Computerized Breast Cancer Assessment Using Swarm-Intelligent Jellyfish-Optimized Neural Network

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Breast cancer, a potentially deadly condition, necessitates early detection and proper treatment. Computer-aided diagnostic (CAD) technologies are used by healthcare professionals to diagnose breast cancer from mammography images. This paper introduces a novel approach for computerized breast cancer evaluation using Swarm Intelligent Jellyfish Optimized Neural Network (SIJO-NN). This algorithm optimizes neural network's architecture and weights, specifically designed for breast cancer assessment. Swarm intelligent optimization enhances the weights and biases of network, improving its classification accuracy for breast cancer. To enhance the network's capacity for distinguishing between benign and cancerous breast lesions, swarm-intelligent optimization is employed. Jupyter Notebook is used to facilitate the process of using digital mammography images from Hologic Selenia equipment. Results from experiments show, the swarm-intelligent jellyfish-optimized neural network helps to assess breast cancer, Outperforming conventional deep learning models in terms of precision, accuracy, and sensitivity. Improved accuracy is vital for early diagnosis and better patient outcomes. The swarm-intelligent jellyfish-optimized neural network presents a promising approach for enhancing computerized breast cancer assessment. This study showcases the optimizing neural networks through swarm intelligence for superior performance in medical image processing. Further research is necessary to address limitations and refine the model for clinical implementation.

Keywords: Breast Cancer, Swarm-Intelligent Jellyfish Optimized Neural Network (SIJO-NN), Detection, Mammography Images.

1. Introduction

The presence of intratumoral variability has been widely recognized as a reliable biomarker indicating an unfavorable prognosis for tumors. Furthermore, recent research has demonstrated a correlation between intratumoral heterogeneity and a specific genetic profile linked with cancer [1]. Cancer of the breast is a prevalent and significant contributor to global mortality rates among women, being frequently diagnosed and acting as the primary global cause of cancer-related mortality. Most women who receive a breast cancer diagnosis frequently have a complete surgical treatment called full removal, which involves the removal of all lymph nodes located on the same side as the affected breast [2]. Breast tumors are the most common type of cancer found in women, with a yearly rate above two million new cases, despite the fact that mortality rates have decreased in recent decades as a result of advancements in early diagnosis and improved treatment methods [3]. The most common illness is cancer, and breast cancer is the second leading cause of cancer-related death among women. Selecting the best course of treatment for breast cancer requires accurate preoperative staging and to precisely ascertain the disease's prognosis, responsiveness to treatment, and predicted survival [4]. Breast cancer, initially recognized, is regarded as one of the earliest reported kinds of cancer. Despite extensive study conducted over the past few decades, an effective way to completely eliminate this deadly disease is unreachable [5]. Over the past 20 years, the automated breast tumor diagnostic system has been essential in early cancer detection and treatment. When paired with better treatment approaches, it has resulted in a considerable decrease in patient mortality and morbidity rates [6]. A breast tumor is a diverse set of tumors with unique immune histochemistry (IHC) characteristics and subtypes that respond to treatments separately. The finding of predictive surrogate indicators for the categorization of breast tumors into predetermined subgroups at the point of initial diagnosis has become more and more interesting due to this variability [7]. The potential for false negative results and negative results, which can lead to an inaccurate diagnosis, unnecessary concern in patients, or a delay in receiving treatment, is a major disadvantage of computerized breast cancer assessment. The SIJO-NN technique aims to improve the accuracy of breast cancer evaluation while potentially reducing false positive and false negative outcomes by utilizing swarm intelligence to improve decision-making.

The remaining studies can be divided into the following categories: In section 2, discuss related works. In section 3, we lay out our recommended methodology. In section 4, we will evaluate the outcomes of our method. The information in the paper is concluded in Section 5.

2. Related works

According to the author of, [8] suggested a prospective study combining functional testing and CT imaging to confirm the two parameters' predictive significance for initial breast cancer in larger patient population. Study [9] investigated the efficacy of machine learning as a computational tool for radiologists in the prediction task of classifying malignant and benign lesions of the breast using a distinct treatment MRI (magnetic resonance imaging) dataset. To create an advanced deep-learning breast tumor risk model based on mammography that outperformed commercially accessible clinical models in terms of accuracy. Breast density was not widely in use due to limited information, variation between radiologists, and subjective interpretation [10].

Study [11] created a predictive model based on anthropometric information and factors that may be obtained through standard blood analysis that may be utilized as biomarkers for breast cancer. Study evaluated new advancements in digital image processing as well as the application of AI and deep learning to diagnose breast pathology. In the near future, AI has the potential to significantly change the manner in which breast cancer is diagnosed and treated [12]. Research [13] introduced the framework for radiomic feature mapping, which produces radiomic MRI texture representations of images known as radiomic feature maps (RFMs). The RFMs are connected with statistical appearance standards, breast tissue biology through quantitative MRI, and the classification of mild versus cancerous tumors. Study established advanced convolutional neural networks (CNN) [14] for categorizing breast cancer screening test data. When evaluated on the screening population, their network was able to predict the existence of breast cancer with better accuracy. They credited a few technological developments for the excellent precision.

To examined the "early on" use of MR scans in breast tumor survivors undergoing neoadjuvant chemotherapy, which may allow dose adjustments before stopping treatment [15]. The presented a reliable data analyzing model that aims to enhance the comprehension of breast tumor survivability when dealing with missing data [16]. That model provides more information into the variables related to patient survivability and facilitates the identification of patient cohorts with shared characteristics. Study proposed a Shallow-Deep Convolutional Neural Network (SD-CNN) [17]. It employed a deep CNN to extract new features for ensemble models via LE, rearranged, or "virtual" recombined pictures. Deriving "virtual" rearranged images from LE photos required building a shallow CNN. Author [18] created an automated system that uses tissue histomorphology analysis to predict molecular markers of malignancy. To allow that type of structure to be practical, tissue morphology and the relevant epitope's molecular expression need to be initially found to connect. To demonstrated the efficacy of using local binary patterns (LBP) [19] in conjunction with DtG filtering for the purpose of assessing the maturation level of breast stroma, as observed in histological slides stained with hematoxylin and eosin (H&E). Study [20] evaluated the effectiveness of a shortened The magnetic resonance imaging technique as a resource-efficient method for screening individuals are vulnerable to breast cancer and ascertained whether shortened procedure changed the breast cancer screening Report and The Data System (BI-RADS) category was allocated.

3. Method

The procedure consists of the collection of full-field digital mammogram (FFDM) image data, the utilization of Linear Discriminant Analysis (LDA) for extracting features, the application of Recursive Feature Elimination (RFE) for feature selection, and the evaluation of breast cancer through the implementation of the Computerized breast cancer assessment using swarm-intelligent jellyfish optimized neural network method. Figure 1 illustrates the sequential process of computerized breast cancer diagnosis.

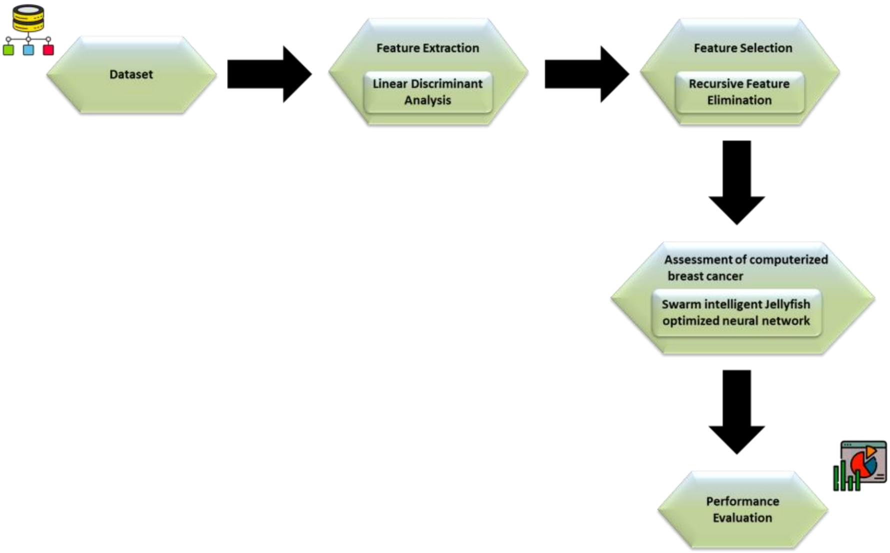

Figure 1: Sequential process of computerized breast cancer diagnosis [Source: Author]

3.1 Acquiring data

Using a pre-assembled FFDM image database from healthcare imaging research, for managed to set up a dataset for this study that included 3654 mammograms taken from 947 patients. In this case, every patient has four mammograms obtained from the breasts on the left and on the right CC (RCC) and Medial Lateral Oblique (MLO) views, which are referred to as the Left Cranial Caudal (LCC), RCC, Left Medial Lateral Oblique (LMLO), and Right Medial Lateral Oblique (RMLO) view pictures, respectively. Hologic Selenia digital mammography equipment was used to obtain each and every mammogram.

3.2 Extracting feature

The LDA approach is employed for the purpose of feature extraction. LDA is capable of effectively managing situations when there is an imbalance in the frequencies of the within-class categories. Furthermore, the performance of LDA has been evaluated using test data that has been randomly produced. This approach aims to optimize the ratio between the variance observed between different classes and the variance observed within each class in a given dataset, ensuring the highest possible level of distinguishability. Although LDA is a relatively straightforward method, it frequently yields reliable, satisfactory, and easily understandable outcomes in classification tasks.

3.3 The process of selecting features

A feature selection technique called RFE model, eliminates the least strong feature or features, and then repeats the procedure with more features until the desired number of features is reached or exhausted. The process involves the removal of some features, followed by the construction of a model utilizing the remaining attributes. Subsequently, the accuracy of the model is calculated. The features are ordered in a relative manner based on the sequence of elimination. After selecting a significance level, all of the attributes are fitted into the model. The highest p-value attributes are chosen, and if the value of p exceeds the significance threshold, it is eliminated. All remaining attributes are again layered on top of the model. This process is continued until the reliability of the created model is impacted by the elimination of an attribute. The attributes are ranked according to their coefficient values. A higher coefficient value indicates a higher rank. RFE can determine which set of characteristics is primarily responsible for the targeted variable's or class's prediction.

3.4 Computerized Breast Cancer Assessment

In computerized breast cancer, jellyfish swarm optimization integrated with convolutional neural networks (CNN) for detect breast cancer. Using this method, the architecture and hyperparameters of the network are adjusted to improve the model's capacity to recognize breast cancer in medical images.

3.4.1 Jellyfish swarm optimization

A swarm of jellyfish is a natural occurrence in which a large number of jellyfish gather in one area of the water. In this instance, the jellyfish travels with the swarm and may be moving in either of two types of motions: passively (type A) or active (type B). The jellyfish moves in passive motion in the area of its present location based on the Equation (1):

$$\mathrm{W_j}(\mathrm{s}+1) = \mathrm{W_j}(\mathrm{s}) + \gamma \times \mathrm{rand}(0{,}1) \times (\mathrm{Va} - \mathrm{Ka}) \qquad (1)$$

The motion coefficient is represented by the positive parameter γ. It is advised to set $\gamma = 0.1$ in light of the findings of numerical trials. The upper and lower limit vectors of the dataset attributes are denoted by Va and Ka. The jellyfish $\mathrm{W_j}$ randomly selects the jellyfish $\mathrm{W_i}$ from a population that differs from $\mathrm{W_j}$ in order to exploit the search space while it is in active motion as shown in Equations (2-4). The present jellyfish moves in the direction of the randomly chosen jellyfish if $\mathrm{W_i}$ is superior to $\mathrm{W_j}$, and retreats from it if it is not.

$$\mathrm{W_j} = (\mathrm{s}+1) = \mathrm{W_j}(\mathrm{s}) + \overrightarrow{\mathrm{step}} \qquad (2)$$

$$\overrightarrow{\mathrm{step}} = \mathrm{rand}(0{,}1) \times \overrightarrow{\mathrm{d\imath rec}} \qquad (3)$$

$$\overrightarrow{\mathrm{d\imath rec}} = \begin{matrix} \mathrm{W_i(s)} - \mathrm{W_j(s)} & \text{if } \mathrm{e(W_i)} \text{ is better than } \mathrm{e(W_j)} \\ \mathrm{W_j(s)} - \mathrm{W_i(s)} & \text{if not} \end{matrix} \qquad (4)$$

The fitness function is represented by e.

3.4.2 Convolutional neural network

CNN remains especially well-suited to handle two-dimensional pictures. Convolution layers (CLs), pooling layers (PLs), and fully connected layers (FCLs) make up CNN. CNNs perform better than more conventional AI techniques (like SVM and DT) because they acquire characteristics from the data set during training, which significantly cuts down on the amount of time required for feature engineering design. Convolution is the most crucial process in CNN, and as a result, the most crucial layer is CL, which performs the 2D convolution of the input data and kernels during the upward pass. Each CL's kernel weights are randomly initialized and adjusted by network training of the loss function. Consequently, the final learned kernels might identify certain kinds of patterns in the input images. Following step 1, the convolution output $\mathrm{D(i)}$is defined as in Equations (5-8)

$$\mathrm{D(i)} = \mathrm{W} \otimes \mathrm{E_i}, \forall \mathrm{i} \in [1, \dots \dots, \mathrm{I}] \tag{5}$$

Where the symbol $\otimes$ stands for the convolution process, which is the filter and inputs' dot product.

$$\mathrm{C} = \mathrm{T}\big(\mathrm{D}(1), \dots \dots, \mathrm{D}(\mathrm{I})\big) \tag{6}$$

Where I is the total number of filters and T is the pile action along the channel direction.

$$\mathrm{P} = \mathrm{NLAF(C)} \tag{7}$$

Three significant matrices (input, filters, and output) are considered to have the sizes S.

$$\mathrm{T(w)} = \begin{cases} \mathrm{U_J \times R_J \times G_J} & \mathrm{w = W} \\ \mathrm{U_L \times R_L \times G_L} & \mathrm{w = E_i}, \forall \mathrm{i} \in [1, \dots\dots, \mathrm{I}] \\ \mathrm{U_P \times R_P \times G_P} & \mathrm{w = P} \end{cases} \tag{8}$$

Where the height, breadth, and channel of the activate map are indicated by the three main variables $\mathrm{(U, R, G)}$in that order. Input, filter, and output are indicated by the subscripts $\mathrm{J, L}$ and P, respectively. Two qualities are present, $\mathrm{G_J = G_L}$first shows that the input channel $\mathrm{(G_J)}$ equals the filter channel $\mathrm{(G_L)}$. Secondly, $\mathrm{G_P = I}$ signifies that the output channel $\mathrm{G_P}$is equal to the amount of filtersI. The values of $\mathrm{(U_P, R_P\, , G_P)}$can be determined by taking B to be the stride and A to be the padding in Equations (9a-b) and (10).

$$\mathrm{U_P} = 1 + \mathrm{e_{ek}}[(2 \times \mathrm{A} + \mathrm{U_J} - \mathrm{U_L}) \div \mathrm{B}] \tag{9a}$$

$$\mathrm{R_P} = 1 + \mathrm{e_{ek}}[2 \times \mathrm{A} + \mathrm{R_J} - \mathrm{R_L}) \div \mathrm{B}] \tag{9b}$$

Where the floor function is denoted by $\mathrm{e_{ek}}$.

$$\sigma_{\mathrm{ReLU}}\big(\mathrm{c_{ji}}\big) = \mathrm{ReLU}\big(\mathrm{c_{ji}}\big) = \max\,(0, \mathrm{c_{ji}}) \tag{10}$$

Where "$\mathrm{c_{ji}}$" denotes an activation map C element. Comparing ReLU to the conventional hyperbolic tangent (HT) and sigmoid (SM) functions, which are defined as in Equations (11a-b)

$$\sigma_{\mathrm{GS}}\big(\mathrm{c_{ji}}\big) = \mathrm{tang}\,\big(\mathrm{c_{ji}}\big) = (\mathrm{f}^{\mathrm{c_{ji}}} - \mathrm{f}^{-\mathrm{c_{ji}}}) \div (\mathrm{f}^{\mathrm{c_{ji}}} + \mathrm{f}^{-\mathrm{c_{ji}}}) \tag{11a}$$

$$\sigma_{\mathrm{SM}}\big(\mathrm{c_{ji}}\big) = (1 + \mathrm{f}^{-\mathrm{c_{ji}}})^{-1} \tag{11b}$$

ReLU's primary benefit lies in its enhanced gradient propagation; that is, ReLU produces less vanishing gradient issues when compared to σ_{SM}. Since ReLU is one-sided, it is more biologically acceptable than σ_{HT}.

3.4.3 Swarm-intelligent jellyfish optimized neural network (SIJO-NN)

An innovative artificial intelligence framework called the Swarm-Intelligent Jellyfish Optimised Neural Network (SIJO-NN) was inspired by the group behaviors of jellyfish. Utilizing the ideas of swarm intelligence, SIJO-NN optimizes neural networks by imitating the synchronized motions of jellyfish in the wild. This novel method improves the decision-making and training capabilities of neural networks, making it more flexible and efficient for a range of applications, including ML and optimization. In Algorithm 1 shows the pseudo code of SIJO-NN Algorithm.

Algorithm 1: Swarm-Intelligent Jellyfish Optimised Neural Network (SIJO-NN)

```
Step 1: Initialize SIJO algorithm parameters
Initialize swarm of jellyfish (population)
Set maximum generations (max_gen)
Set convergence criteria (e.g., fitness threshold)
Initialize neural network parameters (e.g., architecture, learning rate, activation functions)
Step 2: Initialize the neural network for each jellyfish
For each jellyfish in population:
    Create a neural network with random weights
Step 3: Main optimization loop
generation = 0
While generation < max_gen and not converged:
 For each jellyfish in the swarm:
        Step 4: Evaluate the fitness of the jellyfish (Neural Network)
        Train the neural network with the training data
        Evaluate the neural network on the validation set to calculate fitness
        Step 5: Update jellyfish's position and velocity
        Update the jellyfish's position based on fitness
        Update the jellyfish's velocity
    Step 6: Update the swarm's global best jellyfish
    Update the global best jellyfish based on the best fitness
    Step 7: Update convergence criteria
    Check if the convergence criteria are met
    Step 8: Increment generation counter
    generation = generation + 1
```

```
Step 9: Use the best jellyfish (optimized neural network) for testing
Test the best neural network on the testing set
Step 10: Evaluate the performance of the SIJO-NN
Calculate performance metrics (e.g., accuracy, sensitivity, specificity)
Step 11: Output the results
Print or store the results and performance metrics
Step 12: End
End the algorithm
```

4. Result

To assess the effectiveness of the proposed methodology, it is important to employ various quantitative measures such as F-measure, recall, precision, and accuracy. The efficacy of the suggested method is assessed by comparing it to established methods, namely Support Vector Machines (SVM) [21], Naive Bayes (NB) [21], and Logistic Regression (LR) [21].

4.1 Experimental setup

Processing was done on a Core i7 Intel PC with 32 GB of RAM. Python is used in conjunction with Scikit-learn, an open-source machine-learning library. We achieve our objective with the aid of Jupyter Notebook, an open-source web program that makes it possible to create and share reports with live code.

A model's accuracy determines the overall accuracy of its predictions. It determines the proportion of precisely calculated instances to all occurrences in the dataset. Table 1 and Figure 2 create contrasts and evaluate the accuracy of the suggested method in relation to existing methods. The accuracy rates achieved by (SVM), (LR), and (NB) were 96%, 97%, and 95%. Comparing the suggested methodology (SIJO-NN) to existing methodologies, the accuracy percentage is 98.2%. The results indicate that our proposed method is superior to existing methods as shown in Equation (12).

$$\text{Accuracy} = \frac{\text{TP}+\text{TN}}{\text{TP}+\text{TN}+\text{FP}+\text{FN}} \tag{12}$$

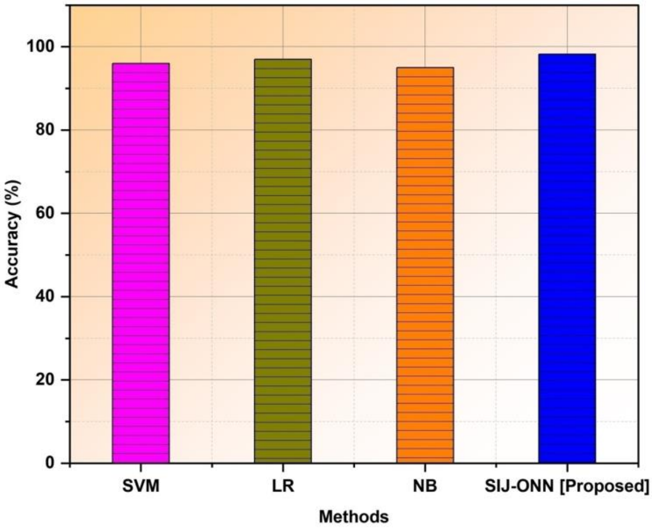

Figure 2: Result of accuracy [Source: Author]

Table 1: Result of accuracy [Source: Author]

Methods	Accuracy (%)
SVM	96%
LR	97%
NB	95%
SIJO-NN [Proposed]	98.2%

The capacity of a model to accurately identify favorable happenings between events that the model predicts as favorable is measured by its precision. It is calculated as the actual positives divided by the sum of the negatives and true positives. Figure 3 and Table 2 present an overview of the precision of the proposed method with the current methodology. The values that were achieved are 95%, 96%, and 94% for (SVM), (LR), and (NB), in that order. On the other hand, the 97.3% precision value is reached by the proposed approach (SIJO-NN). It states that our proposed approach is superior to the existing approach as shown in Equation (13).

$$\text{Precision} = \frac{\text{TP}}{\text{TP+FP}} \tag{13}$$

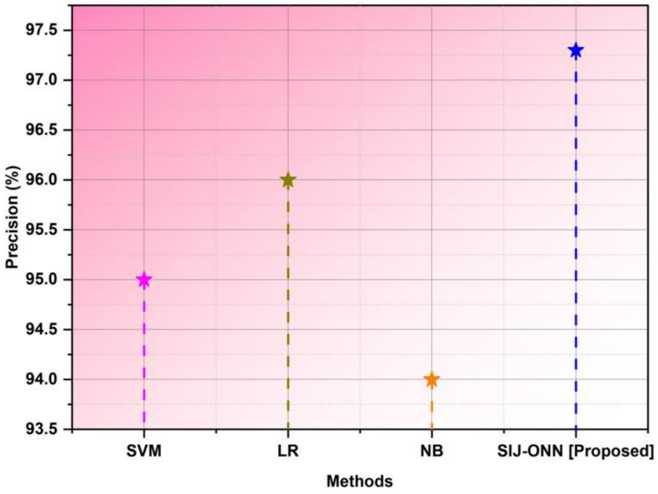

Figure 3: Result of Precision [Source: Author]

Table 2: Result of Precision [Source: Author]

Methods	Precision (%)
SVM	95%
LR	96%
NB	94%
SIJO-NN [Proposed]	97.3%

Recall evaluates a model's accuracy in properly identifying every positive case. It is also known as true positive rate or sensitivity. It is calculated as the ratio of a positive outcome to the sum of true positives and false negatives. Figure 4 and Table 3 display the recall of the proposed methodology and the recall of the existing method, respectively. Recall rates for the (SVM), (LR), and (NB) were 97%, 98%, and 96%, respectively. (SIJO-NN), the recommended method attains a 98.5% recall rate. It demonstrates that our recommended strategy is better than the existing approach as shown in Equation (14).

$$\text{Recall} = \frac{\text{TP}}{\text{TP+FN}} \tag{14}$$

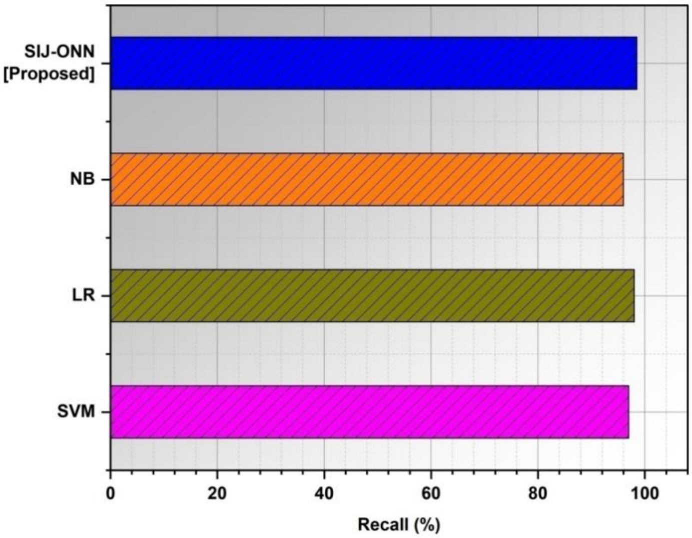

Figure 4: Result of Recall [Source: Author]

Table 3: Result of Recall [Source: Author]

Methods	Recall (%)
SVM	97%
LR	98%
NB	96%
SIJO-NN [Proposed]	98.5%

The F1-score offers a fair evaluation of the performance of a model since it is a harmonic average of precision and recall. It aids in striking a balance between recall and precision. The F1-Scores of the suggested strategy and the existing method are contrasted in Figure 5 and Table 4. It produced values for (SVM), (LR), and (NB) of 96%, 97%, and 95%, respectively. The proposed approach, known as SIJO-NN, showed superior results, with an F1-score average of 98.3%. Our proposed method performs much better as shown in Equation (15).

$$\mathrm{F1-Score} = 2 \times \frac{\mathrm{Precision} * \mathrm{recall}}{\mathrm{Precision} + \mathrm{recall}} \tag{15}$$

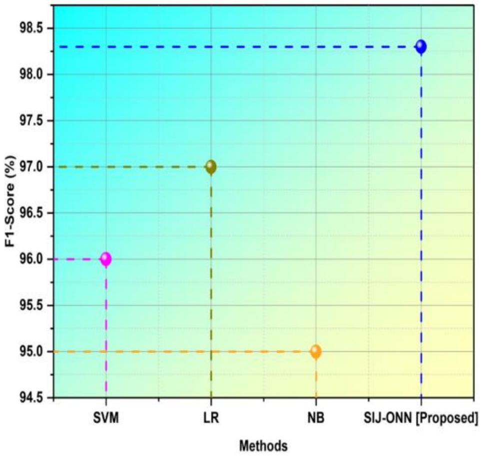

Figure 5: Result of F1-score [Source: Author]

Table 4: Result of F1-score [Source: Author]

Methods	F1-Score (%)
SVM	96%
LR	97%
NB	95%
SIJO-NN [Proposed]	98.3%

5. Conclusion

A promising development in breast cancer diagnosis is the computerized breast cancer assessment using swarm-intelligent jellyfish optimized neural network technique. It provides a comprehensive approach by combining the collection of data from FFDM, feature extraction using LDA, feature selection using RFE, and a novel neural network architecture based swarm-intelligent jellyfish optimization. This approach shows for a more accurate and effective assessment of breast cancer. Python programming and the open-source Scikit-learn ML toolkit were used for development. Jupyter Notebook helps us attain our goal. The suggested approach was assessed using experiment metrics, which included accuracy (98.2%), precision (97.3%), recall (98.5%), and F1-score (98.3%). As a result, our suggested approach outperforms existing methods. A significant drawback of computerized breast cancer screening is the possibility of negative results and false negatives, which can result in incorrect diagnosis, needless anxiety for patients, or a delay in getting treatment. By employing swarm intelligence to enhance decision-making, SIJO-NN approach seeks to increase breast cancer assessment accuracy while possibly lowering false positive and false negative results.

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