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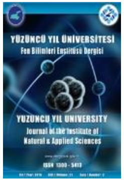

Research Article

Development of a Cost-Effective Novel CNN Model for Breast Cancer Classification in Histopathological Images

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Abstract: Cancer, is a leading cause of disease and death worldwide, affecting both advanced industrialized and developing nations. Breast cancer, specifically among women, is a highly prevalent and serious type of cancer, making it a focal point for extensive research in the field of medicine. In the diagnosis of breast cancer, histopathological images play a crucial role because of the abundance of valuable phenotypic information they contain. To enhance the accuracy and objectivity of breast histopathological image analysis (BHIA), classification, and detection tasks are performed on these images using deep learning architecture approaches. In a preliminary experiment conducted in this paper using the Breast Cancer Histopathological Database (BreakHis), four state-of-the-art and custom CNN architectures were proposed. The experimental results demonstrate the notable performance of the proposed custom model at 40x and 200x magnification factors, reaching accuracies of 97.49% and 97.77%, surpassing other models. The ResNet-50 model achieved higher accuracy at 100x and 400x magnifications, with accuracies of 98.56% and 96.43%, respectively. Compared to other state-of-the-art models, the proposed CNN model not only shows efficient training with a significantly shorter timeframe but also features a reduced number of layers, highlighting its superior computational efficiency. Although the parameter count is higher than that of one of the models, the model strikes a favorable balance between computational efficiency and model capacity. In light of the achieved outcomes and the existing literature, forthcoming studies endeavor can be pursued further to enhance the performance values in breast cancer classification.

Histopatolojik Görüntülerde Meme Kanseri Sınıflandırması İçin Maliyet Etkin Yeni Bir CNN Modelinin Geliştirilmesi

Makale Bilgileri

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Anahtar Kelimeler
CNN,
Derin öğrenme,
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Meme kanseri,
Sınıflandırma

Öz: Kanser, hem gelişmiş sanayileşmiş ülkeleri hem de gelişmekte olan ülkeleri etkileyen, dünya çapında hastalık ve ölümün önde gelen nedenlerinden biridir. Özellikle kadınlar arasında meme kanseri, oldukça yaygın ve ciddi bir kanser türüdür ve bu nedenle tıp alanında geniş çaplı araştırmaların odak noktası olmuştur. Meme kanseri teşhisinde histopatolojik görüntüler, içerdiği değerli fenotipik bilgiler nedeniyle kritik bir rol oynar. Meme histopatolojik görüntü analizinin (BHIA) doğruluğunu ve nesnelliğini artırmak amacıyla, bu görüntüler üzerinde sınıflandırma ve tespit görevleri derin öğrenme mimarisi yaklaşımları kullanılarak gerçekleştirilir. Bu makalede, Meme Kanseri Histopatolojik Veritabanı (BreakHis) kullanılarak yapılan ön deneyde, dört son teknoloji ve özel CNN mimarisi önerilmiştir. Deneysel sonuçlar, önerilen özel modelin 40x ve 200x büyütme faktörlerinde kayda değer bir performans sergilediğini ve sırasıyla %97.49 ve %97.77 doğruluklara ulaştığını, diğer modelleri geride bıraktığını göstermektedir. ResNet-50 modeli ise 100x ve 400x büyütme faktörlerinde daha yüksek doğruluk elde etmiş ve sırasıyla %98.56 ve %96.43 doğruluk oranlarına ulaşmıştır. Diğer son teknoloji modellerle karşılaştırıldığında, önerilen CNN modeli sadece çok daha kısa bir süre içinde verimli eğitim göstermekle kalmamış, aynı zamanda daha az katman sayısı ile üstün hesaplama verimliliğine sahip olduğunu göstermiştir. Parametre sayısı bir modelden daha yüksek olmasına rağmen, model hesaplama verimliliği ile model kapasitesi arasında olumlu bir denge kurmaktadır. Elde edilen sonuçlar ve mevcut literatür ışığında, gelecekteki çalışmalar, meme kanseri sınıflandırmasında performans değerlerini artırmak amacıyla daha da geliştirilebilir.

1. Introduction

Cancer manifests as an ailment characterized by uncontrolled cell proliferation due to the transformation of cells undergoing natural selection (Brown et al., 2023). Among various cancer types, breast cancer is particularly noteworthy, recognized as a prevalent and life-threatening condition affecting women. In 2022, there were 2.3 million reported cases of breast cancer in women, leading to 670,000 deaths globally. In 2022, breast cancer was the most prevalent cancer among women in 157 out of 185 countries. Breast cancer can affect women in any country post-puberty, with higher incidence rates in later stages of life. Men account for approximately 0.5–1% of breast cancer cases (Sadique et al., 2024; WHO, 2024). The geographic distribution of breast cancer occurrences varies greatly, with the majority of instances occurring in industrialized countries. However, transitioning nations experience a disproportionately high number of breast cancer-related deaths. According to predictions, if current trends continue, the worldwide incidence of breast cancer might exceed 3 million new cases and result in 1 million deaths per year by 2040 (Arnold et al., 2022). Various diagnostic techniques are employed in the therapy of breast cancer, such as mammography, magnetic resonance imaging (MRI), and histological testing. Biopsy procedures have consistently been the predominant tool for accurately diagnosing breast cancer when other tests, such as mammography, have produced unclear findings. The inclusion of the biopsy procedure's description, which encompasses the collection of tissue samples, placement onto small glass slides, and application of staining for enhanced visibility, provides more intricacy to the overall process. Pathologists analyze histopathological images to validate the diagnosis (Das et al., 2019; Zerouaoui et al., 2024). Scientists have employed several algorithms and analysis tools to examine breast cancer pictures from diverse perspectives, taking into account elements such as the stage of the disease, image quality, and specific criteria. In recent years, Convolutional Neural Networks (CNNs), a type of deep learning technology, have gained significant recognition as effective instruments in computer-assisted medical image interpretation (Inik et al., 2019). CNNs are deep learning models designed to mimic the organization of the cortical area. Their origins can be traced back to the study 1962 study conducted by Hubel and Wiesel, and they were subsequently enhanced by Fukushima's Neocognitron in 1980. LeCun's introduction of LeNet-5 in 1998 marked a significant advancement in this concept. The CNN architecture comprises convolutional, pooling, and fully connected layers, as described by (Sakib et al., 2019; Suzuki, 2017).

Recently, the utilization of deep learning methods in the processing of medical images has demonstrated considerable potential in enhancing diagnostic precision multiple studies have shown that Convolutional Neural Networks (CNNs) are effective at categorizing histological images of breast cancer. Alom et al. (2019) created the Inception Recurrent Residual Convolutional Neural Network (IRRCNN) using the BreakHis and Breast Cancer Classification Challenge 2015 datasets. The model integrates features from the Inception Network, Residual Network, and Recurrent Convolutional Neural Network. Budak & Güzel (2020) introduced a novel approach for detecting breast cancer in histopathological images by integrating color and texture characteristics. The method combined Shearlet Transform (ST) for breaking down images and the Gray-Level Co-occurrence Matrix (GLCM) for extracting texture. Color features are obtained by extracting information from the red, green, and blue channels, which are then combined into histograms and concatenated to generate a feature vector. The vector, together with texture data, is inputted into a Support Vector Machine(SVM) for classification. The histological Convolutional Neural Network (HCNN) was proposed by Burçak et al. (2021) as a method for identifying breast cancer using histological pictures. The Model employed a Convolutional Neural Network (CNN) for extracting features and was trained using six optimization techniques to improve learning efficiency. Boumaraf et al. (2021b) developed an automated breast cancer classification method for histopathological images, leveraging transfer learning with ResNet-18. They fine-tuned the model and employed global contrast normalization (GCN) and three-fold data augmentation. Another study conducted by Boumaraf, et al. (2021a) compared conventional machine learning (CML) with deep learning (DL) methods for breast cancer classification. CML involved extracting handcrafted features, while DL utilized transfer learning with VGG-19 architecture, fine-tuned on histopathological images. Evaluation of the BreakHis dataset and KIMIA Path960 validation set highlighted DL's superior performance. Wang et al. (2021) introduced a novel approach rooted in the integration of deep features and enhanced routing. The proposed method utilized dual channels to extract features from capsules and convolutions simultaneously. Then, these features are fused, and a routing module and the FE-BkCapsNet classifier are incorporated. Gupta et al. (2021) developed modified residual neural networks, specifically modified Resnet-50 and ResNet-34 architectures for histopathological breast cancer image classification. Notably, the proposed approach results were achieved with ResNet-50. Kallipolitis et al. (2021) proposed a deep learning-based ensemble modeling approach for histopathology image classification, using EfficientNets as the primary components. The study also explored using InceptionNet, ExceptionNet, and ResNet to identify images and produced explainable results with the Grad-CAM technique. Joseph et al. (2022) developed handcrafted feature extraction techniques and Deep Neural Network (DNN) are used on histopathological images from the BreakHis dataset. The characteristics retrieved by handcrafted techniques are then used to train DNN classifiers, which have four dense layers with softmax activation. In the realm of feature extraction using deep learning and classification with machine learning algorithms, Sharma & Kumar (2022) presented a binary classification approach based on magnification that is specific to breast cancer histopathology images. The strategy entailed evaluating five well-known classical machine learning algorithms using handcrafted features with a pre-trained Xception model. The most effective classifier combination was obtained by Xception+SVM R,5. Zerouaoui & Idri (2022) presented and evaluated findings from an empirical comparative study of 28 hybrid architectures for breast cancer (BC) imaging classification. Four classifiers (MLP, SVM, DT, and KNN) and seven deep learning techniques (DenseNet 201, MobileNet V2, ResNet 50, Inception V3, Inception ResNet V2, VGG16, and VGG19) were used. These architectures were evaluated and ranked across two datasets using the SK statistical test and the Borda Count. Chattopadhyay et al. (2022b) developed DRDA-Net, a deep-learning model tailored for histopathology images. DRDA-Net integrates Dense Residual Dual-Shuffle Attention Network architecture, featuring improvements like residual skip connections and multi-scale feature learning. Its key element, the Dual-Shuffle Residual Block (DRB), incorporates ShuffleNet-inspired features, enhancing feature map quality and data flow through Channel Attention (CA) modules and residual skip connections. Krishna et al. (2023) created a decision-support model that effectively classifies breast cancer in histopathological images. They incorporated a trainable attention mechanism into a CNN. This attention branch called the Attention Branch Network (ABN), is connected to the DarkNet19 network. A DarkNet-19 convolutional layer and Global Average Pooling (GAP) contextualize visual properties in the attention branch. By creating a Headmap, it can identify and emphasize photo highlights. The multi-scale and dual-adaptive attention (MDAA) was introduced to recognize histopathological images (Li et al., 2024). This model uses DenseNet and a module for multiscale feature extraction. A dual-adaptive attention block and adaptive balance loss function are included. The network’s tiny and intricate blocks enable feature reuse and improve complex concept communication. The Dual-adaptive attention block improves feature representation by combining channel and spatial adaptive attention to overcome single-attention mechanism limits. Lastly, an adaptive balancing loss is employed to tackle the issue of class imbalance. Chattopadhyay et al. (2022a) developed the MTRRE-Net model, which was specifically designed for breast cancer classification. The model combines dual residual blocks and a recurrent connection, utilizing two-fold residual learning. The method involves extracting features from various network depths with different scales and filter sizes to capture important information from input images while maintaining a balance between depth and learning complexity. Zhou et al. (2022) proposed ADSVM, which combines Anomaly Detection with SVM and Resolution Adaptive Network (RANet), for breast cancer classification. ADSVM detects mislabeled patches in malignant images, which improves classification precision. RANet dynamically selects subnetworks based on image complexity. Kashyap (2022) developed a Stochastic Dilated Residual Ghost (SDRG) model, merging the Multiscale Stochastic Dilated Convolution (MSDC) with a ghost unit, stochastic upsampling, and downsampling units, for accurate breast cancer classification. The MSDC model captures detailed features, whereas the ghost unit reduces redundancy and expands the receptive field of dilated convolution while preserving image information. When combined with stochastic groupings in upsampling, the ghost unit improves model performance. In our study, (Nadr & İnik, 2023) a custom CNN architecture was proposed using only a 100x magnification factor of the BreakHis dataset's histopathological images to classify BC classification. This approach resulted in an accuracy of 92.70. Addo et al. (2024) proposed a lightweight CNN model named "BCHI-CovNet" specifically designed to classify breast cancer using histopathological images. The model employed a novel approach that includes a convolutional operation that is both multiscale and depth-wise separable. In addition, the model includes a second-order pooling module and a multi-head self-attention mechanism.

Despite advancements in deep learning techniques, the necessity persists for models that not only ensure high accuracy but also uphold computational efficiency. This study aims to address this gap by presenting a new CNN model designed exclusively for the binary classification of breast cancer in histopathology images. The primary objective is to design a CNN architecture that is very efficient in terms of both diagnostic accuracy and processing resources. This architecture will be thoroughly evaluated against well-known state-of-the-art architectures such as SqueezeNet, GoogleNet, ResNet-50, and DarkNet-19.

The objective of this study is to investigate the employing of Convolutional Neural Networks (CNNs), a type of deep learning technique, in the classification of breast histopathology images to identify breast cancer. The goal is to utilize the capabilities of deep learning techniques to improve the performance of Breast Histopathological Image Analysis (BHIA). The study seeks to enhance the accuracy of breast cancer diagnosis by enhancing precision and objectivity in the analysis.

2. Material and Methods

This section thoroughly explored the essential elements necessary for creating a proficient deep learning model for the classification of breast cancer in histopathologic images. The exploration commences by introducing the dataset. This section presents the cutting-edge deep learning models that have been proposed in this study. Subsequently, the provided CNN method, specifically tailored for breast cancer categorization, is outlined. Finally, the performance metrics are presented.

2.1. Dataset Description

This study employed the BreakHis dataset, a publically available compilation of histopathological images specifically designed for the examination of breast cancer. The dataset, referred to as the Breast Cancer Histopathological Images dataset, comprises microscopic biopsy images of both benign and malignant breast tumors (Spanhol et al., 2015). The images were acquired as part of a clinical study conducted from January to December 2014 at the P&D Lab in Brazil. The study involved individuals with clinical indications of breast cancer. Institutional review board approval was secured, and all participants provided written informed consent, ensuring their personal information was anonymized to protect privacy. The dataset consists of 9709 pictures gathered by pathologists through surgical (open) biopsy and labeled for histological analysis and is categorized into two classes: benign and malignant, with 2,480 benign samples and 5,429 malignant samples. This classification aids in detailed analysis and model training. Table 1 provides detailed information about the dataset distribution, offering insights into the number of samples in each category. Additionally, Figure 1 showcases representative examples of the histopathological images, illustrating the variety and complexity of the images used in the study.

2.1.1. Data preprocessing

During the preprocessing step, the original 700x460 images were resized to meet the input requirements of various pre-trained deep neural networks used in this study. The images were resized to 224x224x3 for ResNet-50 and GoogleNet, 227x227x3 for SqueezeNet, and 256x256x3 for DarkNet-19. For the proposed method, the images were resized to 64x64x3. This resizing ensured compatibility with the input size constraints of each network, enabling efficient processing while preserving essential diagnostic features. Adjusting the image sizes was crucial for maintaining the performance and applicability of each neural network model.

Table 1. Dataset Distribution by magnification factors and classes

Magnification factor	Benign	Malignant	Total
40 X	625	1370	1995
100 X	644	1437	2081
200 X	623	1390	2013
400 X	588	1232	1820
Total	2480	5429	7909
Pateints	24	58	82

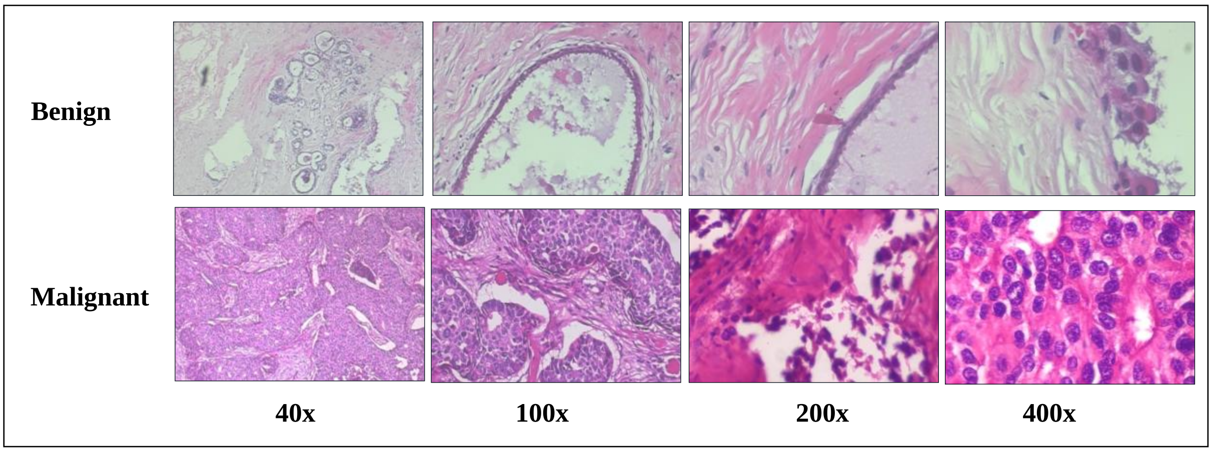

Figure 1. Histopathological image samples of BreakHis dataset.

2.2. State-of-the-art models

Four renowned CNN models were utilized in this study. The selection of these models was based on their extensive usage and exceptional precision in various image classification tasks. The aim is to achieve a harmonious equilibrium between minimizing the number of parameters and acceptable accuracy. The main objective was to attain a high level of accuracy while maintaining a compact model size for the categorization of histopathologic images. To obtain comprehensive information regarding the image input size, model layers, and parameter counts for each model, please refer to Table 2. By elucidating the attributes and details of these models, it gets more straightforward to appreciate them and evaluate their appropriateness for a certain categorization task.

In 2016, Iandola et al. (2016) developed SqueezeNet, an 18-depth deep learning network. Model architecture maximizes efficiency while minimizing parameters and model size. The model starts with a single convolution layer, conv1, and goes through eight fire modules, fire 2-9. Every fire module has a squeeze convolution layer with 1x1 filters and an expanded layer with 1x1 and 3x3 filters. As filters grow, the network’s feature extractions improve. To keep a broad activation map and ensure high accuracy, max-pooling with a stride of 2 is used after conv1, fire4, fire8, and conv10.

GoogLeNet, introduced by Szegedy et al. (2015), is a deep learning model with 22 depths (or 27 depths with pooling). This architecture, which appeared in the ILSVRC 2014 competition, is a customized version of the Inception framework. Despite attempts to expand the Inception network, only minor advances were seen, prompting a concentration on the basic design. The network is made up of around 100 distinct construction components, which vary depending on the layer enumeration inside the machine learning architecture. The figure shows GoogLeNet's layered structure and architecture.

ResNet-50 (Hong et al., 2019) is a 50-layer deep learning model that has been extensively trained on ImageNet. Its main feature, residual learning, tackles degradation difficulties in deep networks. The architecture uses convolutional blocks with a "bottleneck" design for computational efficiency and skip connections to improve information flow. ResNet-50 processes RGB images of size 224x224, gradually reducing spatial dimensions through different layers to a 1x1 output before finishing with a softmax layer for classification.

Darknet-19 (Sankari et al., 2023) is a robust pre-trained network based on the YOLOv2 model that has 19 convolutional layers and five max pooling layers. It predominantly employs 3x3 filters, which double the number of channels following each max pooling layer. The architecture generates 8x8 features, which are then processed by a GAP layer for prediction and feature compression. Darknet-19 implements batch normalization for faster convergence and model regularization, as well as a classification layer with two neurons in place of the softmax layer.

Table 2. An overview of pre-trained models and their parameters

Model	Input size	Layers (depth)	Parameters
SqueezNet	227x227	64(18)	1.24 M
GoogleNet	224x224	144(22)	7 M
ResNet-50	224x224	177(50)	25.6 M
DarkNet-19	256x256	64(19)	20.8 M

2.3. Proposed method

In the proposed method section, four well-known state-of-the-art models are utilized alongside the proposed CNN model for binary classification from histopathological images. Figure 2 shows the diagram of these models. The flowchart starts by providing the BreakHis dataset, followed by image preprocessing where the image is resized to the appropriate dimensions for each model. The preprocessed images extracted features are then inputted into the feature layers of their respective models. The feature outputs are passed through the softmax layer for classification, ultimately identifying images as either benign or malignant.

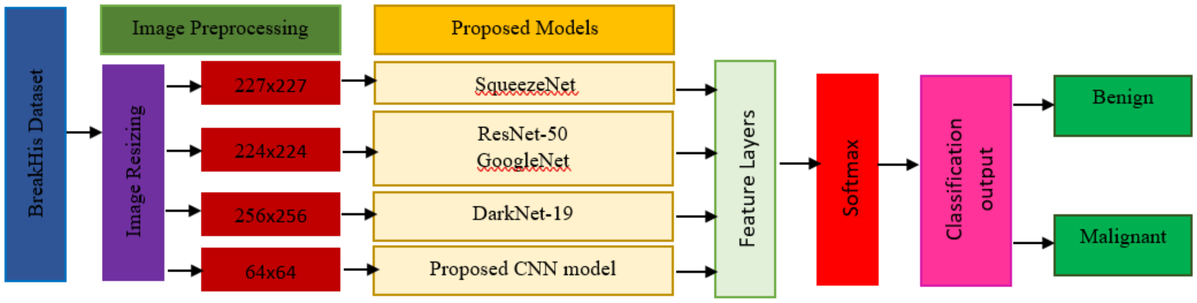

Figure 2. Proposed method diagram.

2.3.1. Proposed CNN model

The provided (CNN) architecture is designed for image classification tasks, specifically to distinguish between benign and malignant images in the BreakHis dataset. The proposed CNN has 23 layers, which include input, convolutional, ReLU, batch normalization, pooling, fully connected, dropout, and softmax layers. Images are resized to 64x64 and sent through various convolutional layers that include batch normalization, ReLU activation, and pooling. The architecture features 198 filters (3x3) in the first convolutional layer with max-pooling (6x6, stride 2), 209 filters (3x3) in the second convolutional layer with max-pooling (6x6, stride 2), 244 filters (3x3) in the third convolutional layer with average pooling (3x3, stride 2), and 256 filters (3x3) in the fourth convolutional layer with max-pooling (6x6, stride 2). The final layers consist of a fully connected (FC) layer with 512 units and ReLU activation, followed by a dropout layer with a rate of 0.2. The purpose of the dropout layer is to prevent overfitting by randomly deactivating neurons during training, as explained (Wu & Gu, 2015). After the dropout layer, there is another fully connected (FC) layer with 2 units, and finally, a softmax layer with 2 neurons for classification, as illustrated in Figure 3. The proposed CNN method involves approximately 1.5 million parameters in total. For a detailed breakdown of these parameters, please refer to Table 3.

Figure 3. Proposed CNN model.

Table 3. Parameter values of each layer in the proposed model

Layer No.	Layer name	Output	Filter No.	Filter size	Stride No.	Learnable properties	No. of Parameters
1	Input layer	64x64x3	-	-	-	-	0
2	Conv2D-1	64x64x198	198	3x3	1x1	3x3x3x198	5 544
3	Batchnorm-1	64x64x198	-	-	-	1x1x198	396
4	Relu-1	64x64x198	-	-	-	-	0
5	Maxpool-1	30x30x198	-	6x6	2x2	-	0
6	Conv2D-2	30x30x209	209	3x3	1x1	3x3x198x209	372 647
7	Batchnorm-2	30x30x209	-	-	-	1x1x209	418
8	Relu-2	30x30x209	-	-	-	-	0
9	Maxpool-2	13x13x209	-	6x6	2x2	-	0
10	Conv2D-3	13x13x244	244	3x3	1x1	3x3x209x244	459 208
11	Batchnorm-3	13x13x244	-	-	-	1x1x244	488
12	Relu-3	13x13x244	-	-	-	-	0
13	Avgpool2D	6x6x244	-	3x3	2x2	-	0
14	Conv2D-4	6x6x256	256	3x3	1x1	3x3x244x256	562 432
15	Batchnorm-4	6x6x256				1x1x256	512
16	Relu-4	6x6x256					
17	Maxpool-3	1x1x256		6x6	2x2	-	0
18	FC-1	1x1x512	-	-	-	512x256	131 584
19	Relu-5	1x1x512	-	-	-	-	0
20	Dropout (0.2)	1x1xx512	-	-	-	-	0
21	FC-2	1x1x2	-	-	-	2x512	1 026
22	Softmax	1x1x2	-	-	-	-	0
23	Classoutput	1x1x2	-	-	-	-	0
							Total 1.5M

2.4. Performance criteria

Different measurements are utilized to assess the performance of deep learning models. Various learning tasks may necessitate distinctive execution measurements to be emphasized. The classification performance of a model was evaluated using a confusion matrix too in this study. This tool, often referred to as an error matrix, is a table representation that provides a concise summary of the effectiveness of a classification or prediction model (Deng et al., 2016).

Accuracy is a commonly used evaluation metric that is often used alongside the confusion matrix. It measures the proportion of properly identified images out of the total number of evaluated images. Equation 1 represents the classification of this metric in binary classification, taking into account the number of true positives (TP) and true negatives (TN) (Gupta & Chawla, 2020).

$$\text{Acurracy} = \frac{(\text{TP+TN})}{(\text{TP+TN+FP+FN})} \text{ X } 100 \qquad (1)$$

To obtain a more comprehensive evaluation of the model's performance, we employed other assessment measures such as precision, recall, and F1-score (Ali et al., 2021).

Precision: is a measure that calculates the proportion of accurately predicted positive outcomes compared to the total number of predicted positive outcomes made by the classifier. Equation 2 represents this metric (Ali et al., 2021).

$$\text{Precision } = \frac{\text{TP}}{\text{TP+FP}} \text{ X } 100 \qquad (2)$$

Recall: this metric as defined in Equation 3, quantifies the accuracy of properly identifying true positive findings out of all the actual positive samples (Ali et al., 2021).

$$Recall = \frac{\text{TP}}{\text{FN+TP}} \text{ X } 100 \qquad (3)$$

F1-Score: F1-score: Also referred to as the harmonic mean, balances precision and recall. It accounts for both false positives and false negatives in its calculation, making it especially useful for evaluating performance on imbalanced datasets. Equation (4) represented the f1-score metric.

$$F1 = 2 * \frac{Precision\ X\ Recall}{\text{Precision+Recall}} \text{ X } 100 \qquad (4)$$

3. Results and Discussion

This section presents the proposed CNN model, the results of state-of-the-art models, a comparison of competitors, the computational complexity of models, and previous studies. The experiment was carried out on a Windows 11 Pro 64-bit OS (version 23H2) using MATLAB R2023a. The system consisted of an Intel Core i7-8850H CPU @ 2.60 GHz (12 CPUs), 16GB DDR4 RAM, and a 500GB SSD. Deep learning computations were enhanced by an NVIDIA GeForce RTX 1050 GPU with 4GB of dedicated RAM.

3.1 Results of the proposed CNN model

The training parameters utilized by the proposed CNN model are as follows: Adam is the optimizer algorithm used, and training is performed on a GPU. The mini-batch size is set to 64, and the initial learning rate is 0.001. The learning rate schedule is piecewise, with a drop factor of 0.1 per ten epochs. The total number of epochs is 40. Shuffling occurs every epoch, and the validation frequency is set to 50. Furthermore, L2 regularization with a value of 0.001. Furthermore, in this study, the dataset was divided into two parts for experimentation. The division of the dataset was not based on random selection. Specifically, 80% of the data was allocated for training and 20% for testing. Figure 4 presents the results obtained by the proposed CNN model in terms of accuracy, recall, precision, and F1-score across all magnification factors. From the figure, we can see that the proposed CNN achieved accuracies of 97.49%, 97.60%, 97.77%, and 94.78 for magnification factors 40x, 100x, 200x, and 400x, respectively.

3.2. Results of state-of-the-art models

In this section, the results obtained from four deep-learning CNN-based models are presented. Figure 5 displays the achieved results of four deep learning models, including SqueezeNet, GoogleNet, ResNet-50, and DarkNet-19, evaluated in terms of accuracy, recall, precision, and F1-score. The figure illustrates a comprehensive performance comparison across different magnification factors. From the analysis presented in Figure 5, it is observed that ResNet-50 outperforms all other models in terms of accuracy across all magnification factors. Specifically, ResNet-50 achieves an accuracy rate of 96.99%, 98.56%, 96.53%, and 96.43% at magnifications of 40x, 100x, 200x, and 400x, respectively. These results underscore ResNet-50's superior capability in accurately classifying histopathologic images of breast cancer.

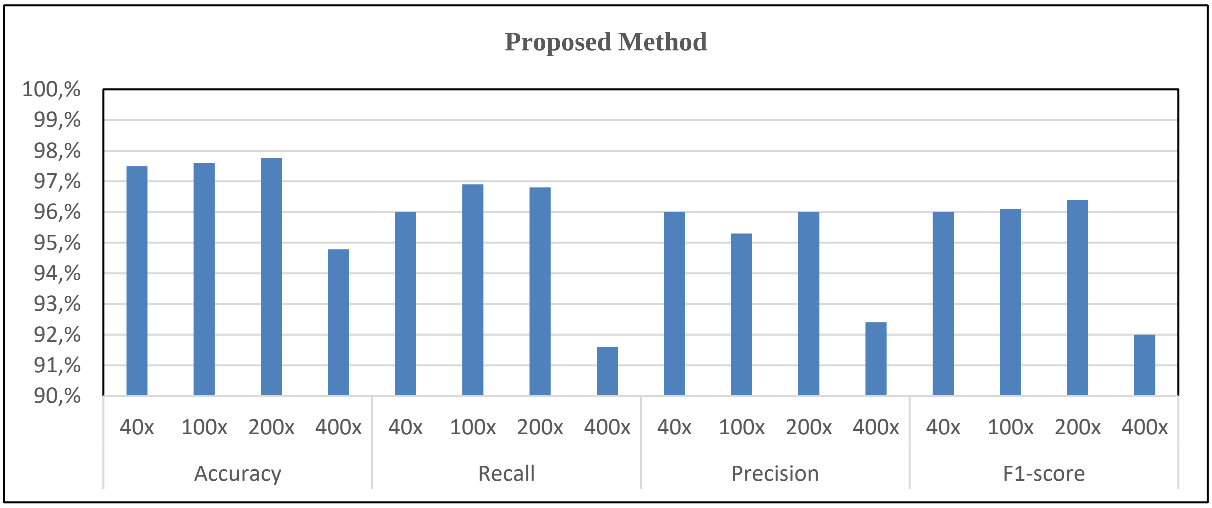

Figure 4. Performance metrics of the proposed CNN model across different magnifications.

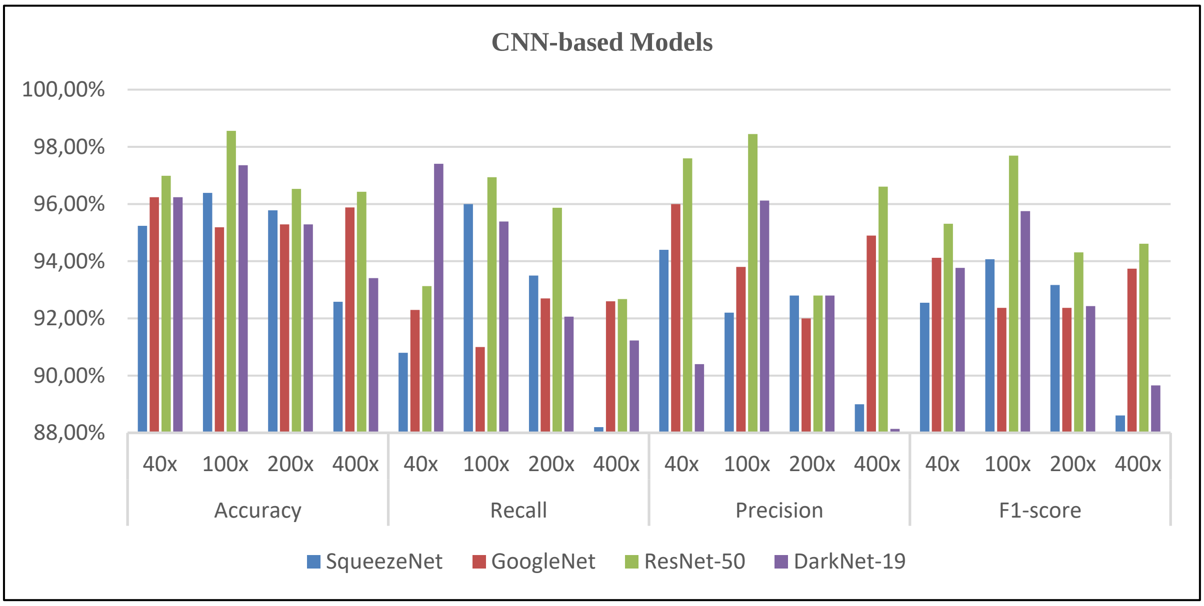

Figure 5. State-of-the-art performance metrics across different magnifications.

3.3. Comparison of competitors

The results obtained from the application of renowned deep learning models, including Sequezenet, GoogleNet, ResNet-50, DarkNet-19, and the proposed CNN model, are presented. Each model's performance is assessed based on accuracy metrics and confusion matrices. A comparison was conducted to demonstrate the performance of the proposed CNN model against established models such as Sequezenet, GoogleNet, ResNet-50, and DarkNet-19. This comparison included various evaluation metrics: accuracy, precision, recall, and F1-score. The objective is to evaluate the strengths and weaknesses of each approach in breast cancer classification by analyzing their respective outcomes. Figure 6 displays the confusion matrices for all the models. Table 4 provides a summary of the results obtained by the different models on the BreakHis dataset, considering four magnification factors, in terms of accuracy, precision, recall, and F1-score.

Summarizing the results of the proposed models, the proposed CNN model demonstrated superior accuracy rates across magnification factors 40x and 200x, achieving accuracies of 97.49% and 97.77%. Additionally, ResNet-50 exhibited a notable accuracy of 98.56% and 96.43% at a magnification factor of 100x and 400x. Turning to recall, precision, and F1-score, DarkNet-19 obtained the highest recall of 97.41% at a magnification factor of 40x, while ResNet-50 yielded the highest recall of 96.94% and 92.68% at a magnification factor of 100x and 400x. The proposed CNN model outperformed other models in the recall at magnification factors of 200x achieving 96.80%. Furthermore, RestNet-50 demonstrated the highest precision rates at magnification factors of 40x, 100x, and 400x with rates of 97.60%, 98.45%, and 96.61% respectively, while the proposed CNN model exhibited precision rates of 96% at magnification factors of 200x. In terms of the F1-score, the proposed CNN model achieved the highest rates at magnification factors 40x and 200x, with scores of 96% and 96.40%, whereas ResNet-50 attained a score of 97.69% and 94.61% at a magnification factor of 100x and 400x.

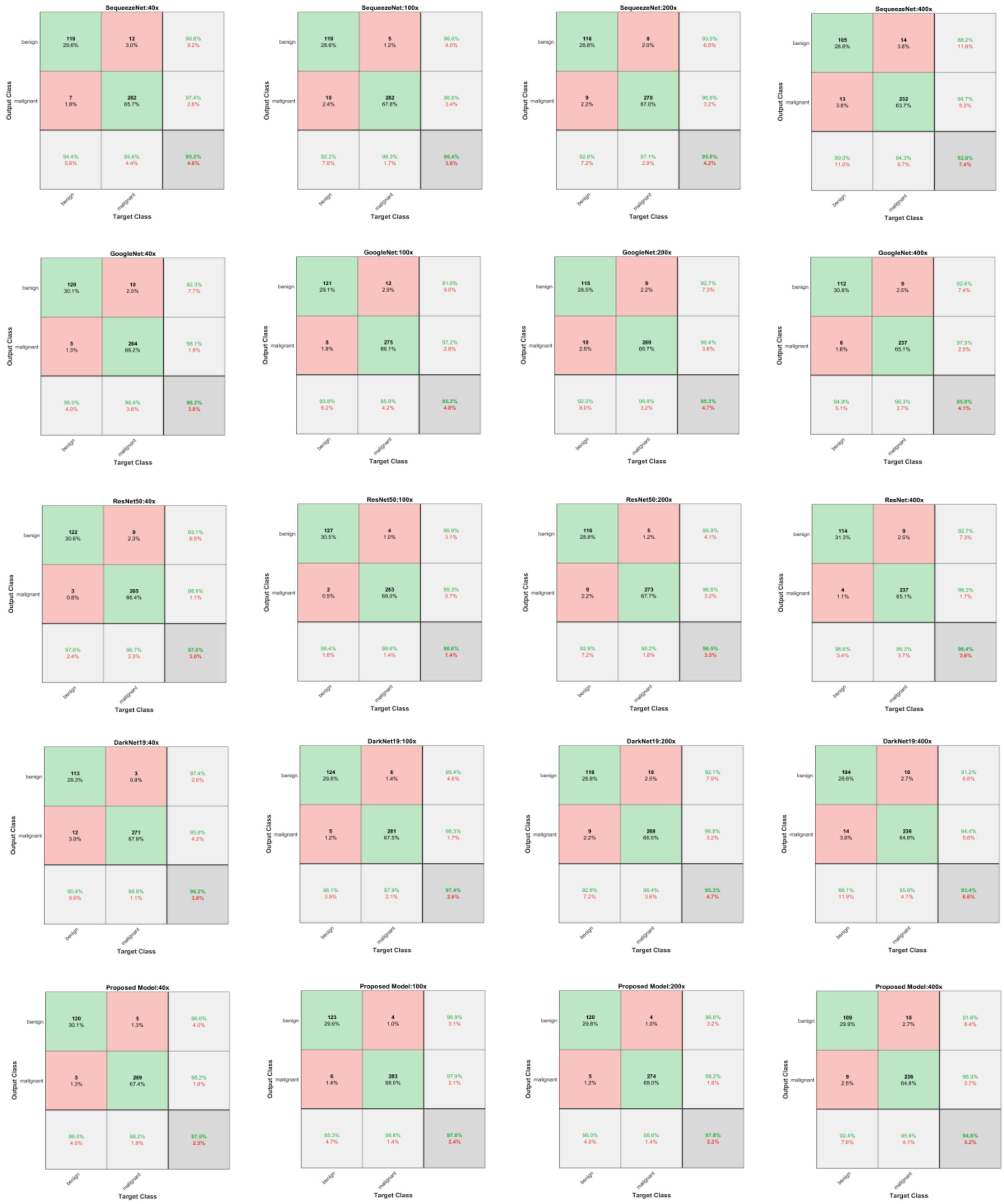

Figure 6. Confusion matrices for models.

Table 4. Models comparison at various magnifications

	Magnification factor	SqueezeNet	GoogleNet	ResNet-50	DarkNet-19	Proposed CNN
Accuracy	40x	95.24%	96.24%	96.99%	96.24%	**97.49%**
	100x	96.39%	95.19%	**98.56%**	97.36%	97.60%
	200x	95.78%	95.29%	96.53%	95.29%	**97.77%**
	400x	92.58%	95.88%	**96.43%**	93.41%	94.78%
Recall	40x	90.80%	92.30%	93.13%	**97.41%**	96.00%
	100x	96.00%	91.00%	**96.94%**	95.39%	96.90%
	200x	93.50%	92.70%	95.87%	92.06%	**96.80%**
	400x	88.20%	92.60%	**92.68%**	91.23%	91.60%
Precision	40x	94.40%	96.00%	**97.60%**	90.40%	96.00%
	100x	92.20%	93.80%	**98.45%**	96.12%	95.30%
	200x	92.80%	92.00%	92.80%	92.80%	**96.00%**
	400x	89.00%	94.90%	**96.61%**	88.14%	92.40%
F1-score	40x	92.55%	94.12%	95.31%	93.77%	**96.00%**
	100x	94.07%	92.37%	**97.69%**	95.75%	96.09%
	200x	93.17%	92.37%	94.31%	92.43%	**96.40%**
	400x	88.61%	93.74%	94.61%	89.66%	92.00%

3.4. Computational complexity comparison of the proposed models

This study examined the computational complexity of different deep learning methods. Table 5 displays a comprehensive study of several elements, including training and testing time, the overall number of parameters, and the number of layers. The proposed method showed superior efficiency compared to all other models when comparing the periods of training and testing, resulting in a shorter overall workflow duration.

The proposed CNN method scored second regarding parameter count, with around 1.5 million parameters. Significantly, out of all the models, SqueezeNet had a lower number of parameters, which makes the suggested CNN approach a noteworthy choice in terms of computational robustness. Nevertheless, despite its commendable parameter efficiency, SqueezeNet's performance was shown to be subpar in comparison to other models. This suggests that SquuezeNet may have difficulties in effectively understanding and categorizing input, highlighting the importance of finding a balance between parameter economy and predictive accuracy.

Furthermore, the simplified architecture of the CNN model, which consists of a reduced number of layers, is particularly notable. This architectural modification improves both computing efficiency and accelerates the training process. The decreased number of layers enables the model to extract significant features from the dataset with greater efficiency, resulting in accelerated training durations and enhanced overall performance. Hence, the CNN model provided successful capability, rendering it a resilient and effective tool for analyzing histopathological images of breast cancer. The equilibrium is essential for constructing models that are simultaneously precise and viable for implementation on computers with restricted hardware capacities.

Table 5. Computational complexity comparison of the proposed models

Models	**Training time / Second**				**Testing time (image/second)**				**Total number of parameters**	**Layer numbers (depth)**
Magnification factors	40x	100x	200x	400x	40x	100x	200x	400x		
SqueezeNet	964	1035	1015	875	0.00203	0.00303	0.00251	0.00201	**723K**	68(18)
GoogleNet	2333	2429	2304	2067	0.00531	0.00578	0,00528	0.00526	5.9M	144(22)
ResNet-50	10126	10892	10559	9268	0.01182	0.01302	0.01191	0.01192	23.5M	177(50)
MobileNet-V2	7179	7731	7456	6574	0.00964	0.01001	0.00918	0.00945	2.2M	154(53)
DarkNet-19	8649	9498	9139	7837	0.01262	0.01229	0.012121	0.12074	19.8M	64(19)
Proposed CNN	**684**	**780**	**710**	**631**	**0.00123**	**0.00121**	**0.00118**	**0.00138**	1.5M	**23(11)**

3.5. Comparative analysis with prior research

The proposed study conducted a comparative analysis of its results to previous research, focusing on accuracy metrics. This study utilized the BreakHis dataset and binary classification. Furthermore, take into account that the comparison was done at the image level, not the patient level, using the binary classification method. Table 6 compares the CNN architecture proposed in this work to other CNN-based methods used in previous studies.

Table 6. Comparative analysis of the proposed methodology to prior research

References	**Method**	**Data Augmentation**	**40x**	**100x**	**200x**	**400x**
(Alom et al., 2019)	IRRCNN	Yes	97.95%	97.57%	97.32%	97.36%
(Budak & Güzel, 2020)	Texture and Color fusion+SVM	No	98.20%	97.20%	97.80%	97.30%
(Burçak et al., 2021)	HCNN	No	96%	99%	97%	96%
(Boumaraf et al., 2021b)	Fine-tuned ResNet-18 with GCN	Yes	**99.25%**	99.04%	99%	98.08%
(Boumaraf et al., 2021a)	Block-wise fine-tuned VGG	Yes	98.13%	97.39%	96.63%	94.05%
(Wang et al., 2021)	Deep feature integration+ enhanced routing	No	92.71%	94.52%	94.03%	93.54%
(Gupta et al., 2021)	Modified ResNet	Yes	99.11%	**99.52%**	98.74	
(Kallipolitis et al., 2021)	Ensemble deep learning with EfficientNets	Yes	98.66%	98.24%	98.59%	96.97%
(Sharma & Kumar, 2022)	Xception+SVM R,5	No	96.25%	96.25%	95.74%	94.11%
(Joseph et al., 2022)	Hybrid feature extraction with DNN	Yes	97.89%	97.60%	96.10%	96.84%
(Chattopadhyay et al., 2022b)	DRDA-Net	No	95.72%	94.41%	97.43%	96.84%
(Krishna et al., 2023)	Interpretable CNN+ABN	Yes	98.40%	98.60%	98.70%	97.80%
(Zerouaoui & Idri, 2022)	28 hybrid architecture+ 4 classifier	Yes	92.61%	92%	93.93%	91.73%
(Chattopadhyay et al., 2022a)	MTTRE-Net	Yes	97.12%	95.22%	96.85%	97.81%
(Zhou et al., 2022)	ADSVM+RANet	Yes	94.43%	98.31%	99.14%	93.35%
(Kashyap, 2022)	SDRG	Yes	98.41%	98.37%	96.26%	97.38%
(Nadr & İnik, 2023)	CNN architecture	No	-	92.70%	-	-
(Addo et al., 2024)	BCHI-CovNet	Yes	99.15%	99.08%	**99.22%**	**98.87%**
(Li et al., 2024)	MDAA	Yes	95.42%	93.79%	94.87%	97.08%
Proposed Method	CNN	No	97.49%	97.60%	97.77%	94.78%

This analysis examines patterns, appraises progress, and analyzes the efficacy of our model within the wider framework of breast cancer classification approaches. The examination and comparison specifically utilized prior work that employed the BreakHis dataset for binary classification. This decision maintained uniformity and impartiality, enabling a precise evaluation of the performance of the suggested approach in comparison to other models under identical dataset settings. The comparison aims to provide a meaningful evaluation of the model's efficacy in diagnosing breast cancer by just focusing on the BreakHis dataset.

After conducting a comprehensive analysis, it was discovered that the proposed CNN model exhibited different accuracy rates in comparison to other approaches, showcasing a competitive performance even in the absence of data augmentation strategies. Data augmentation is an essential process in deep learning that involves intentionally expanding the quantity and diversity of the training dataset to improve the performance of deep neural networks (Motlagh et al., 2018). This is especially significant in medical imaging, as the quantity of accessible images may be restricted, and fluctuations in the dataset are vital for training resilient models. Data augmentation plays a crucial role in training the CNN model efficiently, primarily because of the disparities in the quantity of images across various subtypes of breast cancer. It enhances the model's ability to apply its learned knowledge to new, unfamiliar data and prevents it from becoming too specialized to the training data. While several techniques in the table were enhanced by data augmentation, which can greatly enhance the performance of the model, the CNN model obtained impressive accuracy rates even without utilizing it. This emphasizes the model's effective exploitation of available data to uphold competitive levels of accuracy.

Therefore, the fact that the CNN model can achieve good performance with data augmentation highlights its resilience and the effectiveness of its architecture and training procedure. In comparison to experiments that did not utilize data augmentation, the CNN model earned the third-highest accuracy rate. Thus, the suggested CNN model demonstrated its practical applicability in breast cancer diagnosis, even without the use of data augmentation, which may not always be possible.

4. Discussion

Classifying and categorizing breast cancer is a challenging and time-consuming procedure. When it comes to detecting breast cancer, radiologists commonly rely on mammography pictures to identify malignant tumors. Nevertheless, there is an inherent possibility of human mistakes. To tackle this problem, deep learning (DL) and machine learning (ML) algorithms have been employed to precisely categorize breast cancer and other internal irregularities. Both machine learning techniques and deep learning models are frequently used in this domain. Deep learning models were employed in this methodology. Subsequently, the suggested model underwent evaluation comparison with four cutting-edge models regarding performance metrics and computational complexity. In addition, the new approach was compared to other existing studies.

Upon analyzing the data shown in Table 4 and Table 5, some significant insights can be made when comparing the proposed method CNN model with established deep learning architectures. The CNN model exhibits both exceptional performance and extraordinary adaptability across different magnification factors. This is corroborated by its strong accuracy measures, such as elevated precision, recall, and F1-score values, which demonstrate its dependability and efficacy in breast cancer classification tasks. Although it stood at the second number of parameters and only higher than the SqueezeNet model, the model's simplified structure highlights its computing efficiency. This efficiency is especially beneficial as it results in considerably quicker training and testing durations in comparison to other intricate models. This element is vital in actual applications where computational resources and temporal constraints are frequently encountered. Furthermore, the CNN model being offered is notable for its simplicity, since it possesses an approach that not only enhances its computational speed but also indicates a possible decreased risk of overfitting due to the reduced complexity. The proposed CNN model demonstrates its strengths in competitive performance, versatility across magnifications, robust accuracy metrics, computational efficiency, and a streamlined architecture. These factors highlight its potential for practical implementation in the field of histopathological image analysis for breast cancer classification.

Additionally, after carefully analyzing the previous studies listed in Table 6, we observed that Addo et al. (2024) achieved the highest level of accuracy when using magnification factors of 200x and 400x. On the other hand, Boumaraf et al. (2021b) and Gupta et al. (2021) attained the highest accuracy at magnification factors of 40x and 100x, respectively. Although the proposed method's accuracy results are close to those of the previous research, it is noteworthy that the CNN model has substantially fewer parameters. This feature not only enables our model to generate impressive outcomes without requiring a large number of hardware resources but also highlights its computational efficiency, making it a viable choice for real-world applications. Furthermore, the model’s ability to withstand and recover from challenges is demonstrated when compared to previous research, since it continually achieved competitive levels of accuracy even without the implementation of data augmentation approaches. The resilience demonstrated by our model indicates that it possesses intrinsic robustness and adaptability to various datasets, hence minimizing the need for pre-processing processes that may be necessary for other models. Therefore, the adaptability and effectiveness of this model suggest that it has the potential to be easily incorporated into clinical processes, which often involve heterogeneous data and limited computational resources. Our CNN model’s capacity to consistently and effectively perform well across different levels of magnification and datasets establishes it as a valuable tool for analyzing histopathologic images in the classification of breast cancer.

4.1. Conclusion

This study aimed to improve breast cancer classification using deep learning techniques. Various neural network architectures, including SqueezeNet, GoogleNet, ResNet-50, DarkNet-19, MobileNet-V2, and a custom CNN model designed for binary classification of breast cancer, were used to address the need for better diagnostic tools in breast cancer pathology. Promising results were obtained from experiments conducted on the Breast Cancer Histopathological database (BreakHis), with the custom CNN model performing exceptionally well, achieving accuracies of 97.49% and 97.77% at magnifications of 40x and 200x, respectively. The custom CNN model also showed the highest recall at a magnification factor of 200x. It is worth noting that the proposed method achieved a high precision rate at a magnification factor of 200x and the highest F1-score at 40x and 200x magnification. Furthermore, the proposed CNN model demonstrated efficient training and computational capabilities, with fewer layers compared to other models. Although SqueezeNet, GoogleNet, ResNet-50, and DarkNet-19 were evaluated in this study, the primary focus was on showcasing the performance of the custom CNN model.

One limitation observed in this study is the relatively small size of the dataset, which consisted of 7,909 images. While it provided valuable insights into breast cancer classification, the limited size of the dataset may hinder the generalizability of the findings to larger populations. The limited sample size may hinder the model’s capacity to accurately represent the complete spectrum of histopathological variations and tumor features observed in real-world clinical settings. The lack of data augmentation tools increased this challenge by limiting the variety and inclusiveness of the training data. To overcome this constraint and improve the reliability and applicability of breast cancer classification models future research takes into account the utilization of larger and more varied datasets, in addition to implementing data augmentation techniques. Additional suggestions involve investigating innovative architectures and enhancing training techniques. Through persistent innovation in this field, we can boost the precision of diagnoses and ultimately improve the results for people suffering from breast cancer.

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