

Deep meta-learning framework with U-Net segmentation and optimization-based feature selection for breast cancer detection in MRI images

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Background: Breast cancer is one of the most prevalent cancers worldwide and continues to pose significant challenges to global healthcare systems. The survival rate of patients largely depends on early detection, accurate diagnosis, and timely treatment. Medical imaging techniques such as mammography, ultrasound, and magnetic resonance imaging (MRI) are widely used for detecting abnormalities in breast tissue. However, many existing breast cancer detection approaches suffer from limitations such as high computational complexity, long tumor detection time, inaccurate predictions, and high false-positive rates. These challenges highlight the need for more reliable and efficient automated diagnostic systems. The aim of this study is to develop an efficient deep meta-learning framework for accurate breast cancer detection and classification using MRI images. The proposed system integrates preprocessing, tumor segmentation, feature extraction, optimization, and deep learning models to improve diagnostic accuracy, reduce false-positive rates, and support early clinical decision-making in computer-aided diagnosis systems.

Methods: This work proposes a deep meta-learning framework for precise breast cancer detection and classification using MRI images. The framework integrates multiple stages to improve diagnostic accuracy. Initially, Adaptive Median Filtering (AMF) is applied to enhance image quality and remove noise during preprocessing. Subsequently, U-Net-based segmentation is used to accurately identify tumor regions. Growth Distribution Depth (GDD) is employed to extract discriminative features from the segmented regions, and Salp Swarm Optimization (SSO) is used to select the most relevant features. Finally, deep meta-learning-based classification is performed using pre-trained convolutional neural network (CNN)

models, including AlexNet, VGG16, and LeNet, which are fine-tuned on breast cancer datasets to improve classification performance.

Results: Experimental results demonstrate that the proposed framework achieves superior performance compared to existing methods. Among the evaluated models, the VGG16-based classifier shows the best performance, achieving an accuracy of 98.82%, precision of 97.1%, recall of 99.11%, and an F1-score of 98.25%. The integration of tumor-focused segmentation and optimization-based feature selection significantly improves classification accuracy and reduces false detections.

Conclusions: The proposed deep meta-learning framework provides an effective and reliable approach for automated breast cancer detection from MRI images. By combining advanced preprocessing, segmentation, feature extraction, optimization, and deep learning classification techniques, the framework enhances diagnostic accuracy and efficiency. The results suggest that the proposed method has strong potential to support computer-aided diagnosis systems and assist clinicians in early breast cancer detection.

Keywords: Deep meta-learning; Adaptive Median Filtering pre-processing (AMF pre-processing); U-Net-based segmentation; Growth Distribution Depth (GDD); Salp Swarm Optimization (SSO)

Submitted Feb 21, 2026. Accepted for publication May 28, 2026. Published online Jul 06, 2026.

doi: 10.21037/qims-2026-1-0388

View this article at: <https://dx.doi.org/10.21037/qims-2026-1-0388>

Introduction

Cancer is regarded as the second greatest cause of death worldwide, making it a serious public health concern, subsequent to cardiovascular diseases. A significant impact is created by cancer, as millions of people and their families are affected every year. Breast cancer is characterized by the uncontrolled proliferation of abnormal cells within the breast tissue. If it is left untreated, cancerous tumors are allowed to grow and spread to different organs or tissues, leading to more advanced stages of the disease. Breast cancer is usually initiated in the milk ducts or the milk-producing lobules of the breast. Invasive breast cancer is associated with the formation of tumors that cause lumps or thickening in the breast tissue, and these tumors are known to spread to adjacent organs or lymph nodes. Treatment is typically provided through a combination of approaches, including surgery for tumor removal, radiation therapy for targeting cancer cells, and medications such as chemotherapy, hormonal therapy, and targeted therapy. In 2020, an estimated 2.3 million new cases of breast cancer were reported worldwide. By 2040, 2.08 million new cancer cases are projected to be reported in India. This projection is considered to represent a substantial rise of 57.5% in cancer cases in India from 2020 to 2040. According to predictions provided by the Global Cancer Observatory (GLOBOCAN), a significant increase in cancer cases in India is expected. India is ranked in the third position in

terms of cancer incidence, following China and the United States of America, which highlights the substantial cancer burden within the country. Early detection is associated with more successful treatment outcomes, and the prognosis for individuals with early-stage breast cancer is generally more favorable due to higher survival rates.

Various diagnostic methods are employed to identify breast cancer at the primary stage, and procedures such as biopsy, mammography, breast self-examinations (BSE), ultrasound, magnetic resonance imaging (MRI), genetic testing, and liquid biopsies are regarded as the most definitive means of confirming cancerous tissue. Breast MRI is typically reserved for women who are considered to be at heightened risk of developing breast cancer, including those with a family history of the disease or specific genetic mutations such as BRCA1 or BRCA2. MRI is considered more expensive and time-consuming than mammography, making it less practical for large-scale population-based screening programs. The large volume of medical images, including mammograms and breast MRIs, is often overwhelming for radiologists; therefore, computer-aided diagnostic (CAD) systems are used to support healthcare professionals in detecting potential breast cancer lesions. Research in deep learning for medical imaging is continuously being advanced. New architectures, techniques, and applications are being explored to enhance the capability of CAD systems further. Deep learning models are employed to process multimodal medical

imaging data, allowing information from different imaging modalities to be integrated, which improves diagnostic accuracy. Convolutional neural networks (CNNs) have been recognized as having a transformative impact on disease diagnosis due to their strong image-recognition and classification capabilities, thereby improving the precision and efficiency of medical image analysis. Machine learning algorithms are trained on extensive MRI datasets, enabling them to identify subtle patterns and features that may be difficult for human observers to detect. Through this data-driven learning process, suspicious regions can be recognized and classified more effectively. Transfer learning techniques are widely considered highly effective in the classification of breast images and many other domains. Pre-trained models such as VGG16, AlexNet, and DenseNet are utilized after initially being trained on large and diverse datasets for image-recognition tasks. These models are regarded as having learned highly valuable features and representations from breast images. Despite the existing challenges, ongoing research and development in breast cancer classification are viewed as highly promising.

Microwave-based diagnostic methods gained considerable attention because microwave signals interact differently with normal and cancerous tissues due to variations in electrical properties (1). Techniques such as metasurfaces were explored to improve the sensitivity and accuracy of microwave imaging systems. Mammography-based classification systems using custom ResNet architectures were employed for BI-RADS classification by assigning mammograms to appropriate categories based on detected abnormalities (2). Ultra-Wideband (UWB) microwave technology, employing extremely narrow microwave pulses across a broad frequency spectrum, provided deeper penetration into breast tissue and enabled the identification of structural anomalies (3). Advanced Computer-Aided Diagnosis (CAD) systems integrated deep CNN-based features with morphological, textural, and density characteristics to facilitate early detection and improve diagnostic accuracy (4). Comparative evaluations of data-mining and machine-learning algorithms were conducted to identify suitable methods for handling large datasets with higher predictive precision (5). Hard-attention-based approaches were designed to identify potential lesion regions without scanning the entire image, thereby reducing computational cost (6). The integration of deep learning and machine-learning techniques for genetic sequencing tasks using histopathological imaging has also been investigated (7). MRI-based approaches were explored extensively for cancer detection (8). Breast cancer detection was enhanced

by merging mammography images with clinical records through artificial intelligence (AI)-based classifiers (9). Comprehensive reviews highlighted current and future trends in applying AI to therapeutic and diagnostic domains (10). Deep learning architectures such as GoogLeNet and residual blocks were introduced to improve diagnostic accuracy (11). Attention-based multimodal AI models integrating gene expression, copy-number variation, and clinical data improved cancer-related prediction tasks (12). Several studies concentrated on breast cancer detection by applying a range of AI-based algorithms to multiple datasets, including clinical information and mammography images, with the objective of improving patient care in real-world diagnostic scenarios (13). Deep-learning-based frameworks were proposed for anomaly identification to distinguish benign from malignant breast abnormalities (14). Cascade deep learning networks addressed tumor detection and characterization challenges (15). Meta-learning strategies combined with multiple CNNs enabled accurate breast cancer classification using ultrasound images (16). ResNet50-centered computational frameworks were introduced for mammogram image classification (17). AI-driven deep learning approaches integrating mammography data demonstrated effectiveness for early breast cancer detection (18). Conditional Generative Adversarial Networks (CGANs) and CNN-based dimension-reduction methods were employed to handle data imbalance and high-dimensionality issues (19). Transfer-learning models such as DeepBreastCancerNet were designed to reduce overfitting problems (20).

Hybrid algorithms combining Advanced Elman Recurrent Neural Networks (AERNN), Wild Horse Optimization (WHO), and Linear Discriminant Analysis (LDA) were proposed for disease detection and classification (21). SIFT-CNN integrated machine learning frameworks demonstrated promising performance in breast cancer detection (22). Different machine-learning methods, including Extreme Gradient Boosting (XGBoost), neural networks (NNs), logistic regression (LR), and random forests (RF), were analyzed for breast cancer prediction (23). Several machine-learning models were further explored to forecast breast cancer risk (24). Feature selection and classification approaches integrating Gradient Boosting Decision Trees (GBDT) with the Mayfly Optimization (MO) algorithm achieved improved predictive capability (25). Hybrid CNN and random forest classifiers improved breast cancer detection and classification performance (26). Earlier studies combined AI techniques

with multivariate statistical models to enhance prediction accuracy in specialized applications (27). AI-driven approaches integrating digital health records with mammography data demonstrated effectiveness for early breast cancer detection (28). Ensemble algorithms and ML models demonstrated the benefits of model aggregation for accurate cancer prediction (29). In addition, new Dynamic Contrast-Enhanced MRI datasets such as Breast-DM were released to support breast tumor classification and segmentation research (30). In the proposed framework, meta-learning is implemented through a hierarchical learning strategy that combines multiple CNN models and a higher-level aggregation mechanism. Initially, several pre-trained CNN architectures, namely LeNet, AlexNet, and VGG16, are fine-tuned using the extracted breast MRI features obtained after preprocessing, segmentation, and feature selection. Each CNN model functions as a base learner and independently produces probabilistic predictions for benign and malignant tumor classes. These predictions capture complementary feature representations learned by different network architectures. Subsequently, the outputs generated by the base CNN models are aggregated using a meta-level classifier implemented through logistic regression. This meta-learner learns to optimally combine the predictions of the individual base learners to generate a more reliable final classification. We present this article in accordance with the STARD-AI reporting checklist (available at <https://qims.amegroups.com/article/view/10.21037/qims-2026-1-0388/rc>).

Methods

Proposed deep meta-learning for breast cancer detection and classification

The study was conducted in accordance with the Declaration of Helsinki and its subsequent amendments. The deep meta-learning is a promising research area with the potential to significantly enhance the development of efficient machine learning models. It addresses challenges related to data scarcity, domain adaptation, and rapid learning in dynamic environments. The proposed deep meta-learning-based breast cancer detection and classification framework is illustrated in *Figure 1*. In breast cancer classification, the model takes breast cancer images as input, with each image associated with a label (benign or malignant). The images are resized to a uniform resolution before training. The BreastDM MRI dataset used in this work contains a relatively limited number of labeled

samples as 232 images which make very deep architectures prone to overfitting when trained on small datasets. The dataset was divided into training, validation, and testing subsets using an 8:1:1 ratio, which is a commonly used split in machine learning studies when the available dataset size is limited. The splitting process was performed randomly while preserving the class distribution (benign and malignant) across all subsets to avoid class imbalance and ensure fair evaluation of the model. The resulting test set contains a relatively small number of samples, which limit the statistical robustness of the evaluation. Data augmentation techniques such as rotation, flipping, and scaling were applied during training to increase the diversity of the training data and improve the model's generalization capability. Second, a validation set was used during training to monitor model performance and prevent overfitting through early stopping. These 2D slice images are directly used as input to the preprocessing, segmentation, feature extraction, and classification stages. The selection of 2D slices follows the dataset annotations, which identify slices containing relevant tumor regions. This approach is commonly adopted in medical image analysis when the dataset provides slice-level annotations which represents a relatively limited sample size and may not capture the full variability encountered in clinical practice. Potential sources of bias include variations in MRI acquisition protocols, scanner configurations, patient-specific anatomical characteristics and the distribution of benign and malignant cases within the dataset. Additionally, the images originate from a restricted clinical setting, which limit demographic diversity and introduce sampling bias. These factors influence the generalisability of the proposed model when applied to broader clinical populations. To partially address this issue, preprocessing and data augmentation techniques are employed to improve model performance.

To improve the diversity of the training dataset, data augmentation is applied by transforming the original images through flipping, rotation, and scaling. Image normalization is then performed, typically by converting pixel values to a range between 0 and 1. A set of pre-trained CNN models is considered, including LeNet, VGG16, and AlexNet. These established CNN architectures have been trained on large-scale datasets and are fine-tuned for the breast cancer classification task. The primary motivation for selecting these models is related to the characteristics of the available dataset and the design objective of the proposed framework. In contrast, LeNet, AlexNet, and VGG16 provide stable training behavior and require comparatively fewer training

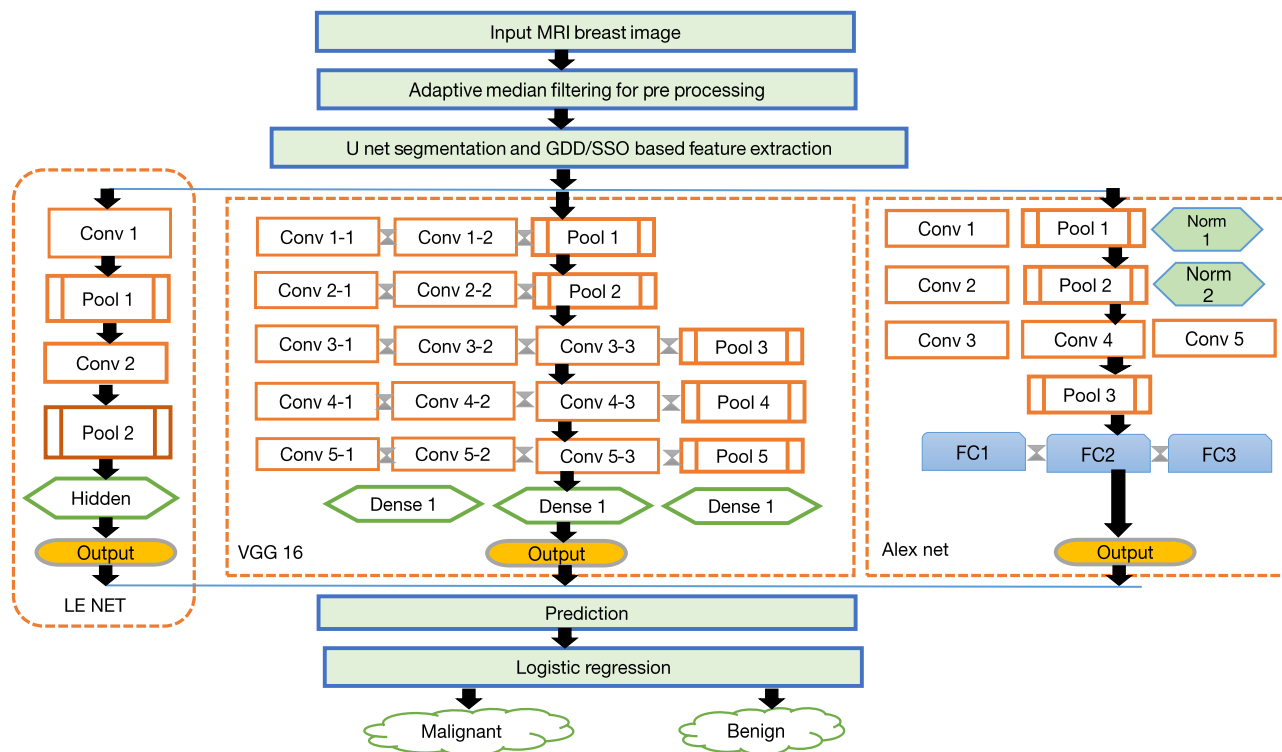


Figure 1 The proposed deep meta-learning for breast cancer detection and classification. FC, fully connected; GDD, Growth Distribution Depth; MRI, magnetic resonance imaging; SSO, Salp Swarm Optimization.

samples while still capturing meaningful spatial features. Furthermore, these architectures have widely available pre-trained weights and well-understood feature extraction capabilities, making them suitable as heterogeneous base learners in the proposed meta-learning ensemble framework. For each CNN model in the set, the training loop is executed for a specified number of epochs. Training is performed using mini-batches drawn from the training dataset, and the model parameters are updated to minimize the binary cross-entropy loss. A condition is applied to check whether the validation accuracy has failed to improve for consecutive epochs. If no improvement is observed, training for that model is stopped early. This early-stopping mechanism prevents overfitting and improves generalization. After all models are trained, the algorithm enters the testing phase. For each breast image in the test dataset, the outputs from all previously trained models are combined. These aggregated outputs are then fed into a logistic regression classifier to obtain the final classification result. Algorithm 1 describes the proposed meta-learning framework for breast cancer detection, which integrates preprocessing, U-Net segmentation, Growth Distribution Depth (GDD) feature

extraction, Salp Swarm Optimization (SSO)-based feature optimization, and CNN-based ensemble classification. The GDD has ability to capture discriminative structural and texture characteristics from tumor regions, which are critical for distinguishing benign and malignant tissues in MRI images. The distance metric used within the descriptor was selected because it effectively measures feature similarity and enhances class separability in high-dimensional feature spaces. Similarly, the model parameters and architecture choices for the CNN base learners (LeNet, AlexNet, and VGG16) are determined based on their proven effectiveness in medical image analysis and their ability to provide complementary feature representations due to differences in network depth and receptive fields. The parameters of the SSO algorithm are chosen according to commonly adopted configurations in the literature to ensure stable convergence and effective feature selection.

Algorithm 1 proposed meta-learning-based breast cancer detection framework

Input: Breast MRI image dataset $D=\{I_1, I_2, \dots, I_n\}$

Output: Classification label $C \in \{\text{Benign}, \text{Malignant}\}$

Step 1: Load the breast MRI dataset D .

Step 2: For each image $I_i \in D$ and perform preprocessing

- a) Convert the image to grayscale
- b) Apply Adaptive Median Filtering (AMF) to remove noise
- c) Normalize pixel intensity values

Step 3: Apply U-Net segmentation to extract the tumor region

- a) Input preprocessed image I_i
- b) Generate segmentation mask M_i
- c) Extract Region of Interest ROI_i .

Step 4: Perform feature extraction using the GDD

- a) Compute texture and structural features from ROI_i
- b) Form feature vector F_i .

Step 5: Apply SSO for feature selection

- a) Initialize Slap population
- b) Evaluate feature subsets using classification fitness
- c) Select optimal feature subset F_{opt}

Step 6: Train base CNN classifiers using optimized features

- a) Train LeNet model
- b) Train AlexNet model
- c) Train VGG16 model

Step 7: Generate prediction probabilities from each CNN model

$$P_{LeNet}, P_{AlexNet}, P_{VGG16}$$

Step 8: Apply meta-learning aggregation

- a) Use Logistic Regression as the meta-classifier.
- b) Combine base learner predictions.

Step 9: Produce final classification output

$$C = \text{MetaClassifier}(P_{LeNet}, P_{AlexNet}, P_{VGG16})$$

Step 10: Return predicted label C for each MRI image.

Adaptive Median Filtering (AMF) based preprocessing

The input breast cancer image contains several noise elements because MRI acquisition often introduces distortions that degrade image quality and disrupt texture properties. MRI-based breast cancer images may include different types of noise and artifacts, which can negatively affect diagnostic accuracy. Therefore, filtering is applied to normalize the image by removing these noise components or artifacts. Several filtering techniques such as mean

filtering, Gaussian filtering, and median filtering have been proposed by various researchers. To eliminate black-and-white speckle noise, a median filter is typically applied. In this research work, an AMF technique is adopted to enhance the images in the dataset. Compared with conventional median filtering, the AMF divides the window region into four sub-windows based on axial characteristics and computes the mean value for each sub-window. This mean value is calculated by averaging the distances along the axial coordinates, consistent with the principle of distance-weighted averaging in the axial direction. The pixel value is then modified according to the computed axial mean distance values, which improves image sharpness and enhances edge characteristics essential for feature extraction. Similarly, the axial mean value for each axial window is measured, and the window with the lowest mean value is selected. The technique then computes the average mean gray value (AMGV) for the selected window. If the difference between the current pixel value and the AMGV exceeds a predefined threshold that is determined by the number of pixels in the window, the pixel value is adjusted to match the AMGV; otherwise, the original pixel value is retained. This process is repeated for every pixel in the image window, resulting in improved pixel quality and smoother image representation. When the distance with respect to the AMGV is greater or less than the number of pixels in the window, the pixel value is accordingly modified to reflect the computed AMGV. By applying this adaptive filtering technique, a normalized and contrast-enhanced breast image is produced, which is subsequently used for segmentation and feature extraction tasks.

U-NET segmentation

The U-Net segmentation model is used to segment the breast region from the preprocessed image. It operates on a CNN architecture and accepts images of variable size. Additionally, the model is extended to handle multiple classes. The CNN component of U-Net represents a significant advancement in image recognition and analysis. The primary layers used in the U-Net architecture include convolutional layers, ReLU activation layers, pooling layers, normalization layers, fully connected layers, and dense layers. Compared with other image classification algorithms, CNN-based models require relatively few preprocessing steps. After each convolution layer, a ReLU activation layer is applied. This activation function removes negative values from the feature maps, thereby enhancing

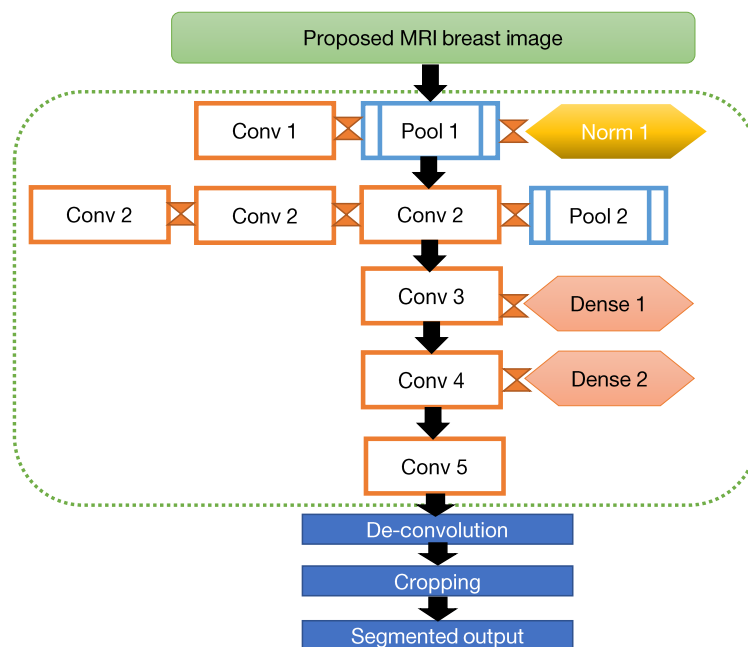


Figure 2 Architecture model of U-Net segmentation algorithm. MRI, magnetic resonance imaging.

nonlinearity within the network and enabling the extraction of more complex features. During the pooling stage, the spatial dimensions of the input are progressively reduced, which decreases computational complexity and helps retain essential structural information. In the sequential layer arrangement, the pooled feature map is normalized using a normalization layer to stabilize learning and improve network performance.

Dropout is applied to fully connected layers because these layers contain a large number of parameters and are more prone to overfitting. By randomly disabling a subset of neurons during training, dropout reduces excessive co-adaptation and improves model generalization. In the dense layer, every neuron is fully connected to all neurons in the previous layer, enabling the network to combine high-level abstracted features. This capability allows U-Net to measure variations between different sets of image features effectively. The deconvolutional upsampling layer, which forms part of the decoder path, precedes the softmax layer. The softmax function generates a probability distribution across the output classes by converting the non-normalized network outputs into values between 0 and 1. A probability is assigned to each possible class, enabling the model to produce interpretable segmentation outputs. The layered flow diagram of the U-Net architecture is illustrated in *Figure 2*. Typically, U-Net is developed following the

standard principles of CNN-based architectures. In this model, image interpretation, feature redistribution, and probability estimation are performed to achieve accurate segmentation of the breast region and shown in Algorithm 2.

Algorithm 2 U-Net segmentation algorithm

Input: Segmented image D_{seg} , coordinate D_c ;

Output: image Segmentation C_i

Start

To calculate the value segmentation,

For $i=1: D_{n_para}, 1$

For $j=1: D_{n_fea}, 1$

$G = \text{determinant}[r] - k(\text{segment}(\text{Number}))^2$

End

End

data segmented $dseg = [q_{n_fea}, \text{distance}]$

$k = \text{class label length}$

For $m=A:z$

$\text{temp} = \text{sum} - \text{mean}(A, :)$

$X(A, m) = -0.8 * \text{temp} * \text{mean} + \log(i)$

$X(A, 2, :) = \text{temp}$

$$H = \beta_1 \beta_2 - V(\beta_1 + \beta_2)^2$$

End

$$G = \text{determinant}[r] - k(\text{segment}(\text{Number}))^2 \quad [1]$$

where, G is the feasible area, r is irregular feature, $\beta_1 \beta_2$ are the segmented areas.

$$\text{Determinant}[r] = \beta_1 \beta_2 \quad [2]$$

$$\text{Segment}(r) = \beta_1 \beta_2 \quad [3]$$

The segmentation is represented as in the following model:

$$H = \beta_1 \beta_2 - V(\beta_1 + \beta_2)^2 \quad [4]$$

where, V is a constant.

GDD feature extraction

After segmentation, the most important and relevant texture features are extracted from the segmented image by using the GDD feature extraction model. The GDD properties of the texture are obtained by calculating various features and values. During this stage, the textures of the segmented image are considered for feature extraction. Features related to the texture and dimensions of the image are computed. When these features are not present, the growth value is approximated based on the coverage area and the number of pixels occupied throughout the entire breast region. Additionally, the Growth Tumor Support Factor (GTSF), which represents the growth characteristics, is calculated as follows:

$$GTSF = \frac{\text{Dist}(\sum \text{pixels} \in T, \sum \text{pixels} \in PT)}{\text{Ims}} \times GTSF(PT) \quad [5]$$

In this context, PT denotes the texture obtained from the patient's previous image, T represents the texture from the current image, and Ims indicates the dimensions of the image. When the roughness value from the previous image is not available, the GTSF is approximated by using the following model:

$$GTSF = \frac{\sum \text{pixels} \in T}{\text{Ims}} \quad [6]$$

In this context, PT is denoted as the texture obtained from the patient's previous image, T is represented as

the texture extracted from the current image, and Ims is specified as the dimensional information of the image. When the roughness value from the previous image is unavailable, the GTSF is approximated by employing the following model:

$$DTSF = \frac{\sum_{i=1} \text{pixels}(\text{Image}(i)) \cdot \text{value} > \left(Grmax \times \frac{1}{3}\right)}{\text{Size}(\text{Image})} \quad [7]$$

In this setting, Grmax is defined as the greatest gradient value of the image. The distribution characteristic is used to denote the extent to which the breast is affected by the tumor. Although certain tumor regions may exhibit limited coverage, they may still possess a greater spread. The depth of the tumor is subsequently assessed based on the particle density within the region. If the tumor area exhibits minimal depth, it is indicated that the tissues in that region are not proliferating and may be classified as benign. This depth information is utilized to evaluate the progression of the disease within the breast, enabling more accurate diagnosis and survival prediction. To facilitate these assessments, the Depth Tumor Support Factor (DeTSF) is computed by the proposed technique, as delineated in Eq. [8].

$$DeTSF = \frac{\sum T(i) \text{value} = Grmax}{\text{Size}(T)} \quad [8]$$

where, T represents the texture, the size of T represents the pixel number present in the texture.

Salp Swarm Optimization (SSO) based feature selection

After feature extraction, the most relevant features are selected from the image subset to minimize dimensionality and improve classifier performance with reduced computational complexity. Typically, a larger number of features is chosen to achieve more accurate prediction. In existing research, several optimization techniques such as Whale Optimization (WO), Bee Colony (BC), Swarm Intelligence (SI), and Simulated Annealing (SA) have been widely employed for developing breast tumor detection frameworks. However, these approaches exhibit certain limitations, including algorithmic complexity, low convergence rates, and slow processing speeds. Therefore, in the proposed work, a more sophisticated and recent optimization method is adopted for optimal feature selection. A SSO algorithm is utilized to provide an optimal

solution for identifying the features most relevant to the tumor. The algorithm is inspired by the natural behavior of salps belonging to the family Salpidae, in which the population is divided into leader and follower groups. In an N-dimensional search space, where n represents the number of variables, salp positions are defined accordingly. After the food source is identified, the positions of the salps are updated, as expressed in Eq. [9].

$$a_j^l = \begin{cases} ps_j + w_1((u_j - l_j)w_2 + l_j)w_3 \geq 0 \\ ps_j - w_1((u_j - l_j)w_2 + l_j)w_3 < 0 \end{cases} \quad [9]$$

where, a_j^l is the leader salp's position in dimension j , ps_j indicates the position of food source, u_j and l_j are the upper and lower bounds respectively, and w_1 , w_2 and w_3 represents the random numbers. The leader salp adjusts its location in response to the availability of food. Here, the exploration and exploitation capabilities are represented as shown the Eq. [10].

$$w_1 = 2e^{-\left(\frac{itr}{\max_{itr}}\right)} \quad [10]$$

where, itr stand for the current iteration, and $\max_{itr}$ is the maximum number of iterations. Consequently, the position update is performed based on Eq. [11].

$$a_j^i = \frac{1}{2}kT^2 + S_p(t) \quad [11]$$

where, T indicates the time, S_p indicates the initial speed, and k value is computed by Eq. [12]

$$k = \frac{S_f}{S_p} \text{ and } S = \frac{a - a_0}{T} \quad [12]$$

Moreover, the position of follower can be updated as shown in Eq. [13].

$$a_j^i = \frac{1}{2}(a_j^i + a_j^{i-1}) \quad [13]$$

Based on this Algorithm, the best optimal solution is computed for choosing the optimized features for classifier training.

Results

The performance of the proposed model is experimentally verified and compared by evaluating various parameters. Moreover, the results are assessed using a publicly available and widely used benchmarking dataset, the Breast DM

Dataset. This dataset contains 232 labelled breast tumor images, including 85 benign and 147 malignant samples. Eighty percent of the images are used for training, during which the model learns patterns, textures, breast volume, tumor size, and their relationships to perform detection and classification. Ten percent of the data is allocated for validation to optimize the proposed model during the training process. The validation step assists in hyper parameter selection, performance monitoring, and overfitting detection. The remaining ten percent of the dataset is reserved for testing the proposed algorithm. In this section, the proposed model is analyzed the entire MRI images including all relevant sequences. Specifically, the focus was placed on the post-contrast subtracted sequences, which provide optimal visualization of tumor regions by enhancing contrast between malignant tissue and normal breast tissue. These sequences were chosen because they highlight the vascular characteristics and structural details of tumors, which are critical for accurate segmentation and feature extraction. All cases included in the dataset were acquired on MRI scanners with comparable imaging protocols, ensuring consistency in spatial resolution, slice thickness, and contrast enhancement timing. Any minor variations between scanners were accounted for during the preprocessing stage, which included AMF and intensity normalization, to minimize variability and standardize the input for the deep meta-learning model. In the preprocessing stage, the AMF computes the mean value of each sub-window or axial window. Contrast and brightness play an essential role in overall image quality. Contrast enhancement is quantified by measuring the changes in pixel intensity differences between the enhanced and original images. Similarly, brightness improvement is evaluated by analyzing the variation in average pixel intensity. Pixel values are adjusted to improve contrast and sharpen edges for more effective feature extraction. The AMF begins the filtering process by selecting a neighborhood around each pixel. The neighborhood size is adaptive and depends on the characteristics of the MRI breast cancer image. For each pixel, the values within the selected window (4×4 size) are sorted to determine the median. The central pixel is compared with the median and with the minimum and maximum values in the window. If the central pixel value is lower than the minimum value, it is treated as impulse noise and replaced with the median. If the central pixel value falls within the valid range, it is preserved. After adaptive mean filtering, the mean value of the axial window's central pixel is observed to be 90, whereas

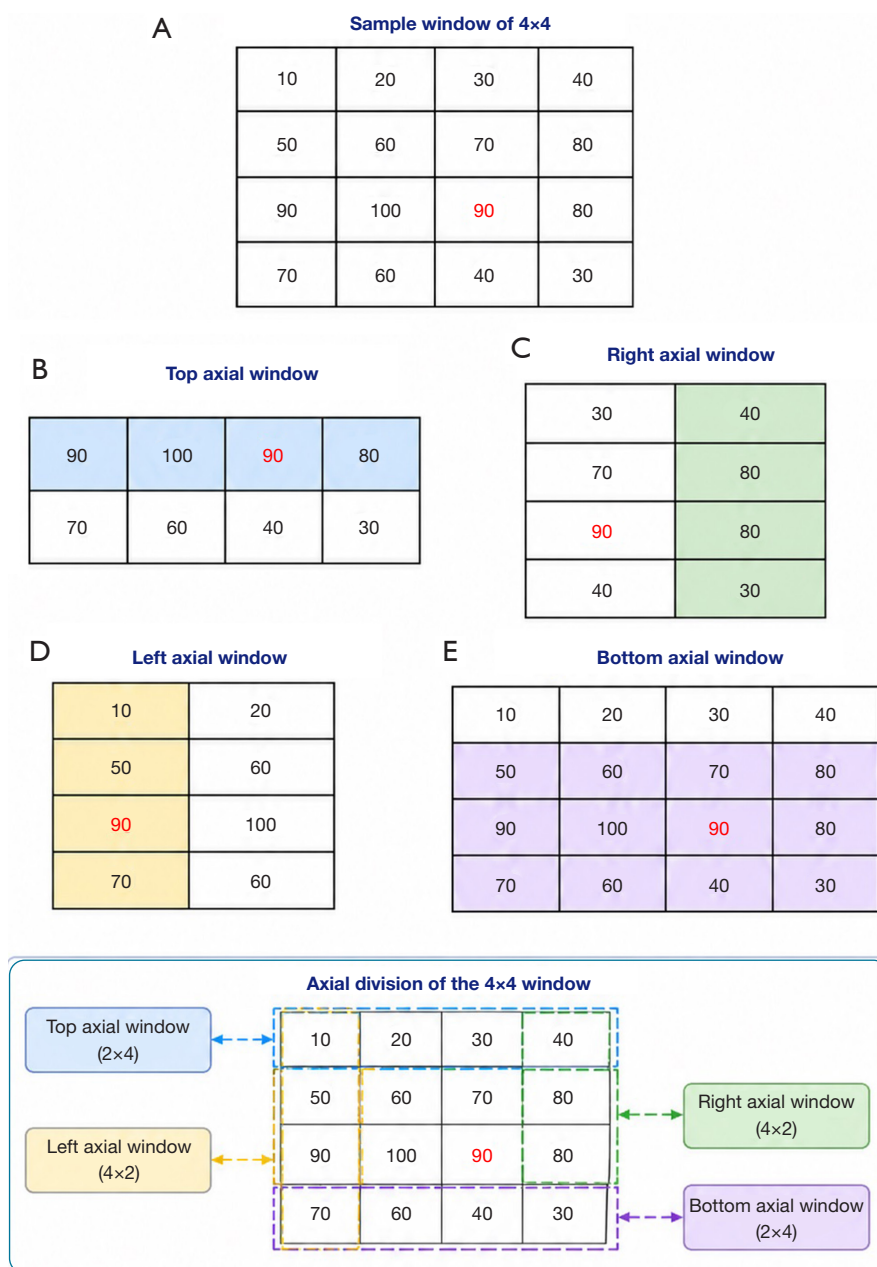


Figure 3 The stages of adaptive mean value filtering process. (A) Sample window of 4×4. (B) Top axial window. (C) Right axial window. (D) Left axial window. (E) Bottom axial window.

the bottom axial pixel exhibits a value of 26. The distance with respect to the AMG_V is computed using the central pixel value of 90 and the neighborhood average of 77. Since the difference between the actual and estimated values (13) is greater than the number of pixels in the window, the pixel is adjusted to match the corresponding AMG_V value. This procedure is repeated for every pixel in the image window,

resulting in improved pixel quality. Ultimately, a normalized and contrast-enhanced breast image is produced, which is then used for segmentation and feature extraction. The stages of the adaptive mean value filtering process are illustrated in *Figure 3*. The image demonstrates the division of the window into four axial sub-windows, namely top, right, left, and bottom axial regions, for adaptive mean

value computation and noise reduction during MRI image preprocessing.

The mean distance value with other pixels are computed using the following procedure. For instance, the distance is computed according to the top axial window and is represented as follows:

$$\begin{aligned} \text{❖} \quad \text{Axial mean } Am &= \text{Dist} \left(\frac{(90-80)+(90-30)+(90-40)+(90-60)}{+(90-70)+(90-90)+(90-100)} \right) / 7 \\ &= (10+60+50+30+20+0+10) / 7 = 26 \end{aligned}$$

Likewise, the axial mean value is computed for the bottom axial window as shown in below:

$$\begin{aligned} \text{❖} \quad \text{Axial mean } Am &= \text{Dist} \left(\frac{(90-10)+(90-20)+(90-30)+(90-40)+(90-50)+(90-60)}{+(90-70)+(90-80)+(90-100)+(90-80)+(90-90)} \right) / 11 \\ &= (80+70+60+50+40+30+20+10+10+10+0) / 11 = 35 \end{aligned}$$

For instance, the value of AMGV is estimated for the pixel with value 90 as shown in below:

- ❖ For top axial window, $AMGV = (100+60+70)/3 = 230/3 = 77$
- ❖ For bottom axial window, $AMGV = (80+80+70)/3 = 230/3 = 77$

For U-Net segmentation, the training process is conducted for 70 epochs, with an initial learning rate of 0.0002. This learning rate determines the step size used by the optimization algorithm when updating model parameters. A batch size of 20 is used, meaning that 20 training samples are processed per iteration. A smaller batch size introduces controlled randomness into the stochastic gradient descent process, which can improve generalization. The learning rate is reduced by a factor of 0.2 at the 35th epoch to refine convergence. Training is terminated early if the loss remains constant for 20 consecutive epochs, thereby preventing overfitting by halting training when further learning becomes ineffective. Based on the results, the lowest performance is observed for the original U-Net model. The weakest performance occurs when the model is trained using non-overlapping original patches and tested under the same condition, achieving Dice, recall, and specificity scores of 82.25%, 76.81%, and 73.62%, respectively, with a false positive rate (FPR) of 30.13%. The best outcomes are obtained using the proposed deep meta-learning approach. The model is trained on overlapping patches with reflection padding, where overlap enhances feature robustness and reflection padding preserves spatial context at patch boundaries. This configuration achieves a Dice similarity coefficient (DSC) of 97.53%, indicating excellent overlap between predicted and ground-truth segmentations. The recall value is 95.24%, demonstrating effective identification of true positives, while the specificity

score of 93.12% reflects accurate identification of negative cases. The FPR is reduced to 12.42%, and the overall DSC of 97.53% confirms highly accurate pixel-level segmentation of breast tissue. After segmentation, the breast texture features are extracted using the GDD feature extraction model, which computes the Distributed Tumor Support Factor (DTSF) and DeTSF to evaluate tumor size and growth. Feature selection is then performed using the SSO algorithm to reduce dimensionality while retaining the most informative features. This process enhances classifier performance, reduces overfitting, and minimizes computational complexity. The SSO is executed with ten search agents, a maximum of 100 iterations, α_1 , α_2 , and α_3 values ranging from 0 to 1, and variable bounds determined by tumor size. Ten features including breast mass, size, shape, texture, smoothness, depth variations, number of dips, and lesion complexity are selected to distinguish benign from malignant tumors. By analyzing these features, the proposed method predicts tumor type with high accuracy. The selected features are used to train and test meta-learning models. Based on the different classes of breast images and the extracted features, the results are validated and compared across multiple performance metrics. Sample MRI slices, filtered images, and segmented regions for both benign and malignant cases are shown in *Figure 4*. Confusion matrix values are used to compute recall, accuracy, precision, and F1-score, enabling reliable classification of positive and negative cases.

For the LeNet model, an accuracy of 87% is achieved. Precision for malignant images is 87.5%, slightly higher than that for benign images (87.17%). The recall for benign cases is 95.77%, while malignant cases achieve 98.36%. The F1-score is 91.24% for benign and 92.48% for malignant samples, indicating slightly better performance for malignant classification. For AlexNet, an accuracy of 92.85% is achieved. The precision values for benign and malignant images are 92.85% and 91.27%, respectively. Recall values are 97.36% for benign and 97.71% for malignant images. The corresponding F1-scores are 95.05% (benign) and 94.38% (malignant). For VGG16, an accuracy of 98.82% is obtained. Precision for benign and malignant images is 96.51% and 97.27%, respectively. Recall values are 98.79% for benign and 99.29% for malignant cases. The F1-scores are 97.64% (benign) and 98.27% (malignant). These results indicate that VGG16 performs exceptionally well in identifying both benign and malignant tumors, showing strong balance between precision and recall. The overall performance of the deep meta-learning algorithm on the

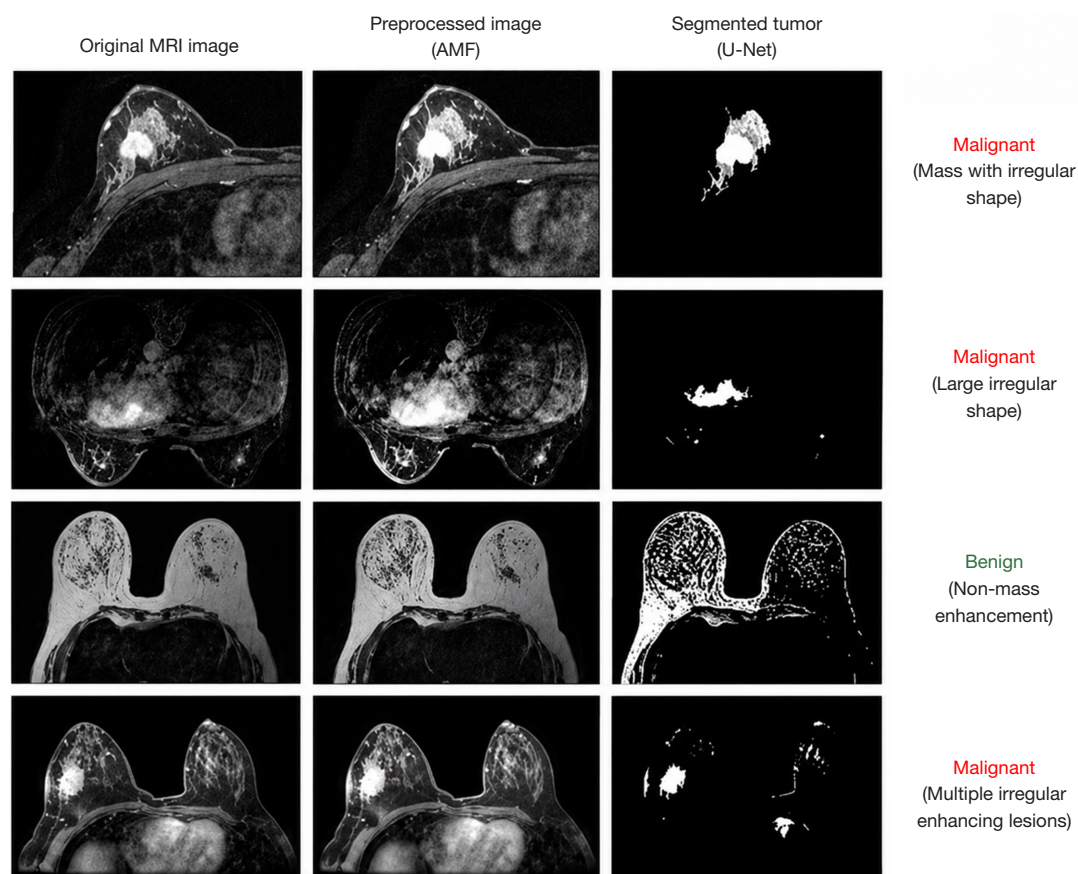


Figure 4 Sample inputs and predicted results for malignant and benign tumor detection. AMF, Adaptive Median Filter; MRI, magnetic resonance imaging.

MRI breast image dataset is presented in *Figure 5* and *Table 1*.

Figure 6 validates and compares the root mean squared error (RMSE) of the proposed deep meta-learning models. The error rate is one of the most widely used parameters to evaluate the performance of a classifier. The overall effectiveness of the tumor detection system is reflected by a lower error rate. It is observed that the proposed VGG16 model achieves the minimum error rate of 0.85, compared to LeNet (1.27) and AlexNet (1.15) on the input dataset. This reduction in error is attributed to the extraction of essential features from the segmented output, which improves classification efficiency and produces a lower error rate.

Discussion

Figure 7 shows the various performance metrics comparison of proposed deep meta-learning techniques using dataset

of breast cancer. The comparative evaluation presented in *Table 2* highlights the performance of the proposed deep meta-learning framework against several existing state-of-the-art approaches for breast cancer detection across different imaging modalities and datasets. The proposed method integrates multiple processing stages, including AMF for noise reduction, U-Net-based segmentation for tumor localization, GDD for feature extraction, SSO for feature selection, and CNN-based classification using LeNet, AlexNet, and VGG16 architectures. Among the evaluated configurations, the VGG16-based model demonstrates the best performance by achieving an accuracy of 98.82%, precision of 97.1%, recall of 99.11%, and F1-score of 98.25% on the BreastDM MRI dataset. This result indicates that deeper convolutional architectures combined with optimized feature selection and meta-learning strategies can effectively capture discriminative patterns in breast MRI images. The AlexNet and LeNet

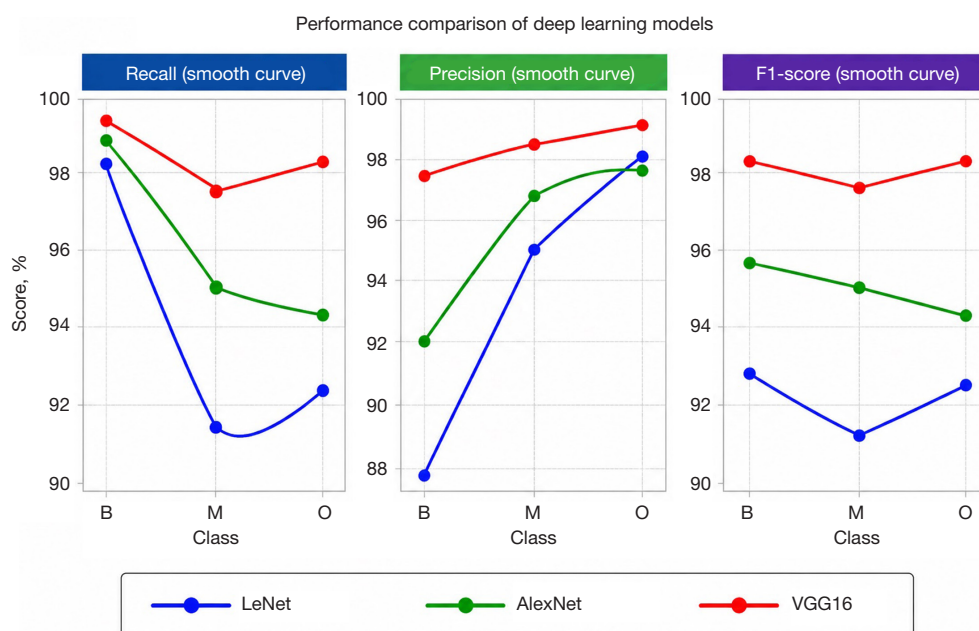


Figure 5 Performance analysis of proposed deep meta-learning algorithm using MRI breast image dataset. B, benign; M, malignant; MRI, magnetic resonance imaging; O, other.

Table 1 Performance analysis of proposed deep meta-learning algorithm

Models	Accuracy (%)	Precision (%)			Recall (%)			F1-score (%)		
		B	M	O	B	M	O	B	M	O
LeNet	87	87.17	87.5	87.7	95.77	98.36	98.4	91.24	92.48	92.74
AlexNet	92.4	92.85	91.27	92.24	97.36	97.71	99.04	95.05	94.38	95.52
VGG16	98.82	96.51	97.27	97.41	98.79	99.29	99.11	97.64	98.27	98.25

B, benign; M, malignant; O, other.

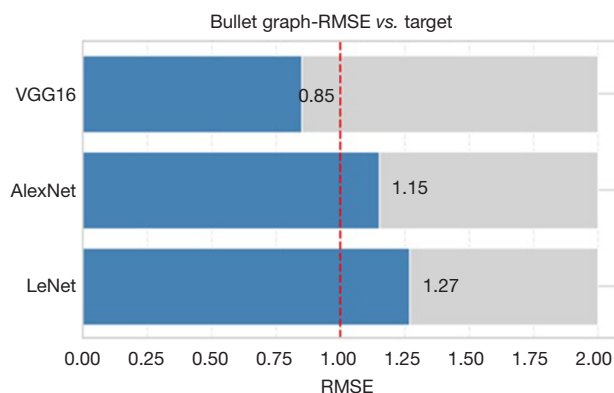


Figure 6 Error rate estimation of proposed deep meta-learning algorithm. RMSE, root mean squared error.

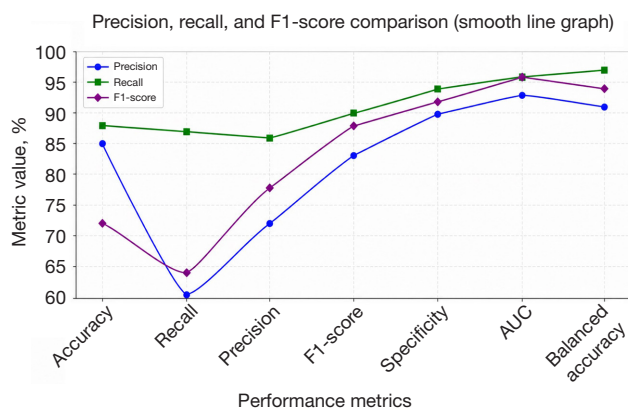


Figure 7 Performance metrics comparison of proposed method. AUC, area under the curve.

Table 2 Performance comparison of proposed deep meta-learning algorithm with other techniques

Study/authors	Method	Dataset/modality	Accuracy (%)	Precision (%)	Recall (%)	F1-score (%)
Proposed Work (VGG16)	Deep meta-learning + AMF + U-Net + GDD + SSO	MRI (BreastDM)	98.82	97.1	99.11	98.25
Proposed Work (AlexNet)	Deep meta-learning + AMF + U-Net + GDD + SSO	MRI (BreastDM)	92.85	92.85	97.36	95.05
Proposed Work (LeNet)	Deep meta-learning + AMF + U-Net + GDD + SSO	MRI (BreastDM)	87.0	87.5	98.36	92.48
Trang <i>et al.</i> , 2023	AI-based classifier (mammography + clinical)	Mammography + clinical records	92.5	90.8	91.7	91.2
Rahul Kumar Yadav <i>et al.</i> , 2023	Conventional CNN	Mammography + clinical data	94.3	92.5	93.1	92.8
G. Rajasekaran <i>et al.</i> , 2023	Hybrid (AERNN + WHO + LDA)	Clinical + imaging data	95.2	93.9	94.5	94.2
Ali Bou Nassif <i>et al.</i> , 2022	DL + ML (histopathology)	Histopathological images	96.1	94.8	95.5	95.1
Adam <i>et al.</i> , 2023	MRI-based CNN	MRI	95.8	94.2	95.0	94.6
H. Rahman <i>et al.</i> , 2023	Deep CNN	Mammographic images	97.5	96.8	97.0	96.9
Shen <i>et al.</i> , 2019	Deep learning CNN	Screening mammography	92.5	91.2	90.8	91.0
Xu <i>et al.</i> , 2023	Integrated dimensionality reduction CNN	Breast MRI	94.8	93.5	94.0	93.7
A. Raza <i>et al.</i> , 2023	DeepBreastCancerNet (CNN)	Ultrasound images	95.2	94.6	94.8	94.7
G. Rajasekaran & P. Shanmugapriya, 2023	Hybrid DL + optimization (AERNN + WHO + LDA)	Clinical + imaging data	95.2	93.9	94.5	94.2
Vimala Mannarsamy <i>et al.</i> , 2025	SIFT-BCD (SIFT + CNN)	Mammography	96.1	95.2	95.5	95.3

AERNN, auto-encoder recurrent neural network; AI, artificial intelligence; AMF, Adaptive Median Filter; BCD, breast cancer diagnosis; CNN, convolutional neural network; DL, deep learning; GDD, Growth Distribution Depth; LDA, linear discriminant analysis; ML, machine learning; MRI, magnetic resonance imaging; SIFT, scale-invariant feature transform; SSO, Salp Swarm Optimization; WHO, World Health Organization.

variants of the proposed framework also show competitive performance, achieving accuracies of 92.85% and 87.0%, respectively. While these models provide slightly lower accuracy compared to the VGG16-based approach, they still demonstrate the effectiveness of the proposed preprocessing, segmentation, and feature optimization pipeline. When compared with recent studies such as those by Trang *et al.* [2023] (9), Yadav *et al.* [2023] (13), and Rajasekaran and Shanmugapriya [2023] (21), which report accuracies ranging from 92.5% to 95.2%, the proposed VGG16-based framework achieves superior classification performance. Similarly, deep learning approaches such as Adam *et al.* [2023] (8), Rahman *et al.* [2023] (17), and Xu *et al.* [2023] (19), which use MRI or mammography images, report accuracies between 94.8% and 97.5%. The numerical comparison with results reported in prior studies are challenging when different datasets, preprocessing strategies, and experimental protocols are used. In this study, the comparison with existing methods was intended to provide a general perspective on the effectiveness of the proposed framework relative to previously reported approaches in breast cancer image classification. Among the evaluated models, the VGG16-based classifier achieved the highest performance, with an accuracy of 98.82%, precision of 97.1%, recall of 99.11%, and an F1-score of 98.25%. This indicates that deeper convolutional architectures are capable of learning more discriminative patterns from segmented tumor regions when combined with optimized feature selection. The high recall value demonstrates that the proposed model is highly effective in identifying cancerous cases, which is particularly important in medical diagnosis where missing a malignant case have severe consequences. The AlexNet-based model achieved 92.85% accuracy, while the LeNet-based model achieved 87% accuracy, demonstrating that even relatively simpler CNN architectures benefit from the proposed preprocessing, segmentation, and feature optimization pipeline. However, the performance gap between these models and VGG16 suggests that deeper networks are better suited for capturing complex spatial and texture patterns present in breast MRI images. Another key finding is the importance of tumor-focused segmentation. By using U-Net to isolate the region of interest before feature extraction, the model reduces the influence of irrelevant background tissue, thereby improving the discriminative capability of extracted features. Additionally, the SSO algorithm effectively selects the most relevant features, reducing redundancy and improving classification efficiency. Comparative analysis

with recent studies shows that the proposed VGG16-based framework outperforms several existing approaches that report accuracies between 92% and 97.5% across different datasets and modalities. Although direct comparison must be interpreted cautiously due to dataset differences, the results suggest that integrating segmentation, optimized feature extraction, and deep learning classification substantially enhance automated breast cancer detection performance. These findings highlight the potential of the proposed framework as a reliable CAD tool for assisting radiologists in clinical breast cancer screening. From the results, it is noticed that the proposed deep meta-learning models overwhelms the existing models by increasing an average accuracy to 98.82%, precision to 97.1% and recall to 99.11% and F1-score to 98.25%. The VGG16 model outperforms other models like LeNet and AlexNet in a classification task using breast dataset.

From a clinical perspective, the proposed framework functions as a CAD support system that assists clinicians in detecting and classifying breast lesions from MRI images. By automatically segmenting suspicious regions and extracting discriminative features, the propose system helps radiologists focus on potentially abnormal areas during image interpretation. This approach aligns with existing diagnostic workflows where imaging findings are combined with radiological assessment and pathological confirmation. The high recall achieved by the model indicates its capability to minimize missed malignant cases, which is particularly important in early cancer detection. However, integration into real-world clinical practice requires further validation on larger, multi-center datasets to ensure robustness across different imaging protocols and patient populations. Additionally, practical deployment requires compatibility with clinical imaging systems such as PACS, as well as compliance with regulatory and ethical standards.

Ablation study

An ablation study was performed by gradually incorporating the main components of the framework. The baseline model consists of the CNN classifier applied directly to the input images without preprocessing, segmentation, or optimization. In the second configuration, AMF was introduced to enhance image quality and suppress noise. In the third configuration, U-Net-based segmentation was employed to isolate tumor regions from surrounding tissue. Subsequently, the GDD was applied to extract discriminative

features from the segmented regions. Finally, SSO was utilized to select the most informative feature subset before classification. The experimental results demonstrate that each component contributes to performance improvement, and the complete framework yields the highest accuracy, indicating the effectiveness of integrating preprocessing, segmentation, feature extraction, and optimization within the proposed meta-learning framework.

Conclusions

Breast cancer is the most common cancer among women worldwide. The integration of computer-aided image analysis into breast MRI diagnosis represents a significant advancement in medical imaging, enhancing both the accuracy and efficiency of breast cancer detection and characterization. The proposed research focuses on the integration of deep meta-learning with AMF, U-Net-based segmentation, GDD feature extraction, and SSO for feature selection in MRI images. This approach provides precise information to medical practitioners for accurate breast cancer classification. The computational complexity of the proposed method is reduced by leveraging pre-trained LeNet, AlexNet, and VGG16 models, which achieved error rates of 1.27, 1.15, and 0.85, respectively. Among these, the VGG16 model outperforms LeNet and AlexNet in classifying breast cancer images. The proposed deep meta-learning framework surpasses existing methods, achieving an average accuracy of 98.82%, precision of 97.1%, recall of 99.11%, and F1-score of 98.25%. In future work, the proposed methodology will be extended to Quantum-based CNNs (QCNN) for further improvement in breast cancer detection.

Acknowledgments

The authors extend their appreciation to the Deanship of Research and Graduate Studies at King Khalid University for funding this work through Large Research Project under grant number RGP2/424/46.

Footnote

Reporting Checklist: The authors have completed the STARD-AI reporting checklist. Available at <https://qims.amegroups.com/article/view/10.21037/qims-2026-1-0388/rc>

Funding: The study was supported by the Deanship of

Research and Graduate Studies at King Khalid University through Large Research Project under grant number RGP2/424/46.

Conflicts of Interest: All authors have completed the ICMJE uniform disclosure form (available at <https://qims.amegroups.com/article/view/10.21037/qims-2026-1-0388/coif>). The authors have no conflicts of interest to declare.

Ethical Statement: The authors are accountable for all aspects of the work in ensuring that questions related to the accuracy or integrity of any part of the work are appropriately investigated and resolved. The study was conducted in accordance with the Declaration of Helsinki and its subsequent amendments.

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Cite this article as: Marimuthu BP, Kumar PR, Sundaramurthy A, Jayabalan J, AlGhamlas NA, Alablani BA, Alam MM, Kwee WK. Deep meta-learning framework with U-Net segmentation and optimization-based feature selection for breast cancer detection in MRI images. *Quant Imaging Med Surg* 2026;16(8):605. doi: 10.21037/qims-2026-1-0388