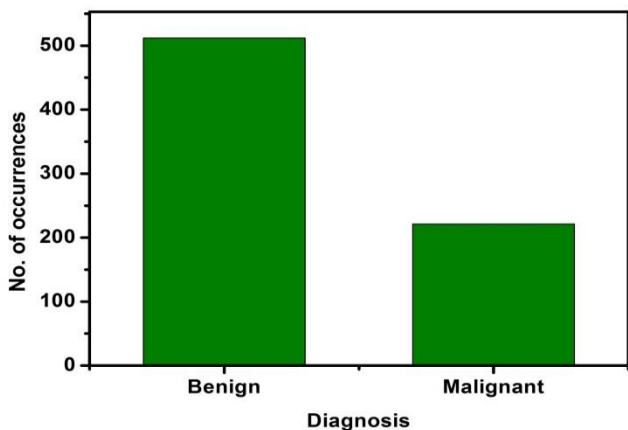


Fig. 2. No. of occurrences of benign and malignant diagnosis in Wisconsin Breast cancer dataset.

The following are some of the formulations that have been undertaken in this article for necessary evaluation of the device parameters. Accuracy and Mean Square Error have been identified here.

$$\text{Accuracy} = \frac{\text{TN} + \text{TP}}{\text{TN} + \text{TP} + \text{FN} + \text{FP}} \tag{9}$$

$$\text{MSE} = \left[\frac{1}{PQ} \sum_{c=0}^{P-1} \sum_{d=0}^{Q-1} [F(c, d) - \hat{F}(c, d)]^2 \right] \tag{10}$$

In Fig. 3, the average training accuracies of LM algorithm is displayed for various samples. The accuracy in average is calculated by calibrating SR's accuracy across several initialization parameters. As shown, both algorithms were extremely accurate, with all tests showing accuracy of greater than 80%.

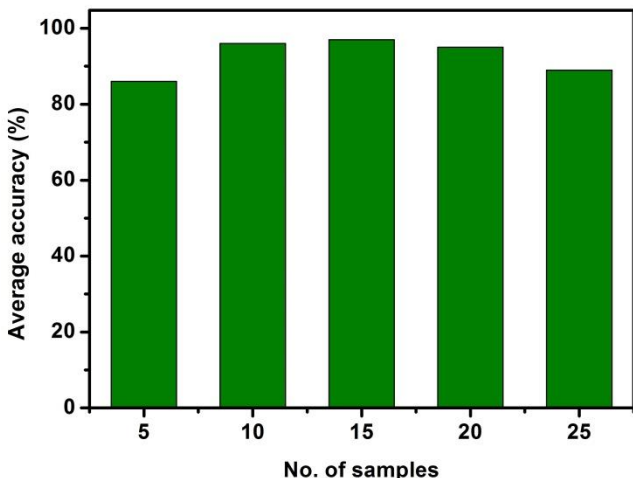


Fig. 3. Average training accuracy measured using the training algorithm Levenberg-Marquardt (LM).

Fig. 4 illustrates the average MSE vs the number of samples. A lower MSE suggests that the remainders are minute, indicating that SR fit the data effectively. As can be shown, for both training procedures, some SR structures converged to a relatively minimal MSE value. MSE was quite large at sample 3, implying that the sample size is inadequate to simulate the data's input-output relationship, restricting its exclusionary potential.

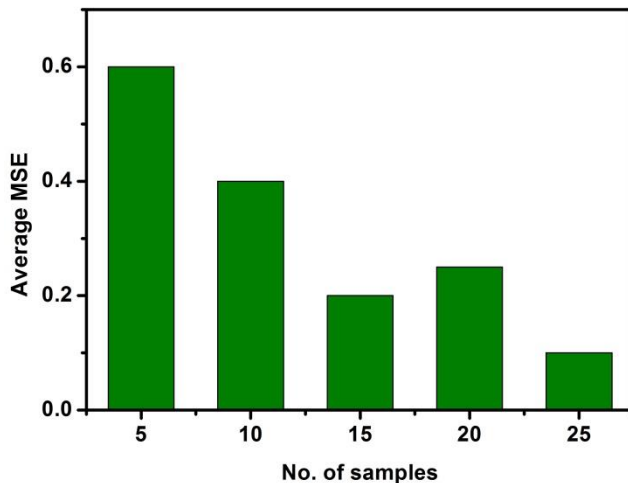


Fig. 4. Average MSE measured using LM and SR classifier.

Fig. 5 demonstrate the no. of training iterations in average vs the samples. Because the LM algorithm noticed that SR was over-fitting the data, all training runs were terminated prematurely.

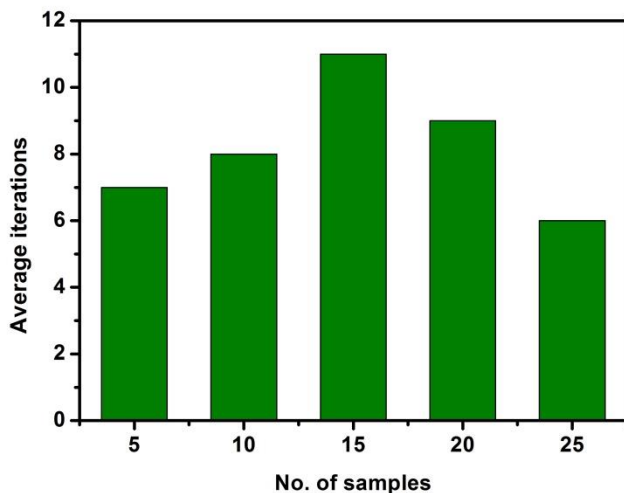


Fig. 5. Average iterations used by the training algorithm LM

Table II shows the accuracies acquired using various training techniques from literature. The proposed LM training algorithm produced enhanced accuracy of 99.3%.

Table II: Performance measure of different ML algorithms on Wisconsin dataset

Training algorithm	Percentage accuracy	Reference
Light Gradient Boosting Model	97	[21]
CAT Boost Extreme Gradient Boosting Scaled Conjugate Gradient	96	[21]
Quasi Newton	97.13	[22]
Resilient Back-Propagation	97.6	[22]
Levenberg-Marquardt	99.3	This work

The performance measures for the proposed method using classification algorithm SR is represented for around 8 samples, as given in Fig. 6.

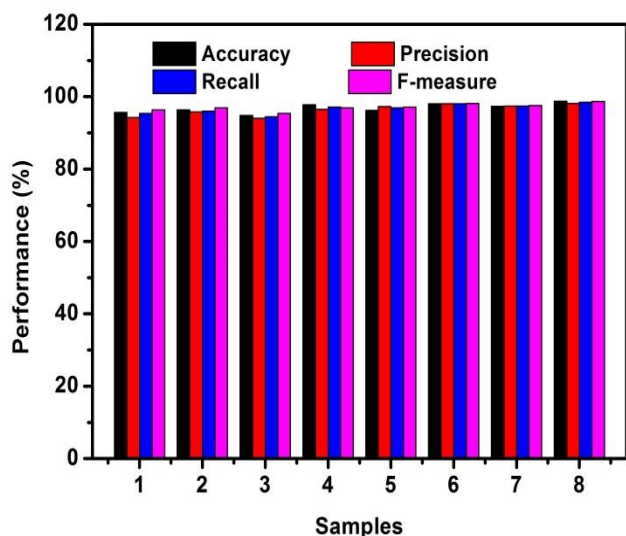


Fig. 6. Performance measures of proposed model using composite LM-SR technique for 8 samples.

Fig. 7 shows the accuracies acquired using several training methodologies from the existing works. The proposed LM training algorithm produced enhanced accuracy.

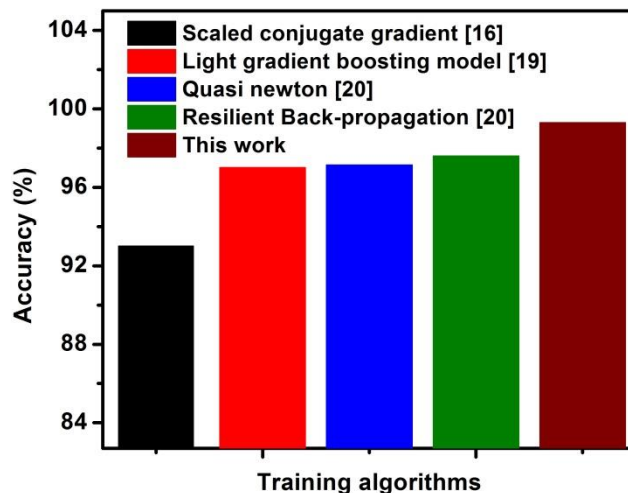


Fig. 7. Accuracy comparison of the proposed LM training algorithm with other conventional models from literature.

The Receiver Operating Characteristics (ROC) curve showing the performances of contemporary classifiers like CNN, BPNN, ANN, SVM with the proposed composite LM-SR have been shown in Fig. 8. All classifiers obtain fine true positive rates though initially starting at several points.

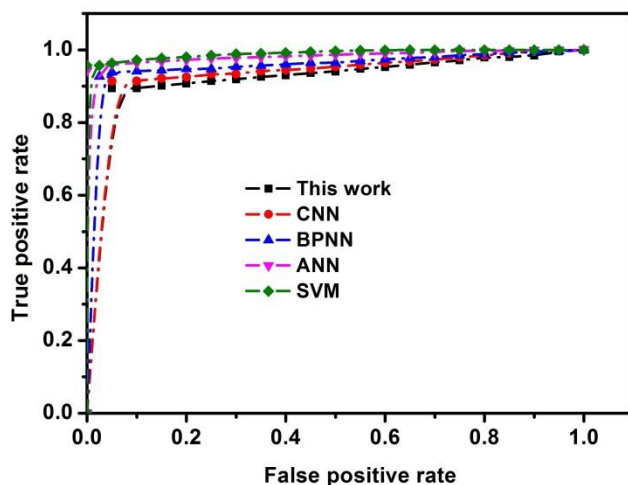


Fig. 8. ROC curve for the proposed model using LM-SR classifier.

Table III describes the confusion matrix for test samples 1 to 8, using the proposed algorithms.

Table III: Confusion matrix for test samples.

Samples	Actual	Prediction	
		Benign	Malignant
1	Benign	205	10
	Malignant	5	96
2	Benign	208	6
	Malignant	4	98
3	Benign	204	9
	Malignant	8	95
4	Benign	207	9
	Malignant	7	93
5	Benign	203	10
	Malignant	6	97
6	Benign	205	8
	Malignant	6	98
7	Benign	206	8
	Malignant	6	96
8	Benign	204	9
	Malignant	5	98

Table IV shows the quantity of training iterations in average with another article. Because the LM algorithm noticed that SR was over-fitting the data, all training runs were terminated prematurely.

Table IV: Comparison of iterations for the proposed work with other methodologies.

Method	Reference	Accuracy	Iterations
LM and SCG training algorithms	Mohamad et al. [16]	93%	13
NN with RBP	Azami et al. [22]	97.6	50
NN with Quasi Newton algorithm	Azami et al. [22]	97.02	50
LM and SR	This work	99.52	11

A comparison of the proposed composite LM-SR technique when compared to the accuracy level of various other contemporary machine learning classifiers using Wisconsin Dataset (WD) is presented in Table V.

Table V: Comparison with existing systems in classification

Authors	Method	Classifier	Accuracy
Razaeipanah and Ahmadi [12]	LM, RBP, GD with MLP classifier	Multi-stage Weights Adjustment	99.35
Shailaja et al. [14]	KNN algorithm	K-nearest neighbour	98.14
Derangula et al. [21]	LGBM, CAT Boost, XGB with NB	Naïve Bayes	96
Azami and Escudero [22]	Ensemble training algorithms with RBP	Resilient Back-Propagation	97.68
Assiri et al. [23]	Ensemble classifiers such as LG, RDL, RDF, SVM, NB, KNN	Ensemble classifier	99.42
This work	LM and SR	Composite LM-SR	99.52

An average of 8 samples are tested and analyzed during this process. Due to higher spatial allocations and segmentation preciseness, the accuracy and the other prominent parametric values like sensitivity, precision, recall and f-measure attain optimized conditions and hold superior to the conventional models.

CONCLUSION

Many research teams around the world have used various strategies to transform medical data for identifying breast cancer because several of the data sets employed are difficult to comprehend with various structures considering several

attributes, making the identification of abnormality extremely difficult. This article determines a breast cancer diagnosis methodology built on Levenberg-Marquardt (LM) training algorithm and Sparse Representation (SR) as the classification approach. A composite of the LM and SR algorithms have been incorporated into this article to be used

as a novel classification methodology. The Wisconsin Database (WD) is used for performing the work, through which the benign and malignant data occurrences are classified efficiently. After a thorough evaluation of the models, it is observed that LM-SR technique exceeds all other methods with a 99.5 and 98.2 % accuracy and precision correspondingly, with minimal mean square error value of 0.1. The results obtained are specific to the WD database, that could be viewed as a limitation for this work. It will therefore be essential to apply these techniques to other databases in the future. The outcomes, however, show a superior performance to other contemporary training and classification algorithms such as KNN, MLP, RBP, SVM, NB etc. The most critical task for the future is to create benchmark breast cancer data sets. This will aid in the evaluation and comparison of the various algorithms' results.

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