Magnetic Resonance Imaging for Breast Cancer Classification Using Convolutional Neural Networks

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Article Info

ABSTRACT

Breast cancer remains a leading cause of mortality among women worldwide, emphasizing the urgent need for accurate diagnostic methods. This research addresses the challenges of early detection by leveraging Convolutional Neural Networks (CNNs) for the classification of Magnetic Resonance Imaging (MRI) data. Using a publicly available Kaggle dataset consisting of 54,676 MRI images categorized into "Normal" and "Cancer" classes, the dataset was split into 80% for training and 20% for validation. A modified CNN architecture was developed, incorporating optimized layers and hyperparameters, such as the ADAM optimizer, a learning rate of 0.0001, and a mini-batch size of 128. The proposed model achieved exceptional performance, with an accuracy of 99.72%, precision and recall of 99.98% and 99.97%, respectively, and an F1-score of 99.98%, as evaluated through a confusion matrix. These results demonstrate the model's robustness in distinguishing between healthy and cancerous tissues, providing a reliable and efficient diagnostic tool. This study highlights the potential of CNNs to improve diagnostic precision in medical imaging, aiding clinicians and advancing AI applications in healthcare.

I. INTRODUCTION

Breast cancer is one of the most common cancers affecting female patients throughout the world. It involves uncontrolled growth of breast tissue cells [1]. The WHO reports that breast cancer contributes to about 25% of all cancer diagnoses among women and is first in the cause of cancer burdens worldwide [2]. This makes it a health priority for many low- and middle-income countries where early detection and access to advanced care are hard to come by. Given these challenges, selecting the appropriate imaging modality is crucial for improving diagnostic accuracy. Magnetic Resonance Imaging (MRI) was chosen as the imaging modality in this study due to its superior soft tissue contrast and high sensitivity in detecting breast abnormalities [3]. While mammography is widely used for early detection due to its cost-effectiveness and accessibility, it has limitations in imaging dense breast tissues, which can lead to false negatives. Ultrasonography (USG) is another alternative,

often used as a complementary tool, but it is highly operator-dependent and may not provide sufficient details in some cases. MRI, although more expensive and typically used as a secondary diagnostic tool, is advantageous in detecting small and invasive tumors, particularly in high-risk patients. This study leverages MRI to explore its potential in deep learning-based breast cancer classification, emphasizing its ability to enhance diagnostic accuracy in complex cases. Whereas great strides have been achieved both in screening and in therapeutic approaches, equal access to health care with good diagnostics and proper patient management remains an unfulfilled dream [4], [5]. The WHO demands immediate implementation of integrated approaches, increasing awareness, early detection, and the use of new technologies, including artificial intelligence, to enhance diagnostic precision with consequential improved outcomes in this respect [6], [7], [8]. Such a measure is bound to reduce mortality rates and consequently disparity in care for this condition.

From the challenges of diagnosis and management of breast cancer that are at critical dimensions, the integration of advanced technological solutions offers a very promising pathway. Computer vision is one aspect of Artificial Intelligence serving with tremendous potentials in bringing greater precision and efficiency into the analyses related to medical imagery [9], [10]. Automation systems that will assist healthcare providers in detecting abnormalities within mammograms or MRI can surmount hurdles for early detection mainly where facilities are restricted to a minimal degree [11], [12]. It decreases the need for professional radiologists, reduces diagnosis errors, and fast-tracks treatment planning. Application of computer vision can facilitate bridging gaps in access to quality diagnostics for improving outcomes in breast cancer management worldwide [13].

In computer vision, Convolutional Neural Networks (CNNs) form a very important constituent in image analysis and interpretation in medical diagnostics [14], [15], [16]. CNNs are deep learning models that are elaborately developed to process pixel data in images; therefore, they are very useful in the detection of patterns that may be very intricate and indicative of breast cancer [17]. These networks are good at feature extraction, segmentation, and classification, hence enabling them to differentiate between healthy and cancerous tissues with precision [18]. Continuous learning and large-scale dataset training through CNNs have contributed to the development of robust diagnostic tools that enhance sensitivity and specificity, with informed decisions supported by clinicians [19], [20], [21]. The integration of CNNs into the workflow of breast cancer detection is representative of a paradigm shift in the use of artificial intelligence toward global health improvements.

Pathan et al. (2022) [17] proposed an AI-based method for breast cancer detection using the Breast Ultrasound Images Dataset (BUSI), which includes benign, malignant, and normal categories with both grayscale and masked images. Their multi-headed CNN framework achieved a notable accuracy of 92.31% (±2) with a Mean Squared Error (MSE) of 0.05 by combining raw and masked image inputs, significantly improving diagnostic precision. Additionally, a web interface was developed to make the model accessible to non-technical users, highlighting its practicality and potential in reducing human diagnostic errors.

Amadea et al. (2023) [2] proposed a deep convolutional neural network (CNN)-based model for detecting breast cancer from mammogram images. Their approach leverages the advanced capabilities of CNNs to analyze low-dose X-ray mammograms and identify tumor cells with high precision. The model was evaluated on a mammogram image dataset, achieving impressive performance metrics, including an accuracy of 99.52%, precision of 99.72%, recall of 99.31%, specificity of 99.72%, and an F-measure of 99.50%. These results demonstrate the model's effectiveness in breast cancer detection, offering a reliable and advanced diagnostic tool to support radiological examinations and improve early diagnosis outcomes.

Alqahtani et al. (2022) [22] proposed a deep learning-based approach for breast cancer histopathology image classification using a multiscale recalibrated channel model, msSE-ResNet34. This model refines feature channels through multiscale calibration, utilizing learned channel weights to minimize redundant features and improve classification accuracy. By combining multiscale channel properties and fusing them into successive calibration models, msSE-ResNet34 enhances the recalibration process and boosts performance. Experiments conducted on the publicly available BreakHis dataset demonstrated its efficacy in benign/malignant classification across various magnifications, achieving an accuracy of 88.87%. The findings highlight msSE-ResNet34's robustness in handling pathological images under different magnifications, making it a reliable tool for automatic histopathological image classification.

This research is inspired by various approaches that leverage artificial intelligence, particularly CNN, for breast cancer detection using different types of medical images. Several previous studies have used CNNs to analyze breast ultrasound, mammogram, and histopathology images, demonstrating impressive results in cancer detection accuracy. Based on the success of CNN methods applied to these image types, this study aims to implement CNN training on breast MRI data obtained from a public Kaggle dataset. The MRI data will be divided into 80% for training and 20% for validation, with the expectation of achieving higher accuracy compared to the results obtained in previous studies. To enhance the model's performance, this research uses modified layers for adjusting the CNN training model to the chosen MRI dataset, optimizing the learning process and improving detection outcomes.

II. METHOD

Based on flow of Figure 1, the proposed method begins by utilizing a public dataset, which is split into 80% training data and 20% validation data. The training data is used to configure and train a model, where specific training parameters and CNN layer configurations are optimized to achieve the desired performance. Once the CNN model is trained, the reserved validation data is used to fine-tune and validate the model, ensuring its accuracy and robustness. After the training and validation process, the model enters the prediction phase, where it analyzes testing data to classify inputs as either "Normal" or "Cancer." The performance of the model is then evaluated using a confusion matrix, which provides metrics such as accuracy, precision, recall, and F1-Score, ultimately concluding the process with a reliable classification result.
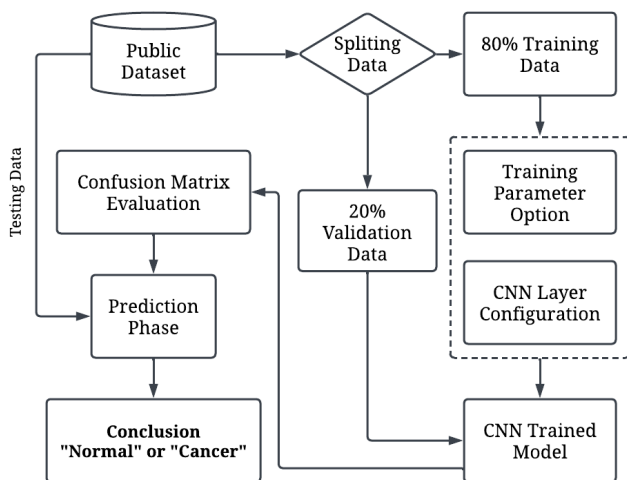
Figure 1. flow of proposed method

A. Datasets

The dataset used in this research consists of MRI images of breast tissue, gathered from the Kaggle open-source dataset. In all, the dataset contains 54,676 images, each with 256 x 256 pixels in size. Their classes are "Normal" and "Cancer," which represent healthy breast tissues and cancerous tissues, respectively. Data were collected by downloading this dataset from Kaggle and preprocessing the data to train and validate the model. To ensure balance during model training, the data is evenly distributed, with 26,000 images for the "Normal" class and 26,000 images for the "Cancer" class used for training. The remaining 2,676 images are allocated for testing. With this balanced distribution, the risk of model bias toward one class is minimized, allowing the model to better recognize relevant patterns in both categories. Sample datasets used in this research can be seen in Figure 2.
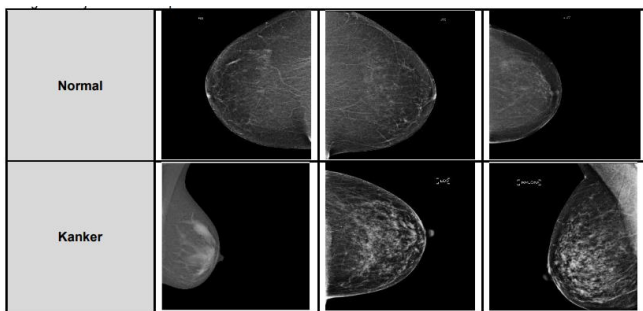

Figure 2. Sample of datasets

This dataset is variegated, with a proper balance between the number of images representing the normal and cancerous conditions; thus, it should be quite efficient in performing comparative studies among its classes during classification. Definitely, this dataset can be used as a base for this research into the development of deep learning models in the classification of MRI images. Meaningful and comprehensive analysis is assured through the vastness of this dataset,

opening up ways for more use of machine learning techniques in the screening of breast cancer and further improving the automated diagnostic tools.

B. Training Parameter Option

Based on Table 1, the training parameters utilized in this study include the ADAM optimizer, which is well-suited for handling sparse gradients and adaptive learning rates. A fixed learning rate of 0.0001 was chosen to ensure stable convergence during the training process. The mini-batch size was set to 128, allowing for efficient training while maintaining memory efficiency. The model was trained over a maximum of 16 epochs to prevent overfitting and to strike a balance between computational efficiency and performance. Additionally, the validation frequency was set to every 30 iterations, enabling regular monitoring of the model's performance on the validation set. These parameter choices aim to optimize the training process, ensuring robust convergence and accurate classification results on the MRI dataset.

The implementation of these training parameters was conducted prior to the deep learning training process. This step involved configuring the optimizer, learning rate, mini-batch size, maximum number of epochs, and validation frequency to establish the foundational settings for the model.

TABEL I
TRAINING PARAMETER

Optimizer	ADAM
Max Epoch	16
Mini Batch Size	128
Learning Rate	0,0001
Validation Frequency	30

The implementation of these training parameters is also intricately connected with the configuration of CNN layers, ensuring a harmonious integration between the model's architecture and the training process.

C. Modified Layer Convolutional Neural Networks

CNN is a type of artificial neural network architecture that is very important in image processing and pattern recognition [23]. CNN is specifically designed to handle image or grid data, such as medical images, and has made tremendous progress in various fields, including classification tasks [24]. The convolutional layers in this study were modified and tailored specifically to align with the characteristics of the dataset and the selected training parameters [25]. These adjustments were made to ensure that the CNN effectively learns the most relevant features from the MRI images while optimizing performance during training [26]. By fine-tuning the architecture, such as the number of filters, kernel sizes, and activation functions, the layers were configured to better capture critical patterns and distinctions between the "Normal" and "Cancer" categories. Modified CNNs Layer can be seen in Figure 3.
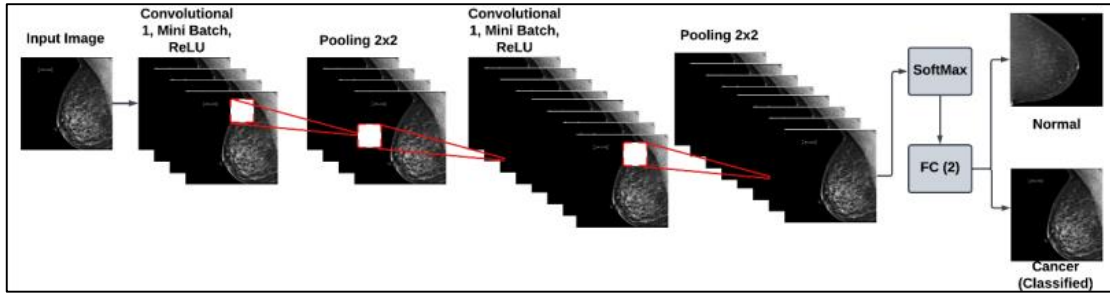
Figure 3. CNN Layers

As see in figure 3, the proposed modified CNN layers were designed to process input images I of size $256 \times 256 \times 3$, where W_{in} is the image width, H_{in} is the height, and $D_{in} = 3$ represents the RGB color channels. The first layer applies convolution operations to extract spatial and texture information. Using K convolutional filters F, each of size $256 \times 256 \times 3$, the convolution operation generates a feature map C. This equation can be seen in eq (1).

$$C_{(i,j,k)} = \sum_{u=0}^{K_{size}-1} \sum_{v=0}^{K_{size}-1} \sum_{d=0}^{D_{in}-1} F_{(u,v,d,k)} \cdot I_{(i+u,j+v,d)} + b_k \qquad (1)$$

where i, j represent spatial positions in the input image, k indexes the filter, and b_k is the bias for filter k. After obtaining C, the ReLU activation function $\sigma(x) = max(0, x)$ is applied element-wise to introduce non-linearity, helping the network to learn complex patterns effectively.

The feature map C is then passed through a pooling layer, typically max pooling, which downsamples the spatial dimensions, reducing C from $W_C \times H_C \times K$ to a smaller size, e.g., $W_C/2 \times H_C/2 \times K$. This reduces computational complexity and aids in feature generalization. The features are then flattened and passed through fully connected (FC) layers. The FC layer maps the pooled features F_C to a higher-level representation using weights W_{fc} and bias b_{fc} as seen in eq (2).

$$F_{fc} = W_{fc} \cdot \text{Flatten}(C) + b_{fc} \qquad (2)$$

Finally, the output layer applies a softmax function for classification. The probabilities for each class p_i are calculated as seen in eq (3).

$$p_i = \frac{\exp(z_i)}{\sum_{j=1}^{N} \exp(z_j)} \qquad (3)$$

where z_i is the output of the last FC layer for class i, and N is the total number of classes. These modifications in the CNN architecture ensure better learning from the MRI dataset while optimizing accuracy in distinguishing between "Normal" and "Cancer" classes.

D. Confusion Matrix Evaluation

The confusion matrix is one of the most important types of evaluation metrics that helps in understanding the efficiency of the proposed CNN model on the classification task [27], [28]. It gives a complete breakdown of the predicted classes, which get organized into four classes: TP, FP, TN, and FN [29]. In this study, the confusion matrix presents the capability of the model in correctly identifying "Normal" and "Cancer" MRI images. The metrics derived from the confusion matrix, such as accuracy, precision, recall, and F1-score, are computed as seen in eq (4) – (7).

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \qquad (4)$$

$$Precision = \frac{TP}{TP + FP} \qquad (5)$$

$$Recall = \frac{TP}{TP + FN} \qquad (6)$$

$$F1 - Score = \frac{2 \times Precision \times Recall}{Precision \times Recall} \qquad (7)$$

It integrates various advanced layers, custom parameters, and specially designed preprocessing techniques for fast feature extraction and a robust model. It also contains several metrics for evaluating the capability of the classifier with respect to true positive rate or accuracy, precision, and recall, which are calculated from the confusion matrix. In this way, the methodological approach adopted has all the ingredients for high accuracy in classification with less computational cost.

III. RESULTS AND DISCUSSION

The results in this section are obtained by implementing the proposed method described in the previous chapter. Systematic training was done with the hyperparameter setting in Table I, Adam optimizer with a learning rate of 0.0001, a mini-batch size of 128, maximum 16 epochs, and validation frequency of 30 iterations. In doing so, the model was ensured not to be overfitted but to converge efficiently. This ensures the best learning of the features of the MRI dataset. More importantly, as highlighted in Figure 3, the modified CNN layers played a big role in the extraction of meaningful feature representations from input images. Indeed, this has improved the performance of the model. The whole training pipeline

was performed in MATLAB, using the MATLAB framework of deep learning, and the implementation and optimization process was eased.

The MATLAB software allowed us to give one holistic approach to the workflow of training by embedding the selected hyperparameters with the custom-designed CNN architecture. First, the dataset was split into 80% for training and 20% for validation; further preprocessing was done on it for unifying the dimensions and enhancing the quality of images. The changed convolutional layers became able to grab the minute patterns of MRI images, whereas the pooling

and fully connected layers optimized dimensionality and the mapping of features accordingly. These obtained results are highlighted in detail below, along with the performance evaluation for the model related to accuracy, precision, recall, and overall classification efficiency. The progression and effectiveness of the training process are visualized in the training graph, as shown in Figure 4, which illustrates the model's loss reduction and accuracy improvement over successive epochs.
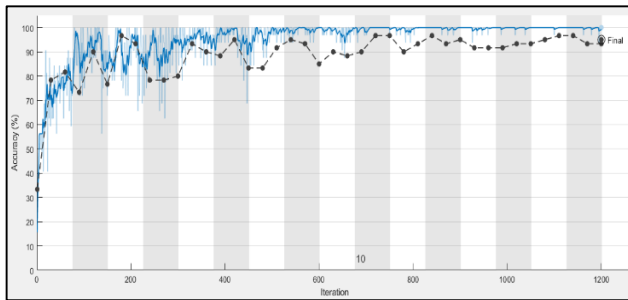
(a) Training progress
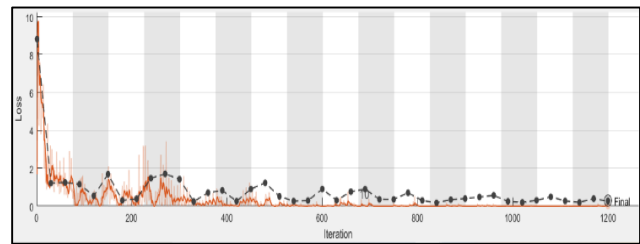
(b) Loss validation

Figure 4. Training and loss graph

Based on Figure 4 (a), The graph depicts the accuracy of a model over iterations (or epochs) during the training process. The blue line represents the accuracy for each iteration, showing fluctuations as the model learns and adjusts its parameters. The black dashed line likely represents the smoothed or average accuracy, providing a clearer trend over the training process.

In the earlier epochs (0-200 iterations), there is significant variability in accuracy, indicating the model is still in the initial stages of learning. As training progresses (200-800 iterations), the accuracy stabilizes and begins to increase consistently, reflecting the model's improved ability to generalize patterns in the data. In the later epochs (800-1200 iterations), the accuracy approaches its maximum and fluctuates minimally, suggesting the model has largely converged to an optimal performance. The final point indicates the model's accuracy at the end of training.

The loss graph depicted in Figure 4 (b) illustrates the relationship between the iteration number and the model's loss during the training phase. Initially, the loss starts at a high value, reflecting the unoptimized state of the model. However, as the number of iterations increases, a significant decrease in loss is observed, indicating that the model is learning and adjusting its parameters to minimize error. After the training process is complete, as shown in the accuracy graph, the model reaches a stable and optimal level of accuracy. The evaluation model is performed using data testing, and the results are displayed in the form of a confusion matrix as shown in Table 2.

TABEL II
CONFUSION MATRIX EVALUATION

Matrix Evaluation	Class	
	Cancer	Normal
Accuracy	**99.72%**	
Precision	99.98%	99.98%
Recall	99.97%	99.97%
F1-Score	99.98%	99.98%

Based on Table 2, the matrix evaluation highlights the exceptional performance of the trained model in classifying data into "Cancer" and "Normal" categories. The model achieved an overall accuracy of 99.72%, indicating that the vast majority of predictions were correct. The precision for both "Cancer" and "Normal" classes is 99.98%, showing that almost all instances predicted as "Cancer" or "Normal" were correct. Similarly, the recall for both classes is 99.97%, demonstrating the model's ability to correctly identify nearly all actual instances of each class. Furthermore, the F1-Score for both "Cancer" and "Normal" is 99.98%, reflecting a balanced and outstanding combination of precision and recall. These metrics confirm that the model is highly reliable and effective in detecting and classifying cancer with minimal errors.

After obtaining the evaluation results in Table II, a testing phase is carried out to determine whether the input data being tested is detected as TP or TN. If the input data is cancer and the model correctly predicts it as cancer, it is categorized as TP. Conversely, if the input data is normal and the model correctly predicts it as normal, it is categorized as TN. The results of this test are presented in Table III, which provides details of the number of correct predictions for each category.

Image Name	Class		Conclusion
	Actual Class	Predicted Class	
Glioma1.jpg	Cancer	Cancer	TP
Glioma7.jpg	Cancer	Cancer	TP
Glioma28.jpg	Cancer	Cancer	TP
Glioma71.jpg	Cancer	Cancer	TP
Glioma1003.jpg	Cancer	Cancer	TP
Normal21.jpg	Normal	Normal	TP
Normal356.jpg	Normal	Normal	TP
Normal11.jpg	Normal	Normal	TP
Normal95.jpg	Normal	Normal	TP
Normal721.jpg	Normal	Normal	TP

Based on Table III, the independent dataset used for testing was sourced from the TCGA-BRCA MRI dataset, a publicly available breast cancer MRI dataset from The Cancer Genome Atlas (TCGA). This dataset was selected to validate the generalizability of the model on MRI scans obtained from a different medical institution. for the Cancer class, the testing phase results demonstrate that all input images labeled as "Cancer" were accurately predicted as "Cancer" by the model, resulting in TP outcomes. For instance, images such as Glioma1.jpg, Glioma7.jpg, and Glioma1003.jpg represent cases where the model successfully identified the presence of cancer.

For the Normal class, the model also performed accurately, correctly predicting all input images labeled as "Normal" as "Normal," resulting in TN outcomes. Images like Normal21.jpg, Normal356.jpg, and Normal721.jpg exemplify cases where the model effectively recognized the absence of cancer. This indicates the model's robustness in correctly identifying normal cases, minimizing false negatives and false positives, and further confirming its reliability in distinguishing between normal and cancerous conditions.

Researcher	Deep Learning Methods	Accuracy	Precision	Recall	F1-Score
Amadea et al. [2]	Deep CNN (Classic Layers)	99.52%	99.72	99.31%	99.50%
Our	Deep CNN (Modified from Classic Layers)	99.72	99.98%	99.97%	99.98%

Table IV compares the results of this study with previous research conducted by Amadea et al. (2023) [2]. Their study utilized a traditional Deep CNN architecture to detect breast cancer from mammogram images, while this research implements a modified CNN architecture for breast cancer classification based on MRI images. The comparison highlights a notable improvement in accuracy, with this study achieving 99.72%, compared to 99.52% in the previous research. Furthermore, the proposed model demonstrates superior performance in precision (99.98%), recall (99.97%), and F1-score (99.98%), surpassing the results obtained by Amadea et al. [2].

To further determine whether the developed CNN model is genuinely superior to other existing models, the current results indicate significant improvements over a traditional CNN, evaluating its performance against more advanced architectures would help validate its effectiveness more comprehensively. Furthermore, testing the model on diverse datasets, including different imaging modalities like mammograms and histopathology slides, would ensure its robustness and generalizability.

IV. CONCLUSIONS

In this research study, a public MRI dataset consisting of 54,676 images, equally distributed between "Normal" and "Cancer" classes, was used for training and validation of the Convolutional Neural Network (CNN) model. The dataset was preprocessed and then divided into 80% for training and 20% for validation. Results showed outstanding performance of the model by using an optimized CNN architecture with the ADAM optimizer, learning rate 0.0001, and mini-batch size of 128. According to the confusion matrix, the model showed an accuracy value of 99.72%, precision-99.98%, recall-99.97%, and F1-score value of 99.98% for the respective classes. This substantiates that the model is highly reliable and robust for classifying MRI images of breast tissues as "Normal" and "Cancer," therefore, this research will be of great importance in assisting diagnostic experts toward the early detection of this type of cancer and sharing with readers advanced AI techniques applied in medical imagery.

Eventually, some proposals for future research involve implementing transfer learning to enhance the model's performance and efficiency. It allows using some pre-trained networks like ResNet, VGG, or DenseNet as a baseline, thus reducing the time taken for training and thus generalizing well on different datasets. Increasing the dataset to the involvement of more types of imaging modalities, such as mammography or ultrasound examinations, may further increase the model's versatility in medical diagnostics. All these developments, in turn, will allow developing a more complete and efficient automated diagnostic system for the detection of breast cancer.

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