

## RESEARCH ARTICLE

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# Advanced feature learning and classification of microscopic breast abnormalities using a robust deep transfer learning technique

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## Abstract

Breast cancer is a major health threat, with early detection crucial for improving cure and survival rates. Current systems rely on imaging technology, but digital pathology and computerized analysis can enhance accuracy, reduce false predictions, and improve medical care for breast cancer patients. The study explores the challenges in identifying benign and malignant breast cancer lesions using microscopic image datasets. It introduces a low-dimensional multiple-channel feature-based method for breast cancer microscopic image recognition, overcoming limitations in feature utilization and computational complexity. The method uses RGB channels for image processing and extracts features using level co-occurrence matrix, wavelet, Gabor, and histogram of oriented gradient. This approach aims to improve diagnostic efficiency and accuracy in breast cancer treatment. The core of our method is the SqE-DDConvNet algorithm, which utilizes a  $3 \times 1$  convolution kernel, SqE-DenseNet module, bilinear interpolation, and global average pooling to enhance recognition accuracy and training efficiency. Additionally, we incorporate transfer learning with pre-trained models, including mVVGNet16, EfficientNetV2B3, ResNet101V2, and CN2XNet, preserving spatial information and achieving higher accuracy under varying magnification conditions. The method achieves higher accuracy compared to baseline models, including texture and deep semantic features. This deep learning-based methodology contributes to more accurate image classification and unique image recognition in breast cancer microscopic images.

## Research Highlights

- Introduces a low-dimensional multiple-channel feature-based method for breast cancer microscopic image recognition.
- Uses RGB channels for image processing and extracts features using level co-occurrence matrix, wavelet, Gabor, and histogram of oriented gradient.
- Employs the SqE-DDConvNet algorithm for enhanced recognition accuracy and training efficiency.
- Transfer learning with pre-trained models preserves spatial information and achieves higher accuracy under varying magnification conditions.

- Evaluates predictive efficacy of transfer learning paradigms within microscopic analysis.
- Utilizes CNN-based pre-trained algorithms to enhance network performance.

**KEYWORDS**

cancer, deep semantic feature, feature classification, microscopic breast images, transfer learning

## 1 | INTRODUCTION

Recent global cancer research shows breast cancer has surpassed lung cancer to become the most prevalent cancer worldwide. Approximately 685,000 deaths were attributed to breast cancer in 2020, accounting for one-fourth of female cancer cases and one-sixth of fatalities. In the United States alone, around 420,000 new breast cancer cases were reported in 2020, resulting in approximately 120,000 deaths (World Health Organization, 2021). Early detection and diagnosis of breast cancer are crucial to reduce disease progression and improve patient outcomes. Various breast cancer screening techniques, including clinical examination, ultrasonography, mammography, and magnetic resonance imaging, are frequently employed (Iqbal, Qureshi, Li, Choudhry, & Mahmood, 2023; Öztürk & Çukur, 2023). However, none of these methods alone can conclusively diagnose breast cancer. Instead, a breast biopsy involving surgically removing diseased tissue is required. The excised breast tissue is processed through fixation, dehydration, purging, and paraffin infiltration, producing pathological images. These images are examined by a pathologist, representing the “gold standard” for breast cancer diagnosis (McCann et al., 2014). This comprehensive diagnostic approach ensures accurate and reliable identification of breast cancer, enabling timely and appropriate medical interventions.

Globally, breast adenocarcinoma emerges as a paramount health concern for women, causing significant mortality each year (Mahmood et al., 2020; National Health Service, 2023). The International Health Organization's Agency for Research on Cancer highlights the severity of breast cancer, attributing it to a significant portion of female cancer-related deaths, surpassing other malignancies such as colorectal, lung, cervical, and stomach cancers (Stewart & Kleihues, 2014). With annual diagnoses surpassing 1.6 million, the death toll exceeds 500,000 (WHO Cancer Fact Sheets, 2023). Forecasts suggest a potential escalation to 27 million new cases by 2030. Genetic factors, hormonal shifts, and modern-day stressors are primary contributors. The urgency for early detection is further amplified by healthcare resource constraints and the growing demands on women's health. While imaging techniques like mammograms, MRIs, and ultrasounds have been used for decades, biopsy-based pathological imaging remains the definitive diagnostic tool, providing clinicians with a robust platform for treatment decisions (Yaqub et al., 2022). Breast cancer image classification spans traditional techniques, which rely on artificial features, and contemporary deep learning approaches. The former requires specialized feature identification and

classification expertise using machine-learning tools, making it labor-intensive (Zhang et al., 2020). Traditional methods for diagnosing breast cancer are inefficient and time-consuming, leading to the rise of digital pathology technology. Artificial intelligence can automatically analyze microscopic images, promoting the development of digital pathology CAD technology and reducing pathologist workload (Zhu et al., 2019).

In contrast, deep learning techniques offer a more streamlined approach, allowing for inherent feature recognition and eliminating manual intervention (Lichtblau & Stoean, 2019). The evolution of automated medical image analysis aimed to address the limitations of manual examination (Branchatine & Riccio, 2018). Early efforts were based on basic processing and mathematical models to create rule-specific systems. This research, however, presents advanced CAD models that leverage deep learning algorithms for breast cancer diagnostics (Zou et al., 2022). While earlier CAD techniques, grounded in standard machine learning algorithms, had their merits, they were limited by dataset size, manual feature extraction needs, and lack of standardized benchmarks. This paper advocates using deep convolutional neural networks (CNNs) to tackle these challenges, specifically for breast cancer image classification. CNN models, with their automated feature extraction capabilities, outperform traditional methods. However, the intricate design of CNNs increases the risk of overfitting, necessitating extensive training datasets, which can be resource-intensive. Fine-tuning hyperparameters, especially the learning rate, is essential, often requires manual adjustments, and poses challenges for those unfamiliar with the field.

This study presents a deep-learning strategy for autonomously classifying breast cancer microscopic images, highlighting the need for high-quality training and validation datasets for image analysis. Improved cure and survival rates for breast cancer patients depend critically on early detection. It introduces a novel method for visualizing staining patterns to deal with the complexities of microscopic variations on large digital transparencies. The study introduces a low-dimensional multiple-channel feature extraction method for learning and classifying microscopic breast cancer image characteristics by dividing the original image into R, G, and B channels. The deep learning-based SqE-DDConvNet algorithm improves recognition precision and training efficiency. The Breast Cancer microscopic image classification model incorporates global pooling and interconnected layers, utilizing pre-trained networks to identify pertinent features and achieve accurate classification. Transfer-learning-based pre-trained methods, such as mVVGNet16, EfficientNetV2B3,

ResNet101V2, and CN2XNet, attain greater classification accuracy and precision under magnification. The study examines factors influencing breast cancer microscopic image recognition using BreakHis datasets and evaluates the efficacy of five proposed methods. The method achieves higher accuracy compared to baseline models, including texture and deep semantic features. This deep learning-based methodology contributes to more accurate image classification and unique image recognition in breast cancer microscopic images.

## 1.1 | Research motivation

Breast cancer tissue pathology image recognition faces challenges such as the diversity and complexity of these images, the need for experienced pathologists, and the subjective nature of pathologist diagnoses. This makes it difficult to diagnose breast cancer, as there is no uniform pattern or standard for tumor types and stages. Pathologists' diagnoses are subjective, relying on their prior knowledge and experience, leading to poor average diagnostic consistency and increased workload. Unpredictable situations during tissue section preparation and defects in image acquisition can also affect subsequent diagnosis. Digital pathology images are large and high in resolution, making diagnosis labor-intensive and prone to fatigue and misdiagnosis. Misdiagnosis can have serious consequences, such as missing optimal diagnosis and treatment time and even loss of life. Improving the accuracy of imaging diagnosis can reduce unnecessary suffering for subjects and alleviate their psychological and economic burdens. To achieve computer-aided diagnosis of breast cancer tissue pathology images, reasonable methods for recognizing these images can provide theoretical support for computer-aided diagnosis systems and provide objective and scientific diagnostic results for pathologists. However, issues such as limited public datasets for deep learning, the complexity of labeling tissue pathology images, the need for large operating memory and high-performance computers, and uncertainty in tissue preparation processes need to be addressed.

## 1.2 | Novel contribution

The study explores the challenges of recognizing breast cancer microscopic images, emphasizing the importance of timely diagnosis. It proposes a novel approach using artificial features and deep learning to improve microscopic image recognition accuracy, achieving superior accuracy at both image and patient levels. The novel contribution is under:

1. To develop a deep learning-based method for breast cancer microscopic image recognition and classification, enhancing feature learning and classifying images with unique characteristics.
2. Employing the SqE-DenseNet module, featuring a  $3 \times 1$  convolution kernel, enhances recognition accuracy by integrating global pooling and interconnected layers and accelerating computations.

3. To systematically evaluate the predictive efficacy of transfer learning paradigms within microscopic analysis by juxtaposing five pre-trained algorithms, each fine-tuned across two distinct datasets.
4. The study utilizes CNN-based pre-trained algorithms such as mVGGNet16, ResNet101V2, EfficientV2B3, and CN2XNet to enhance network performance, modifies the last pooling layer with GAP, BN, FC1, FC2, and SoftMax layers.

The paper's organization is as follows: Section 2 a concise overview of pertinent research on advanced techniques and innovative advances in medical image analysis is provided. Section 3 demonstrates the proposed method, which includes microscopic image processing and data enhancement. Section 4 demonstrates the feature extraction and classification techniques. Section 5 demonstrates the proposed architecture and transfer learning paradigm based on deep learning. Section 6 employing microscopic images, describe the findings of the investigation using the suggested framework. Section 7 concisely explains the results and concentrates on the advancements of deep learning and its applications in microscopy image analysis. Finally, Section 8 the study's conclusions are recapitulated.

## 2 | BACKGROUND KNOWLEDGE BASED ON THE MICROSCOPIC IMAGES

### 2.1 | Breast cancer microscopic image classification based on BreakHis dataset

Gu & Yang (2018) introduced the extended version of VGG-Net called DCMMH (Densely Connected Multi-Magnification Hashing) that incorporates dense blocks and leverages low and high-magnification images to guide the learning of image features mutually achieving an average accuracy of approximately 95%. Song, Zou, and Chang (2017) developed a Fisher vector encoding of VGGNet to enhance classification accuracy compared to AlexNet-based models. They used a supervised embedding algorithm to address FV's high dimensionality and burst effect. GoogLeNet tackled gradient disappearance by incorporating two distinct losses at different depths, enabling deeper network architectures and increased learning capacity. Wei et al. (2017) developed BiCNN, a breast cancer microscopic image classification model that uses class and subclass labels to constrain image features' distance, resulting in a 97% improvement in classification accuracy compared to previous methods. Wang et al. (2020) developed a breast cancer histopathological image classification model using ResNet-50 and an ELM classifier. The model was pre-trained on natural images and fine-tuned twice on breast cancer histopathological images, achieving an impressive accuracy of 98.18%. Gour and Jains (2020) developed Res-Hist, a breast cancer microscopic image classification model using ResNet-152 and data enhancement techniques. The model achieved a classification accuracy rate of 92.52%, significantly improving breast cancer microscopic image classification. Addo et al., (2024) developed a sequential DenseNet framework for extracting multi-layer depth features using the XGBoost classifier on each

convolutional layer. This method outperformed models relying solely on high-level features, achieving a classification accuracy of around 96.76%. Vo et al. (2019) utilized the Inception-ResNet-v2 architecture and a gradient-enhanced tree classifier for breast cancer image histopathological classification. The model extracted global and local information from images with an accuracy of approximately 99.5%, thereby substantially enhancing histopathological image classification techniques for diagnosing breast cancer. Mehra (2018) tackled the challenge of training networks from scratch using transfer learning and evaluated its effectiveness on VGG-16, VGG-19, and ResNet-50. The experimental findings indicated that transferring learning improved the trained networks' robustness.

Deniz et al. (2018) utilized AlexNet and VGG-16 combined with a support vector machine (SVM) classifier to classify breast cancer histopathological images, achieving an accuracy rate of approximately 91%. Khan et al. (2019) integrated VGGNet, GoogLeNet, and ResNet to develop a breast cancer histopathological image classification model, achieving an impressive classification accuracy rate of about 97.52%. Ozturk and Akdemir (2019) developed HIC-net, a convolutional neural network model that uses window-based classification and pre-processing to identify cancerous areas on histopathological images, outperforming other CNN algorithms with an AUC score of 97.7%. Similarly, Spanhol et al. (2016) used DeCAF features, reusing a pre-trained CNN architecture and parameters and feeding the output of a specific layer into a new classifier, achieving a classification accuracy rate between 82% and 86%. Sudharshan et al. (2019) demonstrate that integrating CNN and multi-instance learning can improve classification accuracy by 83%–87% without instance-specific labeling. The research emphasizes the importance of data enhancement in enhancing classification accuracy, highlighting the need to transition from shallow models to deeper architectures like ResNet and DenseNet. Akalin and Yumuşak (2022) conducted a study on real-time white blood cell detection in the medical field using YOLOv5s, YOLOv5x, and Detectron 2 R50-FPN pre-trained models. They improved recognition rates by 0.006 and success rates by 3.44%–14.7%. Researchers have explored alternative methodologies like transfer learning, data enhancement, and innovative network structures. Model fusion, leveraging different networks' strengths, has also proven effective in improving classification accuracy. Although some attempts may not achieve the same accuracy levels, they offer valuable insights for future research.

## 2.2 | Breast cancer histopathological image classification based on BACH dataset

The BACH dataset faces a significant limitation due to its small number of breast cancer histological images, which proves insufficient for effectively training high-performance CNN models that typically require a larger dataset. To tackle this issue, Weiss et al. (2018) researched the interactive classification of breast cancer histopathological images, utilizing Xception (Malve & Vijay, 2023) and

incorporating a logistic regression (LR) classifier. They applied data augmentation techniques, such as horizontal and vertical rotating, to achieve an accuracy of 72% on the BACH hidden test set. To overcome the challenges posed by the limited dataset, Iesmantas and Alzubas (2018) proposed a convolution-based optimization parameter. Consequently, most studies employing the BACH dataset have turned to transfer learning techniques. In the realm of image preprocessing, it is customary for most studies to apply standard staining modifications. Considering the scale of the BACH dataset  $2048 \times 1536$  pixels, image cropping has emerged as a prevailing practice. Roy et al. (2019) explored three distinct cropping sizes for images,  $64 \times 64$ ,  $128 \times 128$ , and  $512 \times 512$ . Their comprehensive experimentation revealed that the model trained with  $512 \times 512$  image fragments outperformed others in classification accuracy. Notably, the cropping process was executed non-overlapping to eliminate redundant information effectively. However, despite the primary objective of eliminating redundancy, most studies utilizing the BACH dataset persisted in adopting segmentation techniques that involve both large and small sizes with overlap.

## 2.3 | Challenges in the manual classification of breast cancer microscopic images

Currently, pathologists face significant challenges in manually classifying breast cancer microscopic images. These challenges include subjectivity in interpretations, the time and labor-intensive nature of the process, limited access to specialized expertise, potential pathologist fatigue, lack of standardization, cost and resource constraints, and extensive training requirements. Alternative methods, such as incorporating artificial intelligence and machine learning, are being explored for breast cancer microscopic image classification to overcome these issues and improve accuracy and efficiency. These advancements hold great promise in enhancing breast cancer diagnosis and treatment, leading to better patient outcomes and advancements in breast cancer research.

1. The global scarcity of pathologists poses a significant challenge, particularly in underdeveloped regions and smaller healthcare institutions.
2. The accuracy of pathological diagnosis heavily relies on the expertise of pathologists and diagnostic tests. However, this process is highly subjective, leading to disagreements among expert pathologists and a mere 75.3% agreement among identified reference diagnoses.
3. Pathologists' susceptibility to fatigue and decreased attention when dealing with complex pathological images heighten the risk of misdiagnosis. To address this, an urgent need is to develop an automatic and precise CAD system that can support pathologists in breast cancer histopathological image classification. Such a system can improve diagnostic efficiency, reduce costs, lessen the burden on pathologists, and ultimately decrease the misdiagnosis rate, allowing them to concentrate on the most suspicious cases.

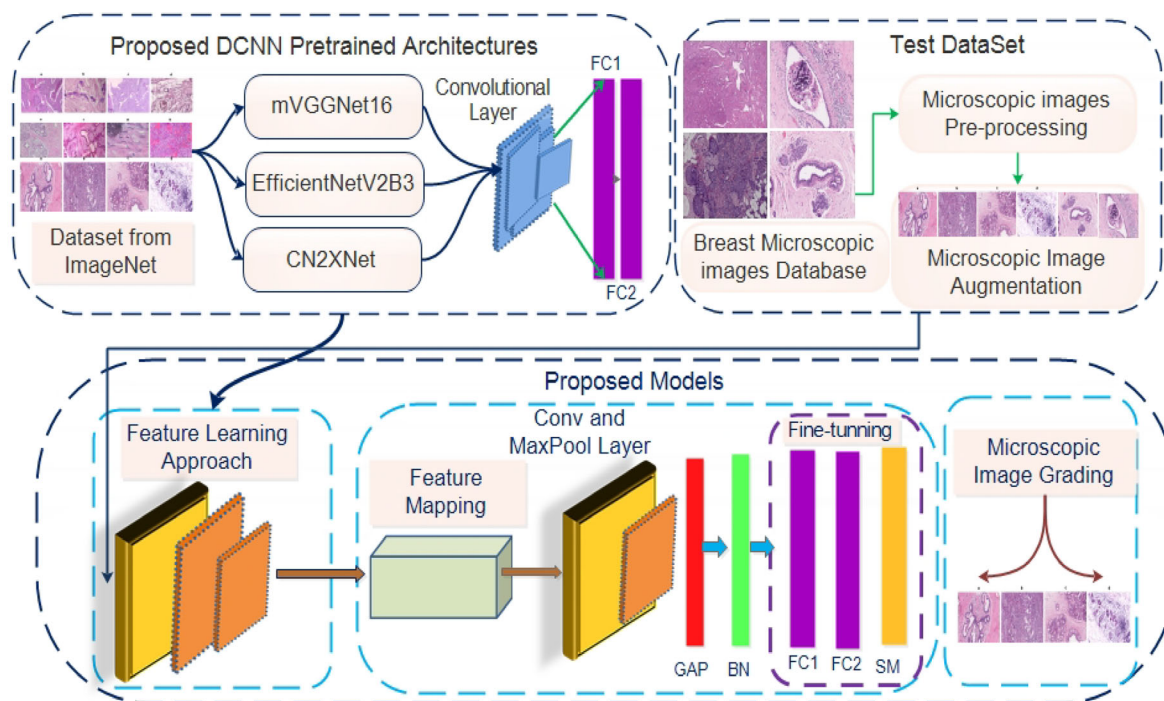


**FIGURE 1** The step-by-step transfer learning process in deep convolutional neural network (DCNN)-based architectures involves pretraining models, preprocessing data, enhancing, augmenting, fine-tuning models, and obtaining predictions by modifying lower and higher layers' weights.

### 3 | PROPOSED METHODOLOGY

Deep learning is a powerful approach to detecting and classifying malignant breast tissues in microscopic images. This method involves preprocessing, including scaling, scrambling, and normalizing the data. Filtering techniques like Median, Gaussian, and Bilateral filtering mitigate irregularities like staining variations, blurring, and artifacts. The Contrast Limited Adaptive Histogram Equalization (CLAHE) method improves image contrast, allowing for more accurate visualization of lesions. A threshold-based segmentation method identifies and isolates the region of interest in breast lesions, enabling comprehensive characterization and evaluation. The dataset is expanded using flipping, rotation, resizing, and brightness adjustment techniques. A novel framework is proposed using hybrid models SqE-DCCConvNet and deep CNN (DCNN)-based pre-trained architectures. The step-by-step process of transfer learning-based architectures is depicted in Figure 1. The proposed framework captures low-level features using CNN-based architectures, including mVGGNet16 (Simonyan & Zisserman, 2014), EfficientNetV2B3 (Tan & Le, 2021), ResNet101V2 (He et al., 2016), and DenseNet-121 (Huang et al., 2017). The study focuses on automating feature engineering and exploring transfer learning paradigms across DL-based algorithms. The model's performance is improved through iterative training with different hyperparameter values. The method integrates deep semantic features from pre-trained networks with GLCM features from the original image, preserving spatial information. The hybrid breast cancer histopathological image recognition model is trained using SqE-DCCConvNet and DCNN pre-trained models. The

technique achieves superior accuracy at image and patient levels compared to multiple baseline models.

1. To conceptualize and implement an innovative methodology for the automated diagnosis, localization, and categorization of breast cancer microscopic images leveraging the CNN architecture.
2. To delineate and segment Regions cancerous employing a comprehensive global thresholding strategy amalgamated with morphological operations to circumvent the inefficacious segments inherent in microscopic.
3. To prognosticate regions of paramount concern utilizing a region-centric max-pooling schema, integrated with a miniature kernel dimension, to attenuate potential overfitting intricacies.
4. To assess the proposed models' performance using a novel manually labeled dataset and compare it to other state-of-the-art schemes.

#### 3.1 | Breast cancer microscopic image dataset

Publicly accessible large marker breast cancer histopathology datasets are scarce, and the datasets researchers use are widely dispersed. Among the most frequently utilized public datasets are BreakHis (Spanhol et al., 2015) and BACH (Aresta et al., 2019). These datasets are comprehensive collections of breast cancer microscopic images encompassing various magnifications and cancer stages. BreakHis contains 7909 images from 82 patients, and

BACH includes 100 high-quality histopathological images of each category. The choice of these datasets provides a balanced representation of different breast cancer types and stages. However, the limitation is their focus on specific demographic groups, potentially affecting the model's performance across diverse populations. Research based on the BreakHis dataset focuses on binary classification, distinguishing between benign and malignant tumors, such as adenosis, fibroadenoma, tubular adenoma, and phyllodes tumors. Some studies have also attempted the dataset's eight categories, which include adenosis, fibroadenoma, tubular adenoma, phyllodes tumor, ductal carcinoma, lobular carcinoma, mucinous carcinoma, and papillary carcinoma. On the other hand, the BACH dataset's study aims to categorize it into four groups: normal, benign, carcinoma in situ, and invasive carcinoma. Due to the two datasets' differing research objectives and evaluation criteria, making explicit comparisons between studies based on them is inappropriate. Consequently, the research progress based on each dataset will be discussed separately in the following sections.

### 3.2 | BreakHis dataset

The BreakHis dataset comprises a rich collection of 7909 unique images of breast tumor tissue sourced from 82 patients diagnosed with breast cancer. These images are acquired at varying magnifications ranging from 40 $\times$  to 400 $\times$ . Among the dataset samples, 2480 are classified as benign, while 5429 are classified as malignant, as represented in Table 1. The images are presented in a 3-channel RGB format, each with an 8-bit depth per channel, resulting in 700  $\times$  460 pixels size. These images are saved in the widely used PNG format. The specimens utilized for the dataset were extracted from breast biopsies and subsequently stained with hematoxylin and eosin H&E. Expert pathologists from a Brazilian P&D laboratory meticulously labeled the images to ensure accuracy. This comprehensive dataset is valuable for researchers exploring and analyzing breast cancer histopathology images, enabling advanced studies and developing robust classification models. Figure 2 visually represents the BreakHis dataset's characteristics.

**TABLE 1** Image distribution of BreakHis dataset.

| Magnification | A   | F    | TA  | PT  | Total | DC   | LC  | MC  | PC  | Total |
|---------------|-----|------|-----|-----|-------|------|-----|-----|-----|-------|
| 40 $\times$   | 114 | 253  | 109 | 149 | 625   | 864  | 156 | 205 | 145 | 1370  |
| 100 $\times$  | 113 | 260  | 121 | 150 | 644   | 903  | 170 | 222 | 142 | 1437  |
| 200 $\times$  | 111 | 264  | 108 | 140 | 623   | 896  | 163 | 196 | 135 | 1390  |
| 400 $\times$  | 106 | 237  | 115 | 130 | 588   | 788  | 137 | 169 | 138 | 1232  |
| Total         | 444 | 1014 | 453 | 569 | 2480  | 3451 | 626 | 792 | 560 | 5429  |
| Patients      | 4   | 10   | 3   | 7   | 24    | 38   | 5   | 9   | 6   | 58    |

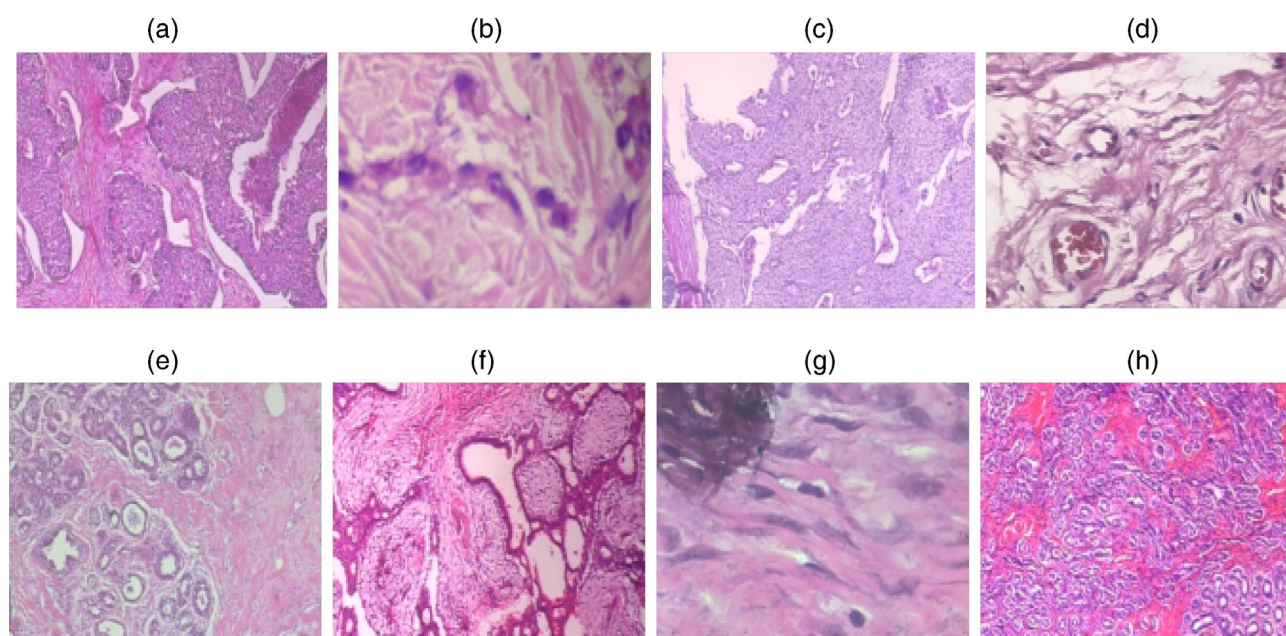


**FIGURE 2** The figure illustrates a selection of histopathological images sourced from the BreakHis dataset, encompassing different categories, including (a) adenosis, (b) fibroadenoma, (c) tubular adenoma, (d) phyllodes tumor, (e) ductal carcinoma, (f) lobular carcinoma, (g) mucinous carcinoma, and (h) papillary carcinoma.

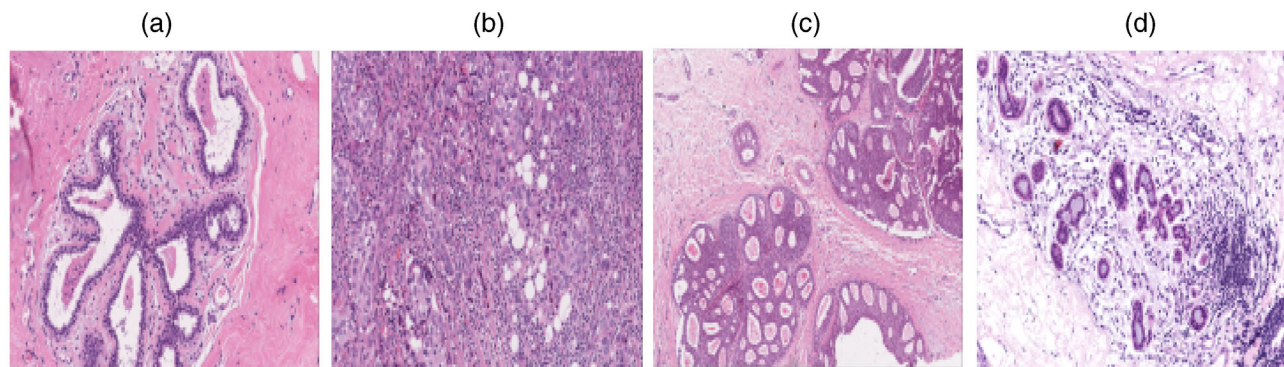


**FIGURE 3** The figure illustrates a selection of histopathological images sourced from the BACH dataset, encompassing different categories, including (a) normal, (b) invasive, (c) carcinoma in situ, and (d) benign tumor.

The BreakHis dataset is used in a study to evaluate the proposed model's performance in accurately classifying breast tumor images as benign or malignant. The effectiveness of these models is assessed using metrics like accuracy, sensitivity, specificity, and precision. 5-Fold cross-validation techniques are used to ensure robustness and generalizability. The dataset is divided into training and testing subsets, allowing for training and evaluation of models. The research aims to improve breast cancer diagnosis and treatment planning by enhancing early detection and accurate characterization, impacting patient outcomes, and guiding appropriate treatment strategies. The Patient Recognition Rate (PRR) can be calculated using the formula presented in Equation (1).

$$PRR = \frac{\sum \frac{Nr_{pa}}{N_{pa}}}{N_{npa}}, \quad (1)$$

$Nr_{pa}$  is the count of correctly classified images for patient  $pa$ , while  $N_{pa}$  is the total images of patient  $pa$ .  $N_{npa}$  is the patient count. PRR assesses patient recognition accuracy in a dataset. It calculates the average percentage of correctly identified images per patient, which is valuable for evaluating algorithm performance in medical imaging. A higher PRR indicates better patient identification. The Image Recognition Rate (IRR) can be calculated using the formula presented in Equation (2).

$$IRR = \frac{Nr_{pi}}{N_{npi}}, \quad (2)$$

$Nr_{pi}$  is correct image count, while  $N_{npi}$  is the total count. IRR evaluates image recognition accuracy by measuring a dataset's correct image identification percentage. A higher IRR signifies better accuracy, crucial in computer vision, pattern recognition, and machine learning for algorithm and model assessment.

### 3.3 | BACH dataset and evaluation criteria

The BACH dataset, also known as the ICIAR2018 Breast Cancer Histology Challenge dataset, is an expanded version of the Challenge

dataset presented in 2017 (Araújo et al., 2017). This dataset comprises microscopic images of breast tissue stained with hematoxylin and eosin H&E. The images are categorized into four classes: normal, benign, carcinoma in situ, and invasive carcinoma, as illustrated in Figure 3.

To ensure the accuracy of the categorization, two medical professionals independently assigned the images to their respective classes. In cases of disagreement, the images were excluded from the dataset to maintain consistency and reliability. The BACH dataset contains 100 images for each category, resulting in 400 images. These images have dimensions of  $2048 \times 1536$  pixels and are stored in 3-channel RGB format, saved in TIFF file format. The dataset is valuable for researchers and practitioners in breast cancer histology analysis. It provides a diverse and well-labeled set of images representing different breast tissue conditions, facilitating the development and evaluation of DL-based algorithms for accurate breast cancer classification.

#### 3.3.1 | Microscopic image preprocessing and augmentation

The preprocessing stage of imaging is crucial for addressing noise in deep-learning models for breast cancer microscopic image classification. Common noise types, such as Gaussian, salt-and-pepper, and speckle noise, can obscure critical image features, affecting model accuracy and reliability. To counter this, advanced noise reduction techniques like adaptive filtering and robust feature extraction methods are used. These techniques ensure the clarity and precision of input images before analysis by deep learning models. Moreover, the research introduces a new image preprocessing technique that uses color detection to delineate gland boundaries in breast microscopic images (Rehman et al., 2021). The method focuses on identifying purple and dark pink shades standard at gland borders to enhance the deep learning model's capability for gland detection. The process involves manually collecting color pixels and formulating a statistical probability model for color, which removes pixels associated with target colors using a maximum likelihood ratio. Non-target pixels are assigned a white value of 255. The collected pixel colors are

**TABLE 2** Different ques of augmenting data with in-variance parameters.

| S. No. | Augmentation approaches           | In-variance parameters             |
|--------|-----------------------------------|------------------------------------|
| 1      | Sharpness (lightness adjustment)  | 0.5, 1, 1.5, 2                     |
| 2      | Emboss (strength adjustment)      | 0.5, 1, 1.5, 2                     |
| 3      | Gaussian blur (sigma adjustment)  | 0.25, 0.5, 1, 2                    |
| 4      | Rotation                          | 45°, 90°, 135°, 180°               |
| 5      | Edge detection (alpha adjustment) | 0.25, 0.5, 0.75, 1.0               |
| 6      | Skew (tilt)                       | Forward, Backward, Left, Right     |
| 7      | Flipping                          | Top, Bottom, Left side, Right side |
| 8      | Shear (axis & value adjustment)   | X-axis 10° and Y-axis 10°          |

categorized into segments within the RGB histogram, and probability values for each RGB color division are computed using a histogram-based technique (Ali et al., 2022). The model then expands the gland boundary pixels and increases the contrast between the gland boundary and its background, addressing potential gaps in coverage. This technique enhances the model's accuracy and efficiency in precisely outlining the gland boundary, facilitating a more comprehensive analysis.

The study aims to address the challenges of CNN-based algorithms for medical image classification by utilizing data augmentation techniques to boost the dataset size. The input dataset undergoes horizontal flipping, random rotation angles, brightness and contrast adjustments, random cropping, random aspect ratios, and blurring to minimize noise. This approach enlarges the dataset and enhances the model's generalization ability by training on original and augmented images. The study also seeks to balance the microscopic dataset using varied augmentation techniques to minimize error rates and enhance generalization. Overfitting in CNN-based architecture occurs when models extensively learn features from training data but struggle to generalize effectively to make accurate predictions on unseen data. To counter this, the research artificially augments the dataset eightfold, employing diverse data augmentation methods as shown in Table 2. The expanded dataset is crafted through geometric transformations applied to the initial dataset, including scaling, flipping, rotating, translations, and cropping. Images are rotated within  $\pm 45$  degrees to mitigate overfitting effects during training epochs. Keras' ImageDataGenerator library is harnessed to generate tensor image data batches with real-time data enhancement.

### 3.3.2 | Patches cropping and normalization

This study employs patch cropping and normalization techniques to prepare microscopic images for analysis. The study focuses on

cropping breast microscopic images to preserve essential information while excluding irrelevant elements. This systematic approach reduces computational load, optimizes processing speed, and enhances feature analysis precision. The cropped segments undergo further processing analysis and may be input for diagnostic tools. The study also cropped patches to a size of  $224 \times 224$  pixels, contributing to accurate diagnosis and nuanced interpretation of microscopic observations. A sliding window technique was used to analyze microscopic images, generating patches of suspicious regions. A horizontal reflection data augmentation approach was applied to enhance dataset diversity and robustness. Patches of distinct classes were kept separate for feature extraction and model accuracy. Subsequently, normalization ensures consistency in pixel intensities through contrast normalization, subtracting intensity impacts, and minimizing illumination variations. Together, these processes optimize the dataset for accurate analysis and facilitate standardized comparisons within our study's context.

## 4 | DEEP-LEARNING-BASED FEATURE LEARNING

Breast cancer is prevalent in women, requiring diagnostic procedures to identify benign and malignant lesions. The study proposes a breast cancer histopathology image recognition method based on three-channel low-dimensional features, addressing insufficient feature utilization and high-dimensional features' potential to increase calculation time. The model integrates methods like GLCM, Wavelet Transform, Gabor, and HOG, each contributing to its effectiveness, addressing the issue of increased redundancy and reduced resolution in breast cancer histopathology. The proposed dataset independently considers image-level and patient-level breast cancer histopathological image recognition, addressing insufficient feature utilization and potential time-consuming high-dimensional features. The proposed methods enhance breast cancer image accuracy and robustness but also present challenges like increased computational demand and increased sensitivity to image quality variations. This study aimed to improve computational efficiency and enhance the model's robustness to diverse image data variations, thereby enhancing its applicability and reliability in real-world diagnostic settings.

### 4.1 | Gray level co-occurrence matrix

Haralick et al. (1973) introduced a pioneering method for quantifying image texture using a gray level Co-occurrence matrix (GLCM). This technique analyzes spatial relationships between gray-valued pixels to extract texture features. By calculating the occurrence of pixel pairs at specified distances, the GLCM unveils intricate texture details. The GLCM method generates co-occurrence matrices that provide a nuanced representation of complex textural patterns in microscopic images. Its relevance lies in its application in medical diagnostics, where it extracts detailed textural information to identify subtle variations in tissue structure, crucial for accurate diagnosis and study of

diseases like breast cancer. The detailed textural analysis facilitated by GLCM enhances the diagnostic capabilities of computational models in distinguishing between benign and malignant tissue patterns. The research aims to optimize GLCM with advanced feature extraction techniques like Wavelet Transform, Gabor filters, and HOG to enhance the accuracy and robustness of a model for comprehensive analysis of histopathological images, thereby expanding its applicability in various diagnostic settings.

## 4.2 | Wavelet transform

The study employs a two-dimensional wavelet transformation to derive texture features from microscopic images (Mahmood, Li, Pei, Akhtar, Imran, & Yaqub, 2021; Song, Zou, & Chang, 2017). This transformation technique, widely used for texture analysis, plays a crucial role in capturing frequency changes across various scales and orientations within the image. Specifically, our approach focuses on extracting the energy of high-frequency components, which are represented by the detailed sub-images derived from the Wavelet Transform. The research focuses on high-frequency details in microscopic image analysis to improve breast cancer detection accuracy. The *coif5* wavelet function is selected for its favorable attributes, including symmetry, support length, and vanishing moments, making it well-suited for assessing energy distribution along the frequency axis. The study optimizes Wavelet Transform for computational efficiency while preserving its efficacy in capturing essential textural features. The goal is to strike a balance between computational demands and analytical accuracy, enhancing the model's applicability in real-world clinical settings. This approach is expected to significantly contribute to microscopic image analysis and improve breast cancer detection accuracy for clinical practitioners.

## 4.3 | Gabor

The research employed the Gabor feature extraction method, a crucial technique in microscopic image analysis, to comprehend intricate texture details. Similar to the two-dimensional reflective region of the human cerebral cortex, the Gabor filter can analyze images across multiple frequencies and orientations, capturing localized frequency information and exhibiting strong direction selectivity. The Gabor feature extraction method is a powerful tool in histopathology image analysis, enhancing classification outcomes and understanding microscopic images. It involves creating customized Gabor filters that match specific frequencies and bandwidths for specific textures. These filters amplify the energy of textures aligned with their frequencies while reducing the energy associated with unrelated textures (Alom et al., 2019; Spanhol et al., 2016). This method captures the nuances of texture patterns within microscopic images, providing a profound understanding of the intricate texture characteristics. The subsequent phase of our methodology encompasses the extraction of texture features across multiple dimensions and orientations. This comprehensive

approach provides a profound understanding of the intricate texture characteristics present in histopathology images. Moreover, it significantly aids in the analysis and diagnosis of diseases, particularly in the context of breast cancer detection. The Gabor feature extraction method is a powerful tool in histopathology image analysis, improving classification outcomes and understanding microscopic images. This research enhances disease classification accuracy and contributes to a deeper understanding of textural patterns in histopathological images, furthering the capabilities of computational models in medical diagnostics, especially in breast cancer detection and diagnosis.

## 4.4 | Histogram of oriented gradient

The study leverages the HOG method, renowned as a texture feature descriptor, to facilitate object detection. The histogram of oriented gradient (HOG) technique captures the target object's edge characteristics, local image appearance, and geometry intricacies. While traditionally employed in applications such as pedestrian detection and facial recognition, HOG may encounter challenges when applied to images with intricate texture information, as noted in prior research (Zhang et al., 2020; Zou et al., 2022). Nevertheless, its utility in object detection remains invaluable. The procedural workflow contains various stages, including Gamma-correction, computation of horizontal and vertical gradients, partitioning images into discrete cells, tabulating cell-level attributes, and subsequent amalgamation of block features to engender the final image's distinctive features. The HOG method follows a procedural workflow that includes gamma-correction, computation of horizontal and vertical gradients, partitioning images into discrete cells, tabulating cell-level attributes, and amalgamating block features to generate distinctive representations of the image's texture characteristics. The study incorporates HOG to enhance object detection capabilities in complex visual environments, particularly in breast cancer detection. HOG captures critical features, aiding in the accurate identification of objects of interest, thereby improving the effectiveness of the computational model. This approach is widely recognized for its efficacy in pedestrian detection and facial recognition.

## 4.5 | Breast cancer microscopic image recognition model based on low-dimensional multi-channel features

This research presents a novel approach to breast cancer microscopic image recognition, utilizing low-dimensional multi-channel imaging. The study addresses the challenge of underutilized features in recognition and the computational overhead associated with high-dimensional features. The methodology involves segmenting the original image into R, G, and B channels, extracting GLCM, wavelet, and Gabor features, and combining them with HOG features. DL-based is employed for recognizing breast cancer microscopic images. Despite a maximum dimension of 264 for the three-channel features, this study demonstrates their efficacy by achieving comparable results to four

### Algorithm 1 Breast cancer microscopic image recognition

- 1: **procedure** Image Recognition ( $X_{\text{train}}, Y_{\text{train}}, X_{\text{test}}, Y_{\text{test}}$ )
- 2: **Input:** Training samples  $X_{\text{train}}, Y_{\text{train}}$ , test samples  $X_{\text{test}}, Y_{\text{test}}$
- 3: **Output:** Image-level accuracy, patient-level accuracy, sensitivity, specificity, precision,  $F1\_score$
- 4: **Step 1:** Separate the training and test samples into R, G, and B channels
- 5: **Step 2:** Employ diverse feature extraction techniques to derive channel-specific features
- 6:  $F_{\text{train}_R}, F_{\text{train}_G}, F_{\text{train}_B}, F_{\text{test}_R}, F_{\text{test}_G}, F_{\text{test}_B}$
- 7: **Step 3:** Combine features from the three channels
- 8:  $F_{\text{train}} = [F_{\text{train}_R}, F_{\text{train}_G}, F_{\text{train}_B}]$
- 9:  $F_{\text{test}} = [F_{\text{test}_R}, F_{\text{test}_G}, F_{\text{test}_B}]$
- 10: **Step 4:** Input  $F_{\text{train}}, Y_{\text{train}}$  and  $F_{\text{test}}, Y_{\text{test}}$  into SVM for recognition.
- 11: **Step 5:** Calculate image-level accuracy, patient-level accuracy, sensitivity, specificity, precision,  $F1\_score$
- 12: **Returns:** Image-level accuracy, patient-level accuracy, sensitivity, specificity, precision,  $F1\_score$
- 13: **end procedure**

other feature extraction techniques. Remarkably, the extracted low-dimensional features, averaging values from the three channels, sufficiently characterize the original  $700 \times 460$  pixel image, attaining a successful recognition outcome. Algorithm 1 represents the pseudo-code of breast cancer microscopic image recognition model based on three-channel low-dimensional features.

## 5 | PROPOSED ARCHITECTURE FOR BREAST CANCER MICROSCOPIC IMAGE CLASSIFICATION

In recent studies, deep learning has been used to analyze microscopic images to identify diverse disease subgroups. This model has shown success in disease diagnosis by enhancing decision-making in complex diagnostics by extracting and analyzing medical image properties. This approach is particularly beneficial in managing large data volumes that traditional methodologies often struggle with effectively. Despite the significant progress made in managing large datasets, challenges persist due to the limited availability of image data. Small datasets and resizing needs of pre-trained models can hinder precise classification, leading to potentially unreliable outcomes. Furthermore, the complexity of cancerous and healthy cell image classification and the limitations of models trained on non-medical images present additional difficulties. A promising approach could be developing models from

scratch, explicitly incorporating images of cancerous and healthy cells to enhance classification accuracy. CNN has swiftly become the preferred approach for analyzing medical images due to its exceptional accuracy in image recognition. A standard CNN architecture comprises an input layer, a convolutional layer, a pooling layer, a fully connected layer, and an output layer. In 1998, Lecun et al. (1998) effectively utilized LeNet-5 for handwritten digit recognition, but CNN received limited attention. However, the landscape changed dramatically in 2012 with the introduction of AlexNet by Krizhevsky et al. (2012), which secured the ILSVRC (classification) championship and sparked the accelerated growth of CNN. Following AlexNet, in 2014, Simonyan and Zisserman (2014) introduced VGGNet, a more sophisticated version of AlexNet. The same year saw the emergence of GoogLeNet by Szegedy et al. (2016), based on Inception-v1. The Inception structure expanded the network's dimensions, leading to improved performance. Subsequent iterations, including Inception-v2 (Ioffe & Szegedy, 2015), Inception-v3 (Szegedy et al., 2016), and Inception-v4 (Szegedy et al., 2016), further refined the efficacy of GoogLeNet. In 2015, He et al. (2016) introduced ResNet, introducing the concept of the residual unit as a groundbreaking network structure. Later, a new variation of the residual unit concept was proposed (Huang et al., 2016). In 2017, Huang et al. (2017) presented DenseNet, built upon dense blocks, significantly enhancing network performance and leading to further advancements. Additionally, Szegedy et al. (2016) combined Inception with the residual unit, proposing Inception-ResNet-v1 and Inception-ResNet-v2.

### 5.1 | Convolutional neural network

This study aimed to design a robust deep-learning architecture to extract the in-depth features for all the microscopic images and compute malignant lesion probability. Large image patches retain valuable information to classify pixels associated with distinct breast tissues accurately. The current lightweight model encompasses nine weighted layers, out of which three convolution layers memorize the full region of the microscopic image for feature mapping (extractions) interleaved with rectified linear unit (ReLU) activation and followed by max-pooling layers to obtain vector representation from extracted deep-feature to reduce the data capacity or perform data reduction, and followed by a dense layer (fully connected layers) and softmax activation layer, used for tumor classification by reducing the overfitting problem. Convolutional layers also sequentially downsize the dimensional resolution of microscopic images while expanding their feature maps' depth. The sequence of convolutional transformations can produce much lower-dimensional and more convenient spectacles of images than what could feasibly be handcrafted. However, the first convolution layer is followed by the max-pooling layer, and the same pattern is repeated for the subsequent three layers. This architecture's motivation is using  $3 \times 3$  kernel size of all convolution layers and  $2 \times 2$  max-pooling of all convolution layers. The stride of size one was used in all convolution layers. The distribution of input in each layer has been changing in the training process, making the training process

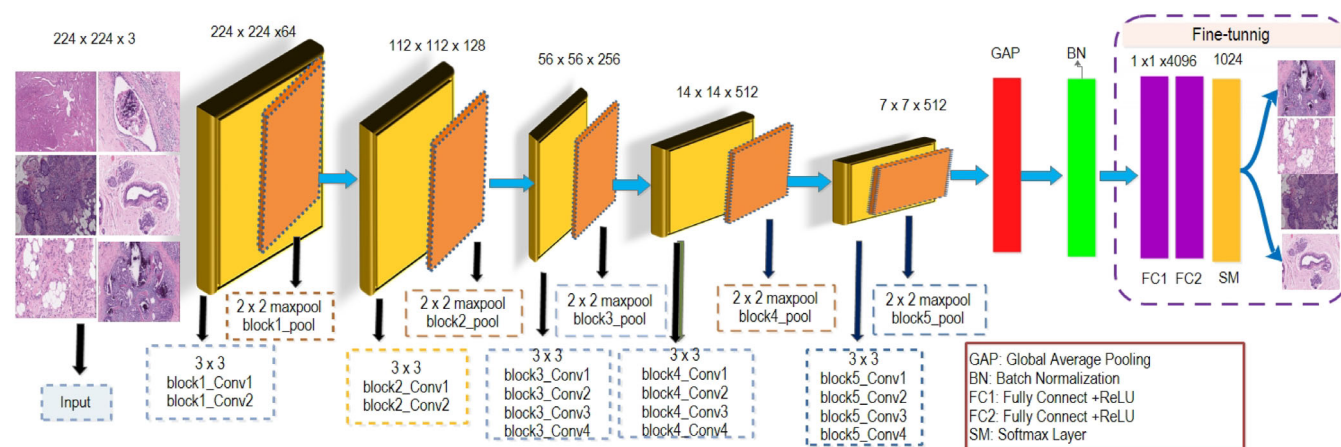


**FIGURE 4** The mVGGNet16 architecture, which includes 16 layers, is presented. In fully trained mVGGNet16 models, all five blocks are trainable. GAP and BN are incorporated, followed by two fully connected layers (FC1, FC2) and SoftMax. The weights are optimized during model training to facilitate learning for specific tasks.

more difficult. It is imperative to add a normalization layer after the convolution layer to make the distribution of the input data of each layer more consistent. To reduce the feature dimension calculations, accelerate the convergence speed, and increase the nonlinearity of the network, an activation function & ReLU function is exercised after the pooling layer corresponding to Conv1, Conv2, and Conv3. The reduction of neurons in a fully connected layer dramatically reduces the storage space of the network model. However, we changed the weights of the dense layers of the proposed model and activated them with the concept of transfer learning for pattern recognition, feature mapping, and feature classification.

## 5.2 | Transfer learning-based architecture

In the realm of medical image analysis, transfer learning emerges as a highly advantageous approach for augmenting the efficacy of deep learning models (Iqbal, Qureshi, Li, & Mahmood, 2023). The process entails initializing a model using pre-trained parameters derived from an extensive dataset, such as ImageNe, and then fine-tuning the target dataset, such as BreakHis and BACH datasets. By leveraging knowledge from pre-training, the model learns essential features related to color and edges, leading to improved classification results on the target dataset. Obtaining substantial training data in medical image analysis can be challenging. To tackle this issue, this study employs data augmentation techniques that expand the dataset, balancing its distribution and mitigating overfitting. By combining transfer learning and data augmentation, this study effectively increases their dataset size and improves the effectiveness of medical image analysis (Mahmood, Li, Pei, & Akhtar, 2021). Feature extraction and fine-tuning are two prominent methods for transfer learning that have garnered widespread recognition in deep learning. Feature extraction utilizes pre-trained models trained on standard datasets.

This study utilized a transfer learning approach with pre-trained models, including mVGGNet16, EfficientNetV2B3, ResNet101V2, and

CN2XNet, to enhance breast cancer histopathological image classification. To adapt these models, we adjusted input layers to fit image dimensions, customized output layers for binary classification, and fine-tuned convolutional layers to capture cancerous tissue patterns. Additionally, we optimized network performance with modifications of the last layers of each model with GAP, BN, FC1 and FC2, and SoftMax layers, resulting in accurate feature extraction and classification. Detailed discussions on the structure of these models are anticipated in the subsequent section.

### 5.2.1 | Modified version of VGGNet16

Simonyon and Zisserman (2014) suggest that a VGGNet16 network has 13 convolutional layers and 03 fully connected layers. As part of our research, we introduced modifications to the VGGNet-16 model by integrating the initial 13 layers of the VGGNet-16 model and incorporating global average pooling, flattening, and a dense layer that utilizes the ReLU activation function, as depicted in Figure 4. This study uses a small convolution kernel  $3 \times 3$  instead of a  $5 \times 5$  convolution kernel. It uses the stack of small convolution kernels to achieve the same receptive field effect as the large convolution kernel. At the same time, the amount of calculation is reduced. Although the performance of CNN is excellent, its limited local receptive field limits its performance. The modified VGGNet-16 model comprised 143,667,240 parameters, of which 138,357,544 were trainable and 5,309,696 were not. The features of mVGGNet-16 are divided into three levels, with the first level consisting of VGG's extracted features, which include 18 feature sets with 64, 128, 256, and 512 Convolution features each. In the second level, the feature set is labeled Conv, where  $n$  is the feature module, and there are five convolution feature sets with 128, 256, 1024, and 2048 features each. The feature set at the third level comprises a convolution feature set and a fully connected feature set, with the convolution feature set containing 5504 features and the fully connected feature set containing 8192 features.

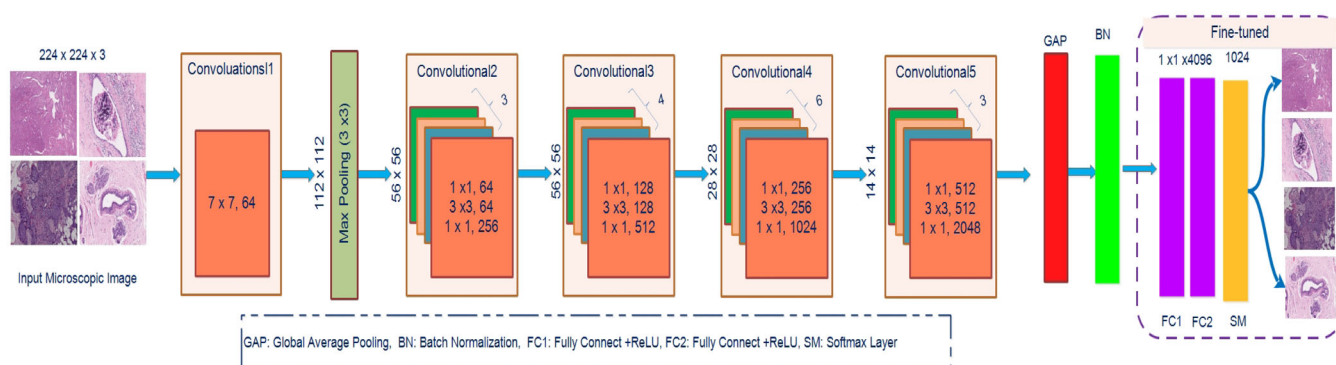


**FIGURE 5** A cutting-edge ResNet101V2 architecture incorporates GAP and BN to improve its effectiveness. Two fully connected (FC1, FC2) and output layers are included to enhance the architecture's performance further.

### 5.2.2 | EfficientNetV2B3

The study introduces EfficientNetV2B3, an enhanced version of the original EfficientNetV1 model developed by Tan and Le (2021). This architecture uses neural architecture search (NAS) techniques to find an optimal compound scaling factor, balancing network width, depth, and resolution. This balance enhances the network's understanding of intricate features and streamlines training across various tasks. EfficientNetV2B3 differs from traditional models by incorporating width and resolution scaling, enabling the model to capture nuanced patterns and details. It is particularly effective in handling larger datasets due to increased resolutions. The research also uses transfer learning techniques to improve model performance, incorporating GAP and BN layers to classify microscopic images. The FC layer architecture is linked to the number of classes associated with the network's final transferred layers and intermediate stages, enabling the training of a robust network with fewer parameters and efficient use of computational resources.

### 5.2.3 | ResNet101V2

ResNets (He et al., 2016), a foundational neural network for computer vision tasks, have revolutionized deep learning by enabling the successful training of profound networks with over 101 layers. This breakthrough was made possible by introducing skip connections, allowing for the training of over 23 million parameters. This study restructured the architecture by fine-tuning the final block layers, replacing top layers with GAP, BN, two fully connected, and Softmax layers for diagnostic class detection, as depicted in Figure 5. The input images were resized to achieve a dimension of  $224 \times 224$  for seamless integration with the model. The study employed the Adam optimizer with a  $Lr^{-3}$  learning rate during training. The identity function is crucial for establishing parameter mapping that preserves original values without modifications. The output generated from the ultimate layer is integrated with the preceding layer.

### 5.2.4 | CN2XNet

CN2XNet is a powerful deep-learning model with proficiency in multiple computer vision applications, including object detection and segmentation. This model utilizes convolutional layers enriched with residual connections, group normalization, and efficient channel attention strategies. Its training on an extensive dataset enhances its remarkable precision and generalization ability. CN2XNet can be seamlessly tailored for specific tasks and serves as an effective feature extractor. Its compact design and computational prowess make it ideal for mobile deployment and embedded systems with constrained processing capabilities. The CN2XNet model encompasses 28,021,092 parameters, of which 28,019,556 are trainable and 1536 are fixed.

### 5.2.5 | DenseNet-121

DenseNet, a relatively novel architecture, has accomplished notable feats in the ImageNet classification challenge while operating with fewer parameters (Huang et al., 2017). It can be a complex task to train CNNs with numerous convolutional layers due to the issue of vanishing gradients. DenseNet effectively tackles this problem by ensuring each layer is connected to all prior layers, enhancing gradient flow and boosting classification precision. Instead of having  $L$  connections in a typical  $L$ -layer network, DenseNet boasts about  $L(L+1)/2$  connections, facilitating dense links between initial and subsequent layers. Each following layer gets inputs from the initial layer and the preceding layer, but the output of each layer remains consistent. However, as the network deepens, DenseNet encounters specific difficulties. For instance, in a 10-layer network, the tenth layer accepts input from all the previous nine layers' feature maps, potentially leading to operational challenges. To overcome the issue, fixed output feature maps are allocated for each layer, and compact blocks are created. Every dense block houses a certain number of layers, and its output is transferred to a transition layer that uses a bottleneck-like mechanism to downsize feature maps. This transition layer usually implements the Maxpool operation for feature map size reduction.

The study introduces DenseNet-121, an architecture featuring four dense blocks and 121 weighted layers. The critical feature is dense connectivity, which establishes direct connections between each layer and all subsequent layers. The architecture is fine-tuned through transfer learning, incorporating GAP, BN, FC1, FC2, and SoftMax layers. The dense connectivity facilitates efficient feature extraction by concatenating feature maps, removing the necessity for manual feature extraction and ultimately enhancing the network's performance.

### 5.2.6 | Squeeze-and-excitation network

Squeeze-and-excitation network (SqE-Net), standing for Squeeze-and-Excitation Network, emerged as the ImageNet 2017 classification challenge champion. This network integrates a SqE module to refine its structure, determining the importance of each feature channel through squeezing and excitation techniques. The SqE module amplifies crucial features while diminishing less relevant ones. The SqE module initiates its three-step process with compression, transforming feature channels into individual scalar values. The following excitation phase utilizes a threshold mechanism and a series of operations, encompassing an FC layer, ReLU activation, another FC layer, and concluding with a Sigmoid function. This progression aids the network in identifying channel relationships. During the reweighting phase, the module recalibrates weights derived from the excitation process, prioritizing more prominent features. The SqE module then adjusts the initial features by performing element-wise multiplication using these weights, effectively scaling the features based on their channel-wise significance. This innovative method adaptively modifies

feature maps, evaluating channel importance, emphasizing key features, and minimizing less crucial ones, thus sharpening the network's focus on vital dataset components.

### 5.3 | Proposed hybrid SqE-DCCConvNet architecture

The proposed SqE-DCCConvNet architecture, as depicted in Figure 6, is a refined version of the original DenseNet. In the proposed variant, a  $3 \times 3$  convolutional squeeze-and-excitation (SqE) unit, derived from the SqE-DCCConvNet framework, is incorporated within every dense section. A SqE unit is strategically positioned ahead of each dense and transition layer. SqE-DCCConvNet is a structure for deep learning that contains multiple internal layers. The proposed architectural blueprint captures and stores vital data across feature channels, ensuring uniform information dissemination throughout the network. By recognizing the significance of individual features, the design can emphasize essential attributes, minimize secondary ones, and fluidly customize the responses of feature channels. SqE-DCCConvNet is distinguished from conventional DenseNet models by the following novel enhancement.

1. The SqE module, after convolution in each block, improves weight recalibration across feature channels, enabling the network to assign more weight to salient features and less weight to less vital ones.
2. Implementing a max pooling layer immediately after initial convolution reduces feature loss in lower layers, a potential side effect of pooling, and enhances the model's overall potency by retaining early-stage feature information.

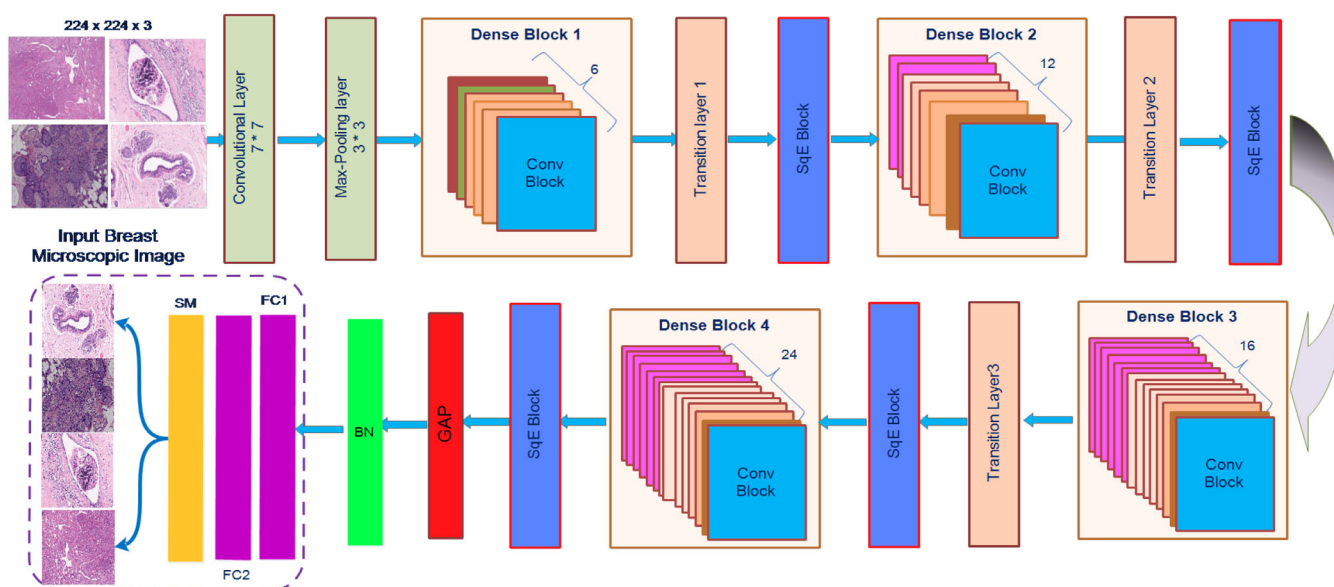


**FIGURE 6** Depicts the proposed SqE-DCCConvNet includes DenseBlock, Transition layers, GAP, BN, FC1, FC2, and SoftMax layers, leading to a substantial improvement in the network's performance for breast cancer classification.

**TABLE 3** Optimal configurations of hyperparameters combined with data augmentation for the suggested models.

| Hardware                  | Software                        |
|---------------------------|---------------------------------|
| Memory capacity 32 GB     | Python 3.7                      |
| GPU (GeForce GTX 1080 Ti) | NumPy 1.24                      |
|                           | PyTorch 3.7                     |
|                           | TensorFlow 2.11                 |
|                           | Keras 2.11                      |
| Configuration             | Value                           |
| Number of iterations      | 100                             |
| Step per iterations       | 100                             |
| Batch size                | 32                              |
| Activation function       | Adam                            |
| Learning rate             | 0.0001                          |
| Activation function       | ReLU                            |
| Momentum                  | 0.9                             |
| Convolution               | 3 × 3 with stride 1             |
| Dropout                   | 0.5                             |
| Loss function             | Binary Cross entropy            |
| Pooling                   | 2 × 2 max-pooling with stride 2 |
| Weight decay              | 0.0005                          |
| Architecture              | Fine-tuned and fully trained    |

SqE-DCCConvNet combines DenseNet's dense connectivity with dynamic feature recalibration, resulting in a more efficient and adept deep learning model. The entire process of breast microscopic image classification is depicted in [Algorithm 2](#).

## 6 | RESULT AND DISCUSSION

### 6.1 | Experimental set

The study aimed to enhance breast microscopic image classification accuracy using a comprehensive experimental approach. Preprocessing was performed to ensure image consistency, and data augmentation methods were used to handle noise and enhance model accuracy. Real-time data augmentation was implemented to mitigate overfitting during model training. The study used an initial learning rate of  $Lr^{-3}$  for network training and a stochastic gradient descent technique with a batch size of 32 for optimal loss function optimization. The dataset was randomly shuffled to prevent unintentional pattern learning. A momentum factor of 0.9 was applied to facilitate convergence towards the global minimum while avoiding local minima. Keras (Chollet, 2015), a freely accessible deep learning framework, is employed in conjunction with TensorFlow (2021) as the base framework for importing and modifying the pre-trained structures using the ImageNet repository. The hardware configuration used was an Intel Core™ i7-4590 CPU, 32GB memory, and NVIDIA GTX 3080 Ti graphics card. The Table 3 depicted the optimal configuration of hyperparameters for the suggested models.

### 6.2 | Evaluation measures

Breast cancer microscopic image classification relies on specific metrics to assess its performance and reliability. Accuracy measures the proportion of images correctly classified as benign or malignant, indicating the model's effectiveness in diagnosis. Sensitivity measures the model's ability to identify malignant cases, preventing potential cancers from being overlooked. Specificity evaluates the model's proficiency in identifying benign cases and preventing unnecessary alarms and medical interventions. Precision indicates the likelihood of a case classified as malignant being truly malignant. The F1 score balances precision and recall, providing a holistic view of the model's performance. The Area Under the Curve measures the model's ability to discriminate between benign and malignant cases. The Confusion Matrix provides a detailed breakdown of the model's predictions. The study assesses the performance of a proposed model using parameters to evaluate its strengths and limitations in real-world applications, aiding researchers and practitioners in optimizing performance for desired outcomes. The computation formula for evaluation parameters is presented in Equations (3)–(7).

$$\text{Accuracy (ACC)} = \frac{TP + TN}{TP + TN + FP + FN}, \quad (3)$$

$$\text{Sensitivity (SEN)} = \frac{TP}{TP + FN}, \quad (4)$$

$$\text{Recall} = \frac{T_p}{T_p + F_N}, \quad (5)$$

$$\text{Precision} = \frac{T_p}{T_p + F_P}, \quad (6)$$

$$F1 \text{ score} = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}}. \quad (7)$$

TP represents the number of predicted positive classes, while TN represents the number of predicted negative classes, and FN represents the number of predicted positive classes.

### 6.3 | Comparative analysis of low-dimensional multi-channel feature extraction techniques

The study presents a breast cancer microscopic image recognition method using low-dimensional multi-channel features to address the insufficient utilization of breast cancer microscopic features. The study uses four feature extraction methods to extract features from three image channels, fuse them, and implement breast cancer histopathology image recognition using SVM. The results show that the recognition effect of GLCM can exceed 90% at both the image and patient levels, with three-channel features being significantly superior to gray-scale features. The R channel significantly impacts recognition results for 40×, 100×, and 200× images, while the B channel significantly affects 400× recognition results. The study evaluates performance, specificity, accuracy, and FScore using Wavelet transform, Gabor, and

**Algorithm 2 SqE-DCCConvNet training**

```

1: procedure SqE-DCCConvNet Training (Training data, Network depth, Configurations)
2:   Initialize: Network weights and epoch  $\leftarrow 0$ 
3:   while not converged do
4:     for each input image in Training data do
5:       Pass through initial convolutional layer
6:       for each Dense Block in the network do
7:         Concatenate outputs of preceding layers
8:         Process through BN, ReLU, and Conv.
9:         SqE Module:
10:        Squeeze: Apply Spatial Pyramid Pooling
11:        Excitation: Process through two FC layers with ReLU and Sigmoid activations
12:        Scale: Multiply feature maps by Excitation output
13:        Concatenate output with input to current Dense Block
14:      end for
15:      Process through Transition Layer using BN, ReLU,  $1 \times 1$  Convolution, and  $2 \times 2$  average pooling
16:      Process through global average pooling and FC layer with softmax
17:      Compute loss and backpropagate to update weights
18:    end for
19:    Increment epoch
20:  end while
21: end procedure

```

**TABLE 4** Microscopic image recognition results of different gray-level features.

| Feature | Magnification | IRR (%)    | PRR (%)    | SEN (%)    | SPC (%)     | ACC (%)     | F score (%) |
|---------|---------------|------------|------------|------------|-------------|-------------|-------------|
| GLCM    | 40×           | 94.1 ± 2.1 | 93.4 ± 2.7 | 94.9 ± 1.5 | 91.7 ± 5.5  | 97.0 ± 2.3  | 95.9 ± 1.7  |
|         | 100×          | 92.6 ± 3.0 | 91.7 ± 3.8 | 95.6 ± 4.8 | 83.0 ± 5.6  | 94.5 ± 1.5  | 95.0 ± 2.4  |
|         | 200×          | 94.6 ± 2.0 | 94.2 ± 2.8 | 97.1 ± 3.4 | 86.3 ± 7.7  | 95.8 ± 2.0  | 96.4 ± 1.5  |
|         | 400×          | 90.9 ± 2.1 | 91.4 ± 2.1 | 91.8 ± 4.0 | 89.0 ± 7.3  | 95.7 ± 3.0  | 93.6 ± 1.8  |
| Wavelet | 40×           | 80.9 ± 4.2 | 80.0 ± 7.1 | 97.6 ± 4.2 | 30.9 ± 28.0 | 80.7 ± 8.0  | 88.3 ± 4.8  |
|         | 100×          | 80.3 ± 3.6 | 80.2 ± 1.0 | 97.0 ± 4.6 | 30.2 ± 14.5 | 80.8 ± 4.3  | 88.0 ± 2.5  |
|         | 200×          | 78.9 ± 4.4 | 76.5 ± 3.3 | 97.3 ± 3.6 | 22.7 ± 16.6 | 79.4 ± 4.2  | 87.4 ± 2.8  |
|         | 400×          | 76.0 ± 2.2 | 76.7 ± 1.4 | 89.6 ± 4.3 | 39.1 ± 12.3 | 80.2 ± 3.9  | 84.5 ± 1.7  |
| Gabor   | 40×           | 86.1 ± 4.4 | 84.8 ± 4.8 | 97.0 ± 1.3 | 53.7 ± 21.0 | 86.4 ± 6.9  | 91.2 ± 3.2  |
|         | 100×          | 89.9 ± 2.1 | 89.7 ± 2.7 | 93.4 ± 2.8 | 80.6 ± 9.7  | 93.3 ± 3.7  | 93.3 ± 1.3  |
|         | 200×          | 91.0 ± 2.6 | 89.6 ± 3.9 | 97.1 ± 1.8 | 72.9 ± 11.7 | 91.5 ± 3.7  | 94.2 ± 1.7  |
|         | 400×          | 88.9 ± 2.8 | 87.8 ± 2.6 | 96.9 ± 1.7 | 67.2 ± 6.6  | 88.9 ± 3.0  | 92.7 ± 1.9  |
| HOG     | 40×           | 76.5 ± 4.4 | 76.8 ± 7.2 | 95.4 ± 2.9 | 23.1 ± 35.7 | 78.6 ± 10.2 | 85.9 ± 4.7  |
|         | 100×          | 76.0 ± 4.0 | 75.5 ± 2.6 | 95.1 ± 5.3 | 19.7 ± 20.5 | 78.2 ± 5.8  | 85.5 ± 2.5  |
|         | 200×          | 76.8 ± 3.3 | 76.2 ± 2.1 | 93.3 ± 3.3 | 27.1 ± 12.4 | 79.6 ± 4.3  | 85.8 ± 2.3  |
|         | 400×          | 77.8 ± 3.2 | 78.2 ± 1.7 | 89.6 ± 4.2 | 46.9 ± 16.5 | 82.2 ± 5.9  | 85.5 ± 1.9  |

HOG. GLCM performed exceptionally well at image and patient levels, with the highest recognition accuracy at 200×

Despite the recognition accuracy being greater than 82%, more recognition time is required due to the high feature dimension. Gabor

and HOG classification performance was inferior to other feature extraction techniques. The difference in feature distribution derived from various feature extraction methods explains the results. The study focuses on recognizing grayscale features in microscopic images

| Architecture     | ACC (%) | PRE (%) | F score (%) | REC (%) | AUC (%) | SEN (%) |
|------------------|---------|---------|-------------|---------|---------|---------|
| mVGGNet16        | 95      | 94      | 94          | 94      | 94      | 95      |
| ResNet101V2      | 96      | 95      | 95          | 95      | 96      | 96      |
| EfficientNetV2B3 | 95      | 96      | 97          | 95      | 96      | 96      |
| CN2XNet          | 97      | 96      | 96          | 97      | 97      | 97      |
| SqE-DCCovNet     | 98      | 99      | 98          | 98      | 98      | 99      |

| Architecture     | ACC (%) | PRE (%) | F score (%) | REC (%) | AUC (%) | SEN (%) |
|------------------|---------|---------|-------------|---------|---------|---------|
| mVGGNet16        | 94      | 94      | 93          | 93      | 94      | 94      |
| ResNet101V2      | 95      | 96      | 96          | 95      | 96      | 96      |
| EfficientNetV2B3 | 96      | 96      | 97          | 96      | 97      | 97      |
| CN2XNet          | 97      | 98      | 98          | 97      | 98      | 98      |
| SqE-DCCovNet     | 99      | 98      | 99          | 98      | 99      | 99      |

using multiple techniques. The recognition accuracy of Wavelet and HOG does not vary significantly, but GLCM does. Gabor three-channel features are superior to grayscale features, with most methods increasing recognition accuracy by over 10% at image and patient levels. The color channel's significant role in recognition remains unknown. The fusion of GLCM with other features enhances recognition effects for 40× and 100× compared to the separate method, while the accuracy of 200× and 400× is marginally reduced. The combination of GLCM improves image-level accuracy, but the recognition accuracy of 40× and 100× is marginally lower than that of GLCM. Table 4 highlights the optimal values of each evaluation index. GLCM achieved the highest image-level recognition accuracy of 94.1%, while wavelet achieved the highest patient-level recognition accuracy of 80.9%. GObar came in second with 86.1% and a patient-level accuracy of 84.8%. For 100×, the image-level and patient-level accuracy of GLCM, wavelet, Gabor, and HOG were 92.6%, 80.3%, 86.1%, 89.9%, 76.0%, 91.7%, 80.2%, 89.7% and 75.5%. GLCM achieved the highest image-level accuracy of 92.6%, 0.3% higher than Gobar, followed by wavelet. GLCM obtained the highest image-level and patient-level accuracy for 400×, 90.9%, and 91.4%, respectively. GLCM and Gabor performed exceptionally well at both image and patient levels, followed by Wavelet. Table 4 reveals that while all features have high sensitivity, their specificity is low, particularly for wavelet and HOG features. These features have a specificity of less than 60%, with Gabor's at 40× at 53.7%. This indicates that these methods often misidentify benign samples as malignant, increasing the misdiagnosis rate and causing mental stress in patients.

## 6.4 | Breast lesion classification based on deep learning paradigm

The study aims to develop transfer learning-based models, including mVGGNet16, EfficientNetV2B3, ResNet101V2, and CN2XNet, and optimized fused methods SqE-DCCovNet to distinguish breast cancer pathology images accurately. Ablation experiments were

**TABLE 5** Performance Comparison of proposed architectures, namely mVGGNet16, ResNet101V2, EfficientNetV2B3, CN2XNet, and SqE-DCCovNet based on BACH data for the robust classification of BACH microscopic images.

**TABLE 6** Performance comparison of proposed architectures, namely mVGGNet16, ResNet101V2, EfficientNetV2B3, CN2XNet, and SqE-DCCovNet based on BreakHis data for the robust classification of BreakHis microscopic image.

conducted on the BreakHis dataset to determine the function and significance of each proposed component. The model has been evaluated against four well-known CNN-based architectures in an unbiased manner, as observed in Table 5 based on BACH dataset and Table 6 based on BreakHis dataset. The DCNN algorithms were fine-tuned using a transfer learning approach, obtaining local and global features through low/high-level learning. The model's performance was significantly improved by iterating over various hyperparameter configurations during training.

This study investigates the influence of freeze layers on the transmission of the mVGGNet16 model from the ImageNet dataset to breast histopathological images. The study revealed that incorporating transfer fusion and global average pooling enhanced performance, with accuracy rates of 94% on both the BreakHis and BACH datasets. However, suspending additional convolutional layers reduced the model's sophisticated features, making them less suitable for breast histopathological images. This is due to the interaction between convolutional neural network layers and their layered layering. Freezing specific strata can impair migration outcomes. The model initialized with random parameters had an accuracy rate of 87%, and the transferred model showed a significant improvement in classification capabilities compared to the non-transferred model. On the other hand, the ResNet101V2 model significantly improves image classification accuracy on the BreakHis dataset, with an accuracy rate of 95%. The mVGGNet16 model's accuracy increases by 0.157–0.9424, while the ResNet101V2 model's accuracy rate is 95%. Both models show significant enhancements by replacing the pooling layer with global average pooling, as depicted in Figure 7a,b. The mVGGNet16 model outperforms conventional pooling by 0.157, while the ResNet101V2 model improves by 0.53%–96%, surpassing the traditional performance of pooling. However, the model's block-by-block freezing effect during migration from the ImageNet dataset to the BACH dataset results in a decrease in classification accuracy rate, indicating negative migration. Besides that, the study uses the EfficientNetV2B3 network for breast cancer microscopic image classification due to its robust performance in minimizing error rates and false negatives while enhancing model

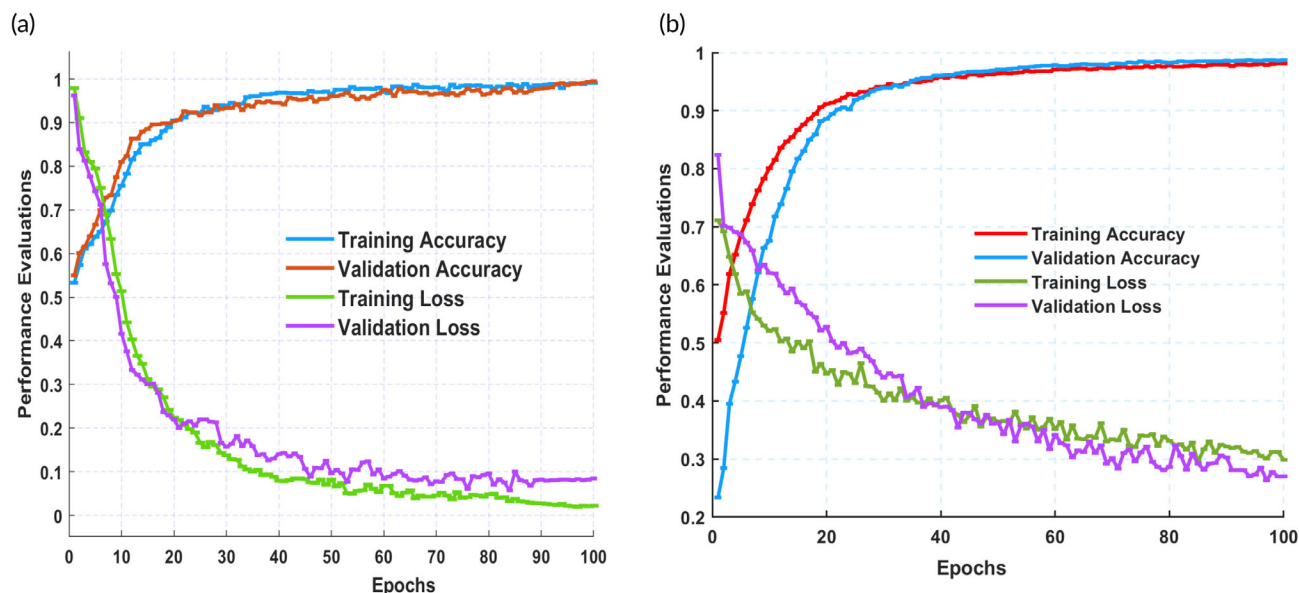


**FIGURE 7** The figure depicts the suggested system's precision and cross-entropy loss. The ascending plot depicts the accuracy of the presented models, whereas the descending plots depict the loss values on the training and validation datasets (BreakHis). The similarity between the training and testing curves indicates effective model training. The diagram illustrates two system variations: (a) CN2XNet architecture and (b) SqE-DCCConvNet architecture.

generalization. Key parameters were optimized through extensive tests, resulting in rapid training and satisfactory network convergence. The EfficientNetV2B3 model showed high accuracy rates of 96% on BreakHis breast cancer images, with an impressive Area Under the Curve (AUC) score of 0.978. This model outperformed lightweight neural network and deep learning models, highlighting its convergence, speed, and accuracy effectiveness.

The CN2XNet model was compared to other advanced classification methods on two datasets. The results showed that the CN2XNet model achieved superior classification performance 97 on BreakHis compared to the alternative approach, as depicted in Figure 7a. The training and validation arcs were visualized using the softmax layer after 100 iterations. The CN2XNet model achieved the highest overall classification performance, surpassing the state-of-the-art ResNet101V2 model by a margin of 0.512 percentage points. The pre-trained models mVGGNet167, ResNet101V2, and EfficientNetV2B3 achieved accuracies of 94, 95, and 96, respectively, as shown in Tables 5, 6. The CN2XNet model achieved an overall accuracy of 3%, 2%, and 1%, higher than mVGGNet16, ResNet101V2, and EfficientNetV2B3 on the BreakHis dataset. The model exhibited minimal overfitting, making it a well-fitted solution for the datasets. The research also highlighted the superiority of the integrated feature map in achieving better results compared to traditional CNN methods. The study evaluates the CN2XNet model with a softmax layer on the BreakHis dataset, focusing on training and testing cross-entropy loss. The Figure 7a shows a steady decrease in training loss with each epoch, reaching a minimum of 0.041 at the final epoch. However, when applied to the BACH dataset, the model achieves a training loss error rate of 0.638. The model also shows lower loss values than other DCNN models, indicating its excellent fit to the BreakHis dataset. The

model consistently decreases training loss with each epoch on the BACH dataset, outperforming other models with a training loss of less than 0.041. The CN2XNet model's performance evaluation uses a confusion matrix representation, with actual categories depicted vertically and predicted categories represented horizontally. The Figure 8a,b represents the confusion matrix of eight classifications where the actual categories are depicted vertically, and the predicted categories are represented horizontally, (a) CN2XNet and (b) SqE-DCCConvNet architecture. The model's accuracy for tubular adenocarcinoma and PC is below 97%, with TA often misclassified as PC. Fibroadenoma (F) shows better classification but is prone to confusion with lobular carcinoma (LC) and Phyllodes tumor (PT). Fibroadenomas (F) have a 1% chance of being incorrectly classified as malignant. In contrast, mucinous carcinoma (MC) has a 2% chance of being misclassified as adenoma (A), as illustrated in Figure 8a.

The CN2XNet model, a proposed clinical diagnostic system, was evaluated using the area under the curve (AUC) value, assessing its performance based on true-positive, false-positive, true-negative, and false-negative results. The model achieved the highest AUC value of 0.98 on the BreakHis and 0.97 on the BACH dataset, outperforming other architectures like mVGGNet16, ResNet101V2, and EfficientNetV2B3, as depicted in Figure 9a,b. The model also reduced false-positive and false-negative rates while recognizing numerous genuine positives. The model's category-specific ROC curves demonstrated its effectiveness in detecting true positives.

The CN2XNet model showed high accuracy, precision, recall, and F1 scores with F scores of 96%, precision 96%, recall 97%, and sensitivity 97% using the BreakHis dataset, while the proposed method achieved Fscores of 98%, precision 98%, recall 98%, and sensitivity using the BACH dataset, as plotted in Figure 10a,b. The proposed

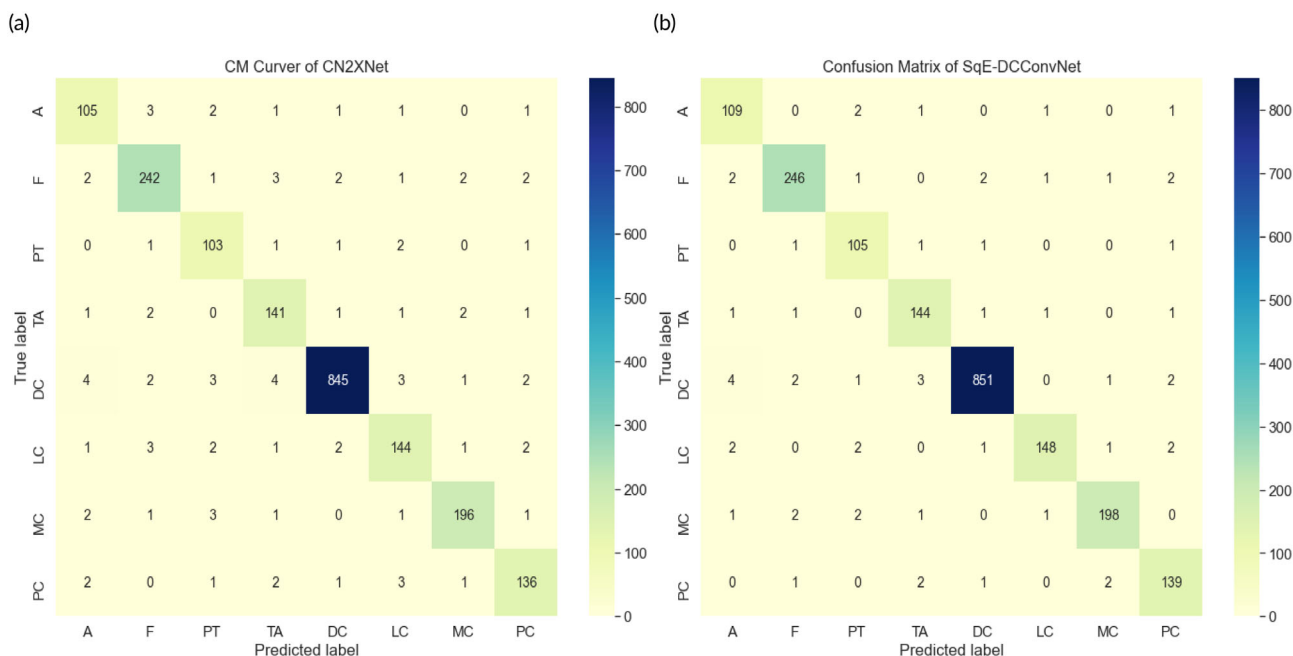


**FIGURE 8** Representation confusion matrix of eight classifications where the actual categories are depicted vertically, and the predicted categories are represented horizontally. (a) CN2XNet and (b) SqE-DCCConvNet architecture.

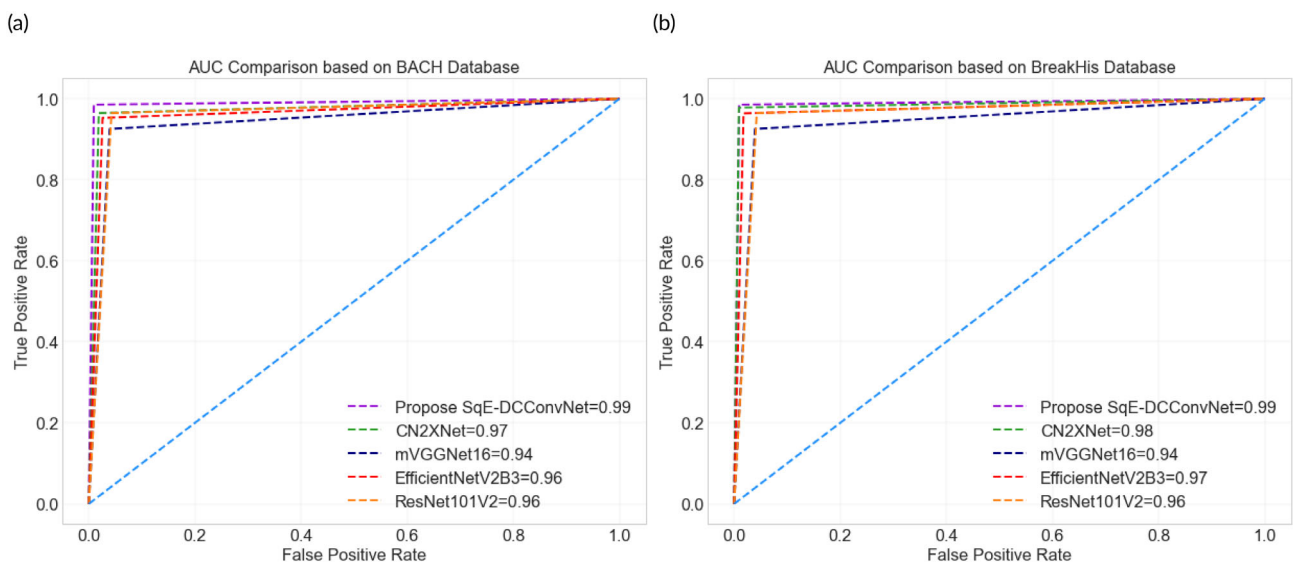


**FIGURE 9** Comparison of the AUC using the BACH and BreakHis datasets for the proposed model. The graph depicts the AUC performance of the DDC-DenseNet and SqE-DCCConvNet models, demonstrating that the DDC-DenseNet model earned an optimal AUC of 99% on BreakHis and 98% on BACH. In contrast, the SqE-DCCConvNet model attained the highest AUC of 99% on BreakHis and 99% on BACH.

method outperformed three pre-trained models regarding F-score, precision, and sensitivity. However, it performed slightly better on the BreakHis dataset due to the size and blurriness of microscopic images in the BACH dataset. The CN2XNet model outperformed the current system in all classes, indicating its superiority in classification tasks. These findings suggest that DL-based models can help physicians and radiologists predict breast lesions earlier. The study assesses the proposed SqE-DCCConvNet model's ability to differentiate breast tumor types and its feature discrimination effectiveness. Existing algorithms

struggled to classify breast histopathology images accurately, and there was a slight overlap between lobular and ductal carcinoma, leading to the misclassification of a small percentage of ductal carcinomas. The proposed SqE-DCCConvNet model outperforms the alternative approach in distinguishing different types of breast cancers, with outstanding accuracy rates of 99% on the BACH and 99% on the BreakHis dataset, as examined in Table 5 and plotted in ACCLOS (Figure 7b). In contrast, other models such as CN2XNet, mVGGNet16, ResNet101V2, and EfficientNetV2B3 attained lesser accuracy of 97%,

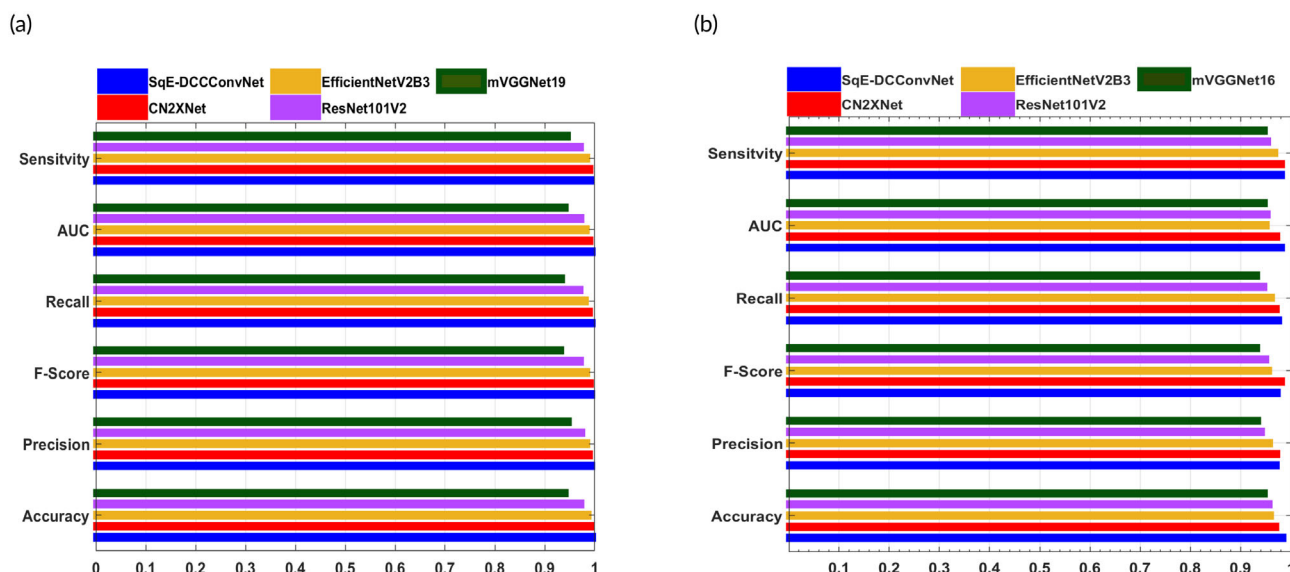


**FIGURE 10** (a) The suggested architecture outperforms BreakHis on the BACH dataset. The suggested model improves the average accuracy, AUC, precision, and sensitivity of BreakHis. It also produces less false-negative findings than deep convolutional neural network (DCNN) algorithms. (b) The BACH dataset training accuracy, loss, sensitivity, AUC, and AUC of the recommended design and DCNN algorithms. The suggested approach outperforms the most sophisticated conventional models.

94%, 95%, and 96%, respectively. The model's 99% accuracy on the BreakHis dataset following the 100 epoch demonstrates effective regularization and a decent fit. On the BACH dataset, the proposed model achieved an impressive 99% accuracy, while other DCNN models such as CN2XNet, mVGGNet16, ResNet101V2, and EfficientNetV2B3 achieved accuracies of 97%, 94%, 95%, and 96%, respectively. The proposed model outperforms CN2XNet, mVGGNet16, ResNet101V2, and EfficientNetV2B3 by 1%, 4%, 3%, and 2% in overall accuracy on the BreakHis dataset. The SqE-DCCConvNet exhibits the highest accuracy and lowest cross-entropy loss, indicating minimal overfitting and a well-fitted dataset approach. The study also shows that feature maps in the proposed model outperform CNN approaches. The model has a minimal training loss of 0.021 on BreakHis and 0.038 on BACH datasets, as shown in ACCLOS (Figure 7b). It retains high training accuracy and reduces training loss superior to other DCNN models on both datasets. The findings show the model's excellent fit to BreakHis and higher performance on BACH compared to other pre-trained techniques.

The SqE-DCCConvNet model was tested in a binary classification experiment to differentiate between benign and malignant breast tumors. The model's complementary confusion matrix, based on magnification factors, was used to provide insights, with the brown diagonal line in the Figure 11a-d representing the accuracy of correct classifications. The top-left quadrant shows the proportion of correctly predicted benign cases (true negatives) at different magnifications. The top-right quadrant shows the minimal rates of incorrectly predicted benign cases (false negatives). The lower-left quadrant shows the proportion of falsely predicted malignant cases (false positives) at different magnifications. The lower-right quadrant shows the proportion of accurately predicted malignant cases

(true positives) at different magnifications. The overall accuracy rate is 99%. In contrast, eight classification experiments were conducted, and a comparison of the confusion matrices was obtained, as shown in Figure 8b. The SqE-DCCConvNet model focuses on four classes due to its significant number of samples, neglecting training of other types. The highest classification accuracy was found for adenoma, Phyllodes tumor, lobular carcinoma, and PC, with lower accuracy rates for other classes.

In terms of AUC values, the SqE-DCCConvNet model outperforms other architectures such as CN2XNet, mVGGNet16, ResNet101V2, and EfficientNetV2B3 on both the BreakHis and BACH datasets, as illustrated in Figure 9a,b. The model's robustness is evident in its ability to reduce false-positive and false-negative rates, accurately identify true positives, and distinguish between all classes, indicating its potential for precise medical data classification in clinical applications. The SqE-DCCConvNet model beats other models concerning accuracy, specificity, F-scores, precision, and sensitivity, with marginally greater accuracy on the BreakHis dataset, as shown in Figure 12a-d. These results demonstrate the efficacy of deep learning-based models in classifying breast microscopic images and their potential for early breast cancer prediction, rendering the proposed model a plausible solution for breast cancer classification tasks.

## 6.5 | Analysis comparison with cutting-edge approaches based on BreakHis dataset

Extensive research and development over the years have led to integrating significant knowledge from neurology, statistics, and applied mathematics into deep learning methods. With the continuous

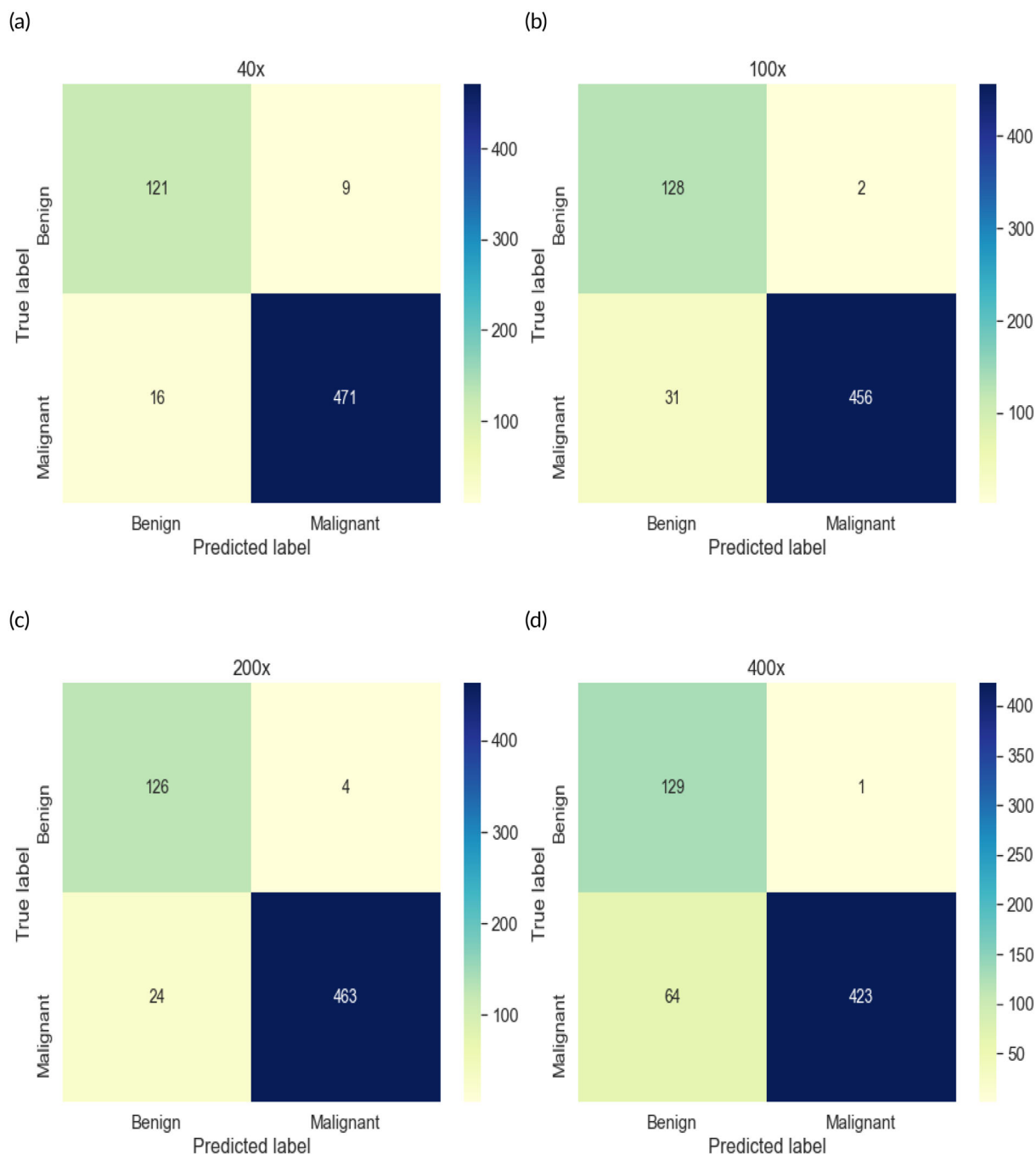


**FIGURE 11** The confusion matrix for binary classifications on the BreakHis dataset, with actual categories on the vertical axis and predicted classes on the horizontal. 40 $\times$ , 100 $\times$ , 200 $\times$ , and 400 $\times$ .

progress in computer performance, recent advancements have facilitated the widespread adoption of more extensive datasets and novel training techniques for deep neural networks, particularly in image recognition and classification domains. Song, Chang, and Huang (2017) designed a supervised embedding algorithm using a multi-layer neural network to improve the feature representation of Fisher vectors. This enhancement resulted in better categorization of the BreakHis dataset. Wei et al. (2017) introduced a DCNN-base BiCNN model for clinical breast cancer applications. Their binary classification

system achieved an impressive accuracy of 97%, but the method required complex architecture and high computational resources. Kwok (2018) developed an Inception-ResNet-v2-based mammary gland network for image classification in cancer histopathology. The network trained a classifier using microscopic and segment images and used rotations, and random horizontal or vertical flipping to enhance data quality. The test set achieved an accuracy rate of 87% using the BACH concealed dataset. In contrast, Kohl et al. (2018) developed a DenseNet-161-based breast cancer histopathological

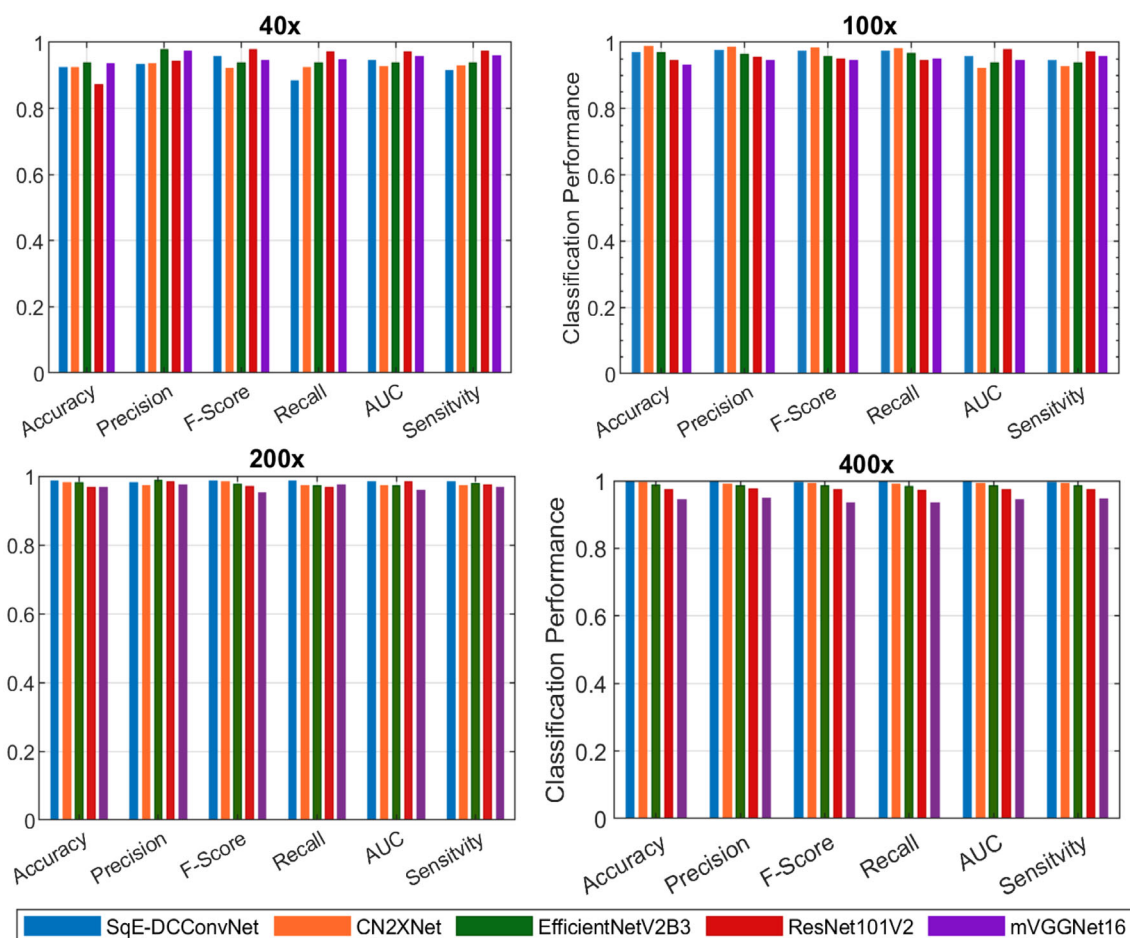


**FIGURE 12** The proposed architecture on the BreakHis dataset showed improved accuracy, AUC, precision, and sensitivity compared to existing deep convolutional neural network (DCNN) models, and a significant reduction in false-negative instances, demonstrating its superior performance on the dataset at various magnifications.

image classification model, which achieved an 83% accuracy rate on the BACH hidden test set after incorporating random rotation, twisting, dimension changes, and adjustments. Li et al. (2019) developed a classification model for breast cancer histopathological images using Inception-v3. The model was tested using horizontal and vertical flipping, random flipping, and movement, achieving an average accuracy rate of 85%. Li et al. (2019) developed two models for breast cancer histopathological image classification: Deep-Reverse Active Learning (DRAL) and Atrous DenseNet (ADN). DRAL improves CNN accuracy by removing incorrectly labeled image segments, while ADN combines dilated convolutions with dense blocks for multi-scale feature extraction. Data augmentation techniques like rotations, mirror images, and vertical reflections were used. The study found 94.1% accuracy.

The primary goal of this study was to evaluate and compare the performance of proposed models that integrated DenseNet into the backbone network for breast cancer classification. The classification results on the BreakHis dataset are presented in Table 7 for both image and patient levels. The CN2XNet model achieves high classification accuracies at different magnifications, specifically 98.2%,

98.6%, 98.2%, and 98.9% on the image-level classification, and 98.1%, 98.5%, 98.2%, and 98.3% on the patient-level classification, for magnifications of 40 $\times$ , 100 $\times$ , 200 $\times$ , and 400 $\times$ , respectively. Compared to the AHoNet model, the CN2XNet consistently outperforms it with improvements of 2.3%, 0.8%, 0.8%, and 1.4% on image-level classification, and 1.7%, 0.9%, 1.0%, and 0.8% on patient-level classification, for the corresponding magnifications. Similarly, the SqE-DCCovNet achieves classification accuracies of 99.4%, 99.2%, 99.6%, and 97.7% on image-level classification and 99.3%, 99.2%, 99.5%, and 99.5% on patient-level classification for breast cancer microscopic images. The SqE-DCCovNet model demonstrates accuracy improvements of 1.9%, 1.8%, 0.6%, and 3.3% on image-level classification and 2.5%, 1.8%, 0.3%, and 2.4% on patient-level classification, compared to AHoNet on the respective datasets. Although the performance of the SqE-DCCovNet is slightly lower on the 200 $\times$  datasets, it outperforms the backbone model across all four magnifications. Combining the basic model with either the SqE-DCCovNet or CN2XNet results in improved classification performance, and integrating both modules simultaneously into a single network further enhances accuracy.

TABLE 7 Comparing the performance of the suggested framework with the baseline techniques using the BreakHis dataset.

| Ref.                          | Methods          | Image recognition rate (IRR) |              |              | Patient recognition rate (PRR) |               |              |              |              |
|-------------------------------|------------------|------------------------------|--------------|--------------|--------------------------------|---------------|--------------|--------------|--------------|
|                               |                  | 40×                          | 100×         | 200×         | 400×                           | 40×           | 100×         | 200×         | 400×         |
| Bayramoglu et al. (2016)      | CNN              | 83.0 ± 3.70                  | 83.1 ± 5.20  | 84.6 ± 2.40  | 82.1 ± 3.70                    | 81.87 ± 3.06  | 83.39 ± 5.17 | 82.56 ± 3.49 | 80.69 ± 4.23 |
| Song, Chang, and Huang (2017) | FV + CNN         | 87.70 ± 2.40                 | 87.60 ± 3.90 | 86.50 ± 2.40 | 83.90 ± 3.60                   | 90.00 ± 3.20  | 88.90 ± 5.00 | 86.90 ± 5.20 | 86.30 ± 7.0  |
| Spanhol et al. (2016)         | Improved AlexNet | 85.6 ± 4.8                   | 83.5 ± 3.80  | 82.7 ± 1.0   | 80.7 ± 7.1                     | 83.80 ± 4.10  | 82.10 ± 4.90 | 85.10 ± 3.10 | 82.30 ± 3.80 |
| Song, Zou, and Chang (2017)   | VGGNet           | 87.00 ± 2.60                 | 86.20 ± 3.70 | 85.20 ± 2.10 | 82.90 ± 3.70                   | 890.00 ± 3.20 | 88.90 ± 5.00 | 86.90 ± 5.20 | 86.30 ± 7.00 |
| Addo et al. (2024)            | DenseNet         | 95.3 ± 3.20                  | 95.6 ± 2.0   | 95.9 ± 3.0   | 86.5 ± 4.4                     | 94.71 ± 0.88  | 95.90 ± 4.20 | 96.76 ± 1.09 | 89.11 ± 0.12 |
| Han et al. (2017)             | CSDCNN           | 9580 ± 3.10                  | 96.9 ± 1.90  | 96.70 ± 2.00 | 94.90 ± 2.80                   | 97.10 ± 1.50  | 95.70 ± 2.80 | 96.50 ± 2.10 | 95.70 ± 2.20 |
| Benhammou et al. (2018)       | Inception V3     | 90.2 ± 2.9                   | 85.6 ± 2.15  | 86.1 ± 2.32  | 82.5 ± 2.47                    | 91.5 ± 2.65   | 85.1 ± 2.53  | 86.8 ± 2.32  | 82.9 ± 2.30  |
| Lichtblau and Stoean (2019)   | Ensemble Model   | 85.62.53                     | 87.4 ± 2.7   | 89.80 ± 2.1  | 87.0 ± 2.8                     | 83.9 ± 4.20   | 86.0 ± 7.73  | 89.1 ± 3.20  | 86.6 ± 4.28  |
| Alom et al. (2019)            | IRR-CNN          | 97.1 ± 3.6                   | 96.8 ± 3.62  | 96.6 ± 1.5   | 95.7 ± 2.80                    | 96.6 ± 1.7    | 96.3 ± 2.80  | 96.2 ± 1.8   | 96.2 ± 2.3   |
| Zhang et al. (2020)           | VGGVD            | 95.0 ± 2.4                   | 90.1 ± 3.2   | 88.4 ± 2.8   | 85.0 ± 5.30                    | 95.5 ± 3.4    | 91.5 ± 3.20  | 89.2 ± 4.20  | 89.22.53     |
| Zhu et al. (2019)             | InceptionV4      | 85.7 ± 6.9                   | 84.2 ± 4.8   | 84.9 ± 4.20  | 80.1 ± 4.2                     | 85.2 ± 4.46   | 83.5 ± 5.30  | 84.1 ± 7.7   | 79.3 ± 4.4   |
| Zou et al. (2022)             | AHoNet           | 96.5 ± 1.74                  | 97.4 ± 1.88  | 99.0 ± 0.73  | 96.5 ± 2.80                    | 96.8 ± 3.4    | 97.4 ± 2.31  | 99.2 ± 1.77  | 97.1 ± 0.84  |
| Sudharsan et al. (2019)       | CNN              | 86.10 ± 4.20                 | 83.80 ± 3.10 | 80.20 ± 2.60 | 80.60 ± 4.60                   | 86.90 ± 5.40  | 85.70 ± 4.80 | 85.90 ± 3.90 | 83.40 ± 5.30 |
| Wei et al. (2017)             | Bi-CNN           | 97.89 ± 3.10                 | 97.64 ± 3.90 | 97.56 ± 3.60 | 97.97 ± 3.70                   | 97.02 ± 3.90  | 97.23 ± 3.10 | 97.89 ± 3.70 | 97.50 ± 3.60 |
| Proposed                      | CN2XNet          | 98.2 ± 1.54                  | 98.6 ± 0.94  | 98.2 ± 1.59  | 98.9 ± 0.73                    | 98.1 ± 2.80   | 98.5 ± 1.60  | 98.2 ± 2.31  | 98.3 ± 3.4   |
| Proposed                      | SqE-DCCConvNet   | 99.4 ± 0.43                  | 99.2 ± 1.19  | 99.6 ± 0.30  | 99.7 ± 0.16                    | 99.3 ± 0.74   | 99.2 ± 1.43  | 99.5 ± 0.98  | 99.5 ± 0.66  |

**TABLE 8** Accuracy comparing of the suggested framework based on fusion network on BACH testset.

| Author                         | Method                                              | Accuracy |
|--------------------------------|-----------------------------------------------------|----------|
| Sujatha et al. (2023)          | VGG16, VGG19, InceptionResNetV2, DenseNet201        | 0.92     |
| Iesmantas and Alzbutas (2018)  | CapsNet                                             | 0.72     |
| Kwok (2018)                    | Inception-ResNet-v2                                 | 0.87     |
| Kohl et al. (2018)             | DenseNet-161                                        | 0.83     |
| Xu et al. (2023)               | MDF-FNet                                            | 0.86     |
| Sarker et al. (2022)           | EfficientNetV2                                      | 0.96     |
| Koné and Boulmane (2018)       | ResNeXt-50                                          | 0.81     |
| Talpur (2022)                  | CNN                                                 | 0.92     |
| Zhou et al. (2022)             | RANe-ADSVM                                          | 0.97     |
| Malarvizhi and Nagappan (2022) | Improved Mask-RCNN                                  | 0.96     |
| Kumaraswamy et al. (2021)      | ResNet-50, ResNet-101, DenseNet201 and NASNetMobile | 0.72     |
| Cao et al. (2018)              | VGG-16, ResNet-18, ResNet-152, ResNeXt, NASNet-A    | 0.79     |
| Branchatine and Riccio (2018)  | ResNet-34, ResNet-50, ResNet-101                    | 0.86     |
| Abunasser et al. (2023)        | BCCNN                                               | 0.98     |

## 6.6 | Comparing the performance of the suggested framework based on fusion network

A fusion network can extract image features more comprehensively than a singular network, allowing for more informed decisions and enhanced classification accuracy. Fusion networks require less data enhancement and network structure complexity, but more data and a better-adapted structure can improve their performance. Studies based on the BACH dataset show that methods like CNN + Softmax and CNN + SVM can classify breast cancer histopathology images but may result in the loss of crucial spatial correlation data. Employing more data and designing a structure better adapted to the classification task is essential to maximize performance. Table 8 provides comparisons of cutting-edge fusion methods using microscopic images.

Awan et al. (2018) used ResNet-50 and an SVM classifier to classify breast cancer histopathological images. They used data enhancement techniques like rotations and image flips, resulting in an accuracy rate of 71% on the BACH hidden test set. The capsule network (CapsNet) model was also enhanced, achieving a 72% accuracy rate. Ferreira et al. (2018) developed a classification model for breast cancer histopathological images using Inception-ResNet-v2. They used rotations, scaling, twisting, and shifting and achieved a 76% accuracy rate with data augmentation using the BACH concealed test set. Koné and Boulmane (2018) developed a classification model for

breast cancer histopathological images using ResNeXt-50 binary tree structure. The model divides the input image into cancerous or non-cancerous categories and into carcinoma in situ, invasive, and benign normal. Reflection and random rotation were used to augment data, achieving an accuracy rate of 81% on the BACH hidden test set. Mar-ami et al. (2018) developed a classification model for histopathological images of breast cancer using Inception-v3. The models were trained on different subsets and grouped. Random rotation and color perturbation enhanced data during the experimentation phase. The BACH concealed exam set achieved an accuracy of 84%, demonstrating data enhancement's effectiveness.

Zhou et al. (2022) developed a new image processing technique to assist pathologists in accurately diagnosing breast cancer. The technique combines anomaly detection using a support vector machine (ADSVM) method and a resolution adaptive network (RANet) model. The RANe-ADSVM approach was evaluated using two public datasets, achieving 98% on BACH and 99% on BreakHis for binary classification at 200x magnification. Malarvizhi and Nagappan (2022) proposed the improved Maks R CNN (-IMRCNN) method for segmentation using the region proposal network to predict objectless scores and bounds. Region of interest align is used for feature extraction resolving conventional ROI pooling issues, and eliminating quantization issues. The Bayesian interactive Adaboost CNN classifier is used for classification employed in the BACH dataset, achieving an average segmentation accuracy of 96% and 96% accuracy. Mahbod et al. (2018) merged ResNet-50 and ResNet-101 for adenocarcinoma histopathological image classification. Data enhancement was performed by rotating and inverting the data, resulting in a 77% accuracy rate for the BACH concealed testset. Cao et al. (2018) improved breast cancer histopathology image classification by extracting features from various networks and combining them with manual features. The method achieved an accuracy rate of 79%, demonstrating multiple feature extractors' potential. Branchatine and Riccio (2018) proposed a combination of ResNet-34, ResNet-50, and ResNet-101 for breast cancer histopathology image classification, using horizontal and vertical flips and three 90° clockwise rotations. The experiment achieved an accuracy rate of 86%. Abunasser et al. (2023) developed a deep learning model (BCCNN) to classify breast cancers into eight types. The model was trained on ImageNet and used on breast cancer MRI images from the Kaggle depository. The model's accuracy was evaluated using 30 experiments with the best results achieved at 98% accuracy at 400X magnification due to the high image resolution. Yan et al. (2020) proposed integrating Inception-v3 with a recurrent neural network (RNN) to address spatial correlation issues in histopathological images of breast cancer, suggesting this combination could be crucial for future research on adenocarcinoma histopathology images.

## 7 | DISCUSSION

Cancer anomalies are crucial in breast cancer management, serving as indicators for detection, diagnosis, treatment, and monitoring. These anomalies, often seen as lumps, tissue irregularities, or distinctive

findings on mammograms, are the first signs of breast cancer and are essential for timely treatment. Their specific characteristics, such as cancer cell type, hormone receptor status, and HER2 status, guide personalized treatment plans. Histopathological image analysis is essential for breast cancer management, providing a detailed view of cancer anomalies at the cellular level, aiding in accurate diagnosis, distinguishing between benign and malignant lesions, identifying subtypes, determining tumor grade, predicting aggressiveness, and formulating treatment plans. Histopathology also provides definitive evidence of the cancer's response to treatment, as changes in cancer cell and tissue characteristics post-treatment offer conclusive information about the effectiveness of therapy and the possibility of recurrence. Recent deep-learning model advances have significantly increased image categorization accuracy, with models like VGGNet, ResNet, and EfficientNet providing promising breast cancer and microscopic image classification.

In this study, we present the SqE-DCCConvNet model, a novel approach that integrates the SqE module with DenseNet to improve recognition rates for classifying microscopic images of breast cancer. DenseNet has proven effective at preventing gradient disappearance and reducing the complexity of feature extraction. By incorporating the SqE module as an additional layer, the proposed SqE-DCCConvNet model outperforms other models and effectively overcomes the obstacles presented by deeper networks. The hybrid model performs exceptionally well by correctly classifying pathological breast cancer tissues misclassified by the DenseNet backbone network. The process involves utilizing microscopic images' topographical information and categorizing misclassified images into groups with large empty areas and dense, intricate tissue structures. Integrating dense modules into the backbone improves the accuracy with which these images are differentiated, resulting in enhanced performance. Even with limited feature information, the SqE-DCCConvNet model demonstrates robust classification abilities. Compared to other studies on the multiclassification of breast cancer pathological images, the proposed network architecture obtains a 99% classification accuracy, 6% higher than the backbone model. In addition, the model outperforms other approaches on the challenging BACH dataset, further validating its superior performance in multiclassifying breast cancer pathological images, as shown in Table 7. The findings of this study demonstrate the importance of the SqE-DCCConvNet model in improving computer-assisted diagnosis and meeting the requirements of clinical applications. The hybrid approach proposed effectively resolves existing obstacles, resulting in a more accurate and reliable breast cancer diagnosis and classification instrument.

In future research, the research aims to refine the technique for recognizing microscopic breast cancer images by distinguishing between benign and malignant tumors at specific magnifications. The goal is to enhance recognition accuracy and provide valuable tumor information, aiding clinicians in locating lesions more efficiently and reducing workload. Despite challenges like irregular data distribution, the system shows promise for clinical diagnosis and early detection. To ensure the robustness of the methods,

rigorous validation will be conducted, including incorporating diverse external datasets, applying stringent cross-validation techniques, and comparing the results with baseline methods. The research will also involve medical professionals in the validation process, emphasizing interpretability and clinical relevance. These steps will strengthen the credibility of the findings and reaffirm the effectiveness of deep learning techniques in breast cancer microscopic image classification.

## 8 | CONCLUSIONS

Breast cancer microscopic image classification is complex due to factors like improper specimen fixation, lack of publicly accessible large labeled datasets, and the complexity of classification assignment. Researchers use large datasets like natural images from ImageNet to pre-train their networks and fine-tune them using a small number of labeled medical images. However, the lack of large datasets makes it difficult to validate and compare algorithm benchmarks, impeding the development of new algorithms. To advance research in breast cancer microscopic image analysis, rigid training and standardizing operation procedures can resolve the issues. Deep learning in image analysis offers autonomous feature learning and eliminates the limitations of traditional algorithms. CNN-based methods are effective in various domains, including breast cancer microscopic image detection and classification. The study introduced an improved transfer learning-based SqE-DCCConvNet network to classify breast cancer microscopic images, achieving 99.09% with binary classification and 99.47% accuracy in eight-class classification. The study enhances the original Dense Block's convolutional layer by introducing a SqE module, extracting multi-layer features while reducing computational complexity. A novel learning rate optimizer is proposed to improve performance without complex fine-tuning. Additionally, feature migration of convolutional networks using pre-training models is explored, showing that freezing specific layers during migration enhances classification accuracy. Developing a large-scale labeled breast cancer group could enhance deep learning in medical image processing and analysis. Moreover, the collaboration between hospitals, universities, and scientific research institutions is needed to address the lack of publicly accessible large breast cancer histopathology image datasets.

## AUTHOR CONTRIBUTIONS

**Amjad Rehman:** Conceptualization; methodology; formal analysis; supervision; writing – original draft; writing – review and editing. **Tariq Mahmood:** Methodology; software; data curation; formal analysis; investigation; writing – original draft; writing – review and editing; conceptualization. **Faten S. Alamri:** Validation; investigation; conceptualization; formal analysis; project administration; visualization; writing – review and editing; funding acquisition; resources. **Tanzila Saba:** Formal analysis; project administration; funding acquisition; conceptualization; supervision; writing – review and editing. **Shahid Naseem:** Supervision; project administration; investigation; validation; formal analysis; writing – review and editing; data curation.

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## CONFLICT OF INTEREST STATEMENT

The authors declare that they have no conflict of interest.

## DATA AVAILABILITY STATEMENT

The data that support the findings of this study are available from the corresponding author upon reasonable request.

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