AI-Assisted Early Detection of Breast Cancer Using Histopathological Image Analysis

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Abstract

Breast cancer is one of the most common cancers among women worldwide with more than 2.3 million new breast cancer cases diagnosed each year [1], where early detection has a significantly positive effect on patient survival rates. Examination of histopathological features remains the gold standard [2] in the diagnosis of breast cancer, however, clinical histopathological assessment is labor-intensive, time consuming and can potentially have inter-observer variability in the determination of the final clinical diagnosis. The current paper presents an AI-assisted deep learning framework for automatic breast cancer detection using histopathological images. Multiple transfer learning models, including VGG16, ResNet50, DenseNet121, EfficientNetB0, and EfficientNetB5, were evaluated. The proposed framework incorporates data augmentation, mixed precision training, and Binary Focal Loss to improve performance and computational efficiency. Experimental results on a dataset of over 14,000 histopathological images demonstrate that DenseNet121 achieves the best performance, with a test accuracy of 81%, sensitivity of 80.8%, specificity of 76.7%, and ROC-AUC of 0.87. VGG16 also shows stable performance, while ResNet50 suffers from low specificity due to over classification of malignant classes. EfficientNet models exhibit poor generalization and strong class bias. The result highlights the importance of evaluating multiple performance metrics beyond accuracy in medical image classification. The proposed frameworks can assist pathologists by improving diagnostic consistency and reducing workload, making it a practical tool for clinical applications.

Keywords: Deep Learning, Breast Cancer Detection, Histopathology, Transfer Learning, Densenet121, Explainable AI

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1.Introduction

Breast cancer remains a major public health concern and is the most commonly diagnosed cancer among women worldwide [1]. Early and accurate detection is critical for reducing mortality rates. Histopathological image analysis is considered the gold standard for diagnosis [2]; however, manual examination is time-consuming, labor-intensive, and subject to inter-observer variability, which can affect diagnostic consistency. Recent advancements in Deep Learning (DL), particularly Convolutional Neural Networks (CNNs), have demonstrated significant potential in automating medical image analysis and improving diagnostic accuracy [3], [4], [5], [6]. Transfer learning enables the use of pre-trained models to effectively learn from limited medical datasets, making it highly suitable for histopathological image classification tasks. In this study, we propose a deep learning-based framework to classify histopathological images as malignant or normal. Multiple transfer learning architectures, including VGG16, ResNet50, DenseNet121, EfficientNetB0, and EfficientNetB5, are evaluated to identify the most suitable model for this task. The framework incorporates data augmentation, mixed precision training, and Binary Focal Loss to enhance performance and computational efficiency. The experimental analysis demonstrates that DenseNet121 provides the best balance between sensitivity and specificity, making it more reliable for medical diagnosis compared to other models. The proposed framework aims to assist clinicians by improving diagnostic consistency and reducing workload, thereby supporting better clinical decision-making.

The key contribution of this paper are:

- A comparative deep learning framework for breast cancer detection using histopathological images, evaluating multiple transfer learning models including VGG16, Resnet50, DenseNet121, and EfficientNet variants.
- Implementation of data augmentation, mixed precision training and Binary Focal Loss to improve model performance and training efficiency.
- Comprehensive evaluation using multiple performance metrics including accuracy, sensitivity, specificity, F1-score, ROC_AUC, and confusion matrices.
- Analysis of model trade-offs in term of accuracy, generalization, and inference time, highlighting the limitations of deeper architectures such as EfficientNet in the task.
- Identification of DenseNet121 as the most suitable model due to its balanced and reliable classification performance.

2. Preliminaries

Recent advancements in deep learning have significantly improved the performance of medical image analysis systems, particularly in histopathological image classification [4], [7], [8], [9], [10]. Convolutional Neural Networks (CNNs) and transfer learning techniques have been widely adopted for breast cancer detection due to their ability to extract complex spatial features from high-resolution images. Several pre-trained architectures such as ResNet [11], EfficientNet [12], and VGG16 [3], [13] have been successfully applied to classification tasks, achieving high accuracy across various medical imaging datasets. DenseNet-based models have also gained attention due to their dense connectivity, which improves feature reuse and gradient flow, leading to better generalization performance [14], [15]. The BreakHis dataset introduced by Spanhol et al. [2], [16] has become a widely used benchmark for evaluating breast cancer classification models using histopathological images. Additionally, Explainable AI techniques such as Grad-CAM [17] have been employed to visualize model decision regions, improving interpretability and trust in clinical applications. Despite these advancements, many state-of-the-art models, particularly deeper architectures such as EfficientNet and Vision Transformers (ViTs) [18], require large-scale datasets and high computational resources, which may limit their effectiveness in real-world medical scenarios with limited data availability. Furthermore, some models exhibit instability or class bias when applied to smaller datasets [19], [20]. Therefore, there is a need for a comparative evaluation of different transfer learning architectures to identify models that provide a balance between accuracy, computational efficiency, and reliability [21]. This study addresses this gap by analyzing multiple architectures and identifying the most suitable model for breast cancer classification.

3. Methodology

Dataset

This study utilizes a combined dataset consisting of histopathological images from the BreakHis dataset [16] and Paul Mooney's Kaggle dataset [22], totaling approximately 14,020 images. The dataset is categorized into two classes: malignant and normal. The dataset was divided into training (10,010 images), validation (2,000 images), and testing (2,010 images) sets. The distribution ensures a balanced representation of both classes to enable effective model training and evaluation. The dataset distribution is illustrated in Figure 1.

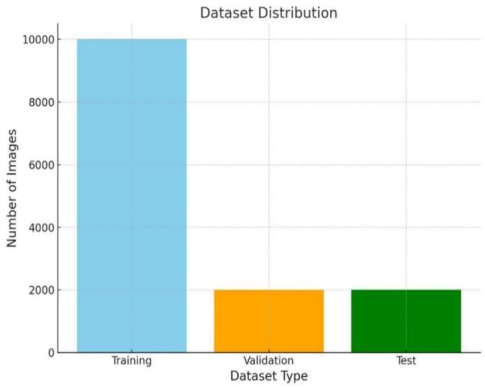

Figure 1. Dataset Distribution

Preprocessing

To enhance model generalization and handle variations in image appearance, preprocessing techniques such as normalization and data augmentation were applied [23], [6]. Images were rescaled to a range of [0,1]. Data augmentation techniques including rotation, width and height shifts, zooming, shear transformations, and horizontal flipping were applied to increase dataset diversity and reduce overfitting [24].

Model Architecture

Multiple deep learning architectures were evaluated using transfer learning, including VGG16 [3], [13], ResNet50 [11], DenseNet121 [14], EfficientNetB0, and EfficientNetB5 [12]. Pre-trained weights from ImageNet were used [24], and the final layers were fine-tuned for the classification task [23]. The convolutional base of each model was partially frozen to retain learned low-level features, while the final layers were fine-tuned to adapt to the dataset

[23]. A custom classification head was added consisting of:

Global Average Pooling → Dense layer (256 units, ReLU activation) → Dropout (0.5) → Dense output layer (1 unit, Sigmoid activation)

This architecture enables efficient feature extraction while reducing overfitting. The overall pipeline of the proposed framework is illustrated in Figure 2.

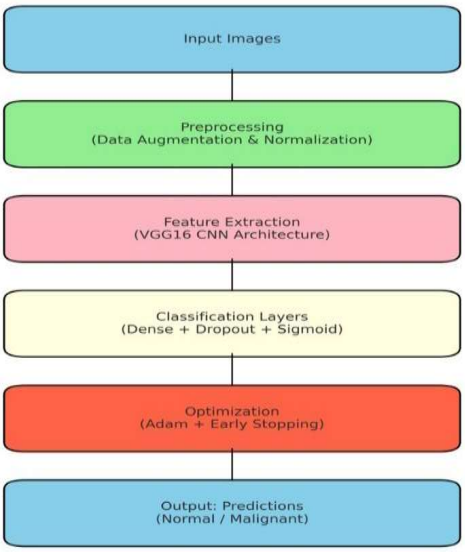

Figure 2. Architecture of proposed deep learning framework

Training setup

The models were trained using the Adam optimizer with a learning rate of 3×10^{-5} [25]. Binary Focal Loss was used to improve classification performance by focusing on difficult samples [26]. Mixed precision training was employed to accelerate computation and reduce memory usage [27]. Early stopping was used to prevent overfitting by monitoring validation loss, with the best model weights restored. A classification threshold of 0.4 was applied during prediction to balance sensitivity and specificity. The training process and convergence behavior are illustrated using accuracy and loss curves in the Results section.

Parameter	Value
Image Size	224 x 224
Batch Size	32
Learning Rate	3 x 10^{-5}
Optimizer	Adam
Loss Function	Binary Focal Loss
Epochs	25
Threshold	0.4

Results

The proposed framework was evaluated using multiple deep learning architectures, including VGG16, ResNet50, DenseNet121, EfficientNetB0, and EfficientNetB5. The performance of each model was assessed using accuracy, sensitivity, specificity, F1-score, and ROC-AUC.

Among all models, DenseNet121 achieved the best overall performance with a test accuracy of 81%, sensitivity of 80.8%, specificity of 76.7%, and ROC-AUC of 0.87, consistent with findings in similar studies [14], [15]. VGG16 also demonstrated stable performance with an accuracy of 77% and balanced classification results.

ResNet50 showed high sensitivity but suffered from low specificity, indicating a tendency to misclassify normal samples as malignant [28]. EfficientNet models (B0 and B5) exhibited poor generalization and strong class bias, predicting most samples as malignant, resulting in near-zero specificity [19], [29].

The training and validation accuracy and loss curves for DenseNet121 are shown in Figure 4 and Figure 5, respectively. The curves demonstrate stable convergence and minimal overfitting, indicating effective learning of meaningful features.

Model	Accuracy	Sensitivity	Specificity	ROC AUC	F1-score
DenseNet121	0.81	0.808	0.767	0.87	0.79
VGG16	0.77	0.789	0.737	0.82	0.76
ResNet50	0.61	0869	0.212	0.67	0.65
EfficientNetB0	0.60	0.62	0.01	0.66	0.66
EfficientNetB5	0.53	0.65	0.00	0.56	0.66

Figure 3. Model Performance Comparison.

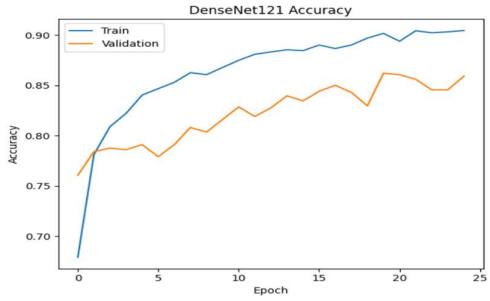

Figure 4. Training vs Validation Accuracy.

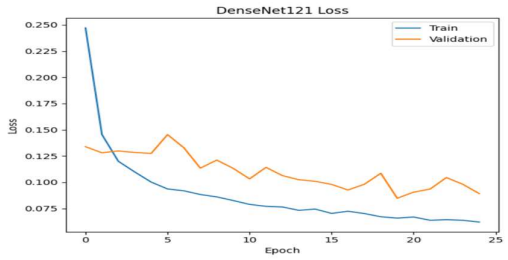

Figure 5. Training vs Validation loss.

The confusion matrix for DenseNet121, shown in Figure 6, highlights the model's ability to correctly classify both malignant and normal samples with balanced performance. Additionally, a comparative analysis of model performance is presented in Table 1, illustrating the trade-offs between different architectures in terms of accuracy, generalization, and computational efficiency

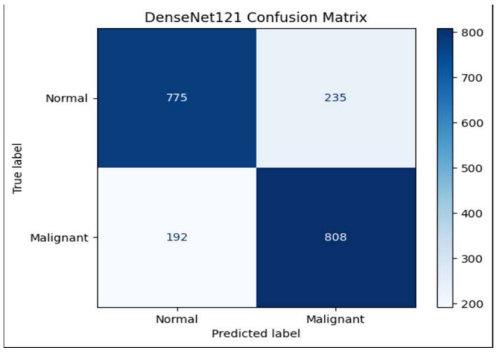

Figure 6. Confusion Matrix on test set.

Discussion and future work

The experimental results demonstrate that model performance varies significantly across different architectures. DenseNet121 achieved the best overall performance with balanced sensitivity and specificity, making it the most reliable model for medical diagnosis [14], [8], [15]. VGG16 also provided stable and consistent results, while ResNet50 exhibited high sensitivity but poor specificity, indicating a tendency to misclassify normal samples as malignant. Efficient Net models (B0 and B5), despite their deeper architecture, failed to generalize effectively on the given dataset and showed strong class bias by predicting most samples as malignant [9], [20]. This highlights that more complex models do not necessarily guarantee better performance, especially when the dataset size is limited. The inference time analysis indicates that lighter architectures such as VGG16 provide faster predictions, whereas deeper models introduce additional computational overhead [21]. However, DenseNet121 achieves a good balance between computational efficiency and classification performance, making it more suitable for practical clinical applications [5], [8].

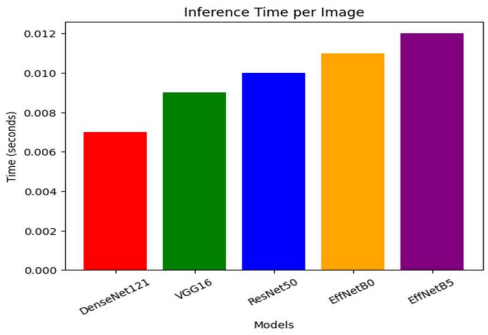

Figure 7. Inference Time per Image.

Limitations

Although the proposed framework achieved strong results, certain limitations remain. The dataset size, while reasonably large, may still be insufficient to fully exploit deeper architectures such as EfficientNet [9]. Additionally, variations in staining, resolution, and image acquisition conditions may affect model generalization in real-world clinical environments [10]. Another limitation is that the models were evaluated on a binary classification task (malignant vs normal), which does not capture the full complexity of breast cancer subtypes [19]. Furthermore, the use of a fixed classification threshold may influence the trade-off between sensitivity and specificity.

Future Work

Future work can focus on improving model robustness and generalization by incorporating larger and more diverse datasets. Ensemble learning techniques combining multiple models may further enhance performance [29]. Exploring advanced architectures such as Vision Transformers and hybrid models could also provide improvements [18]. Additionally, integrating explainable AI techniques such as Grad-CAM can help visualize model decision regions, improving interpretability and trust in clinical settings [17]. Extending the framework to multi-class classification of breast cancer subtypes [20] and optimizing threshold selection based on clinical requirements are also promising directions for future research.

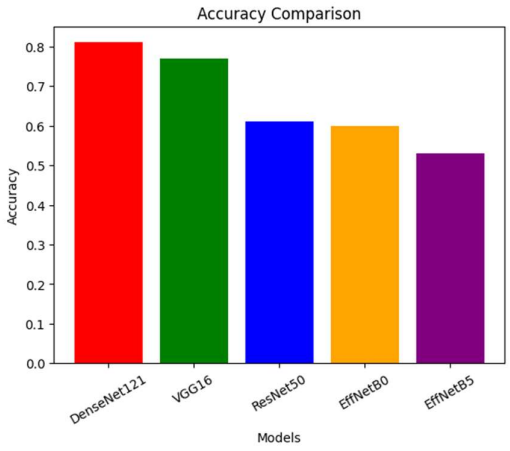

Figure 8. Accuracy Comparison.

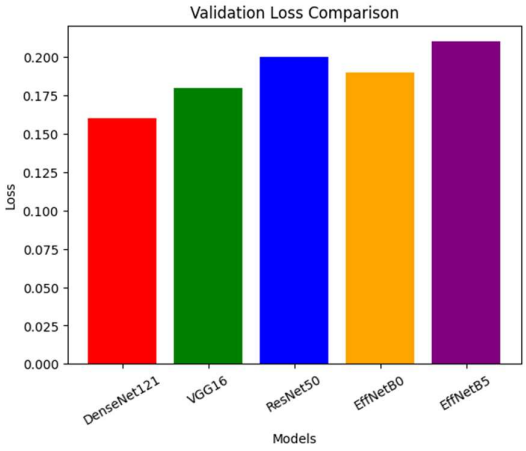

Figure 9. Loss Comparison.

Conclusion

This research presents an enhanced deep learning framework for automated breast cancer classification using histopathological images. Multiple transfer learning architectures, including VGG16, ResNet50, DenseNet121, and EfficientNet models, were evaluated to identify the most effective approach. Among these, DenseNet121 achieved the best overall performance, providing a balanced trade-off between accuracy, sensitivity, and specificity [14], [15]. While VGG16 demonstrated stable and computationally efficient results, deeper models such as EfficientNet showed limitations in generalization on the given dataset [9]. The use of data augmentation, mixed precision training [27], and focal loss [26] contributed to improved model performance and training efficiency. The proposed framework highlights the potential of deep learning as a reliable decision-support tool for assisting pathologists in early and accurate breast cancer diagnosis. By improving consistency and reducing manual effort, such systems can contribute significantly to enhanced clinical outcomes.

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data augmentation, and mixed precision training enables the system to provide accuracy and efficiency. Overall, the framework could be utilized as a useful decision-support tool to aid pathologists in arriving at an early and reliable diagnosis, thus improving patient care.

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