Breast Cancer Detection in Histopathology Images using ResNet101 Architecture

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Abstract: Cancer is a significant challenge in many fields, especially health and medicine. Breast cancer is among the most common and frequent cancers in women worldwide. Early detection of cancer is the main step for early treatment and increasing the chances of patient survival. As the convolutional neural network method has grown in popularity, breast cancer can be easily identified without the help of experts. Using BreaKHis histopathology data, this project will assess the efficacy of the CNN architecture ResNet101 for breast cancer image classification. The dataset is divided into two classes, namely 1146 malignant and 547 benign. The treatment of data preprocessing is considered. The implementation of data augmentation in the benign class to obtain data balance between the two classes and prevent overfitting. The BreaKHis dataset has noise and uneven color distribution. Approaches such as bilateral filtering, image enhancement, and color normalization were chosen to enhance image quality. Adding flatten, dense, and dropout layers to the ResNet101 architecture is applied to improve the model performance. Parameters were modified during the training stage to achieve optimal model performance. The Adam optimizer was used with a learning rate 0.0001 and a batch size of 32. Furthermore, the model was trained for 100 epochs. The accuracy, precision, recall, and f1-score results are 98.7%, 98.73%, 98.7%, and 98.7%, respectively. According to the results, the proposed ResNet101 model outperforms the standard technique as well as other architectures.

Keywords: ResNet101, Augmentation, Bilateral Filtered, Image Enhancement, Color Normalization.

INTRODUCTION

Breast cancer is the most common cancer worldwide, especially in women, caused by abnormal cells in the breast. The disease's most common symptom is a new lump or mass in the breast that is usually hard and painful. Computer-Aided Diagnostic (CAD) models have become a viable strategy for early detection, enhancing treatment effectiveness, and increasing survival chances as computer science has advanced (Gour, Jain, & Sunil Kumar, 2020) (Ghosh et al., 2021). With the advancement in computing power, the Convolutional Neural Network has become one of the most well-known tools for breast cancer diagnosis.

Convolutional Neural Networks have been proven to overcome problems such as classification, segmentation, and detection of various objects (Kumar & Alqahtani, 2022). The successful application of CNN to medical imaging can accelerate experimentation and analysis, leading to future treatments and improving patient care. However, the availability of limited and complex data in medical images may limit the generalizability of existing models (Chowdhury et al., 2022). In State-of-the-art breast cancer (Z. Zhu, Wang, & Zhang, 2023), the CNN model is prone to overfitting when working with limited data, which can worsen the model's generalization performance. There is a need for a

methodology where available data can be used to improve algorithm performance in conditions of scarce and complex data. In addition, determining which layer of the CNN model provides the best features still requires further investigation.

Although computer vision tasks have many advantages, medical imaging cannot always rely on large data sets to train CNNs. This may be due to three things. First, medical images differ from natural images that can be easily created or found online. Histopathological medical images, Ultrasound (US), X-ray mammography, Portion Emission Tomography (PET), Computed Tomography (CT), and Magnetic Resonance Imaging (MRI) require specialized equipment (Nassif, Talib, Nasir, Afadar, & Elgendy, 2022) and highly qualified experts, making these procedures subjective (Eldin, Hamdy, & Adnan, 2021), and time-consuming (Cappello, Richetelli, & Lee, 2019). Because of the variety and complexity of testing, cancer types, and differences in pathologist skill, the procedures done may be prone to many misinterpretations (Sohail, Khan, Nisar, Tabassum, & Zameer, 2021), (Kumar & Alqahtani, 2022). Secondly, it is difficult to get an overview of medical facilities under the 1996 Health Insurance Portability and Accountability Act (HIPAA) law that prevents the release of medical data without prior consent and must remove personal information from patients. This made it challenging to collect medical records. Finally, manual annotation requires expertise from subject matter experts (Al-sayyed, 2021) (Chowdhury et al., 2022) which is costly (Cappello et al., 2019) making it impossible to collect datasets comparable to ImageNet.

Research (Al-sayyed, 2021) By deleting the last layer connected to VGG16 and employing data augmentation to lessen the imbalance between class labels on BreaKHis data, we were able to extract high-level features from breast photos, which consists of two classes, namely benign and malignant. Furthermore, researchers (Alqahtani et al., 2022) created a new CNN model called msSE-ResNet for breast cancer classification. The results obtained are accuracy, precision, and recall of 88.2%, 88.4%, and 95.1%, respectively. Although the method used was a great success, the model still requires a lot of data for good model development (Tiwari, Dixit, & Gupta, 2021) (Saber et al., 2021). In addition, The findings of the research revealed that unique characteristics present in the dataset need to be considered, such as color distribution (Duggento, Conti, Mauriello, Guerrisi, & Toschi, 2021) (Alqahtani et al., 2022) and variations in medical images. This can result in unpredictable errors even when using the best-performing models (Chen et al., 2020). Especially in histopathology medical images, special tuning is needed for further investigation using CNN.

Transfer learning models are important in improving diagnosis performance in the medical field, especially on complex images (Montaha et al., 2021). ResNet101 is a convolutional neural network model that uses bypass to remove blocks from the convolutional layer. It has a clear hierarchical structure (Wu, Xin, Fang, Hu, & Hu, 2019), and is effective in validation, simplicity, and parameter efficiency (Fazari et al., 2021). According to (Mahmud & Abdelgawad, 2023) ResNet101 is a CNN model that helps improve image recognition accuracy and can solve complex tasks. Transfer learning from CNN models that have been previously trained using natural datasets such as ImageNet to medical images can provide a significant improvement in model performance.

Based on the explanation above, this research discusses a deep learning approach to detect breast cancer using CNN on the BreaKHis breast cancer histopathological image dataset. This research aims to improve the accuracy of a study conducted by (Alqahtani et al., 2022) (Ogundokun, Misra, Akinrotimi, & Ogul, 2023) by paying attention to data preprocessing and modifying the ResNet101 model to get optimal results. The treatment of preprocessing and ResNet101 architecture is expected to help doctors and pathologists precisely identify and detect breast cancer to provide accurate diagnoses.

LITERATURE REVIEW

Before beginning study on the detection of breast cancer, the researcher conducted a literature review of past research to use as a reference in formulating the research to be carried out. From the literature review, several previous studies were obtained related to the research to be carried out. As in the research (Chowdhury et al., 2022), the researcher made an Android application, "ABCanDroid," to help users distinguish between malignant and normal tissue by uploading histopathological images. CNN equipped with transfer learning is applied to improve the efficiency and accuracy of early detection of breast cancer. Another study by (Saber et al., 2021) involved a transfer-learning-based deep-learning model

to detect breast cancer using 80-20 and cross-validation techniques. Research conducted (Chen et al., 2020) developed an automatic quality assurance method for automatic segmentation using CNN. The performance of the Resnet101 method with customized parameter settings on augmentation and segmentation methods. Research by (Gupta, Vasudev, Doegar, & Sambyal, 2021) The CNN model was adapted to identify breast cancer. ResNet was modified in three stages. First, a dropout of 0.5 is used. Then, in two CNN layers, adaptive average pooling and adaptive max-pooling are applied. The last step is bottom sampling at 3x3 convolution.

Similar research was also conducted by (Liu, Yi, Wu, Wang, & He, 2022) using bilateral sensitivity to reduce noise and blur effects while maintaining details in the image. Furthermore, (Chaudhury, Rakhra, Memon, Sau, & Ayana, 2021; Liu et al., 2022) applied image enhancement, which aims to reduce the impact of noise and allow CNN models to recognize better and distinguish relevant features. Similarly, some studies have used color normalization to ensure consistency and reasonable interpretation in histopathology image analysis. For example (Sohail, Khan, Nisar, Tabassum, & Zameer, 2021)(C. Zhu et al., 2019) applied color normalization to achieve this goal. The approach uses an RGB histogram that relates the color values of the target image to the source image on a pixel-by-pixel basis. Since BreaKHis has significant variations or high noise levels, additional preprocessing approaches remain important before feeding the images into the artificial neural network (CNN). This study chose methods such as bilateral filtering, image enhancement, and color normalization to reduce the noise level in the histopathology images.

In addition, since tasks involving medical imaging cannot always rely on large datasets, it is necessary to augment the limited data to form a dataset that can be processed to train a CNN and generate a model capable of generalizing to data that has not been seen before. Specifically, data augmentation is used in this research. Data augmentation is a popular way to increase the size of data sets (Saber et al., 2021). Besides being a simple and inexpensive technique, augmentation can significantly improve model performance and robustness (Tiwari et al., 2021).

METHOD

A research design model or workflow is always used to outline a study's research flow. Figure 1 displays the study steps, which include four processes: dataset collecting, data preparation, architectural model development, and testing or evaluation.
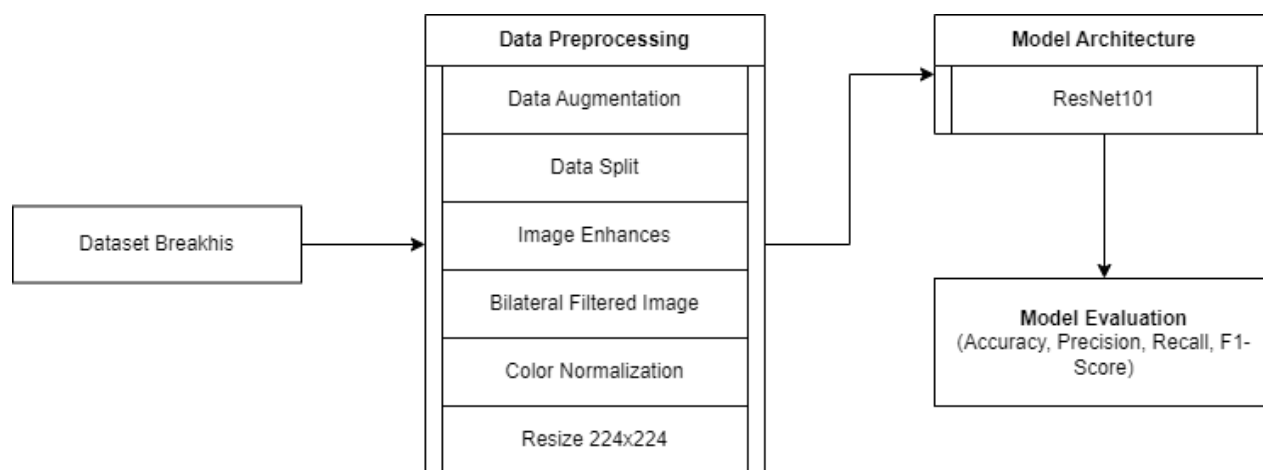

Figure 1. Research Workflow

This research uses the BreaKHis Dataset. Furthermore, entering data preprocessing involves a series of stages performed on the image before it is inserted into the machine learning model. The preprocessing steps carried out are data augmentation and image enhancement. Then, using the ResNet101 architecture that has been pre-trained using ImageNet for breast cancer detection modeling. Next, fine-tuning is done to retrain the dataset on some layers of the pre-trained model. Fine-tuning is to unfreeze the layers near the output by unfreezing certain layers and retraining on the BreaKHis

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dataset. This process is called transfer learning, which is very good for working on relatively small datasets. A more detailed explanation will be provided below.

Dataset

Data collection is carried out to obtain a wide range of information required for research projects. This dataset includes medical drawings of breast cancer histology from earlier studies(Spanhol, Oliveira, Petitjean, & Heutte, 2016). Histopathological medical depictions are derived from cellular staining of biopsy results, which are then processed with hematoxylin and eosin (H&E) staining. This staining technique, which uses hematoxylin and eosin, is extensively used in cancer research, producing pink-colored tissue and blue-colored cell nuclei. Until now, histopathological methods required pathologists to do hand microscopic inspections of stained slides. The scope of the BreaKHis medical imaging dataset is reasonably limited. Such dataset restrictions can limit the applicability of existing models (Chowdhury et al., 2022). The BreaKHis dataset exhibits contrast and color changes (Elmannai, Hamdi, & Algarni, 2021). The many processes used to acquire histopathology data cause distortions and blurriness in medical images (Rashmi, Prasad, & Udupa, 2022). Figure 2 depicts an illustration of the BreaKHis dataset.
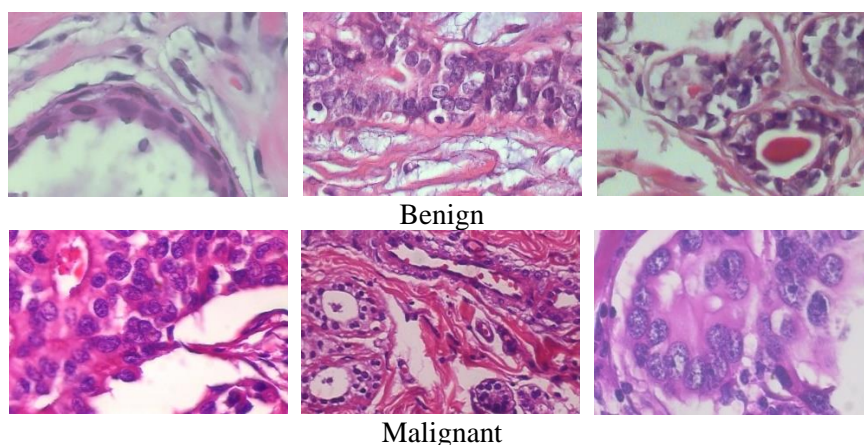

Benign

Malignant

Figure 2. Sample Dataset BreaKHis

The BreaKHis dataset is divided into two categories: benign and malignant. When studied histologically, benign tumors include lesions that do not adhere to the features of malignant tumors. Benign tumors are typically harmless, develop slowly, and are localized. Cancer is synonymous with malignancy. Cancerous lesions have the ability to infiltrate and damage neighboring structures (local invasion), spread to distant locations (metastasis), and finally cause death. The breast cancer histopathology photos (BreaKHis) are a collection of 9,109 microscopic photographs demonstrating breast cancer tissue with increasing degrees of differentiation (magnification levels of 40x, 100x, 200x, and 400x) taken from 82 patients. The database now contains 2,480 benign samples and 5,429 malignant samples (each image measuring 700×460 pixels in PNG format, with RGB including three channels and an 8-bit depth for each channel). However, this study only uses images enlarged at 400x, including 1,146 malignant cases and 547 benign cases.

Preprocessing Data

Preprocessing involves a series of steps performed on the image before it is incorporated into the ResNet101 architecture model. The preprocessing steps performed are data augmentation and image enhancement, such as bilateral filtered, image enhancement, and color normalization chosen to reduce the noise level in the histopathology image.

   a. Data Augmentation

In this research, data augmentation is implemented. Data augmentation is done to expand the amount of training data by creating new variations of existing data. In this research, data augmentation is only applied to the minority data. Histopathology images are characterized by rotation and reflection symmetry. This means that histopathology images can be geometrically transformed. When applied, the transformation will not change the information in the image. Therefore, the transformations in the augmentation used are Rescale, Rotation Range, Brightness Range, Horizontal flip, and Vertical flip. Figure 3 shows the sample data after augmentation. The amount of data used based on the class can be seen in Table 1
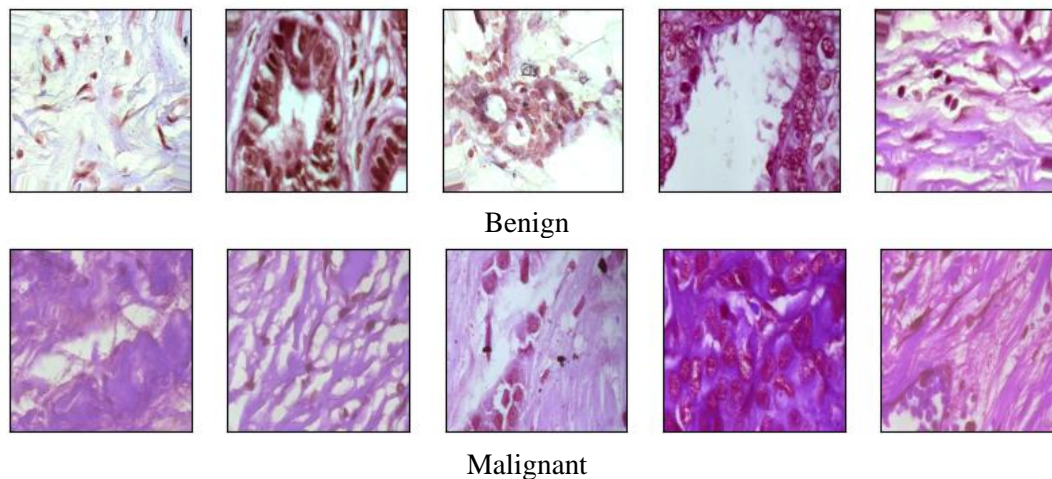
.

Benign

Malignant

Figure 3. Augmentation results from histopathology images

In this research, data augmentation is applied to balance the data. In addition, data augmentation can also overcome the generalization problem using deep learning methods. This is because the network learns variations and generalizes previously unobserved images while preventing overfitting in small data.

Table 1.   400 times detailed Breast Cancer Histopathology Image Dataset

Class of Data BreaKHis	Before Augmentation	After Augmentation
Benign	1146	1146
Malignant	547	1146

b. Splitting Data

Splitting data is essential before applying the Convolutional Neural Network architecture model. This research divides the data into three parts: training data, validation data, and testing data, with a ratio of 80:10:10. The CNN model is trained using training data to extract significant features from images and learn the current model. Validation data is utilized during training to monitor the model's performance and aid in parameter selection. Finally, test data is used to assess the model's performance on previously unknown data objectively, hence validating the model's capacity to categorize or identify real-world scenarios.

c. Image Enhancement

Library Image enhancement in this study is used to enhance the image by improving the color and sharpness to achieve sharper and more attractive image results. By setting the color enhancement factor to 1.25 and the sharpness enhancement factor to 1.25, the clarity and sharpness of the image can be significantly improved. These settings enhance the details in the image, making objects more precise and colors more vivid.

d. Bilateral Filtered Image

The use of bilateral filters on histopathology images plays a vital role in improving and enhancing the image quality and information in histopathology images. Histopathology images are microscopic images of body tissues taken for medical diagnostic purposes. However, these images often contain noise low contrast, and have many important details to analyze. Applying bilateral filtering, a non-linear filtering technique that considers the magnitude and spatial extent of image pixels, can reduce noise while preserving edges and important details in histopathological images. This allows for more precise and more accurate visualization of the observed biological tissues, ultimately allowing pathologists and researchers to conduct further analysis to understand the changes and diseases that may have occurred in those tissue samples.

e. Color Normalization

Color Normalization is used to equalize the color distribution in the image so that the image has consistent characteristics when trained on the model. Histopathology images are often taken in different laboratories or using different equipment, which can result in significant color differences between images. Proper color uniformity is essential in histopathology analysis to ensure consistent and reliable results. This color normalization technique works by calculating the average color intensity of the entire image and then measuring a normalization scale based on the maximum value of that average. By applying this scaling factor to each color channel (red, green, and blue), the image can be modified to achieve better color uniformity. This process removes unwanted color variations and improves the interpretation and visual analysis of histopathology images, allowing the model to focus more on the features in the image and not be distracted by irrelevant variations.

f. Resize

The use of resize techniques on histopathology images, changing the original size of the dataset from 460x460 to 224x224 pixels, is an important step in adapting histopathology images for further analysis, especially in the context of developing machine learning models such as convolutional neural networks (CNNs). In image processing, smaller sizes, such as 224 x 224, are often used to reduce the computational and memory costs required when training or applying models. While larger images may display more details, enhancing them can help retain important information and essential features in histopathology images while maintaining the efficiency and speed of the model training and analysis process.

Figure 4 shows a comparison of data samples before and after going through the preprocessing procedure. This preprocessing stage is critical to clean, organize, and transform the raw data into a more structured form ready for further analysis. The first image shows the raw data that has not gone through the preprocessing stage, which offers some noise, blurring, and non-uniform color distribution. However, the second image shows that the data underwent image enhancement, bilateral filtered image, and color normalization processes. The result is data that is more consistent, more detailed, sharper, and more focused on the image features. This data preprocessing helps prepare the raw data into a more informative and easily processed form, as shown in Figure 4.
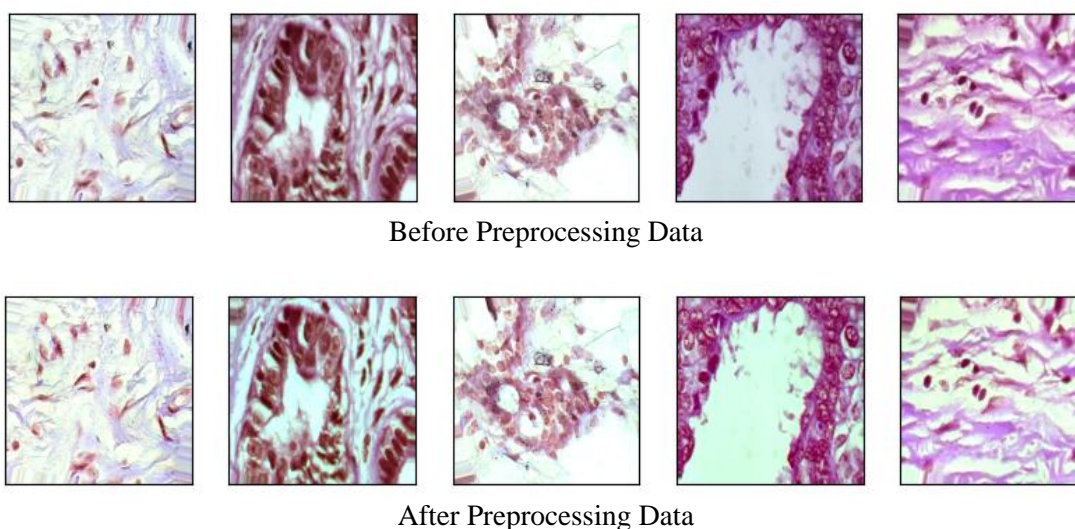
Before Preprocessing Data

After Preprocessing Data

Figure 4. Sample Dataset BreaKHis after Preprocessing Data

Application of ResNet101

In this work, Resnet101 is employed, which is composed of 101 Convolutional layers grouped into 33 blocks, each having a residual connection connecting the first and last blocks. This one-of-a-kind method enhances residual management between the planned convolution and the input function. The use of residual or skip connections enables the model to fine-tune the final layer, which saves training time and improves model performance. (Eldin et al., 2021). ResNet101 is designed to use a bypass link, which allows data to circumvent convolution layer blocks (Mahmud & Abdelgawad, 2023). This method makes obtaining the needed features more effortless and efficient, speeding up neural network training, and boosting the model's accuracy and speed (Aksoy & Salman, 2022). As a result, ResNet101 is a trustworthy and efficient transfer learning model for medical image analysis and other applications. The current work investigates and assesses ResNet101's knowledge concerning the BreaKHis dataset. ResNet101's accuracy architecture is used to create lengthy evaluations.

The ResNet101 model is first trained using the ImageNet dataset in this scenario. The Transfer Learning approach saves computational resources and time because the model does not need to be trained from scratch. As a result, the model already understands the broad task and will adjust when a specific job is assigned. The ResNet101 capability will extract high-level characteristics from histopathological images when combined with transfer learning. Following that, fine-tuning is performed. The first 50 layers are frozen to keep the ImageNet feature representation. The BreaKHis dataset is used to retrain subsequent layers. As a result, the model can mix previous knowledge with fresh data. The approach employs flatten, dense, and dropout layers to improve the model's performance. A thick layer with an activation function in the additional layer construction follows the flatten layer. Then, a dropout layer with a value of 0.2 is added. The dense layer, which has a sigmoid activation function for binary input, is the final layer. Layers enable the trained model to function optimally in the task at hand. Parameters are tweaked during the training cycle to achieve the best model performance. Adam's optimizer was used with a learning rate 0.0001 and a batch size of 32. Furthermore, the model was trained for 100 epochs. This parameter modification increases the model's generalization on BreaKHis data.

In addition to using the previously mentioned parameters, this research also uses checkpoint, early stopping, and reduced learning rate functions. Model checkpoints are used to save duplicate models periodically during the training process. Early Stopping monitors performance metrics such as accuracy or loss on validation data. The training process is stopped early if the model's performance degrades on the validation data after a few epochs. This helps prevent the model from adapting too well to the training data and improves the general ability of the model

to generalize on data that it has not seen before. Furthermore, reducing the learning rate can help the model converge to the minimum loss value. Combining the three techniques will help the model achieve better convergence and produce a stable model.

Evaluation Model Performance.

In this research project, we conducted a series of tests to determine the effect of data augmentation on model performance. We hoped to assess the enhancement brought about by this strategy by contrasting the model's results before and after data augmentation. The model's efficacy was evaluated using a test set partitioned before the model's training phase, guaranteeing a fair evaluation. Using several matrices was critical in demonstrating the robustness of the ResNet101 model. Our method included the use of a variety of indicators to evaluate the performance of the ResNet101 model. The evaluation metrics we used provided a multifaceted perspective, deepening our investigation. Accuracy is used as a model evaluation. The following indicators were used to evaluate the ResNet101 model's efficacy holistically.

$$Accuracy \ = \ \frac{TP+TN}{TP+FP+TN+FN} \qquad \square\square\square$$

Accuracy is a critical parameter for assessing the accuracy of predictions made by the trained model. It provides information about the proportion of correct forecasts among all predictions. The following formula explains how to calculate Accuracy.

$$Precision \ = \ \frac{TP}{TP+FP} \qquad \square\square\square$$

Precision is quantified as a ratio of the correctly predicted cases to the total cases predicted by the model. This metric shed light on the percentage of accurate predictions within the context of positive outcomes. In other words, Precision elucidates the reliability of the model's positive predictions. The mathematical representation of Precision can be observed in the equation provided below:

$$Recall \ = \ \frac{TP}{TP+FN} \qquad \square\square\square$$

Recall describes how frequently the model delivers correct predictions. It provides information on the percentage of true positive cases correctly detected by the model. This indicator displays the proportion of positive occurrences accurately identified from the total number of positive cases in the dataset. The following equation encapsulates the mathematical expression of Recall:

$$F1 - Score \ = 2 \ x \ \frac{Precision \ x \ Recall}{Precision+Recall} \qquad \square 4\square$$

The F-Score is an evaluation metric for the model's performance. It functions as a scoring mechanism, with a higher F-Score indicating a more capable model. The F-Score, also known as the F1-Score, represents the model's performance by encapsulating the balance between Precision and Recall. The following equation depicts the mathematical expression that regulates the calculation of the F1-Score:

A confusion matrix illustrates the features of the classification rule, including the number of elements that have been correctly or incorrectly classified for each unique class. This matrix depicts the associations between true positive, true negative, false positive, and false negative predictions for each class, providing a comprehensive perspective of the model's performance.

RESULT

This section will explain the results of each experiment conducted. Experiments were performed using the ResNet101 architecture model on training and validation data. This experiment used Adam optimizer, learning rate 0.0001, and batch size 32, with training for 100 epochs. To improve the model's performance, flatten, dense, and dropout layers are used. The flatten layer is followed by a thick layer with an activation function in the additional layer construction. A dropout layer with a value of 0.2 is then applied. The dense layer, which has a sigmoid activation function for binary input, is the final layer. Layers enable the trained model to function optimally in the task at hand. To achieve the best model performance, parameters are tweaked during the training cycle.

In training a Convolutional Neural Network model, during the process, the model will be iterative. Iterative in the model aims to make the model better at understanding patterns in the data and making accurate predictions. As demonstrated in Figure 5, the accuracy and loss function in the training and validation data show a flat and constant pattern. This indicates that the model is converging and getting closer to the optimal solution.
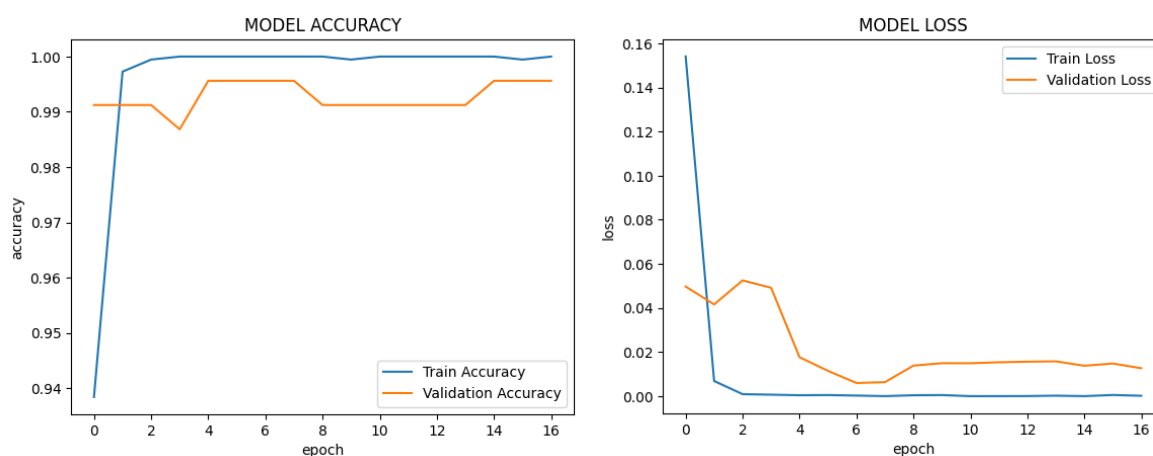

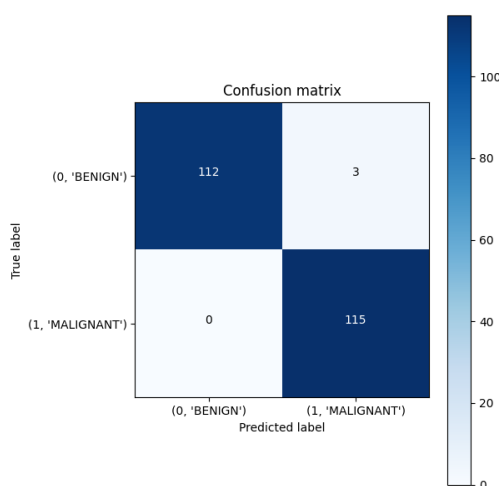Figure 5. Accuracy and Loss Function on ResNet101

Figure 6. Confusion Matrix on ResNet101

To measure the performance of the model, the confusion matrix is used. It shows how well the model can predict the various classes in the dataset. The confusion matrix is handy for understanding where the model makes mistakes and what frequent errors occur. Figure 6 shows the confusion matrix results of the ResNet101 architecture model on the testing data. A total of 112 True Positive values were identified, which means the model correctly predicted benign cases. True Negative as many as 115

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means the model predicts malignant, means is malignant. False Positive shows the model predicts benign, but in fact, it is malignant as much as 3. While in False Negative, the model predicts malignant, in fact, it is a benign case. Based on the confusion matrix in Figure 6, the accuracy, precision, Recall, and F1-Score results are obtained as shown in Table 2.

Table 2. ResNet101 Implementation Results

Model	Accuracy	Precision	Recall	F1-Score
ResNet101	98.7%	98.73%	98.7%	98.7%

DISCUSSIONS

In this section, the performance of the ResNet101 architecture model is compared with previous studies. Table 3 shows the accuracy, precision, recall, and F1-Score values. The accuracy result is 98.7%, precision 98.73%, recall 98.7%, and F1-Score 98.7%. The results show that the ResNet101 architecture model successfully detects breast cancer with the proposed method, namely augmentation, image quality improvement and ResNet101 modification. The model proposed in this study produces more accurate and better results than previous studies (Alqahtani et al., 2022) (Ogundokun et al., 2023) in breast cancer detection.

Table 3. Accuracy Comparison

Method	Recall
(Pandian, 2020)	89%
(Alqahtani et al., 2022)	88.2%
(Ogundokun et al., 2023)	91%
ResNet101 (Proposed Model)	98.7%

CONCLUSION

After experimenting and evaluating the ResNet101 architecture model, the experiments conducted by adding data augmentation, implementing bilateral filtered, image enhanced, and color normalization, and modifying the ResNet101 model exceeded the author's expectations. The findings for accuracy, precision, recall, and the f1-score are 98.7%, 98.73%, 98.7%, and 98.7%, respectively. The results reveal that the suggested ResNet101 model outperforms the conventional technique and other architectures used in earlier studies to detect breast cancer using BreaKhis histopathology pictures. It should be mentioned, however, that the results of this investigation are confined to the conditions and datasets employed in this study. In the future, it is critical to refine the CNN model for further research by using data augmentation techniques such as GAN while keeping image quality in mind.

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