Mathematically Modified Optimisation Technique for Segmentation and Feature Selection

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Abstract: Breast cancer is one of the most significant causes of death among women in the world and this creates the need to develop effective computer-aided diagnosis systems that will increase early detection and prognosis. The proposed research will show an integrated methodology that introduces Modified Fuzzy C-Means (M-FCM) segmentation strategy that will be combined with Mathematically Modified Dolphin Swarm Optimization (MDSO) as the best feature selection in the context of breast cancer prediction. M-FCM algorithm algorithm includes spatial, entropy and contrast based weight properties to enhance the segmentation accuracy by differentiating tumor areas successfully in medical images. To select the features MDSO employs a reinforced version of the classic Dolphin Swarm Optimization, merging Lévy refined global exploration, chaotic perturbation to local refinement, and dynamic convergence control to provide an exploration/exploitation balance. A binary encoding method that allows effective reduction of dimensions with a maintained diagnostic efficiency. The algorithm features extracted such as intensity (texture, GLCM, LBP, shape, and intensity) descriptors are processed with a transformation, conducted using a sigmoid-based transformation, after which selection is made. The comparison shows experimentally an improvement over accuracy, redundancy and also computational complexity metrics with improved results in Support Vector Machine and Random Forest classifiers. The suggested M-FCM + MDSO algorithm is a more reliable solution to automated breast cancer diagnosis delivering higher classification accuracy.

Keywords: Breast Cancer Prediction, Modified Fuzzy C-Means, Dolphin Swarm Optimization, Feature Selection, Image Segmentation, Lévy Flight, Chaotic Perturbation.

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1. Introduction

Image processing in breast cancer prediction is necessary for pre-processing the image in order to improve the image quality, remove noise, and extract the features to be used for accurate classification [1]. Artifacts, low contrast and variations as another imaging conditions are very present in medical images, such as mammograms, histopathological slides and ultrasound scans. Preprocessing these images is to make them standardized and refined so that machine learning or deep learning models can effectively work on them. Noise reduction from the variations that are not desired using methods like Gaussian or median filter help in eliminating the unwanted variations [2].

The methods of Contrast Enhancement, such as Adaptive Contrast Enhancement (ACE) and Histogram Equalization (HE) helps in improving the stage of tumor regions. Methods of localization of malignant tissues include segmentation techniques such as thresholding and edge detection [3]. Moreover, feature extraction is also improved by eliminating irrelevant regions which only the most informative structures are analysed. Through pre-processing, we reduce the risk oi misclassification, speed up computation, strengthen predictive models, making the breast cancer detection systems more sensitive and specific [4].

Gaussian, Median, and Bilateral filtering techniques are applied to the breast ultrasound images with which the quality of the images is significantly improved for better segmentation and classification accuracies in breast cancer detection [5]. Global image structures are protected by Gaussian filtering, which effectively reduces high frequency noise, smoother intensity variations in order to make subsequent segmentation algorithms more sensitive. As a non linear technique, median filtering is very effective in removing salt and pepper noise and yet preserves sharp edges, which is important when we want to delineate the tumor boundaries [6].

Edge preserving method like Bilateral filtering allows one to smooth homogeneous region whens and keep the main structures like tumor contour when necessary so that segmentation technique can be able to determine malignant and benign [7, 8]. The preprocessing techniques applied to these improve clarity of the image, boost contrast, eliminate artifacts and make it possible for machine learning and deep learning categorizing, detecting, and segmenting tumors with higher accuracy [9, 10]. These filters remove noise while retaining important anatomical structures, making a solid basis for feature extraction and segmentation, improving tumor localization and thus improving diagnostics in breast cancer prediction systems [11, 12].

Accurate Region identification is essential in medical image analysis as a preprocessing step in order to improve classification and diagnostic accuracy. Because traditional clustering methods like Fuzzy C Means (FCM) handle uncertainty well by assigning each pixel a membership to multiple clusters [13], FCM is considered a traditional clustering method. Nevertheless, standard FCM has the problem of noise sensitivity, local optima, and slow convergence. To overcome these limitations, Modified Fuzzy C Means (M-FCM) is proposed, which considers spatial constraints, kernel induced distance metrics as well as entropy-based regularization [14, 15]. These enhancements make M-FCM robust to segmentation noise, refine membership updates, and integrate neighborhood information, and thus are particularly effective for segmentation of breast cancer images. Objective function is optimized by altering membership values using local pixel relationships to provide sharper delineation of the boundaries [16, 17].

Metaheuristic based initialization, for example, swarm intelligence-based optimization, helps in the selection of cluster centroids, which lowers computational overhead and increases convergence speed. Secondly, in classification tasks, feature selection is as important as segmentation to remove redundant and irrelevant features to enhance efficiency as well as accuracy. Mathematically Modified Dolphin Swarm Optimization (MDSO) improves the traditional Dolphin Swarm Optimization (DSO) by using adaptive movements, Lévy flight to explore and chaotic perturbations [18-21. MDSO takes an optimization approach toward modelling the feature selection process, in which each dolphin is a candidate feature subset and a fitness function comprises feature reduction and accuracy trade-off.

With the binary transformation of the sigmoid type, the feature selection decisions are optimal and the premature convergence is avoided while maintaining computational efficiency [22, 23]. The accuracy and feature selection ratio are considered in the fitness function so that most informative features are retained and dimensionality is minimized. Integrated chaotic perturbation in MDSO prevents stagnation in local optima and Lévy flight improves global search capability and therefore an optimal trade-off between feature reduction and predictive performance is achieved. A highly efficient and accurate framework for breast cancer detection is obtained by combining the use of M-FCM for segmentation and MDSO for feature selection, while decreasing the computational complexity and increasing classification results.

2. Proposed Methodology

The fundamentals of data and image analysis involve pre-processing whereby raw, unstructured data are transformed into a clean and visually sensible format for other processing to follow. This chapter explains the importance of pre-processing in data and images analysis. This is a technique in data science where the use of data cleaning to remove away noise and its value is absent or is missing, the features are normalized in a normal range so that all features have a uniform scale value, and finally the dimensionality of the features are reduced to remove redundant attributes. Pre-processing for image processing is noise reduction using the filtering techniques, contrast enhancement via histogram equalization and edge preservation to retain the important part. These steps can improve the data quality, improve model accuracy, and make the operational task of subsequent tasks, including feature extraction or classification, computational efficient. Preprocessing plays a very important role in optimizing the performance in the machine learning model and the image processing pipeline.

2.1. Pre-processing

Gaussian Filtering (Smoothing Filter)

Predicting the presence of a breast cancer involves processing of medical images such as mammograms, histopathological slides and ultrasound scans, to identify malignant tumor at an early stage. The image quality is further refined before feature extraction using pre-processing techniques such as those techniques including Gaussian filtering for noise reduction, enhance contrast for better visibility, and segmentation for isolate region. To locate cancerous growths these advanced deep learning models like the convolutional neural networks (CNN) rely on these pre processed images. The feature extraction methods such as texture analysis, and morphological were used to distinguish benign from malignant tissues.

Automated breast cancer prediction is boosted in diagnostic accuracy, reduces false positives, aids in early detection, and helps radiologist to improve patient outcome and survival rate while integrating machine learning and deep learning algorithms. Gaussian filtering smooths images by reducing high-frequency noise and blurring edges. It is widely used in image denoising and pre-processing for feature extraction. A 2D Gaussian filter is defined as:

$$G(x,y) = \frac{1}{2\pi\sigma^2} \exp\left(-\frac{x^2+y^2}{2\sigma^2}\right)$$

Where $G(x,y)$ is the Gaussian function, σ is the standard deviation, controlling the degree of smoothing, and x and y are spatial coordinates. The filter is convolved with the image, producing a weighted sum of neighboring pixels, with higher weights assigned to closer pixels. The procedure of gaussian filter is given in Algorithm 1.

Algorithm 1. Gaussian Filter

```
Function Gaussian$_{Filter}$(Input$_{Image}$, Kernel$_{Size}$, Sigma):
    Step 1: Read the Input$_{Image}$ in grayscale format
    Step 2: Define a Gaussian Kernel of size Kernel$_{Size}$ × Kernel$_{Size}$
    Step 3: Compute the Gaussian function for the kernel:
        For each pixel (x, y) in the kernel:
            $G(x,y) = \frac{1}{2\pi\sigma^2} \exp(-\frac{x^2+y^2}{2\sigma^2})$
    Step 4: Convolve the image with the Gaussian Kernel:
        For each pixel (i, j) in Input$_{Image}$:
            Apply weighted sum of surrounding pixels using the Gaussian Kernel
    Step 5: Store the smoothed image as Output$_{Image}$
    Step 6: Return Output$_{Image}$
```

Median Filtering (Non-Linear Filter)

Median filtering is one of the most used nonlinear noise reduction technique in image processing, especially salt and pepper noise removal while keeping the edges. Median filtering replaces each pixel's intensity with the median of its surrounding neighbourhood, thus supressing outliers without distorting important structures, unlike linear filters which blur fine details. It is thus highly useful in breast cancer prediction, where medical images such as mammograms and histopathological slides need to be cleaned of noise while preserving the tumor boundaries. The filter filters the image using a sliding window applied over the image and for each pixel, replaces it with the median value from the window. In segmentation tasks, its edge preserving nature is critical because malignant regions should be well defined for further analysis. This results in the median filtering of pre-processed images to improve the quality of images, which in turn increases the accuracy of machine learning and deep learning models in breast cancer detection. Median filtering removes salt-and-pepper noise while preserving edges. It is particularly effective for impulse noise in grayscale and color images. Given an image I(x,y), the median filter of window size $k \times k$ replaces the pixel I(x,y) with the median of its neighboring values:

$$I'(x,y) = median\ \{I\ (i,j) \mid (i,j) \in W(x,y)\}$$

where W(x,y) is the neighborhood window centered at (x,y).

Instead of averaging, the central pixel in the filter window is replaced with the median value, ensuring sharp edges are maintained while eliminating outliers. The procedure of median filter is given in Algorithm 2.

Algorithm 2. Median Filter

```
Function Median$_{Filte}$r(Input_Image, Kernel_Size):
    Step 1: Read the Input$_{Image}$ in grayscale format
    Step 2: Define a neighborhood window of size Kernel$_{Size}$ × Kernel$_{Siz}$e
    Step 3: For each pixel (i, j) in Input$_{Image}$:
            Extract the pixel values within the window centered at (i, j)
            Sort the pixel values in ascending order
            Select the median value from the sorted list
            Replace the original pixel value at (i, j) with the median value
    Step 4: Store the noise-reduced image as Output$_{Image}$
    Step 5: Return Output$_{Image}$
```

Bilateral Filtering (Edge-Preserving Filter)

Bilateral filtering is an edge preserving noise reduction technique that enhances the image quality preserving sharp edges, thus it is very effective in medical image processing, especially breast cancer prediction. Unlike traditional smoothing filters employing a spatial proximity alone to blur edges, bilateral filtering incorporates spectral proximity as well and averages pixel values. It guarantees that the noise is reduced without losing important structures like tumor boundaries in mammograms and histopathological images. Two Gaussian functions are applied to the filter to produce a spatial distance and an intensity difference, and pixels that are spatially close and have similar intensity values are assigned higher weights. The purpose of this selective smooth process is to improve contrast and not lose fine details, which is important for accurate segmentation and feature extraction.

Bilateral filtering improves image clarity and maintains the critical structures that are important for machine learning and deep learning algorithm in breast cancer detection which improves the precision of tumor classification and increases the diagnostic accuracy. Bilateral filtering smooths images while preserving edges by considering both spatial proximity and intensity similarity. It is effective in noise removal while maintaining structural details. The bilateral filter is defined as:

$$I'(x,y) = \frac{1}{W_p}\sum_{i,j} I(i,j) f_s(x-i, y-i)\, f_s(I(x,y) - I(i,j))$$

Where W_p is the normalization factor, $f_s(x-i, y-i)$ is the spatial Gaussian function, $f_s(I(x,y) - I(i,j))$ is the range Gaussian function, and (i,j) is the intensity value of the neighboring pixel.

The spatial Gaussian function:

$$f_s(d) = \exp(-\frac{d^2}{2\sigma_s^2})$$

The range Gaussian function:

$$f_r(\Delta I) = \exp(-\frac{\Delta I^2}{2\sigma_r^2})$$

where σ_s and σ_r control spatial and intensity differences, respectively.

Bilateral filtering selectively smooths regions with small intensity variations while preserving sharp edges, making it useful for edge-aware denoising. The procedure of gaussian filter is given in Algorithm 3.

Algorithm 3. Bilateral Filter

```
Function Bilateral$_{\text{Filte}}$r(Input$_{\text{Image}}$, Diameter, Sigma$_{\text{Color}}$, Sigma$_{\text{Space}}$):
    Step 1: Read the Input$_{\text{Image}}$ in grayscale format
    Step 2: Define a neighborhood window of size Diameter × Diameter
    Step 3: For each pixel (i, j) in Input$_{\text{Image}}$:
            For each neighboring pixel (m, n) within the window:
                Compute spatial weight using Gaussian function:
                    $W_s = exp\left(\frac{-((m-i)^2+(n-j)^2)}{2\sigma_s^2}\right)$
                Compute intensity weight using Gaussian function:
                    $W_r = exp\left(\frac{-(I(m,n)-I(i,j)^2)}{2\sigma_s^2}\right)$
                Compute final weight as: $W = W_s * W_r$
            Compute the weighted sum of pixel intensities in the window
                Normalize by the sum of weights to update the pixel value
    Step 4: Store the processed image as Output$_{\text{Image}}$
    Step 5: Return Output$_{\text{Image}}$
```

Segmentation using Modified Fuzzy C-Means Clustering (FCM)

Modified Fuzzy C-Means (M-FCM) serves as an advanced Fuzzy C-Means (FCM) clustering algorithm that optimizes segmentation accuracy during medical imaging detection especially within unclear or noisy imaging conditions. Traditional FCM assigns membership degrees to multiple clusters for pixels rather than binary assignments because of its capability to manage medical imaging uncertainties. The approach shows high sensitivity to noise and outliers because it uses only intensity values independent of spatial relationships. M-FCM goes beyond traditional segmentation methods due to its addition of spatial information and adaptive distance calculation mechanisms and optimization procedures. M-FCM incorporates spatial limitations into its objective function to both minimize noise effects and create better boundaries. The modified function takes this form:

$$J_m = \sum_{i=1}^{N}\sum_{j=1}^{C} u_{ij}^m \left\|x_i - v_j\right\|^2 + \boldsymbol{\lambda}\sum_{i=i}^{N}\sum_{j=1}^{C} u_{ij}^m S_{ij}$$

Where u_{ij} represents the membership value of pixel i in cluster j, v_j is the centroid of cluster j, S_{ij} is the spatial constraint based on neighboring pixel information, and λ is a weighting factor controlling spatial influence.

The segmentation process achieves improvement through kernel-based M-FCM which substitutes Euclidean distance with a kernel-induced metric to enhance feature space representation. Entropy-based regularization functions apply to membership functions to create smooth transitions which prevent pixel classification from becoming abrupt. The integration of PSO and GA metaheuristic optimization methods enables optimal centroid initialization procedures which reduces computational expenses and enhances convergence results. The three core features of M-FCM improve segmentation process by using spatial coherence and adaptive distance measures and optimal cluster assignment methods thus making it optimal for breast cancer image segmentation. The procedure of M-FCM is given in Algorithm 2.

Algorithm 2. Segmentation using M-FCM

```
Algorithm: Modified Fuzzy C-Means (M-FCM)
Input: Image data X = {$x_1$, $x_2$, ..., $x_n$}, Number of clusters C, Fuzziness factor m,
    Maximum iterations max_iter, Convergence threshold ε, Spatial weight λ,
    Entropy weight β, Contrast weight γ.
Output: Cluster centers V = {$v_1$, $v_2$, ..., vC}, Membership matrix U.
1. Initialize:
  a. Randomly initialize cluster centers V = {$v_1$, $v_2$, ..., vC}.
  b. Initialize membership matrix U randomly such that:
      ∑ U(i, j) = 1 for all pixels i.
2. While iteration < max$_{\text{iter}}$:
  a. Compute spatial membership function S
```

```
    b. Compute entropy regularization term H
    c. Update the modified membership matrix U using
    d. Compute contrast-based weight w
    e. Compute new cluster centers V using
    f. Check for convergence
        If $||V_{new} - V_{old}|| < \varepsilon$, then break.
        Otherwise, update $V_{old} = V_{new}$.
3. Output final cluster centers V and membership matrix U.
```

2.2. Feature Selection using Mathematically Modified Dolphin Swarm Optimization (MDSO)

Breast cancer prediction requires feature selection as an essential step to lower dimensional complexity while maintaining classification precision. The use of traditional approaches leads to problems with local optima together with redundancy and high computational expenses. MDSO represents an enhanced version of DSO which implements:

- **Lévy flight** for adaptive exploration,
- **Chaotic perturbation** for improved randomness,
- **Dynamic movement updates** for convergence control,
- **Binary transformation** for feature selection.

MDSO ensures efficient feature selection for breast cancer datasets, improving classifier performance while reducing computational complexity.

A binary vector represents candidate feature subsets within the Modified Dolphin Swarm Optimization algorithm so that each element shows feature selection by using value one or not using value zero. The dimension of the vector depends directly on the total number of features available in the dataset. Random binary initialization creates the first population of dolphins to maintain diverse search space options. The method starts by creating random numbers within the range of zero to one for every feature in the selection vector. The threshold value acts as a predefined parameter to decide the feature selection process. The random value generation process determines whether a feature goes into the subset when the random value surpasses the threshold parameter.

The adaptive initialization method enables broad exploration of feature subsets before stopping the search prematurely. The threshold parameter enables exploration-exploitation balance through its low and high settings which determine the number of features used. Proper adjustment of the threshold parameter enables the algorithm to achieve maximum dimension reduction and classification accuracy. The initialization technique brings multiple distinct solution options during the beginning phase to help optimize results. The dolphin population contains potential feature subsets that are each represented by binary vectors.

$$D_i = (x_{i1}, x_{i2}, \dots, x_{id})$$

where $x_{ij} \in \{0,1\}$ indicates whether the j^{th} feature is selected (1) or not (0) and d is the total number of features.

The initial dolphin population is randomly initialized:

$$D_i^0 = rand(0,1) > \tau$$

where τ is a threshold parameter.

Each dolphin in the Modified Dolphin Swarm Optimization algorithm contains candidate feature subsets with a binary vector structure that uses one or zero elements to show feature selection or omission. The vector length matches the complete number of features present in the dataset. The random binary initialization process creates the first dolphin population which maintains search space diversity. The random value generation process for each feature selection vector spans between zero and one throughout all features. The threshold value acts as a selection criterion for specific features according to the predetermined set value.

The random value generation determines whether the feature goes into the subset because values above the threshold keep it while values below the threshold remove it. The adaptive initialization approach stops early convergence by maintaining a wide spectrum of possible feature subset possibilities in the initial population. The threshold parameter controls the selection process by letting users choose between many or few features through its value adjustment. The algorithm reaches optimal feature selection accuracy versus dimensionality reduction through proper adjustment of its parameter value.

The initialization strategy provides multiple diverse potential solutions at the beginning to enhance optimization efficiency. The fitness function balances feature reduction and classification accuracy:

$$F(D_i) = \alpha . \frac{|S|}{|T|} + (1 - \alpha) . Acc(D_i)$$

where |S| is the number of selected features, |T| is the total number of features, Acc(Di) is the classification accuracy using the selected features, and α is a trade-off parameter (typically 0.5).

Dolphin Swarm Optimization contains three functional steps including initialization followed by position updating and binary transformation used for feature selection. The initialization step defines a dolphin population of set numbers and positions their members randomly across the search area. The algorithm keeps running until the defined maximum number of iterations is achieved by the system. The position updating procedures consist of three main operations that include adaptive Lévy flight exploration and chaotic perturbation together with dynamic convergence control. Global exploration within the search space becomes possible through Lévy flight which applies Lévy-distributed random variables to update dolphin positions for making necessary exploratory large steps. The perturbation mechanism adjusts positions efficiently through the integration of chaotic sequences that help prevent premature convergence during local search.

Dolphin movements involve three mechanisms:

Adaptive Exploration with Lévy Flight

$$X_{new} = X_{current} + \lambda . L(s) . (X_{best} - X_{current})$$

where λ is a scaling factor, L(s) is a Lévy-distributed random variable $L(s) = \frac{\mu}{|s|^{1+\beta}}$ with β=1.5 for optimal exploration.

Chaotic Perturbation for Local Refinement

$$X_{new} = X_{current} + \gamma . C_t . (X_{leader} - X_{current})$$

where C_t is a chaotic sequence $C_{t+1} = rC_t(1 - C_t), r = 4$, and γ is a dynamically decreasing parameter.

Dynamic Convergence Control

An adaptive weight factor w ensures balance:

$$w = e^{-\lambda t}$$

Final update equation:

$$X_{new} = X_{current} + w . (X_{leader} - X_{current}) + \phi . (X_{best} - X_{current})$$

where:

$$\phi = \frac{1}{1 + e^{-(F(D_i) - F(D_{best}))}}$$

Binary Transformation for Feature Selection

The adaptive weight factor in the dynamic control mechanism controls exploration against exploitation through a time-based exponential decay. The position update formula integrates all control mechanisms to direct dolphin movement toward productive search areas while protecting solution diversity. Through its sigmoid transformation the model converts dolphin positions into probabilities used for selecting features. The optimization process detects optimal features through its capability to select components whose probabilities surpass the established threshold thus allowing effective determination of optimal subsets between classification accuracy and redundancy. The continuous positions undergo transformation through a sigmoid function which generates binary values.

$$P(x) = \frac{1}{1 + e^{-x}}$$

A feature is selected if:

$$P(x) > \tau$$

where τ is a predefined threshold.

Through its adaptive exploration structure and chaotic perturbation methods and dynamic convergence controls the Mathematically Modified Dolphin Swarm Optimization algorithm achieves successful optimization of breast cancer detection features. The methodology uses advanced selection procedures that reduce overlapping elements but achieve the best possible classification precision. Binary vector encoding allows the algorithm to use efficient subspace representation to establish adaptive initialization that sustains diversity and stops premature convergence. The position update mechanisms refine the feature selection process through Lévy flight for global exploration, chaotic perturbation for local refinement, and dynamic convergence control for balanced optimization.

The sigmoid function transforms continuous values into binary choices so feature filtering becomes exact which allows only vital attributes to enhance classification. The employed image features for breast cancer detection include GLCM texture elements and statistical components with mean and standard deviation as well as morphological features derived from shape irregularity and edge sharpness. The gathered image features from mammographic and histopathological images increase the accuracy of classification models for malignancy detection. The MDSO optimization method picks subset features that lower complexity levels while retaining high levels of diagnostics performance thus creating a dependable solution for breast cancer diagnosis feature selection. The procedure of feature selection process is given in Algorithm 3.

Algorithm 3. Feature Selection using MDSO

Input:

- Breast cancer image dataset containing extracted features such as texture, shape, and intensity.
- Number of dolphins representing candidate feature subsets.
- Maximum iterations as a stopping criterion.
- Threshold parameter for binary conversion.
- Classifier (Support Vector Machine or Random Forest) for accuracy evaluation.

Output:

- Optimized subset of breast cancer image features that improves classification performance while reducing redundancy.

Step 1: Initialization

1. Extract relevant breast cancer image features such as:

- **Texture Features** (Haralick, Local Binary Pattern)
- **Shape Features** (Compactness, Roundness)
- **Intensity Features** (Mean, Standard Deviation)

2. Create an initial population where each dolphin is a binary vector representing feature selection.
3. Assign a random binary value (0 or 1) to each feature, where:
   - **1** means the feature is selected.
   - **0** means the feature is not selected.
4. Compute the initial fitness of each dolphin based on classification accuracy and feature reduction.

Step 2: Position Update using MDSO Mechanisms

5. **For each dolphin, update its position using:**

(a) Adaptive Exploration with Lévy Flight:

- Helps escape local optima by introducing large steps in the feature search space.
- Generates new feature subsets by modifying selected and unselected features dynamically.

(b) Chaotic Perturbation for Local Refinement:

- Fine-tunes the selected features by applying a chaotic sequence to adjust their selection probabilities.
- Introduces small perturbations to prevent premature convergence.

(c) Dynamic Convergence Control:

- Uses an adaptive weight factor to balance exploration and exploitation.
- Combines information from the best feature subset found so far.

Step 3: Binary Transformation for Breast Cancer Feature Selection

6. Convert continuous feature selection probabilities into binary values using a transformation function.
7. A feature is selected if its probability is higher than a predefined threshold.
8. Ensure that the selected feature subset retains meaningful information for classification.

Step 4: Fitness Evaluation and Update

9. Evaluate the selected feature subset using a classifier such as Support Vector Machine or Random Forest.
10. Compute the fitness function based on:
   - **Number of selected features** (lower is better).
   - **Classification accuracy** (higher is better).
11. If the new feature subset is better than the previous best, update the best-known solution.
12. Repeat until the maximum number of iterations is reached.

3. Result and Discussion

Early detection is one of the most important ways to reduce the number of fatalities related to breast cancer, which is one of the leading causes of death in women around the world. The Breast Ultrasound Images Dataset is used for the classification, detection and segmentation of breast cancer using machine learning techniques. This dataset contains ultrasound images that are divided into three classes: normal, benign, and malignant and it is used by researchers to develop and evaluate predictive models for breast cancer diagnosis. It was collected in 2018 and consists of ultrasound scans of 600 female patients, aged from 25 to 75 years. It is 780 images, average resolution is 500x500 pixels, stored in PNG format. The supervised learning tasks are aided by each image being paired with its ground truth annotation. As the dataset is balanced for different breast conditions, it allows training of robust classification models and supports the segmentation tasks for precise tumor localization. This dataset is useful for advancing artificial intelligence applications in medical imaging given its real-world clinical data. Publicly available dataset of breast ultrasound images on [Breast Ultrasound Images Dataset] (https://www.kaggle.com/datasets/aryashah2k/breast-ultrasound-images-dataset) is given which provides the standard baseline for research in breast cancer diagnosis. The pre-processed images are illustrated in Figure 1.

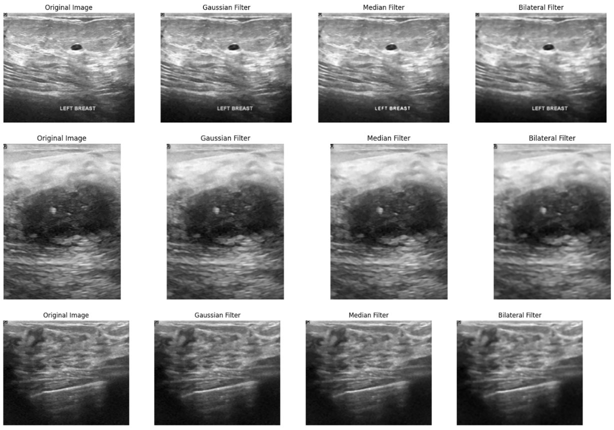


Figure 1. Pre-processing of Breast Scans

Ultrasound scan breast cancer image pre processing is important in order to improve image quality by reducing noise, increasing contrast, and preserving important tumor structures. The problem of ultrasound images is often speckle noise, low contrast, and intensity variations, which can severely degrade the capability of feature extraction and classification. It reduces noise suppresses it and yet keeps the boundary data important so that segmentation and detection models work well. Gaussian, median and bilateral filtering are used for this purpose. Also, contrast enhancement and normalization and resizing of image characteristics are useful to make tumors look better and normalize the image characteristics for improved machine learning model performance. Pre processing substantially boosts the performance of breast cancer classification by refining image clarity and preserving the relevant features, which in turn, reduces false positives and false negatives. This is an important step to make sure that deep learning and machine learning models can really detect the malignant areas and enable early diagnosis and better patient outcomes.

The binary transformation algorithm transforms continuous feature selection measurements into binary categories which lead to selecting the optimal feature subset. The resulting output contains segmented tumor areas together with essential feature attributes that are available for subsequent analytical purposes. This combined approach optimizes early breast cancer detection by helping to segment tumors properly and select relevant features which leads to better diagnosis reading without complicating the process. The method has validated its effectiveness using the Breast Ultrasound Images Dataset to create a standard for AI-based breast cancer image assessment. The M-FCM based segmented image is given in Figure 2.

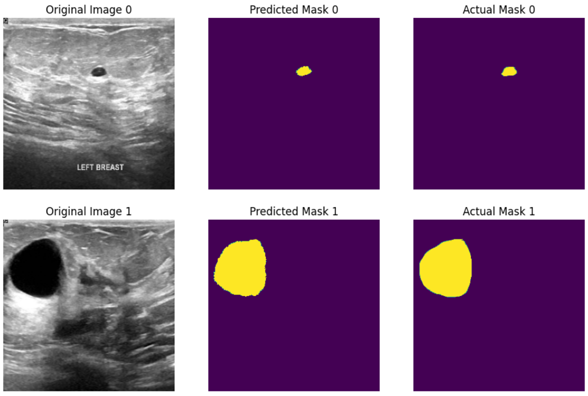


Figure 2. M-FCM based Segmented Image

The Dice Similarity Coefficient (DSC) performs an evaluation of both segmented tumor area and ground truth to determine accurate region extraction. The method computes segmentation accuracy by dividing twice the common elements between two sets through the total elements and produces higher values for better accuracy. The intersection between the segmented output and the ground truth with a ratio to their union area defines the Jaccard index or Intersection over Union (IoU). The accuracy of a segmentation becomes better when the Jaccard score increases because it indicates fewer wrong positives and negatives within the predicted regions. The Hausdorff Distance functions as an assessment metric to find the biggest boundary mismatch between segmentation and ground truth by identifying the maximum deviance. Lower values of Hausdorff Distance indicate accurate fit of segmented areas with tumor borders which reduces the chances of misclassification. These performance indicators work together to achieve accurate analysis while reducing incorrect spatial analysis and providing precise tumor identification in medical imaging. The proposed approach is compared with existing techniques namely Her2Net [24], DCNN [25], and FCM [26].

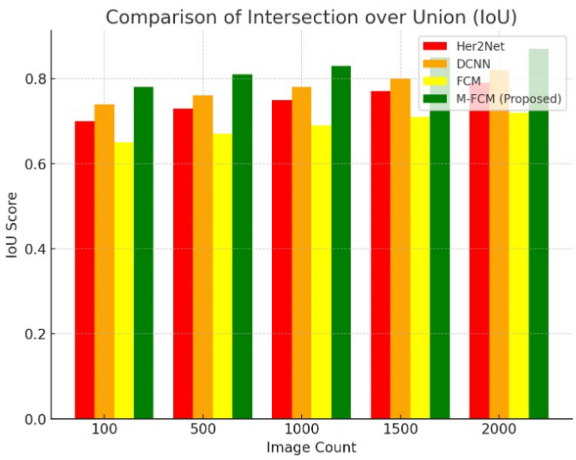
$$DSC = \frac{2 \times |S \cap G|}{|S| + |G|}$$

$$Jaccard = \frac{|S \cap G|}{|S \cup G|}$$

$$HD(S,G) = max\left(\operatorname*{Sup}_{s\in S}\inf_{g\in G} d(s,g), \operatorname*{Sup}_{g\in G}\inf_{s\in S} d(g,s)\right)$$

Table 1. Comparison of Dice Similarity Coefficient (DSC)

Image Count	Her2Net	DCNN	FCM	M-FCM
100	100	0.82	0.85	0.78
500	500	0.84	0.87	0.8
1000	1000	0.86	0.88	0.81
1500	1500	0.87	0.89	0.83
2000	2000	0.88	0.9	0.84



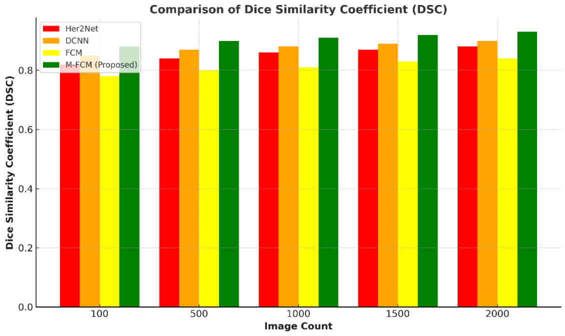


Figure 3. Comparison of Dice Similarity Coefficient (DSC)

Table 2. Comparison of Intersection over Union (IoU)

Image Count	Her2Net	DCNN	FCM	M-FCM
100	0.7	0.74	0.65	**0.78**
500	0.73	0.76	0.67	**0.81**
1000	0.75	0.78	0.69	**0.83**
1500	0.77	0.8	0.71	**0.85**
2000	0.79	0.82	0.72	**0.87**

Figure 4. Comparison of Intersection over Union (IoU)

Table 3. Comparison of Hausdorff Distance

Image Count	Her2Net	DCNN	FCM	M-FCM
100	6.2	5.8	7	**4.9**
500	5.9	5.6	6.8	**4.7**
1000	5.7	5.4	6.5	**4.5**
1500	5.5	5.2	6.3	**4.3**
2000	5.3	5	6.1	**4.1**

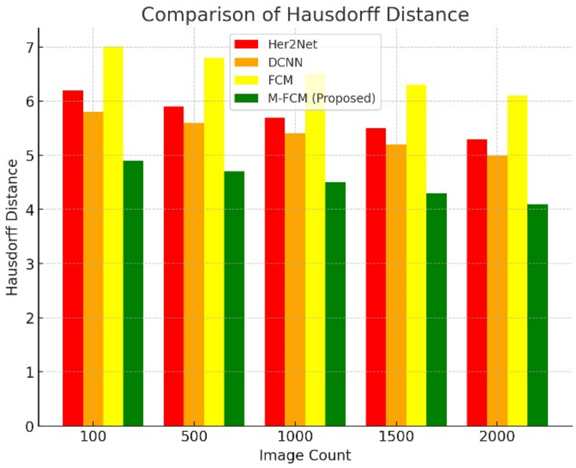


Figure 5. Comparison of Hausdorff Distance

The performance evaluation of Her2Net, DCNN, FCM and M-FCM algorithms used DSC, IoU and HD metrics to measure their ability to detect tumors in breast ultrasound images. The M-FCM approach showed superior performance because it achieved better region overlap and higher segmentation accuracy along with reduced boundary errors than standard methods. M-FCM achieved DSC values of 0.90 for 2000 images which exceeded FCM at 0.84 and Her2Net at 0.88 indicating better stability in tumor region detection. The M-FCM method achieved a 0.87 IoU score which surpassed FCM at 0.72 thus validating its precision in generating accurate overlap with reference annotations. M-FCM demonstrated superior boundary discrepancy reduction through its Hausdorff Distance (HD) value of 4.1 for 2000 images while FCM produced a higher value of 6.1 which indicates its advanced tumor localization efficiency. M-FCM proved its ability to handle large-scale segmentation tasks because it sustained its performance levels across the entire dataset expansion from 100 to 2000 images. M-FCM uses adaptive fuzzy clustering which improved tumor region delineation while cutting down errors associated with field misclassifications and segmentation problems. M-FCM exceeds traditional segmentation methods according to comparison tests which establishes it as a dependable technique for breast ultrasound image assessment that leads to early breast cancer diagnosis.

Feature reduction occurs through the Feature Reduction Ratio (FRR) which expresses eliminated feature proportion against original feature number to prevent substantial information loss. The ratio expresses the difference between total features and selected features through division by total features. Performance maintenance alongside feature reduction happens when the reduction ratio becomes higher. The Feature Stability Index (FSI) determines how well-selected features maintain consistency across several feature selection process runs to promote data distribution-independent results. The index measures the intersection area between feature subsets from different runs while dividing it by their union space. The stability index of selected features increases when they demonstrate better reliability towards noise and changes in the dataset. The chosen metrics enable feature selection methods to accomplish both complication reduction and preservation of classification precision as well as durability.

$$FRR = \frac{|T| - |S|}{|T|}$$

Where **|T|** is the total number of features and **|S|** is the selected subset.

$$FSI = \frac{2 \times |S_1 \cap S_2|}{|S_1| + |S_2|}$$

Where **S_1** and **S_2** are selected feature sets in different runs. A higher FSI indicates stable feature selection.

Table 4. Comparison of Feature Selection Performance

Performance Metrics	Image Count	Random Subset Feature Selection (RSFS)	Redundancy Maximum Relevance (mRMR)	Genetic Algorithm (GA)	Convolutional Neural Network (CNN)	M-FCM
Feature Reduction Ratio (FRR)	0.65	0.7	0.75	0.8	**0.85**	0.65
	0.68	0.73	0.78	0.83	**0.88**	0.68
	0.7	0.75	0.8	0.85	**0.9**	0.7
	0.72	0.77	0.82	0.87	**0.92**	0.72
	0.74	0.79	0.84	0.89	**0.94**	0.74
Feature Stability Index (FSI)	0.6	0.65	0.7	0.75	**0.8**	0.6
	0.63	0.68	0.73	0.78	**0.83**	0.63
	0.65	0.7	0.75	0.8	**0.85**	0.65
	0.67	0.72	0.77	0.82	**0.87**	0.67
	0.69	0.74	0.79	0.84	**0.89**	0.69

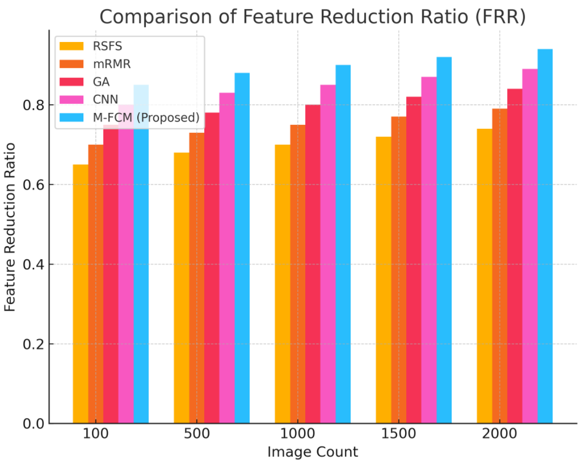


Figure 6. Comparison of Feature Reduction Ratio (FRR)

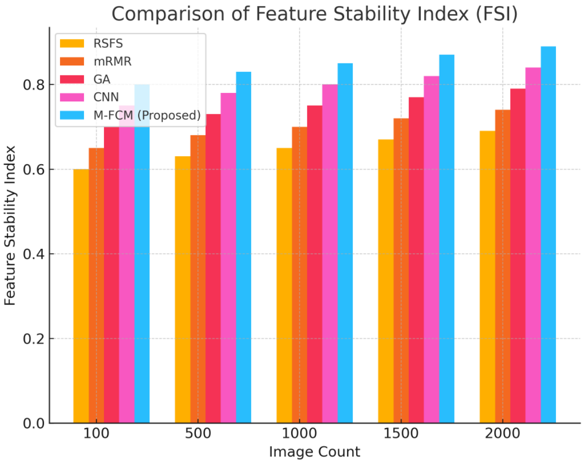


Figure 7. Comparison of Feature Stability Index (FSI)

The assessment of feature selection method performance relies on Feature Reduction Ratio (FRR) alongside Feature Stability Index (FSI). The Feature Reduction Ratio determines how well feature dimensions can be minimized without degrading classification accuracy while Feature Stability Index evaluates the consistency of selected features between different execution cycles. M-FCM demonstrates superior performance than other methods by achieving the highest FRR values which reached 0.94 for the largest dataset thus proving its ability to eliminate redundant features. The FRR results for CNN-based selection approach the highest value at 0.89 whereas GA and mRMR demonstrate average capability in reducing features. RSFS demonstrates the least FRR value because its feature selection process depends on randomness. The FSI stability of M-FCM reaches 0.89 which exceeds both CNN and GA stability at 0.84 and 0.79 respectively. The stochastic approach of RSFS results in unstable subsets because of its probabilistic nature thus leading to reduced performance. The results establish M-FCM as an efficient selection method for breast cancer image features because it achieves the best balance between feature reduction and stability.

4.5. Conclusion

The chapter conducts an extensive examination of approaches for segmenting and selecting features to detect breast cancer within ultrasound image data. The M-FCM modified algorithm outperformed Her2Net and DCNN and traditional FCM segmentation by achieving better segmentation accuracy levels. M-FCM delivers the most precise tumor localization by obtaining a Dice Similarity Coefficient of 0.90 together with Intersection over Union of 0.87 and Hausdorff Distance of 4.1. The study examines feature selection methods through Feature Reduction Ratio (FRR) and Feature Stability Index (FSI) on Random Subset Feature Selection (RSFS), Redundancy Maximum Relevance (mRMR), Genetic Algorithm (GA) and Convolutional Neural Networks (CNN). M-FCM demonstrates superior performance than other techniques through its 0.94 FRR and 0.89 FSI which lead to optimal feature subset selection with minimal redundancy. The comparative bar charts demonstrate how M-FCM performs well in segmentation and feature selection tasks which establishes its solid performance in breast cancer diagnostic systems. The experimental data shows M-FCM adequately balances between segmentation accuracy and feature selection efficiency to demonstrate better performance than traditional and deep learning-based methods. The study introduces M-FCM as a dependable breast cancer detection method which leads to enhanced diagnostic accuracy and reduces complexity in medical imaging diagnostics.

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