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A comparative analysis of convolutional neural networks for breast cancer prediction

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ABSTRACT

Breast cancer continues to be a substantial worldwide health concern, affectingmillions of individuals each year; this emphasizes the critical nature of early detection in order to enhance patient prognoses. The present study aims to assess the classification performance of three convolutional neural network (CNN) architectures-visual geometry group 19 (VGG19), AlexNet, and residual network 50 (ResNet50)-with respect to breast cancer detection in medical images. Thorough assessments, encompassing metrics such as accuracy, precision, recall, and F-score, were undertaken to evaluate the diagnostic performance of the models. ResNet50 consistently outperforms other models, as evidenced by its highest accuracy and F-score. The research highlights the significant importance of carefully choosing suitable architectures for medical image analysis, with a specific focus on the detection of breast cancer. In addition, it demonstrates the capacity of deep learning models, such as ResNet50, to improve the diagnosis of breast cancer with exceptional precision and sensitivity, which is critical for reducing the occurrence of false positives and negatives in clinical environments. In addition, computational efficiency is taken into account; AlexNet is recognized as the most efficient model, which isadvantageous in environments with limited resources. This study advances medical image processing by demonstrating the potential of CNNs in the detection of breast cancer. The results of this study establish a fundamental basis for subsequent inquiries and suggest approaches to improve timely detection and treatment, which will ultimately be advantageous for both patients and healthcare professionals.

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1. INTRODUCTION

In 2020, there were incredible 2.3 million instances of breast cancer diagnosed worldwide, resulting in the unfortunate loss of 685,000 lives. By the end of 2020, over 7.8 million women had been diagnosed with breast cancer during the last five years, solidifying its position as the most prevalent disease globally. Breast cancer is not limited by geographical limits and may impact women at any age after reaching puberty, with the likelihood of occurrence rising significantly in older age [1]. was very little change in the number of deaths caused by breast cancer. During this time, the main treatment method was a surgical procedure called radical mastectomy. Notable advancements in survival rates did not occur until the 1990 s, which coincided with the implementation of breast cancer early detection programs in several nations. These initiatives were

closely linked to complete treatment regimens that included successful medical medications [1]. Breast cancer arises from the cells in the breast and is often identified by the existence of a mass in the breast and several abnormalities compared to typical circumstances. Breast cancer tumors may be classified into two separate categories: benign, which means noncancerous, and malignant, which means cancerous.

Various methods have been used to identify breast cancer, including self-examination, clinical evaluation, and screening instruments like mammography. Identifying breast cancer may be a difficult undertaking, since it encompasses a wide range of complicated disorders [2]. In the field of Histopathology, biopsy is a diagnostic technique used to determine the malignancy of a questionable spot. Pathologists get their diagnosis by visually inspecting histopathological pictures using a microscope, which is a generally accepted and conclusive standard for confirmation [3]. Conventional image recognition algorithms are often used in the interpretation of digital pathology images. Nevertheless, these strategies have mostly been replaced by deep learning methodologies that were first introduced in the ImageNet large scale visual recognition competition (ILSVRC) in 2012 [4]. Scientists have used several algorithms and investigative methodologies to analyze pictures of breast cancer, customizing their techniques to suit the unique needs of the illness, its stage, and the quality of the available photographs [5], [6]. Significantly, the prevailing pattern in computer-assisted medical image analysis in recent years has been the extensive acceptance of deep learning structures, specifically focusing on convolutional neural networks (CNNs). CNNs have become a powerful tool in breast cancer categorization, providing unique benefits in the examination of medical pictures [7]. CNNs, or convolutional neural networks, are a specific kind of deep learning models that are carefully crafted to perform exceptionally well in tasks connected to pictures. They are especially skilled at analyzing mammographic and histological images to detect indications of breast cancer. CNNs have a key benefit in their capacity to automatically extract complicated patterns, features, and pertinent information from sophisticated medical pictures, eliminating the need for time-consuming human feature engineering [8]. This innate capacity alleviates medical experts' workload and improves breast cancer categorization's precision and dependability. In addition, CNNs have shown remarkable ability to generalize, enabling them to effectively process different datasets and adjust to fluctuations in picture quality. This is especially advantageous in real-world clinical environments where data might be intrinsically varied [9]. This research paper explores the significant influence of CNNs, a type of deep learning technique, on breast cancer classification in medical imaging. It aims to investigate the potential of CNNs to transform the field of breast cancer diagnosis and treatment.

2. RELATED WORK

Gour *et al.* [10] presented ResHist, an automated technique that utilizes histopathological images to diagnose breast cancer tumors. A deep convolutional neural network (ResHist) consisting of 152 layers was introduced to classify histopathological images of breast cancer. To enhance the model's efficacy, the authors implemented a data augmentation method consisting of stain normalization, image patch generation, and affine transformation. An analysis of the BreakHis dataset revealed that without data augmentation, it achieved an accuracy of 84.34% and an F1-score of 90.49%. However, with data augmentation, it improved to 92.52% and achieved an F1-score of 93.45%. ResHist outperformed alternative pretrained networks in accurately distinguishing benign from malignant histopathological images, as demonstrated by these outcomes.

In their study, Gupta and Chawla [11] conducted a comparative analysis of the breast cancer classification performance of different convolutional neural networks (CNNs) and conventional classifiers. According to their research, residual network 50 (ResNet50) attained the maximum level of accuracy, 93.27%. By distinguishing benign from malignant breast cancer cases, the CNN + logistic regression (LR) model demonstrated the potential of integrating pretrained CNNs with conventional classifiers, surpassing the performance of CNN + support vector machine (SVM). Notwithstanding the data constraints, the research underscores the potential of machine learning in identifying breast cancer. Subsequent improvements could incorporate more extensive datasets, more precise categorization, and all-encompassing frameworks for analysis.

In their publication, Dabeer *et al.* [12] presented a CNN that effectively automates the detection of breast cancer with a remarkable accuracy of prediction of 99.86%. The CNN-processed labeled input images were extracted directly from raw pixels by distinguishing benign from malignant tissue. By simulating digital staining and employing a classifier network, the CNN accurately classifies breast tissue as benign or malignant, having been trained on a dataset consisting of 2,480 benign and 5,429 malignant samples.

A novel ensemble deep learning-based method for binary classification of breast histology images was presented by Kassani *et al.* [13]. By employing hyperparameter optimization, stain normalization, and pre-trained CNNs (visual geometry group 19 (VGG19), MobileNet, and DenseNet), the ensemble model attained exceptional accuracy when applied to benchmark datasets. Accuracy values of 98.13%, 95.00%,

94.64%, and 83.10% were achieved for the Bioimaging, ICIAR, BreakHis, and PatchCamelyon datasets, respectively. This study highlights the potential of ensemble deep learning in the classification of breast cancer.

Adeshina *et al.* [14] discussed the utilization of an ensemble learning approach and a deep convolutional neural network (DCNN) to classify breast histopathology images within classes. On the BreakHis dataset, the research attained an inter-class classification accuracy of 91.5%. This result underscores the efficacy of DCNNs and ensemble methods in enhancing the automated classification of breast cancer images and diagnostic results.

The subject of Han [15] is automated breast cancer multi-classification from histopathological images. This is a challenging endeavor that requires the identification of numerous classifications of breast cancer. Proposed is a structured deep learning model that achieves an average accuracy of 93.2% when applied to a massive dataset. The study examines the intricacies of multi-classification and emphasizes the criticality of developing an effective instrument for the multi-classification of breast cancer in clinical environments. Table 1 presents an all-encompassing synopsis of the studies above, furnishing significant perspectives on the progressive terrain of methodologies for predicting breast cancer. It details the approaches utilized and the corresponding outcomes of each study.

Table 1. Related work on breast cancer classification

Author (s)	Model (s)	Year	Results
Gour *et al.* [10]	ResHist (residual learning-based 152-layered CNN)	2020	Achieved an accuracy of 84.34% and an F1-score of 90.49% for breast cancer histopathological image classification without data augmentation. With data augmentation, the model achieved an accuracy of 92.52% and an F1-score of 93.45%.
Gupta and Chawla [11]	AlexNet, VGG16, VGG19, GoogleNet, Inception-v3, ResNet50, ResNet152	2019	The highest accuracy of 93.27%.
Dabeer *et al.* [12]	CNN	2019	Achieved an impressive prediction accuracy of up to 99.86% in the automated detection of breast cancer.
Kassani *et al.* [13]	CNN	2019	The ensemble method attained remarkable accuracies of 98.13%, 95.00%, 94.64%, and 83.10% for the BreakHis, ICIAR, PatchCamelyon, and Bioimaging datasets.
Adeshina *et al.* [14]	DCNN	2018	Achieved an impressive interclass classification accuracy of 91.5% when evaluated on the BreakHis dataset.
Han *et al.* [15]	Multi-classification from histopathological images	2017	Achieved an average accuracy of 93.2% for breast cancer multi-classification from histopathological images.

3. MATERIALS AND METHODS

The research methodology comprises a methodical data collection and preparation process employing CNN architectures and k-fold cross-validation to classify breast malignancies accurately. The subsequent detailed explanation provides an exhaustive account of each phase, with particular attention given to the instruments and strategies to ensure reliable and consistent results. Figure 1 illustrates the proposed methodology.

3.1. Data

We evaluated the efficacy of the CNN models utilizing the BreakHis 400X breast tumor dataset [16], which is available to the public. The information was collected at four distinct magnification levels (400X) from a sample size of 82 patients. During this research endeavor, a magnification level of 400X was employed. There are a total of 1,693 microscopic biopsy images in the collection, which depict benign and malignant breast malignancies. The photographs have a resolution of 700 by 460 pixels.

3.2. Preprocessing

The breast cancer biopsy images acquired from the BreakHis database were adjusted during the pre-processing phase to improve the model's performance and ensure uniformity. To ensure that the photographs had a consistent resolution of 360×360 pixels, they were initially resized utilizing the squishy technique. By employing this methodology, the aspect ratio of the original images was compromised, leading to the distortion of the photographs to conform to the specified dimensions; however, this ensured that all photos in the collection had identical dimensions. Following the scaling procedure, normalizing the pixel values of the images was a crucial step. To aid in training deep learning models, the normalization method typically adjusted the pixel values to a standardized range of [0, 1]. The purpose of employing these

preprocessing methodologies was to optimize the convergence of CNNs during training by minimizing disparities in image dimensions. Ultimately, this would lead to more accurate and robust results in the classification of breast cancer [17].

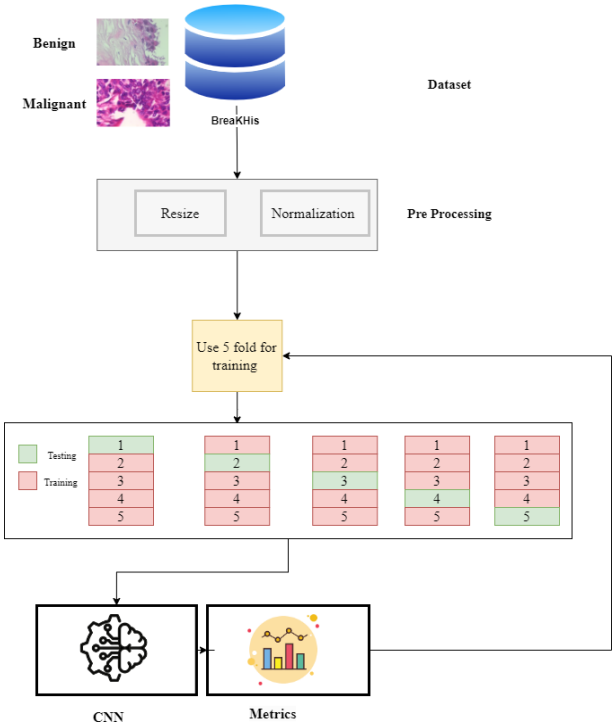

Figure 1. Materials and methods were used for image classification using CNN

3.3. K-fold cross-validation

In order to comprehensively assess the efficacy of our model in processing novel data, we employed a technique called k-fold cross-validation with a value of k=5. By employing this methodology, our dataset is divided into five subsets or 'folds' of equal size. One-fold is designated as the validation set during each iteration; the remaining four folds are utilized for model training. The procedure is executed in five iterations, with each fold being utilized exactly once as the validation set. K-fold cross-validation offers the benefit of conducting an exhaustive evaluation of our model across multiple subsets of the data, thereby reducing the impact of data variability and producing a more reliable evaluation of its performance [18].

3.4. CNN architectures

Our study employed CNNs as robust methodologies. These computer programs are exceptionally intelligent and are inspired by the human brain. Consider them proficient investigators with expertise in discerning intricate patterns within photographs. These entities exhibit remarkable skill in distinguishing shapes, boundaries, and complex components within images, making them highly suitable for detecting cancer in medical imagery. By furnishing these researchers with an extensive collection of microscopic images depicting breast tissue, they can ascertain whether the tissue is in good health or displays signs of malignancy. CNNs serve as dependable partners in the understanding and identification of breast cancer through the utilization of visual depictions [19]. For our investigation, we used two distinct categories of investigators: residual network (ResNet) and VGG. These investigators possess exceptional skills and abilities in technology, akin to superheroes. ResNet is renowned for achieving significant depth and effectively identifying intricate visual patterns in photos. VGG, however, is renowned for its straightforward but efficient methodology in comprehending images. We selected these detectives based on their expertise in image analysis since we need their assistance in identifying indicators of breast cancer in microscopic photos. ResNet excels in processing complex pictures, whereas VGG has exceptional proficiency in analyzing intricate details. In order to correctly determine the health status of a tissue sample, we intended to form a formidable alliance between these two investigators. They are akin to our formidable pair in the realm of picture analysis!

3.4.1. ResNet-50

ResNet-50 represents a unique iteration of the ResNet architecture, widely recognized for its depth and efficacy when applied to the training of complex CNNs. It first appeared in the revolutionary period [20]. The research publication acknowledged the prestigious 2016 ImageNet large scale visual recognition challenge and unveiled ResNet-50, a groundbreaking resolution to the challenges associated with training deep neural networks. Its implementation of residual learning distinguishes ResNet-50. This methodology enables the training of deep networks to acquire knowledge from the residual information, denoting the discrepancy between the predicted and observed outputs. ResNet-50, a model renowned for its innovative architecture and profound profundity, has solidified its position as a foundational instrument in image recognition and achieves consistent superiority across an extensive array of computer vision tasks. ResNet 50's architectural details are presented in Table 2.

Table 2. ResNet 50 architecture

Layer type	Output shape	Number of filters	Kernel size	Stride
Input	224×224×3	-	-	-
Convolutional	112×112×64	64	7×7	2
Residual block	112×112×64	64	3×3	1
Residual block	112×112×64	64	3×3	1
Downsampling	56×56×128	128	3×3	2
Residual block	56×56×128	128	3×3	1
Residual block	56×56×128	128	3×3	1
Downsampling	28×28×256	256	3×3	2
Residual block	28×28×256	256	3×3	1
Residual block	28×28×256	256	3×3	1
Downsampling	14×14×512	512	3×3	2
Residual block	14×14×512	512	3×3	1
Residual block	14×14×512	512	3×3	1
Global average pooling	1×1×512	-	-	-
Fully connected	1×1×1000	-	-	-

3.4.2. VGG-19

VGG-19 is an improved iteration of VGG-16, featuring three additional convolutional layers for nine- teen. VGG-19's enhanced depth capability empowers it to proficiently capture complex features within images, rendering it exceptionally well-suited for tasks requiring sophisticated feature extraction. Like VGG-16, VGG-19 maintains a consistent convolutional kernel size pattern of 3×3. This facilitates the development and training of models due to their homogeneity. VGG-19 is frequently employed when maximum precision is required, and adequate computational resources are available to process its more intricate architecture [21]. The VGG 19 model's architecture is presented in Table 3.

Table 3. VGG19 architecture

Layer type	Output shape	Number of filters	Kernel size	Stride
Input	224×224×3	-	-	-
Convolutional	224×224×64	64	3×3	1
Convolutional	224×224×64	64	3×3	1
Max Pooling	112×112×64	-	2×2	2
Convolutional	112×112×128	128	3×3	1
Convolutional	112×112×128	128	3×3	1
Max Pooling	56×56×128	-	2×2	2
Convolutional	56×56×256	256	3×3	1
Convolutional	56×56×256	256	3×3	1
Convolutional	56×56×256	256	3×3	1
Convolutional	56×56×256	256	3×3	1
Max Pooling	28×28×256	-	2×2	2
Convolutional	28×28×512	512	3×3	1
Convolutional	28×28×512	512	3×3	1
Convolutional	28×28×512	512	3×3	1
Convolutional	28×28×512	512	3×3	1
Max Pooling	14×14×512	-	2×2	2
Convolutional	14×14×512	512	3×3	1
Convolutional	14×14×512	512	3×3	1
Convolutional	14×14×512	512	3×3	1
Convolutional	14×14×512	512	3×3	1
Max Pooling	7×7×512	-	2×2	-

3.4.3. AlexNet

AlexNet, an innovative CNN architecture, brought about substantial changes in deep learning and image recognition. AlexNet won the 2012 ImageNet large scale visual recognition challenge [22]. This development signified significant advancement in the capability of neural networks to discern objects within photographs. AlexNet is composed of three entirely linked levels after five convolutional layers, for a total of eight layers. A pivotal development was implementing rectified linear units (ReLU) as activation functions, substantially accelerating convergence and training. Additionally, implementing dropout regularization to prevent overfitting was a noteworthy feature. The groundbreaking performance and profound architecture of AlexNet laid the groundwork for subsequent developments in deep learning and tasks involving image categorization. The AlexNet architecture is illustrated in Table 4.

Table 4. AlexNet architecture

Layer Type	Output Shape	Number of Filters	Kernel Size	Stride
Input	227×227×3	-	-	-
Convolutional 1	55×55×96	96	11×11	4
Max Pooling 1	27×27×96	-	3×3	2
Convolutional 2	27×27×256	256	5×5	1
Max Pooling 2	13×13×256	-	3×3	2
Convolutional 3	13×13×384	384	3×3	1
Convolutional 4	13×13×384	384	3×3	1
Convolutional 5	13×13×256	256	3×3	1
Max Pooling 3	6×6×256	-	3×3	2
Fully Connected 1	4096	-	-	-
Fully Connected 2	4096	-	-	-
Fully Connected 3	1000	-	-	-

4. RESULT AND DISCUSSION

Using the BreakHis dataset, the primary objective of this study is to assess the performance of each of the trained models described in the preceding section. The dataset comprises 1,693 microscopic biopsy images, consisting of a variety of breast tumor types (malignant and benign). The images have a resolution of 700 by 460 pixels. Two categories were used to categorize the tumors: benign and malignant. Following that, the K-fold cross-validation method was implemented, wherein the value of k was established as 5. The investigation was conducted on a GPU server (Kaggle notebook) utilizing Python 3 and the FastAI platform to construct and assess our approach.

4.1. CNN configuration

Our experiments established a consistent and comparable training environment for all three CNN architectures (VGG19, AlexNet, and ResNet50) [23]. Throughout the optimization procedure, the magnitude of each phase was regulated by a learning rate of 0.01. The CrossEntropyLossFlat loss function was employed to measure the deviation between predicted and observed labels, owing to its appropriateness for classification-oriented tasks. Furthermore, we assessed the model's performance by employing accuracy as the primary metric, enabling us to determine the proportion of accurately classified instances precisely. To ensure comprehensive and reliable evaluation, we implemented a 5-fold cross-validation methodology. By employing this approach, the dataset was divided into five distinct subsets, with a revolving rotation of each subset serving as the validation set while the model was trained on the remaining four subsets. Each fold that the procedure underwent five iterations of was subsequently designated as the validation set. Following this, we computed the average of the outcomes derived from these five iterations, thereby obtaining a comprehensive assessment of the model's efficacy across various subsets of the dataset. By implementing a systematic approach, we successfully enhanced the reliability of our findings and arrived at robust conclusions regarding the effectiveness of the CNN architectures under investigation.

4.2. Metrics

Our experiments established a consistent and comparable training environment for all three CNN architectures (VGG19, AlexNet, and ResNet50). Throughout the optimization procedure, the magnitude of each phase was regulated by a learning rate of 0.01. The CrossEntropyLossFlat loss function was employed to measure the deviation between predicted and observed labels, owing to its appropriateness for classification-oriented tasks [24]. Furthermore, we assessed the model's performance by employing accuracy as the primary metric, enabling us to determine the proportion of accurately classified instances precisely. To ensure comprehensive and reliable evaluation, we implemented a 5-fold cross-validation methodology. The approach involved dividing the dataset into five distinct subsets, with a revolving rotation of each subset

serving as the validation set. On the contrary, the model underwent training using the four remaining subsets. Each fold the method underwent five iterations over was designated the validation set. Following this, the mean of the outcomes derived from these five iterations was computed, enabling a comprehensive assessment of the model's performance across various subsets of the dataset. By implementing a systematic approach, we enhanced the reliability of our findings and arrived at definitive conclusions regarding the effectiveness of the CNN architectures we examined.

4.2.1. Accuracy

The percentage of correctly classified audio samples is referred to as accuracy. It includes all four possibilities: true positives (TP), true negatives (TN), false positives (FP), and false negatives (FN). This formula defines accuracy.

$$\text{Accuracy} = \frac{TP+TN}{TP+TN+FP+FN} \quad (1)$$

4.2.2. The F-score

F-score is a single number that summarizes how well a system or model performs in making accurate positive predictions and finding all positive cases. It combines two key metrics: precision (the accuracy of positive predictions) and recall (the ability to find all positive cases) [25]. The F1-score strikes a balance between these two factors, providing a single measure of performance. It ranges from 0 to 1, with higher values indicating better performance. It is a handy tool for evaluating the effectiveness of classification systems. This formula defines the F-score:

$$F - Score = \frac{2 \times Recall \times Precision}{Recall + Precision} \quad (2)$$

4.3. Result

Table 5 and Figure 2 provide the accuracy scores of multiple CNN designs, namely AlexNet, ResNet50, ResNet32, ResNet18, VGG16, and VGG19. These values are shown for different folds of a cross-validation procedure. Accuracy quantifies the frequency with which the models accurately categorized occurrences within the dataset.

Table 5. Result for 10 epoch

#Epoch	learning rate		Accuracy			F-Score		
		Fold	AlexNet	ResNet 50	VGG 19	AlexNet	ResNet 50	VGG 19
10	0.01	1	0.94	0.97	0.943	0.94	0.979	0.944
		2	0.95	0.98	0.93	0.946	0.979	0.932
		3	0.94	0.97	0.943	0.943	0.973	0.944
		4	0.94	0.96	0.946	0.94	0.979	0.947
		5	0.95	0.98	0.937	0.9496	0.982	0.937
		Mean	0.94	0.98	0.941	0.944	0.979	0.94
	0.001	1	0.94	0.97	0.943	0.94	0.979	0.944
		2	0.95	0.98	0.93	0.946	0.979	0.932
		3	0.94	0.97	0.943	0.943	0.973	0.944
		4	0.94	0.96	0.946	0.94	0.979	0.947
		5	0.95	0.98	0.937	0.9496	0.982	0.937
		Mean	0.94	0.98	0.941	0.944	0.979	0.94
	0.05	1	0.94	0.97	0.943	0.94	0.979	0.944
		2	0.95	0.98	0.93	0.946	0.979	0.932
		3	0.94	0.97	0.943	0.943	0.973	0.944
		4	0.94	0.96	0.946	0.94	0.979	0.947
		5	0.95	0.98	0.937	0.9496	0.982	0.937
		Mean	0.94	0.98	0.941	0.944	0.979	0.94

The table displays the accuracy scores attained by each CNN architecture for every fold, representing distinct splits of the data. The 'Mean' row at the bottom displays the mean accuracy for each architecture's overall folds, allowing us to evaluate the overall performance of each CNN and choose the best one on average. Greater accuracy values signify superior performance in accurately categorizing the data, facilitating the comparison of the efficacy of different CNN models for your particular objective.

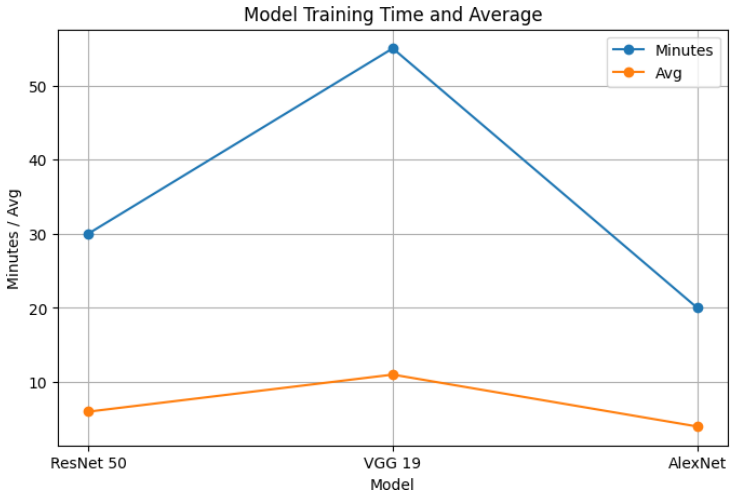

Figure 2. Materials and methods were used for image classification using CNN

5. CONCLUSION

The study conducted insights into the utilization of CNNs in predicting breast cancer through the analysis of microscopic biopsy images. Utilizing the BreakHis dataset and the VGG19, AlexNet, and ResNet50 architectures, this study exhaustively evaluates the models' performance. The results demonstrate that ResNet50 consistently outperformed alternative designs in classifying benign and malignant breast tumors, as measured by F-score and accuracy. Using the 5-fold cross-validation technique, CNN models were rigorously evaluated, resulting in dependable conclusions concerning their effectiveness in detecting breast cancer. The results for ten epochs, each with a distinct learning rate (0.01, 0.001, and 0.05), are presented in the table to illustrate the model's performance in various configurations. Significantly, ResNet50 demonstrated the highest levels of accuracy and F-score across all scenarios, underscoring its efficacy in the prediction of breast cancer. This study makes a substantial contribution to enhancing patient outcomes in breast cancer diagnosis by utilizing cutting-edge technologies. The results emphasize the critical significance of CNNs, specifically ResNet50, in transforming the field of medical image analysis in the context of breast cancer prognosis. ResNet50's rigorous assessment and consistent performance as the superior model establish it as a highly prospective contender for additional investigation and integration into clinical environments.

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