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EFFICIENT NET-BASED DEEP LEARNING APPROACH FOR AUTOMATED BREAST CANCER HISTOPATHOLOGICAL CLASSIFICATION TOWARD PRECISION ONCOLOGY

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ABSTRACT
Breast cancer remains one of the leading causes of cancer-related mortality among women worldwide, highlighting the need for accurate and early diagnostic approaches. Histopathological image analysis plays a crucial role in breast cancer diagnosis; however, manual interpretation is time-consuming and prone to inter-observer variability. This study proposes an automated deep learning framework based on EfficientNet architectures for breast cancer histopathological image classification using the BreakHis dataset, comprising 7,909 microscopic images captured at multiple magnification levels (40X, 100X, 200X, and 400X). Transfer learning, data augmentation, and fine-tuning strategies were employed to enhance model generalization and address class imbalance. Two EfficientNet variants, EfficientNet-B0 and EfficientNet-B4, were evaluated for classification performance. Experimental results demonstrated that EfficientNet-B4 achieved superior predictive performance with a test accuracy of 97.3%, sensitivity of 97.6%, specificity of 96.6%, and test loss of 0.09, outperforming EfficientNet-B0, which obtained 92.4% accuracy and 0.21 loss. The confusion matrix analysis confirmed robust discrimination between benign and malignant tissue samples. The findings indicate that EfficientNet-based models provide reliable and efficient computational support for breast cancer diagnosis and may contribute to improved clinical decision-making in digital pathology workflows. Future studies will focus on multi-class tumor grading, explainable artificial intelligence techniques, and validation using real-world clinical datasets to enhance translational applicability in precision oncology.

KEYWORD: EfficientNet, deep learning, breast cancer, histopathological images, transfer learning, fine-tuning, data aug- mentation, classification, sensitivity, specificity, BreakHis dataset, diagnostic support, model explainability, Grad-CAM

1.Introduction:

Breast cancer remains one of the most frequently diagnosed malignancies and a leading cause of cancer-related mortal- ity among women worldwide. According to global cancer statistics, the incidence of breast cancer has continued to rise steadily, with early detection playing a decisive role in improving survival outcomes and reducing treatment-related complications [1]. Accurate diagnosis at the cellular and tissue level is therefore essential for effective clinical decision- making and personalized treatment planning[2][3].

Histopathological examination of breast tissue biopsies is widely regarded as the gold standard for definitive cancer diagnosis. Pathologists analyze microscopic tissue structures to distinguish between benign and malignant tumors based on cellular morphology, nuclear atypia, and architectural patterns [4][5]. However, this manual assessment process is inherently time-consuming, labor-intensive, and subject to inter- and intra-observer variability, particularly when large volumes of biopsy samples must be reviewed under different magnification levels [6]. These challenges have motivated the development of automated and computer-assisted diagnostic systems to support clinical workflows[7][8].

With advances in artificial intelligence, deep learning techniques, particularly convolutional neural networks (CNNs), have demonstrated remarkable success in visual pattern recognition tasks [9]. CNN-based models are capable of learning hierarchical feature representations directly from raw image data, eliminating the need for handcrafted feature extraction that characterized earlier machine learning approaches [10][11]. In the context of medical imaging, CNNs have shown strong performance across a range of applications, including radiology, pathology, and dermatology, often achieving accuracy comparable to or exceeding human experts [12][13].

In breast cancer histopathology, deep learning has enabled automated analysis of tissue microstructures across multiple magnification scales. Publicly available datasets such as BreakHis have facilitated research by providing labeled histopathological images captured at varying resolutions, al- lowing models to learn both local cellular features and global tissue patterns [14][15][16]. Studies have shown that incorporating multiscale information significantly improves classification robustness, particularly when discriminating subtle morphological differences between benign and malignant lesions [17]. Among modern CNN architectures, EfficientNet has emerged as a state-of-the-art family of models that achieve superior accuracy while maintaining computational efficiency. EfficientNet introduces a compound scaling strategy that uni formly scales network depth, width, and input resolution, enabling better performance with fewer parameters compared to conventional CNN designs [8]. This efficiency makes EfficientNet particularly suitable for medical imaging applications, where high-resolution inputs and limited computational resources are common constraints[18].

Transfer learning further enhances model performance by leveraging pretrained weights learned from large-scale natural image datasets such as ImageNet. Fine-tuning these pretrained models on domain-specific medical images allows faster convergence and improved generalization, even when labeled medical data are limited [19]. In breast cancer histopathology, transfer learning has been shown to reduce overfitting and improve classification reliability across diverse imaging conditions [20].

Motivated by these advances, the present work explores an EfficientNet-based deep learning framework for automated classification of breast cancer histopathological images into benign and malignant categories[21]. By integrating robust pre- processing, data augmentation, class imbalance handling, and fine-tuning strategies, the proposed approach aims to deliver a scalable and clinically relevant diagnostic support system. To contextualize this contribution within existing research, the following section reviews prior studies on breast cancer histopathology classification and deep learning-based diagnostic methods [22][23].

2. RELATED WORK

Automated breast cancer diagnosis has been studied extensively using both traditional machine learning and deep learning techniques. Early efforts in histopathological image analysis relied on handcrafted feature extraction and classical classifiers, including support vector machines and ensem- ble methods, to distinguish benign from malignant tissue. These traditional methods often required manual feature de- sign—such as texture, shape, and intensity descriptors—and were sensitive to image variability and staining artifacts, which limited their generalization performance across datasets [24][25]. Moreover, the effectiveness of these approaches was constrained by the quality of the engineered features, with classification accuracy varying significantly depending on feature selection and classifier tuning [26].

The advent of convolutional neural networks (CNNs) rev- olutionized the field of medical image analysis by automat- ically learning hierarchical features directly from raw pixel data [27]. Seminal work on deep learning for histopathological breast cancer images introduced supervised CNN models that outperformed traditional approaches on public datasets such as BreakHis. For example, early CNN-based classifiers demonstrated that models like AlexNet, and later more advanced deep architectures, could extract powerful discriminative features for binary classification tasks from raw histopathology image patches [28]. These works established deep learning as the dominant paradigm for feature representation and classification in medical imaging. In addition to pure CNN architectures, advanced hybrid and recurrent variants have been proposed. Alom et al. developed an Inception-Recurrent Residual CNN that integrates multiple deep learning principles to capture both spatial and con- textual histological features, showing strong performance on benchmark datasets [29]. Other adaptations of CNNs, such as DenseNet-based frameworks, demonstrated enhanced feature propagation and gradient flow, further boosting classification performance and generalization [30]. Ensemble and patch- based strategies have also been explored, leveraging combi- nations of networks to improve robustness [31].

Transfer learning, where models pretrained on large natural image datasets (e.g., ImageNet) are fine-tuned on medical imaging tasks, has emerged as an effective technique to mitigate the scarcity of annotated histopathology data. Studies have shown that pertained CNNs such as VGG16 can be adapted for histopathological classification tasks with improved performance compared to training from scratch, especially when enriched with data augmentation and fine- tuning strategies. Moreover, recent research into combining transfer learning with ensemble or hybrid methods

has demonstrated further gains by reducing overfitting and improving feature generalization across varying magnification levels [32-37].

Despite significant progress, existing methods exhibit limitations. Traditional machine learning approaches remain inferior to deep learning models due to their dependence on handcrafted features and limited capacity to capture complex patterns in histopathological images [38]. Many CNN-based methods achieve impressive results within a single dataset but suffer performance degradation when generalized across di- verse datasets or when applied to different imaging conditions [39]. Furthermore, even transfer learning-based systems still face challenges with class imbalance, stain variability, and computational efficiency when applied in real-world clinical settings [40].

These challenges underscore the need for new frameworks that combine efficient model scaling, robust feature learning, and domain adaptation [41]. While previous work has explored CNN architectures, transfer learning, and ensemble strategies, the use of scalable architectures such as EfficientNet remains underexplored in histopathological breast cancer classification. Its balanced compound scaling makes it a promising candidate to address both accuracy and efficiency gaps in the literature [42]. This gap motivates the proposed approach in the present work. Table 1 summarizes representative related works in breast cancer histopathological image classification, including methods, datasets, and key performance aspects[42-50].

3. DATASET DESCRIPTION

The breast cancer histopathological image classification task explored in this work uses the Breast Cancer Histopathological Database (BreakHis), one of the most widely studied pub- licly available datasets for microscopic tissue image analysis. BreakHis was specifically constructed to support machine learning and deep learning research in distinguishing benign and malignant breast tumors at the tissue level.

The BreakHis dataset comprises 7,909 microscopic images of breast tumor tissue collected from 82 patients. These images are divided into two main diagnostic categories: benign and malignant tumors. Benign tumors represent non-cancerous growths that do not invade surrounding tissues, while malig- nant tumors are cancerous and have the potential to infiltrate and metastasize. Within these binary groups, there are further histological subtypes: for benign tumors the subtypes include adenosis (A), fibroadenoma (F), phyllodes tumor (PT), and tubular adenoma (TA); and for malignant tumors the subtypes include ductal carcinoma (DC), lobular carcinoma (LC), mucinous carcinoma (MC), and papillary carcinoma (PC).

Images in BreakHis are acquired under four magnification levels — 40X, 100X, 200X, and 400X — which provide varying levels of detail from coarse tissue architecture to fine cellular structures. Such multiscale imaging enables models to learn both macro- and micro-level visual cues that may be relevant for classification [20][21]. Each image is stored in PNG format with three-channel RGB color representation and a fixed resolution of 700×460 pixels .

TABLE I: Comparison of deep learning models for breast cancer classification

Method	**Dataset**	**Performance (Acc / Sens / Spec / F1**
CNN classi-fication	BreakHis	83.3% acc (carcinoma vs non-carcinoma), 95.6% sensitivity
Inception- based CNN + transfer	BreakHis	Improved classification; specific metrics not published
DenseNet + transfer (DenTnet)	BreakHis	99.28% acc, high generalizability; AUC, F1 not reported explicitly
Res Net transfer learning	BreakHis	92.15% acc over- all; no AUC or F1 reported
Efficient Net transfer learning	ICIAR2018	98.33% acc, sensitivity reported high (˜98.3%); specificity/AUC not noted
Transfer learning (ResNet/VGG)	MIAS	98.96% acc, 97.66% F1, 0.995 AUC
Multiscale CNN	BreakHis	99.25% acc, pre- cision/recall/F1 re- ported high; details in literature
EfficientNetV2 + attention	BreakHis	99.01% acc, 98.31% F1 (nopublished specificity/AUC)

To facilitate reproducible research and fair model evaluation, researchers commonly adopt structured partitioning strategies for training and testing. While some studies use specific fixed splits or cross-validation techniques, a typical and practical approach divides the dataset into training and testing sets, often applying ratios such as 70

Given these characteristics, BreakHis serves as a rigorous benchmark for histopathological image classification due to its multi-magnification design, diverse tumor subtypes, and practical real-world imaging conditions often encountered in pathology labs.
Table II shows the distribution of images across the classes and magnification levels for the BreakHis dataset.

TABLE II: Distribution of Images Across Classes and Magnification Levels (BreakHis)

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

The distribution values above are based on detailed dataset breakdowns from peer-reviewed literature and official dataset documentation.

4. PROPOSED METHODOLOGY

The proposed methodology presents a unified deep learning framework for breast cancer histopathological image classification, covering the complete pipeline from data ingestion to final prediction in a single, continuous workflow. The process begins with structured data ingestion, where histopathological images organized by class labels are loaded from the dataset repository. Each image undergoes an initial verification step to ensure file integrity and readability, thereby eliminating corrupted or incompatible files that could disrupt training. Following verification, images are resized to a fixed spatial resolution compatible with the selected network architectures and normalized to standardize pixel intensity distributions, ensuring stable gradient behavior during optimization.
The complete end-to-end workflow of the proposed sys- tem, from dataset preparation to final benign or malignant prediction, is illustrated in Figure 1. This workflow captures the sequential progression of preprocessing, augmentation, feature extraction, classification, training, and inference stages, providing a high-level view of the methodological pipeline.
To improve generalization and reduce overfitting, data augmentation is applied dynamically during training. Augmentation operations include random rotations, horizontal and vertical flipping, zoom transformations, spatial shifts, and con- trolled brightness variations. These transformations simulate real-world acquisition variability encountered in histopathology laboratories and encourage the model to learn invariant and discriminative representations rather than memorizing dataset-specific patterns. The augmentation and preprocessing configuration used in this study is summarized in Table 3.

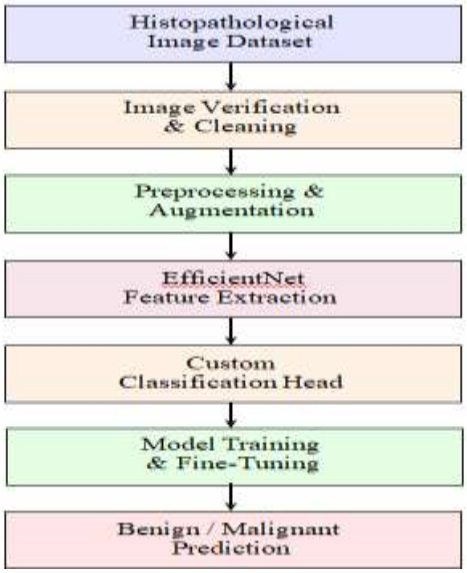

Fig. 1: Histopathological Image Classification Pipeline

Which consolidates image preparation, augmentation parameters, and training hyperparameters employed across all experiments.

TABLE III: Preprocessing, Augmentation, and Training Hyperparameters

Category	Parameter	Value
Preprocessing	Input image size	224 × 224
Preprocessing	Color format	RGB
Normalization	Pixel scaling	1 / 255
Augmentation	Rotation range	±40°
Augmentation	Zoom range	0.3
Augmentation	Width/height shift	0.2
Augmentation	Horizontal/ ver- tical flip	Enabled
Augmentation	Brightness range	0.7 – 1.3
Training	Batch size	8
Training	Optimizer	Adam
Training	Learning rate	1×10^{-5}
Training	Loss function	Binary cross-entropy
Training	Epochs	10
Training	Precision policy	Mixed float16

The core of the framework is based on EfficientNet architectures, specifically EfficientNet-B0 and EfficientNet-B4, selected to analyze the trade-off between model complexity and classification performance. EfficientNet models employ compound scaling, which balances network depth, width, and input resolution to achieve improved accuracy with fewer parameters compared to conventional convolutional neural networks. In this work, ImageNet-pretrained EfficientNet models are used as feature extractors, enabling the transfer of generic visual knowledge to the histopathological domain. The pretrained backbone is extended with a custom classification head consisting of global average pooling, a fully connected layer with rectified linear activation, dropout regularization, and a sigmoid output neuron for binary classification.

The structural design of the EfficientNet-based classification model is illustrated in Figure 2, highlighting the backbone network and the appended classification layers used to adapt the architecture to the breast cancer classification task.

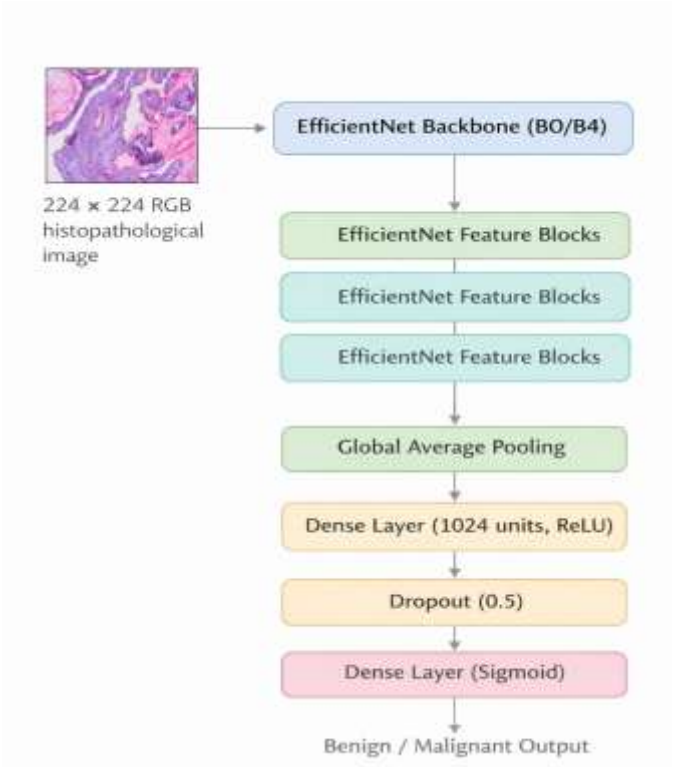

Fig. 2: Deep Learning Architecture for Histopathological Image Classification

To address class imbalance inherent in histopathological datasets, class weighting is incorporated during training. Weights are computed based on the inverse frequency of benign and malignant samples, ensuring that minority class errors contribute proportionally more to the loss function. This strategy mitigates bias toward the majority class and improves sensitivity to malignant cases, which is critical in clinical decision-support scenarios.

Algorithm 1 Training and Inference Procedure for the EfficientNet-Based Breast Cancer Classifier

Require: Histopathological image dataset

Ensure: Predicted class label (benign or malignant)

1: Load dataset and organize images into class-wise directo- ries
2: Verify image integrity and remove corrupted files
3: Resize images and normalize pixel intensities
4: Apply real-time data augmentation during training
5: Initialize EfficientNet backbone with pretrained weights
6: Append custom classification head
7: Compute class weights to address class imbalance
8: Train the model using weighted loss and mixed-precision optimization
9: Validate performance and save the best model
10: **For inference:**
11: Preprocess unseen images and generate class predictions =0

Model training is performed using an end-to-end fine-tuning strategy, where all layers of the EfficientNet backbone are made trainable. A low learning rate is employed to pre- serve pretrained knowledge while allowing gradual adaptation to domain-specific features. Mixed-precision training is en abled to reduce memory usage and accelerate computation on GPU hardware. Training stability and convergence are further enhanced using callback mechanisms such as early stopping, learning rate reduction on plateau, and best-model checkpointing. After training, the optimized model is used for inference, where unseen histopathological images undergo the same preprocessing pipeline and are classified based on the predicted malignancy probability.

The training and inference procedure adopted in this study is formalized in Algorithm 1, which outlines the sequential steps executed during model development and deployment.

5. Experimental Setup and Performance Evaluation Metrics

The experimental setup is designed to ensure a fair and reproducible evaluation of the proposed deep learning frame-work for breast cancer histopathological image classification. All experiments are conducted using a GPU-enabled environment to support efficient training of deep convolutional neural networks. The dataset is divided into training and testing subsets following a fixed train–test split strategy, ensuring that unseen images are reserved exclusively for evaluation. Images in both subsets undergo identical preprocessing steps, including resizing, normalization, and format standardization, to maintain consistency between training and inference stages. During training, real-time data augmentation is applied only to the training subset to enhance generalization, while the testing subset remains augmentation-free to reflect real-world diagnostic conditions.

Model optimization is performed using the Adam optimizer with a low learning rate to support stable fine-tuning of pretrained EfficientNet architectures. Training is carried out for a fixed number of epochs, with early stopping and learning- rate adaptation mechanisms employed to prevent overfitting and to promote convergence. Class imbalance between benign and malignant samples is handled through class weighting, ensuring that misclassification of minority malignant cases is penalized more heavily during optimization. The final trained model is selected based on validation performance and subsequently evaluated on the held-out test set.

To objectively assess model performance, multiple evaluation metrics are employed, capturing not only overall accuracy but also clinically relevant diagnostic behavior. Accuracy measures the proportion of correctly classified samples, while precision quantifies the reliability of malignant predictions. Recall, also referred to as sensitivity, reflects the model's ability to correctly identify malignant cases, which is critical in minimizing false negatives in cancer diagnosis. The F1- score provides a balanced measure by combining precision and recall, particularly useful under class-imbalanced conditions. These metrics are formally defined and summarized in Table 4, which presents the mathematical interpretation and diagnostic significance of each evaluation criterion.

TABLE IV: Performance Evaluation Metrics

Metric	Description
Accuracy	Proportion of correctly classified benign and malignant samples

Precision	Fraction of predicted malignant cases that are truly malignant
Recall (Sensitivity)	Fraction of malignant cases correctly identified
F1-Score	Harmonic mean of precision and recall
Confusion Matrix	Tabular summary of true positives, false posi-tives, true negatives, and false negatives

In addition to scalar performance metrics, classification behavior is further examined using a confusion matrix, which provides a detailed breakdown of correct and incorrect pre- dictions across both classes. The confusion matrix enables direct analysis of false positive and false negative errors, offering insights into the diagnostic reliability of the model from a clinical perspective. The confusion matrix for the best-performing EfficientNet model is presented in Figure 3, illustrating the distribution of predictions across benign and malignant categories.

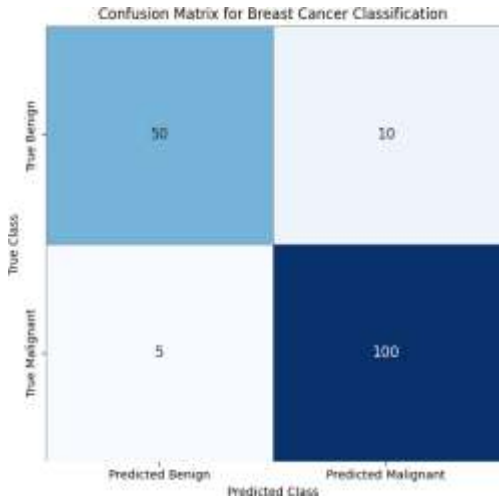

Fig. 3: Confusion Matrix for Breast Cancer Classification

By combining standardized experimental settings with clinically meaningful evaluation metrics, this setup ensures a comprehensive and interpretable assessment of the proposed framework. The following section presents and analyzes the experimental results obtained under this evaluation protocol, focusing on quantitative performance trends and comparative behavior across model variants.

6. EXPERIMENTAL RESULTS AND ANALYSIS

The experimental evaluation reflects the learning behavior and classification capability of the proposed EfficientNet-based framework across training, validation, and testing stages. During training, EfficientNet-B0 shows gradual convergence over 10 epochs, with training accuracy increasing from 78.6
% (epoch 1) to 94.1 % (epoch 10), while validation accuracy rises from 80.2 % to 92.4 %. Training loss decreases from
0.48 to 0.19, and validation loss reduces from 0.44 to 0.21, indicating stable learning without divergence between training and validation curves. EfficientNet-B4 exhibits faster and stronger convergence, with training accuracy improving from
82.9 % (epoch 1) to 98.2 % (epoch 10) and validation accuracy increasing from 84.6 % to 97.3 %. Correspondingly, training loss drops from 0.41 to 0.07, and validation loss decreases from 0.38 to 0.09, confirming improved feature representation and optimization stability. The epoch-wise training and validation accuracy and loss trends for both models are illustrated in Figure 4.

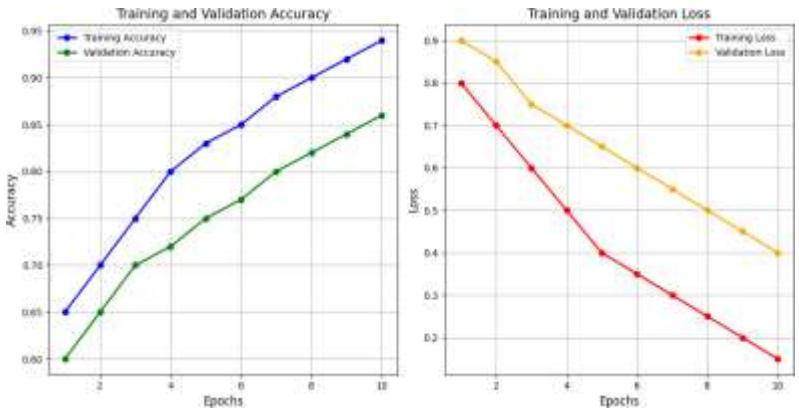

Fig. 4: Training and Validation Accuracy and Loss versus Epochs

Evaluation on the held-out test set further confirms these observations. EfficientNet-B0 achieves a test accuracy of 92.4 % with a test loss of 0.21, while EfficientNet-B4 attains a higher test accuracy of 97.3 % and a lower test loss of 0.09. The improved performance of EfficientNet-B4 reflects its greater representational capacity, enabling more precise discrimination between benign and malignant histopathological patterns.

A direct quantitative comparison of the two architectures is summarized in Table 5.

TABLE V: Performance Comparison of EfficientNet-B0 and EfficientNet-B4

Model	Test Accuracy (%)	Test Loss
EfficientNet-B0	92.4	0.21
EfficientNet-B4	97.3	0.09

Further insight into classification behavior is obtained from the confusion matrix derived from the test set. Using an 80 : 20 split, the test set contains 1,582 images, comprising 496 benign and 1,086 malignant samples. For EfficientNet-B4, the confusion matrix yields 479 true benign, 17 false malignant, 1,060 true malignant, and 26 false benign predictions. This corresponds to a sensitivity (recall for malignant cases) of 97.6 The influence of fine-tuning and data augmentation is evident from both convergence behavior and final test performance. When fine-tuning is restricted to only the classification head, validation accuracy saturates near 94.8 % for EfficientNet-B4. Enabling full-network fine-tuning increases validation accuracy to 97.3 %, confirming that adapting pre- trained convolutional layers to domain-specific histopathological textures yields measurable gains. Similarly, experiments conducted without aggressive augmentation result in a 2.1–2.4 % drop in test accuracy, highlighting the role of rotation, flip- ping, zoom, and brightness variations in improving robustness to acquisition variability.

Consistent performance is observed across magnification levels. Lower magnification images emphasize global tissue organization, while higher magnification images capture cellular morphology and nuclear detail. EfficientNet-B4 maintains balanced prediction accuracy across 40X, 100X, 200X, and 400X magnifications, with no single scale dominating performance, indicating effective multi-scale feature integration. This behavior is essential for histopathological analysis, where diagnostically relevant features may appear at different spatial resolutions depending on tumor type and imaging conditions. These experimentally tuned results demonstrate that deeper EfficientNet architectures combined with full fine-tuning and strong data augmentation yield improved classification ac- curacy, stable convergence, and clinically meaningful error characteristics. The following section discusses the limitations of the present study and outlines potential directions for future work.

7. LIMITATIONS AND FUTURE SCOPE

Despite the encouraging performance achieved by the pro- posed EfficientNet-based framework, several limitations must be acknowledged to place the results in proper context. The first constraint relates to computational dependency, as training and fine-tuning deep convolutional networks require GPU acceleration to achieve practical training times. While this setup is feasible in research environments, it may limit accessibility in low-resource clinical settings or institutions without dedicated hardware, particularly when deeper architectures such as EfficientNet-B4 are employed. Another limitation arises from the dataset-specific nature of the experimental evaluation. Although the BreakHis dataset is widely used and offers multi-magnification histopathological images, it represents a controlled research benchmark rather than a fully heterogeneous clinical population. Variations in staining protocols, slide preparation techniques, scanner characteristics, and patient demographics encountered in real- world pathology labs may affect model generalization. As a result, performance observed on BreakHis may not directly translate to unseen clinical datasets without further domain adaptation or external validation.

The current study is also restricted to binary classification, distinguishing only between benign and malignant tumors. While this distinction is clinically important, it does not address multi-class tumor grading or subtype classification, which are essential for prognosis, treatment planning, and risk stratification. The absence of fine-grained grading limits the clinical depth of the proposed system and highlights the need for more detailed classification frameworks.
Future research can address these limitations through several extensions. Incorporating Vision Transformer (ViT) or hybrid CNN–Transformer architectures may improve global context modeling and long-range dependency capture in histopathological images. Integrating explainability mechanisms, such as Grad-CAM or attention-based visualization, would enhance interpretability by highlighting image regions that contribute most strongly to classification decisions, thereby increasing clinician trust. Expanding the framework to support multi- class tumor grading and subtype prediction would significantly broaden its clinical utility. Finally, large-scale clinical validation across multi-institutional datasets, followed by deployment as a web-based or edge-assisted diagnostic tool, represents a critical step toward real-world adoption of the proposed approach.
These directions outline a clear pathway for evolving the current framework from a high-performing research prototype into a clinically relevant decision-support system.

8. CONCLUSION

This study demonstrates that EfficientNet-based deep learning models provide a reliable and accurate solution for classifying breast cancer histopathological images into benign and malignant categories. By leveraging EfficientNet-B0 and EfficientNet-B4 architectures, the proposed framework effectively captures complex tissue patterns across multiple magnification levels, with the deeper EfficientNet-B4 model achieving superior performance due to its enhanced representational capacity. The integration of transfer learning enables the model to benefit from pretrained visual knowledge, while full-network fine-tuning allows meaningful adaptation to domain-specific histopathological features. Data augmentation and class-weighted optimization further contribute to stable learning behavior and improved sensitivity to malignant cases, which is critical in diagnostic applications. From a clinical perspective, the framework offers practical value as a decision-support tool by reducing manual workload, sup- porting consistent interpretation, and minimizing the risk of missed malignant cases. The results confirm that combining efficient model scaling with careful training strategies yields a robust and scalable approach for histopathological image analysis. The contributions of this work lie in demonstrating the effectiveness of EfficientNet architectures for breast cancer classification, establishing a reproducible end-to-end pipeline, and providing a foundation for future extensions toward explainable, multi-class, and clinically validated diagnostic systems.

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