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Grasshopper-Inspired Deep Neural Network for Enhanced Breast Cancer Classification

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Abstract

Early-stage disease diagnosis is critical for effective treatment, and software-aided design can analyze disease architecture for timely detection. Many fail to identify disease severity before it becomes chronic, contributing to global mortality rates. Breast cancer, a prime reason of death among women, can be treated if detected early. Computer-aided diagnosis aids practitioners in accurately assessing disease criticality. This paper introduces an automated diagnosis system utilizing an enhanced Grasshopper Optimization technique and a Deep Neural Network (DNN) classifier. The Grasshopper Algorithm optimally selects features from segmented images, extracted through SIFT and BRISK hybrid techniques. The DNN classifies breast cancer using a partitioned dataset for training and testing. Performance metrics, including accuracy, precision, F-measure, and recall, demonstrate that the proposed system significantly outperforms existing methods, with an F-measure improvement of 5.1% and an accuracy increase of 11.19%.

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1. Introduction

Breast Cancer (BC) is serious second most reason of deaths among women despite the progress in patient management systems. As stated by American Cancer Association, around 270,000 women were diagnosed with Breast cancer in 2018, out of which 41,760 patients died due to chronic disease due to late detection of the tumour [1, 2]. However, World Health Organization stated 627,000 women expire each year because of this disease. In 2018, more than 2.1 million invasive breast cancer patients were diagnosed [3]. BC is a heterogeneous disease having many types and subtypes [4]. BC disease is classified in three groups of tumours: normal, benign and malignant. A malignant tumour generally expands and reaches neighbouring cells and other parts of the body. However, benign cancer does not expand and is limited to certain regions [5] [6] [7].

It is very difficult to detect BC at beginning, as there are not any symptoms detected in the initial stage. In such situations, the involvement of artificial intelligence has proved to be very beneficial [8] [9]. Early detection saves the lives of women by reducing the death risk [10]. Computer-aided technologies were used to distinguish malignant and benign cancer by analysing the shape of the tumour. The sonographic methods were used for gain setting and morphological characteristics were extracted for contour segmentation [11]. For instance, Michael et al. 2022 proposed a computer-aided system for the recognition of BC [12]. The authors used the machine learning classifier to classify the malignant and benign tumours. The study provides fruitful results in the classification of disease but classification model is not suitable for a large set of data.

In this paper, the dataset has been initialized to load the breast cancer data. Further, pre-processing of image has been accomplished to filter out excessive noise. Further, K-means clustering method is applied to separate foreground from the background. After the extraction of the cancerous region, an optimization technique has been applied to optimize the extracted regions. The optimized regions were further extracted using the feature extraction technique such as SURF, SIFT and BRISK to determine the best technique. After the extraction of features, classification has been done for classifying extracted one features by using Deep Neural Network, Artificial Neural Network, and Naïve Bayes classifier to determine the finest results. The outcomes are in form of various performance metrics have been measured. The key contribution of this new research is as follows:

- A novel behaviour of Grass Hopper algorithm for the feature selection.
- Tuning of DNN in terms of layers and epochs for the appropriate training of the DNN layer
- Evaluation of quantitative parameters and contrast of same with advanced techniques

The presented research article is structured in following way: Section 2 presents the research background connected to breast cancer and the classification techniques used by the researchers. Section 3 presents the research methodology in which dataset, pre-processing, and data classification have been done. Section 4 demonstrates the empirical outcomes and its discussion. Conclusion and future work have been reported in Section 5.

2. Related Work

Tahmooresi et al. 2018 [13] proposed the hybrid model using a combination of Machine Learning techniques for instance SVM, ANN, KNN, and Decision-Tree for the efficient detection of BC. The role of techniques for early diagnosis of cancer considering the symptoms was determined. The maximum accuracy obtained using the SVM was 99.8%. The proposed approach avoids the risk of false detection to save the life of a patient. The limitation of the study was the proposed technique is difficult to apply to other datasets such as mammograms and ultrasound images.

Zeebaree et al. 2019 [14] presented an automatically trained model via the information of local pixels and neural networks to identify the abnormality in the breast. For every window, a set of images has been selected from positive and negative classes. The testing stage includes the scanning of about 250 images to detect the RoI from the image. The success rate of the proposed method is about 95.4% and further segmentation results were compared with the existing techniques such as K-means clustering and the Cascade model. The segmentation of malignant was 93.1% and benign was 90.4%. The limitation of the study was that the working of the proposed technique depends upon certain parameters that make the system cumbersome.

Wu & Hicks, 2021 [15] applied the Machine Learning technique to classify the triple negative BC and non-triple negative BC considering the gene expression data. The authors used four different classifiers such as SVM, Naïve Bayes (NB) technique, Decision tree, and K-nearest neighbour for the selection of features. The simulation results were evaluated and analysed that SVM showed better results to classify the disease for breast cancer. The restriction of the study was that authors were unable to classify finest features and unable to integrate using the cancerous genomics data.

Amrane et al. 2022 [16] studied three different classification machine-learning methods for breast cancer classification. This study's goal is to predict how accurate numerous breast cancer classification schemes are. The main limitation of the study was a classification for multidimensional data using different feature selection and dimension reduction techniques is difficult. Still, there is a need to determine the most suitable ML classification model.

Chaudhury et al. 2022 [17] discussed image processing techniques using the machine learning framework for early detection of BC. The authors used the 322-mammography images for implementation and the histogram equalization technique was used for processing the images. This assists the object identification and boundary delineation, and a confusion matrix was developed for different classifiers. 72 images were used for the testing phase and 250 images were used for training. The results were compared and illustrated that SVM provides better results in terms of accuracy. Although, the results were better using the SVM authors were unable to realize the results using the appropriate graphs and were limited to providing the experimental analysis.

Table 1: Comparative Analysis for Breast Cancer Images

Author	Year	Dataset	Classification Technique	Results	Limitations
Dong *et al*. [8]	2015	DDSM and MIAS	Random Forest	The area under the curve is 0.95.	Datasets of limited sample size were used for experimentation.
Bruno *et al*. [9]	2016	DDSM, BCDRDMR, and BCDR-FMR	Polynomial classifier (PL) was used in association with curvelet	The area under the curve is 0.91 for normal	Unable to detect the most relevant feature using the classifier.

			transform, ANOVA, local binary pattern	malignant and 0.94 for benign malignant.	
de Lima, S. M., da Silva-Filho, A. G., & Dos Santos [10]	2016	IRMA	SVM, Extreme Learning Machine, and Multilayer Perceptron (MLP)	Accuracy is 94.11%	Large training time that limits its applicability. Moreover, the authors do not consider the shape and tumor texture for image analysis.
Jalalian *et al.* [11]	2017	CTLM	Multilayer perceptron neural network (MLPNN)	Accuracy is 95.2%	The authors do not evaluate the performance of the classifier for other CTLM images with different shapes such as ringed and polyploidy.
Cordeiro *et al.* [12]	2017	Mini MIAS	Fuzzy Grow-cut used for segmentation	AUC value is 0.97	The proposed method was not feasible for a large sample size.
Sahran *et al* [13]	2018	Breast UKM	Ensemble Framework SVM	Accuracy is 90.8%.	Due to over-segmentation, the important information in the image is removed.
Jiao *et al*. [14]	2018	DDSM	SVM and using the deep features from different layers	Accuracy is 96.7%	There is a need to improve the iterative learning method, as instances of benign and malignant cancer are required to be considered for more information.
Vijayarajeswari *et al.* [15]	2019	MIAS	Support Vector Machine	Accuracy is 94%	The hyperplane used to separate the cancerous region from the non-cancer may limit the cancerous region.
Yu *et al.* [16]	2019	BCDR	AlexNet, SVM and CNN	AUC is 0.88	Medical Instances are limited to use as still require improvement.
Vijayakumar *et al.* [17]	2021	UCI WDCB	Deep Neural Networks	Accuracy is 98.21, and F1 score is 0.976.	The study was limited to investigating the

					association between the Activation Function (AF)
Veni *et al.* [18]	2022	WBCD	Local linear radial basis function neural network and RNN method	Accuracy is 97.6% using the RNN with precision value 0.989 and F1 score 0.987	The study is limited to providing the desired accuracy for a large database.

Recent years have seen a significant increase in interest in the use of (DNNs) for the categorization of breast cancer. A deep learning method based on multimodal ensemble classification used for predicting the prognosis of human breast cancer was presented by Jadoon et al., 2023 [19]. Their study showed encouraging outcomes in prognostic evaluation and demonstrated the usefulness of utilizing different modalities for classification. Notwithstanding its effectiveness, the practical application of this strategy could provide obstacles because it necessitates a variety of data sources and processing capabilities. Rani et al. 2023 [20-23] presented PCA-DNN, a revolutionary system designed for the categorization of breast cancer. Principal component analysis (PCA) and DNNs were combined in an effort to improve classification interpretability and accuracy. Even with this development, more validation and investigation in various clinical contexts may be necessary due to the unique approach and results of the study [24-26]. In order to classify breast cancer in clinical practice with accuracy and reliability, robust, scalable models need be developed through future research in order to overcome these limitations.

3. Methodology

The empirical methodology is divided into two segments such as optimization and features classification. The proposed methodology is based on the classification of benign and malignant growth in the breast. In first segment, data is extracted using the dataset and further processed using the pre-processing techniques. The different segment of the proposed work is shown in Figure 1.

3.1 Dataset

The dataset is collected from the Kaggle in which the Breast Cancer Histopathological Database is considered for implementation. The cancer dataset comprises of 9,109 images, which are microscopic of breast tumors taken from 82 patients considering the magnifying factors such as 40X, and 10 times to 40X. The dataset holds 2480 benign and 5429 malignant image samples in .png format. In the samples, the benign includes the image samples with disrupted membrane, cellular atypia and metastasise. Thus, it contains four distinct types of benign breast tumors samples and four malignant tumors [27-29]. Depend upon how tumoral cells look under microscope, malignant as well as benign tumors can be classified into several categories. Different types and subtypes of tumor may have changing diagnoses and therapeutic consequences. The dataset is extracted from the Kaggle Repository, 2024 [30].

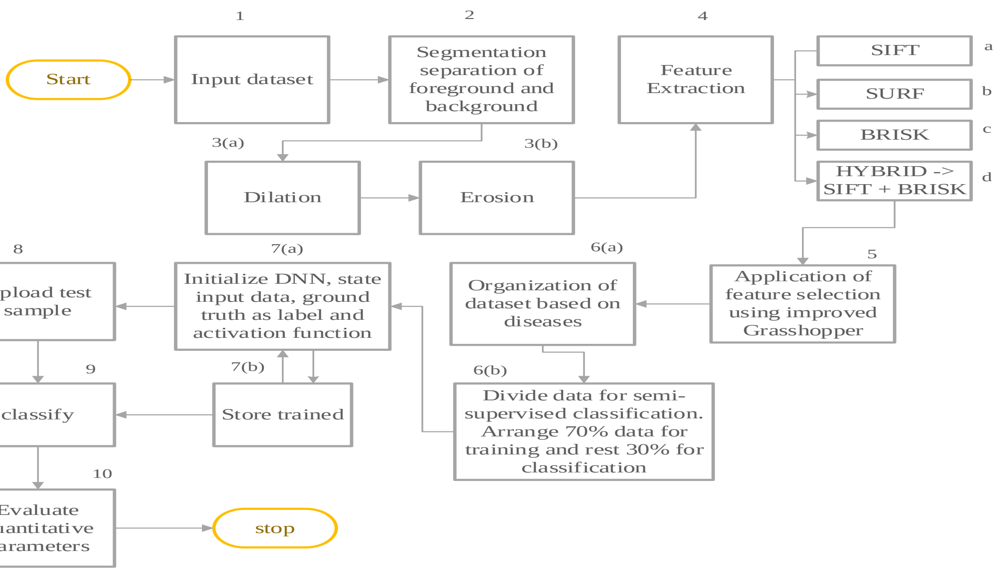

Figure 1. Proposed Methodology for Breast Cancer Classification

3.2 Implementation Platform

The present work is implemented in Matlab 2019a and is used for the simulation analysis of the proposed work. Researchers can efficiently preprocess medical imaging data and extract essential features for classification tasks by utilizing strong toolboxes such as the 'Image-Processing' and 'Statistics and Machine Learning' Toolbox [31-33]. The platform's user-friendly interface allows for the easy integration of algorithms, allowing for the implementation of cutting-edge machine learning models for accurate breast cancer categorization.

3.3 Pre-processing

The initial phase is to formulate the input images using pre-processing techniques. It is very important in any work linked to the analysis of medical images [34, 35]. The images obtained using the dataset have different dimensions that are difficult to fit into the pre-trained classifiers and deep neural networks, which are used in our work for the classification of cancerous breast cancer images. Thus, loaded images have been passed through an editing phase used to eliminate the noise, including the undesired traces and any variations in the image's brightness. The removals of traces allow the resizing of an image into a uniform one, as per the requirements of pre-trained DNNs and ANNs. There are two main filters are used such as the Median filter and the Gaussian filter to remove the unwanted traces, noise and keep the features of original images such as corners and edges with sharp structures. In order to extract the background and the foreground of an input image, a clustering method is required that can separate both the foreground and the background, k-means have been applied as it has been referred to in a lot of articles [2,3,10, 13, 24, 32] for the preliminary segmentation.

3.4 K-means Clustering technique

K-means clustering is a Machine Learning unsupervised technique has been used for data analysis. It has been applied for clustering the extracted data points. There are various applications of K-means clustering in different fields [36]. In this paper, K-means is used for extraction of dominant breast cancer traits. For the Mammographic Image Analysis Society (MIAS) dataset has been extracted from the Kaggle repository [30], two clusters have been selected for malignant and one for benign.

Algorithm 1: K-means clustering with random centroid

Input: Breast Cancer Dataset
Output: Final cluster formed in terms of foreground and background image
Step 1: The clusters selected were 2 such as $N = 2$; for the foreground and the background;
Step 2: Initial partition was positioned for the classification of data into N clusters;
Step 3: **while** *Epoch-1 is not achieved or same centroid is obtained* **do**
    for *each cluster* **do**
        Randomly initialize centroids using random function;
        Update centroids based on cluster information;
    end
end
Step 4: Measure the distance between the centers of the cluster and data points using Euclidean Distance $Ed = \sqrt{\sum_{l=1}^{k}(A_l - B_l)^2}$;
Step 5: Assign data points to the respective cluster based on minimum distance from cluster centers;
Step 6: Compute mean for each cluster;
Step 7: Compute new cluster centers $CC_l = \frac{1}{C_l}\sum_{p=1}^{C_l} A_l$
where A is the selected attribute, C_l is the number of records in the lth epoch, and CC is the center of the cluster in the lth epoch. ;
Step 8: Recalculate distances for determination of new clusters;
Step 9: Obtain thresholds and use centroids to separate the foreground from the background;

Therefore, two clusters are required as there are two clusters, which are computed using the following algorithm. The distance between the center points of the cluster and the pixel data point is measured using the Euclidean distance formula. The two clusters are in the form of foreground and background for each image. The foreground is extracted to analyses the breast cancer in the extracted image as shown in Fig 2. At this stage, region growing is used as a hole filling operation. The region rowing algorithms start from known regions and iteratively expand into neighboring unknown regions based on certain criteria such as pixel intensity similarity or texture coherence.

It is effective for filling small holes within larger regions. The algorithm architecture for the same is given in algorithm 1.

The processes followed in region growing algorithm are described as follows:

- Input Parameters: The algorithm takes as input an image I, seed pixel coordinates (xs, ys) within the image, and a threshold T representing the similarity criterion for pixel intensity.
- Initialization: An empty set R is initialized to store the segmented region, and an empty queue Q is initialized to keep track of pixels to be examined. Seed Pixel Selection: The seed pixel (xs, ys) provided as input is added to the queue Q.
- Region Growing Process: While the queue Q is not empty: Remove a pixel (xc, yc) from the queue Q. Check if the pixel (xc, yc) is within the bounds of the image. If the pixel is within bounds: Check if the intensity of the pixel (xc, yc) is similar to the intensity of the seed pixel (xs, ys) based on the threshold T.
- If the intensities are similar, Add the pixel (xc, yc) to the segmented region R. Add neighboring pixels of (xc, yc) to the queue Q if they are not already in the segmented region R and their intensities are within the threshold T.
- Termination: Repeat the process until all relevant pixels have been examined and added to the segmented region R.
- Output: The segmented region R containing pixels that are similar to the seed pixel within the specified threshold forms the output of algorithm.

Algorithm 2: Region Growing Algorithm for Hole Filling Operation

```
Input: Input image, seed pixel coordinates, threshold
Output: Segmented region
Initialize an empty set Q to store pixels to be checked;
Add seed pixel coordinates to Q;
Initialize an empty set R to store segmented region;
while Q is not empty do
    Remove a pixel (x, y) from Q;
    if pixel (x, y) is within image boundaries and not in R then
        if intensity of pixel (x, y) is within threshold of seed pixel intensity then
            Add pixel (x, y) to R;
            for each 8-connected neighbor of pixel (x, y) do
                Add neighbor pixel to Q;
            end
        end
    end
end
Return segmented region R;
```

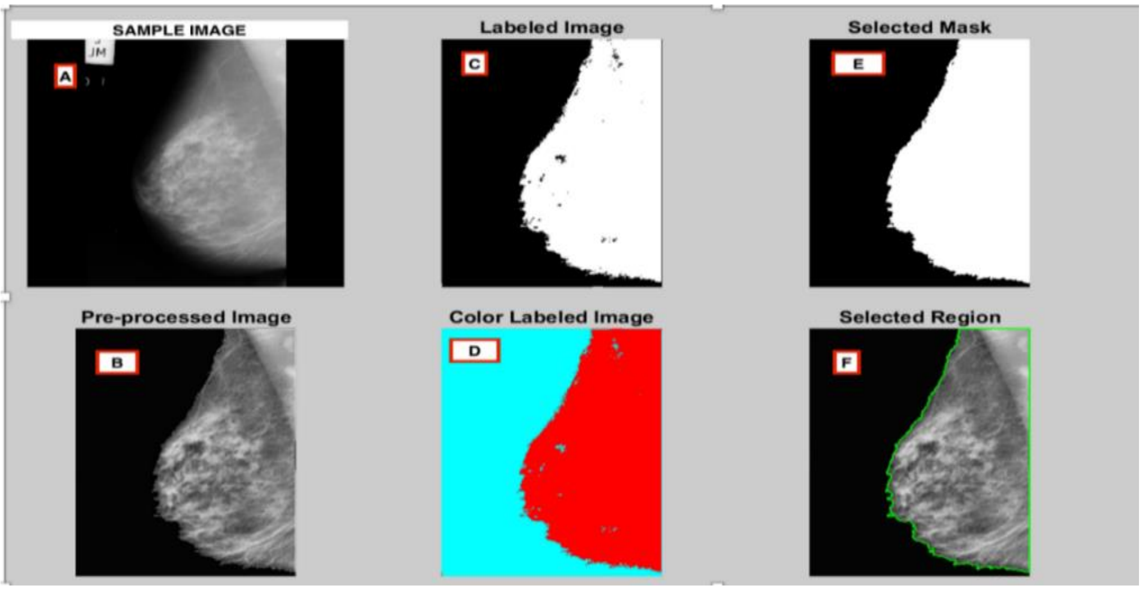

Figure 2. Foreground Extraction of Breast Cancer Image

Figure 2 show that (A) is the raw image is passed to the system-aided design where it is pre-processed using the morphological operators that are shown in (B) part of the image. After the application of k-means, (C) is generated and to find the best suitable patches from each region, masking has been done and as a result, (D) and (E) are obtained. Once the region is selected, it is forwarded for feature extraction.

3.5 Feature Extraction using the descriptors

The proposed workflow uses three different feature extraction techniques i.e. SURF, SIFT and BRISK. As at the initial instance, it was not sure which feature extraction technique would result in a good classification rate, all three features were validated by using Naïve Bayes Classifier and then further a hybrid method was created by observing the best classification rate [37]. Scale Invariant Feature Transform (SIFT) is algorithm which is used for the detection of features in the dominant solution space the location of the key point is determined and the scale at which the key point is located. The location of the key points is determined using the following equation that is linked to the location of the breast cancer region.

$$\theta(a,b) = \tan^{-1}\left(\frac{L(a,b+1) - L(a,b-1)}{L(a+1,b) - L(a-1,b)}\right) \quad (1)$$

In the given equation 1, $\theta(a,b)$ is the direction and L is the solution space for the location of key points. Feature extraction using the SIFT technique is shown in Figure 3. Speeded up Robust Features (SURF) is a robust method used for the detection of features which is inspired by the SIFT technique (Scale-Invariant Feature Transform) and works faster than the SIFT technique [38]. The key points are detected using the determinant of the Hessian blob detector that approximates the integers for data points of an image. Figure 4 shows the features extracted using the SURF method. Binary Robust Invariant Scalable Key-points (BRISK) descriptor is a binary feature extractor method in which there is a scale for each key point that is predicted in the continuous scale space. Figure 5 shows the features extracted using the BRISK technique. The advantages of SIFT and BRISK techniques are hybridized for better extraction of features. The proposed feature extraction method is the hybridization of SIFT and BRISK techniques in which the working mechanism of both techniques has been combined for the better extraction of features. Figure 6 shows the features extracted using the hybrid technique.

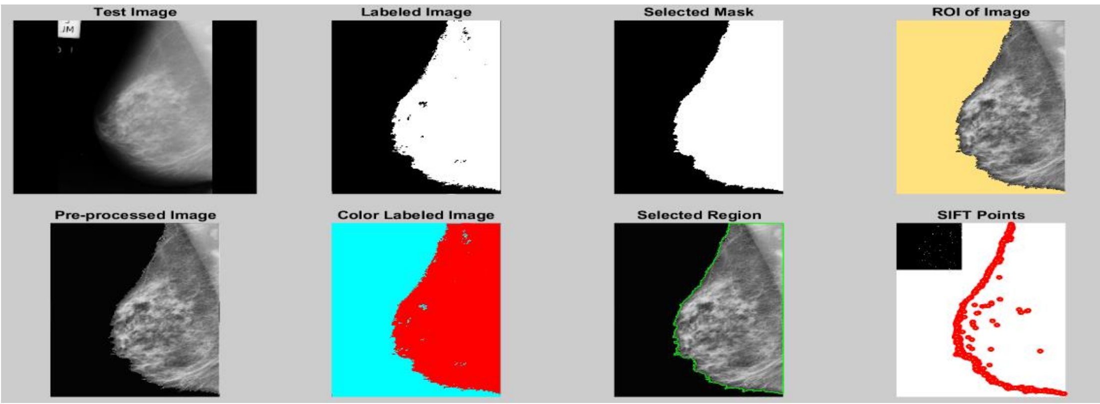

Figure 3. Feature Extraction using the SIFT technique

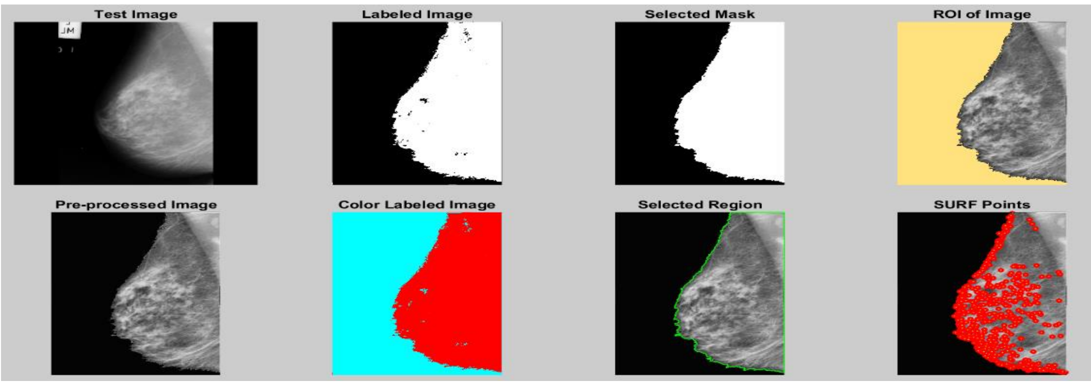

Figure 4. Feature Extraction using the SURF technique

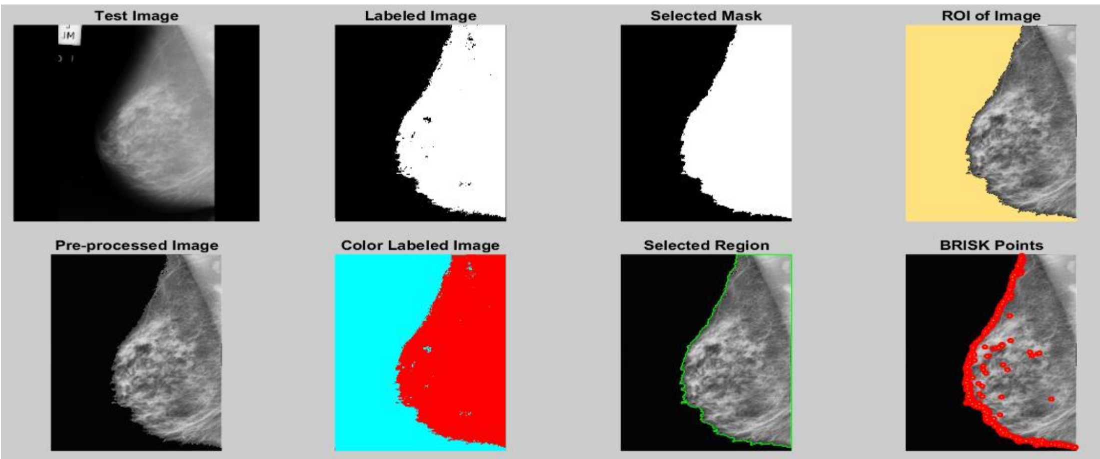

Figure 5. Feature Extraction using the BRISK technique

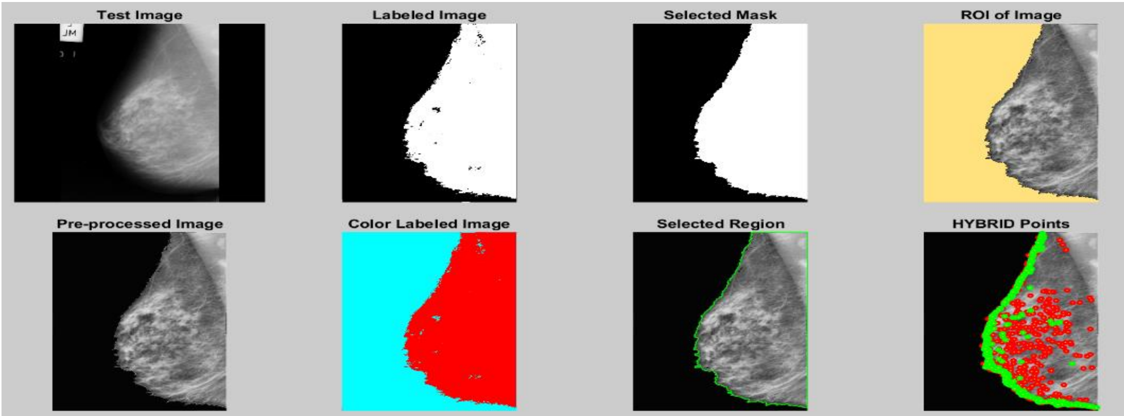

Figure 6. Feature Extraction using the hybrid technique

Algorithm 3: Pseudocode Feature Extraction using the hybrid method

Input: Training images N
Output: Feature hybrid descriptor F_i
Initialization: N training images;
Compute the average height and width for all segments;
while *input image* $i < N$ **do**
  Read the present image I_i with its ground truth image G_i;
  Pre-process the image for contrast setting and filtering;
  Extract n key points using the descriptor $K_i(p, q)$;
  Acquire the point (x_c^i, y_c^i) which are close to the ground truth;
  Calculate the weighted distance between these points and coordinates:
  $D_j = \sqrt{(x_j - x_i)^2 + [\frac{w}{h}(y_j - y_i)]^2}$;
  Add the distance to the feature hybrid descriptor: $F_i(p_j, q+1) = D_j$;
end
Save $F_i(p, m')$, where $m' = m + 1$;

The pseudo-code of proposed feature extraction method shows the extraction of key data points from the dataset. The hybrid algorithm used to extract the required features is given in Algorithm 3. When it comes to selection and rejection architecture, Swarm Intelligence (SI) has been referred to since 1991. SI is a subcategory of the meta-heuristic algorithms that follows the architecture of statistical machine learning. It is built on the food gathering behavior of diverse species worldwide and was first offered in 1991 and until now, numerous modifications and alterations have been presented [39]. More than 50 algorithm architectures have been proposed and the present work uses insect-based SI due to its wide availability in research articles as listed in Figure 7.

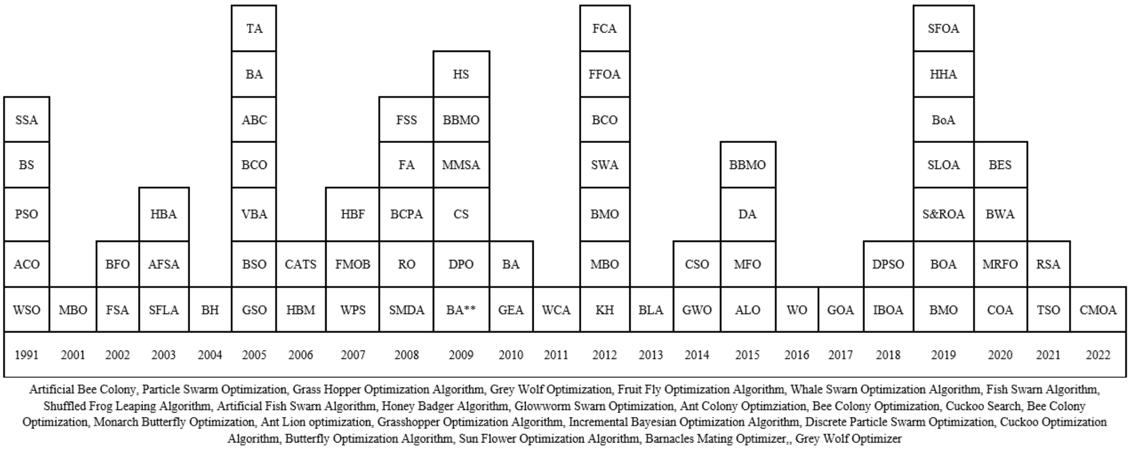

Figure 7. Swarm Intelligence Algorithm list in insect Swarm Category

3.6 Feature Optimization

An accurate and correct diagnosis framework highly relies on strength and relevance of features used in the analysis. Here, feature optimization is used to optimize the features using different optimization techniques such as swarm intelligence and metaheuristic techniques. Feature optimizations performed using GOA which is a stochastic optimization technique inspired by the swarming behavior of the grasshopper insects [39]. In this work, GOA has been used to optimize the features of BC obtained using the K-means clustering. The grasshopper located at the nth position is near enough to objective one grasshopper, which is computed using the following equation as follows: -

$$P_n = G_{F_n} + SI_n + W_{A_n} \tag{2}$$

In the given equation 2, GF signifies the gravity force, SA signifies 'social interaction' and WA signifies 'wind advection'. Here, P_n shows the position of nth grasshopper which is obtained by using the following equation 3.

$$P_n = C_1 G_{F_n} + C_2 SI_n + C_3 W_{A_n} \tag{3}$$

Where C1, C2, and C3 are the random constants whose values fall in interval [0, 1]. However, social interaction for the nth grasshopper commonly depends upon the interaction between the two social forces, which is a repulsion force to avoid and halt the collisions, and it can be an attraction force. The social interaction is computed as shown in equation 4.

$$SI_n = \sum_{i=1}^{q} SI(D_{jk}) D_{jk} \tag{4}$$

Where $(D_{jk}) = X_k - X_l$ (5)

$$\widehat{D_{jk}} = \frac{X_k - X_l}{D_{jk}} \tag{6}$$

Where D_{jk} is the length of the Euclidean of the k[th] with j[th] grasshopper. The social forces are further evaluated using the following equation 7.

$$S_F = f_i e^{\frac{-R}{S_L}} - e^{-R} \tag{7}$$

s_L is the length of the scale of attraction and f_i is the intense force for attraction. Finally, the W_{A_n} is obtained using the following equation 8.

$$S_F = f_i e^{\frac{-R}{S_L}} - e^{-R} \tag{8}$$

Where, D_C is the constant drift and e_g is the unit vector. By computing the different variables, the following equation has been obtained 9.

$$P_n = G_{F_n} + \sum_{i=1}^{q} SI\left(\frac{X_k - X_l}{D_{jk}}\right) D_{jk} + D_C \widehat{e_g} \tag{9}$$

$$c = c_{max} - itr \frac{c_{max} - c_{min}}{T_{itr}} \tag{10}$$

Where, highest c_{max} and lowest c_{min} reducing factor for factor c and itr and T_{itr} are the current and total number of simulation rounds. The proposed Grasshopper algorithm covers both the exploitation and the exploration part of feature set selection.

Algorithm 1 Algorithm Grouped-GrassHopper

```
FeatureSet as fs ClassLabel as Ls Selected Feature set as Selected
for_1 i= 1 : unique(Ls)
Hoppers_(Index)=find(Ls==i)
Hopper_(food)=fs[Hopper_(Index)];
[hypoGH_(index),hypoGH_(GB)]=kmeans(Hopper_(food),2).
lf=10; // levy flights
Reward_(Matrix)=zeros(1,lf);
grp=.20;
for_2 j= 1 :lf
G_m=Index_(of)(Hopper_(Index).grp *100);
Grouping_(Food)=Hopper_(food)[G_m]
Grouping_(Food).Append(Hopper_(food)[j]// Append the current grasshopper
GB_c=hypoGH_(GB)[hypoGH_(index)[j]
[Fit,fitness_t h]=fitness_(fun)(GB_c,Grouping_(Food),Hopper_(food)[j])
if Fit==1
Reward_(Matrix)[lv]=1;
end_(if)
End(for_2)
if Reward_(Matrix)==1 ≥Reward_(Matrix)==0
Selected.Append(j);
end_(if)
End_(for_1)ReturnSelected
```

In order to do so, a novel levy-based group behavior is designed. The proposed algorithm architecture uses a hybrid feature that combines SIFT and BRISK feature sets. Because of its special architecture, the algorithm can go through a variety of feature sets quickly and effectively, which maximizes performance. In addition, the suggested system architecture has a hybrid feature that combines feature sets from BRISK and SIFT, utilizing the advantages of both techniques for improved feature representation. The suggested system is a potential development in feature selection strategies because of this integration, which enhances accuracy and robustness in a variety of applications. The algorithm architecture is given in algorithm 4.

The proposed GOA algorithm is a group behavior-based algorithm for the selection of features. It takes each feature vector from each class category and considers each feature vector as a grasshopper. The update policy of Grasshopper is dependent upon the grouping behavior. 10 levy flights have been considered and each time the grouped population is evaluated against the sole hopper based on the grouped centroid. The step architecture of the proposed algorithm is as follows.

1. Consider the Feature set as the grasshoppers to be selected or rejected, Ls be the label of the features. The label represents the class of the extracted features.
2. For every unique class element in the Ls set, extract each category set features and consider them as grasshoppers and their attribute set as grasshopper food.
3. Divide the entire food into two hypothetical groups using k-means to create the region for exploitation and exploration
4. A 10 levy flights is initiated and for each levy flight, there will be a positive reward 1 or there will be no reward.
5. Take 20% of the total population as the grouping percentage to form Swarm.
6. Create a random index of 20% of the total population
7. Extract the features of the generated indexes, and extract the global best as GB_c, which is the hypothetical centroid value, created by k-means
8. Append the current hopper to the food list
9. Pass the GB_c, and grouped hopper food along with sole hopper food to the fitness function of the proposed grouped GOA algorithm
10. If the fitness value is 1, append the value as a reward into the levy flight value, else it is already 0
11. Repeat the steps until the levy flight finishes and calculate the total number of success rewards as 1 and non-success rewards as 0.
12. If the success rewards are equal to or greater than non-success rewards, accept the feature as an accepted hopper
13. Return all the accepted indexes of features.

In order to compare the presented algorithm with another state-of-the-art SI algorithm, the extracted features are also optimized using other swarm-based techniques such as PSO and the fruit fly technique for better results.

3.7 Feature Classification using the Machine Learning Models

A ML models show an important role in classifying the features using the ANN, DNN and NB classifier. The training and testing have been done to classify the cancerous region or say Region of Interest (RoI). ANN is a computation model that depends upon the structural elements of biological Neural Networks [38]. ANN is widely useful for solving the binary classification problem in the case of a single neuron using the logistic activation function. In the proposed classifier, a densely connected neural network is used with four layers having one-input and two-hidden layers. These layers use a Rectified Linear Circuit (ReLu) function to control the parameters. The classifier works on a sequential basis and is considered as a most straightforward model with a dense 12 neurons-based hidden layer. Each layer is used to deal with its weight matrix and contains the association weight of each neuron and its sources. The neurons are associated with the vector and the initiation work using the ReLu plays a positive role in classifying the cancer and a negative role in case of not detecting the cancerous patches. The architectural measures of the ANN are shown in Table 2.

Table 2: ANN Ordinals

Layers	Type	Units	Output
1	Input	12 units	(1, 12)
2	Hidden Layer 1	6 units	(1,6)
3	Hidden Layer 2	4 units	(1,4)
4	Sigmoid function	1 unit	(1,1)

The layout of Deep Neural Network (DNN) is almost similar to the ANN but still, DNN is a complex model that is used to create a model and define the complex problems in simple form. Moreover, the recent research studies based on image-based cancer study have demonstrated that the deep learning models provide promising outcomes for large sample size. Therefore, DNN is integrated in the present work and there are 'n' hidden layers used to process the data from the previous layer to next layer with a minimum error rate. The error was minimized due to adjustment in weight and backpropagation used for better results. Using DNN, any number of inputs is used in the input layer. To speed up the learning process, there is more count of nodes than the input layers. However, there are unique output nodes in the case of the output layer. The parameters used in DNN are defined in Table 3.

Table 3: Ordinal Measures using DNN

Parameter	Description
Number of nodes in Input layer	12
Number of nodes in Output layer	2
Bias	1
Learning rate	0.15
Initial Weight to adjust the error	Assigned randomly
Number of Hidden layers	6
Number of nodes in a hidden layer	6
Stop condition to terminate the epoch	Until the number of iterations terminates

The algorithm seeks to use DNN for the classification purpose. The topology of the neural network is first established, comprising an input layer with a predetermined number of nodes. The hidden layers that are required for training are set to zero.

Algorithm 7: Classification using the DNN model

```
Input: Training data
Output: Classification accuracy
Parameters: Number of input nodes n, Number of epochs
Define the neural network
    Define input layer with n input nodes;
    Initialize hidden layers required for training;
    Define bias and learning rate for every input node;
    Select initial weights;
Define ReLU activation function: f(y) = max(0, y);
Define number of epochs for back-propagation;
Training
    Train the data using the defined neural network;
Testing
    Pass trained data to test model for classification rate determination;
while Objective not achieved do
    Repeat training process;
Compute accuracy of proposed model using evaluation metrics;
return Classification accuracy;
```

For every input node, initial weights and parameters like bias and learning rate are specified. When the ReLU activation function is set, the network can undergo non-linear changes. When back propagating values from the output node during training, the number of epochs is calculated. Training is carried out using the given information. To evaluate classification accuracy, the data is run through a test model after training. Training is repeated until the intended goal is achieved. Ultimately, a variety of evaluation indicators is used to calculate the model's correctness. The accuracy of the proposed DNN model is defined using the true positive rate and false positive rate.

4. Results and Discussion

In this section, analysis of different performance metrics has been done to determine the robustness of the proposed approach. The analysis results using the aforementioned feature extractor and classifiers are illustrated in the further sections.

4.1 Feature Classification using the Machine Learning Models

The outcomes of the proposed classification is estimated by numerous performance parameters for instance 'accuracy', 'precision', 'recall', and 'F-measure'. The evaluation has been done to ensure that correct classification and segmentation for the detection of BC.

$$Accuracy = \frac{True\ Positive\ (TP) + True\ Negative\ (TN)}{TP + TN + False\ Positive\ (FP) + False\ Negative\ (FN)} \quad (11)$$

$$Precision = \frac{Rate_{True\ Positive}}{Rate_{False\ Positive} + Rate_{True\ Positive}} \quad (12)$$

$$Recall = \frac{Rate_{True\ Positive}}{Rate_{False\ Negative} + Rate_{True\ Positive}} \quad (13)$$

$$F - measure = 2 * \frac{Precision * Recall}{Precision + Recall} \quad (14)$$

The results and outcomes at different stages of breast cancer image processing are presented in this section. The breast cancer segmentation has been done by marking and extracting the cancerous region and selecting the relevant features. To extract the cancerous region, segmentation is performed using K-means followed by feature extraction and feature selection. The optimized feature selection is performed with PSO, FF and GOA and found GOA to be most suitable among all the three-swarm intelligence algorithms. Thus, goal is to combine the strengths of GOA with DNN for a better breast cancer classification architecture.

Table 4 illustrates the results for 100 working samples, which are; depend upon extracted features in terms of classification accuracy without any optimization technique. The analysis reveals that the average accuracy using the SURF method is 85.31%, using the SIFT technique is about 87%, using the BRISK technique is 87.3544% and the hybrid technique shows about 88.25%. It is clear that better results were obtained using the hybridization of SIFT and BRISK technique. In the proposed technique, the advantages of SIFT and BRISK have been merged for better results. The comparative results show that results using the hybrid technique are improved by 3.4%, 1.3%, and about 2% from SURF, SIFT, and BRISK respectively. As demonstrated in Table 4, there is still a margin of improvement and hence a feature selection is performed. As already demonstrated the feature selection is performed using improved GOA discussed in the methodology section. Now, the selected features using improved GOA are passed to different classifiers and evaluated.

Table 4: Accuracy with different feature extraction methods

Number of Image Samples	Using SURF	Using SIFT	Using BRISK	Using Hybrid (SIFT+BRISK)
5	84.1345	85.93163	86.1181	86.32940771
10	84.14126	86.80843	86.19487	86.84696358
20	84.175836	86.48674	86.27164	87.26271809
30	84.5256936	86.58525	86.34841	87.37391026
40	84.8755512	87.15137	86.42518	87.83473523
50	85.2254088	87.21802	87.70195	88.20529442
60	85.5752664	87.24823	87.97872	88.44234418
70	85.925124	87.26906	87.99549	88.88797228
80	86.2749816	87.32652	88.13226	89.38196584
90	86.6248392	87.63901	88.80903	90.01892624
100	86.9746968	88.06718	88.8958	90.19389846

The confusion matrix reflecting the implementation of hybrid technique with DNN classifier is presented in Table 5. To present a balanced dataset distribution, authors have included equal number of benign and malignant image sample for the experimentation.

Table 5: Confusion Matrix for Hybrid + DNN

Total samples	=100	**PREDICTED VALUES**	
	Classes	**Benign**	**Malignant**
ACTUAL VALUES	**Benign**	48	2
	Malignant	1	49

Figure 8 shows that the average precision using the hybrid technique with NB classifier is about 0.94 while using the ANN, it is about 0.95. The result using the DNN classifier is 0.99. Thus, results using the DNN techniques are better and improved by 5% from the ANN classifier. Figure 9 shows that the average recall using the hybrid technique with NB classifier is about 0.93 while using the ANN, it is 0.95. The result using the DNN classifier is 0.98. Thus, results using the DNN techniques are better and improved by 3.11% from the ANN classifier and about 5.28% from the NB classifier.

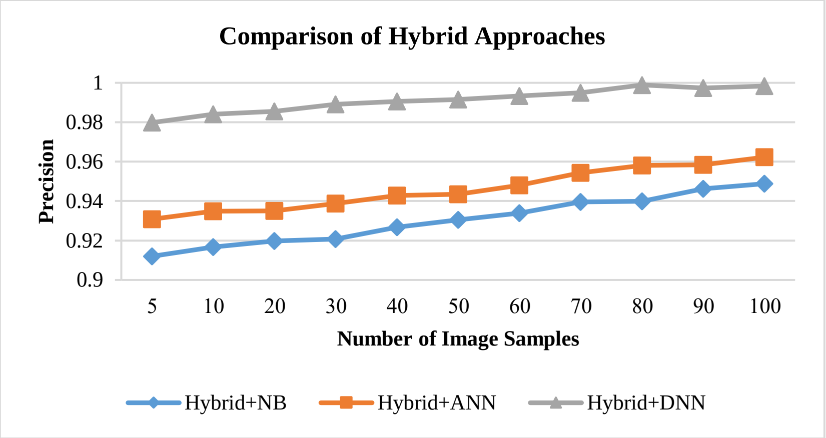

Figure 8. Comparison of Hybrid techniques with different classifiers for precision

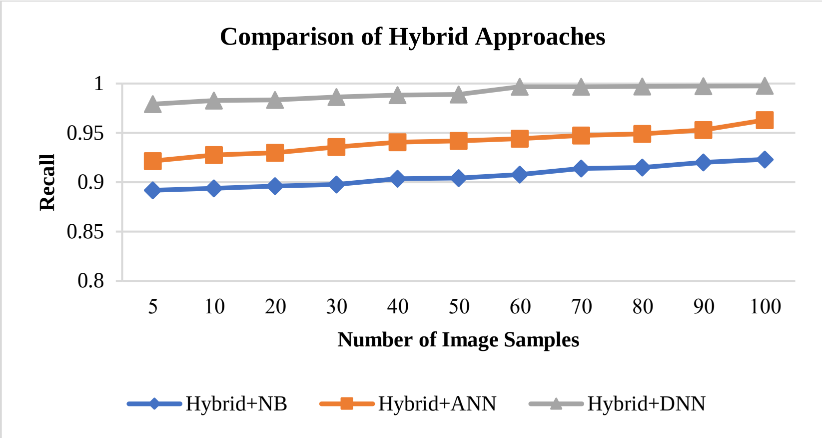

Figure 9. Comparison of Hybrid techniques with different classifiers for recall

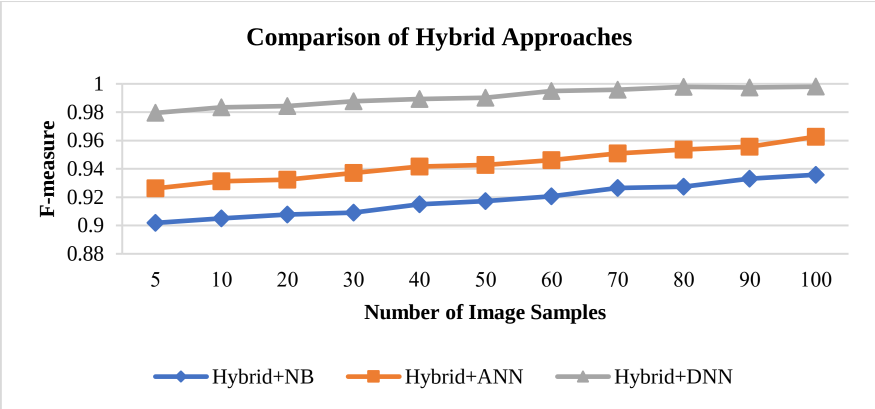

Figure 10. Comparison of Hybrid techniques with different classifiers for F-measure

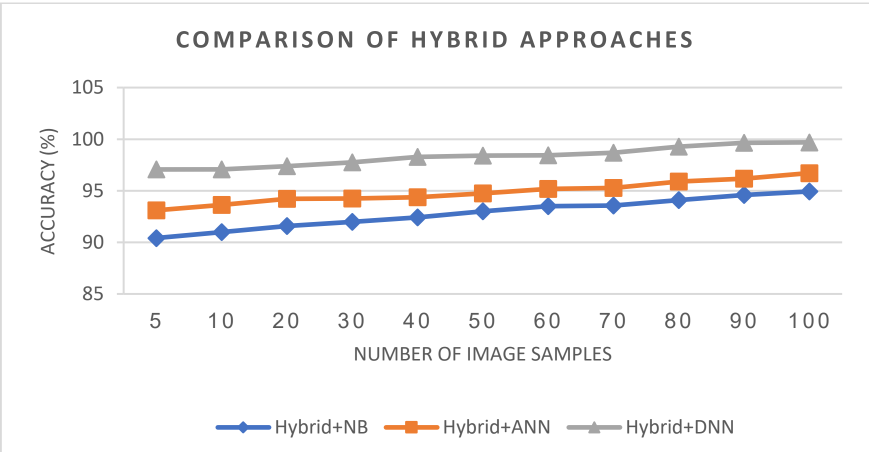

Figure 11. Comparison of Hybrid techniques with different classifiers for accuracy

Figure 10 shows that the average F-measure using the hybrid technique with NB classifier is about 0.93 while using the ANN, it is 0.95. The result using the DNN classifier is 0.985. Thus, results using the DNN techniques are better and improved by 4% from the ANN classifier and 5.1% from the NB classifier. The accuracy analysis of the Hybrid models shows that the Hybrid+DNN approach consistently achieves the highest accuracy, peaking at 99.69% with an average of 98.20%. This outperforms the Hybrid+ANN and Hybrid+NB models, which have maximum accuracies of 96.71% and 94.94%, respectively. The results highlight the superior performance of the Hybrid+DNN model, making it the most effective in the series.

4.2 Comparative Analysis

In this section, results have been compared with the existing techniques for evaluation. The existing techniques using the GOA technique with CNN classifier and Activation Function with DNN classifier have been considered for comparison.

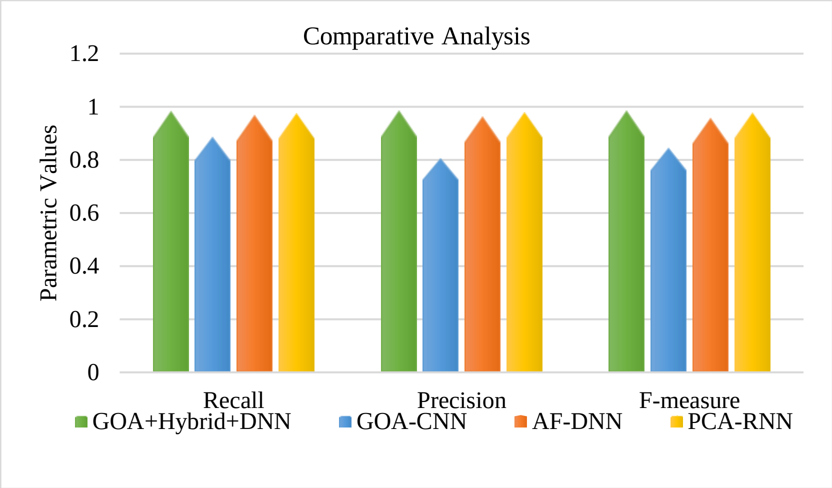

Figure 12. Comparison of Proposed Techniques with Different Classifiers

Figure 12 shows the comparative analysis of the proposed technique with the existing technique for various performance metrics. The analysis results show that precision using the proposed technique is 0.99 while existing technique such as GOA-CNN proposed by Sha et al., 2020 [40], AF-DNN proposed by Vijayakumar et al., 2021 [27] and Veni et al., 2022 [28] shows 0.89, 0.96 and 0.979, respectively. Consequently, the recall value using the proposed technique is 0.99 while existing technique such as GOA-CNN, AF-DNN and PCA-RNN shows 0.89, 0.97 and 0.976, respectively. Similarly, the F-measure of the proposed technique is 0.99 which is better than Sha et al. 2020 (0.848), Vijaykumar et al. 2021 (0.962) and Veni et al. 2022 (0.978). The higher performance values show an improved performance of the proposed technique in comparison to the existing studies.

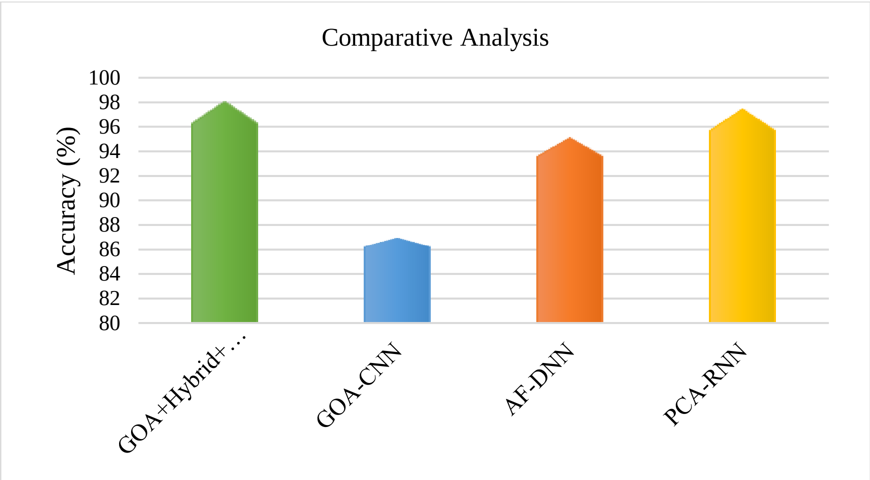

Figure 13. Comparison of Proposed Techniques with Different Classifiers for Accuracy

Figure 13 demonstrates comparative analysis of the proposed technique with the existing technique for accuracy. The analysis results show that accuracy using the proposed technique is about 98.19% while existing technique such as GOA-CNN proposed by Sha et al. 2020 and AF-DNN proposed by Vijayakumar et al. 2021 shows 87% and 95% respectively while PCA-RNN proposed by Veni et al. is 97.6%. Thus, the proposed technique is improved by 11.19% from Sha et al. 2020, 2.95% from Vijayakumar et al. 2021 and 0.6% from Veni et al.

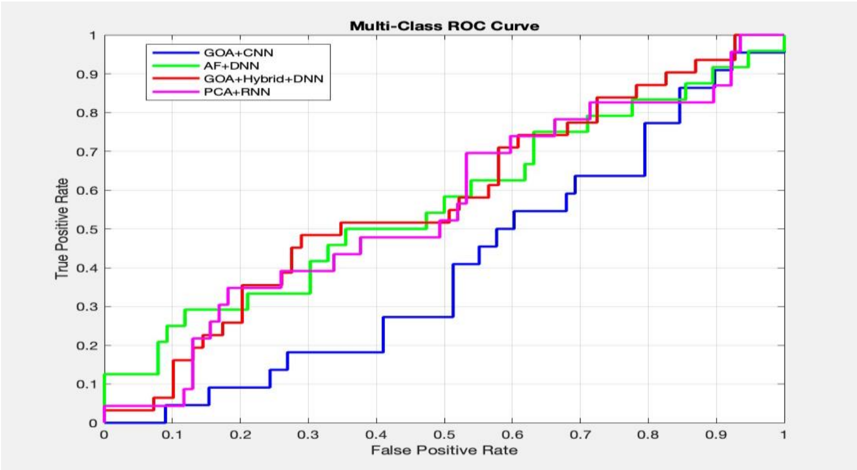

Figure 14. ROC Analysis

Further, ROC analysis is also presented in Figure 14 drawn against true positive rate and false positive rate showing better performance of proposed GOA+Hybrid+DNN.

5. Conclusion

The detection and classification of Breast cancer is a challenging task, which is too time-consuming. The growth of cancerous regions whenever distinguishable can save the lives of hundreds of patients. By investigating, it is advocated that machine learning-based classification techniques had better classify breast cancer with good accuracy. In this paper, feature extraction and classification has been done using the GOA and DNN classifier. The feature extraction is done using the hybrid technique (SIFT and BRISK) for the better extraction of features. The breast cancer dataset was collected and implementation was done to detect the cancerous region. The performance metrics are computed and results show that the average F-measure value using the proposed hybrid technique with DNN classifier is very high. The better value shows the better extraction of features. Furthermore, the average accuracy using the hybrid technique reaches a 99% mark. The outcomes are further compared with existing technique for assessment and show that accuracy is improved by 11.19% from the existing techniques. The work has demonstrated a high success rate, and therefore it has a great scope of experimentation with real time patient data. At present, the work has been experimented over 100 image samples and to overcome a limitation it will be extended with the inclusion of a large image dataset. Further, computation cost was not evaluated at present that may otherwise challenge the present work. Therefore, this parameter will be a part of future research work and attempts will be made to maintain a balance between computation cost and the classification accuracy of proposed work.

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