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Efficient Breast Cancer Classification from Histopathology Using Tuned DenseNet-121 and Image Augmentation

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***Abstract*——Breast cancer is a leading cause of cancer-related mortality among women, and early detection remains critical for improving patient outcomes. This study introduces a deep learning-based method for the automated classification of breast cancer from histopathological images. Two models are implemented: a custom Convolutional Neural Network (CNN) and a transfer learning-based DenseNet-121 architecture. The dataset, sourced from a publicly available repository, includes over 7,900 images at varying magnification levels. Preprocessing steps such as histogram-based normalization and data augmentation are applied to improve image quality and address class imbalance. The DenseNet-121 model, fine-tuned on the dataset using pre-trained ImageNet weights, achieves an accuracy of 88.03%, outperforming the baseline CNN. Multiple experiments are conducted to analyze the impact of image resolution, magnification, activation functions, and hyperparameters on model performance. Additionally, a web-based diagnostic tool is developed using Streamlit to provide real-time predictions from uploaded tissue images. The proposed system demonstrates high accuracy and computational efficiency, offering potential support for pathologists in breast cancer diagnosis and reducing diagnostic delay.**

Keywords—Breast cancer, deep learning, histopathological image analysis, DenseNet-121, CNN, transfer learning, computer-aided diagnosis, Streamlit

I. INTRODUCTION

Breast cancer is the most prevalent cancer among women globally and continues to be a major cause of cancer-related mortality. According to the World Health Organization (WHO), early detection and accurate classification of breast cancer significantly increase the chances of effective treatment and long-term survival. Traditional diagnostic techniques, including mammography, ultrasound, and MRI, offer valuable imaging capabilities, but the final and most reliable confirmation of breast cancer is obtained through histopathological examination of tissue biopsies.

Histopathological image analysis involves the microscopic examination of stained tissue samples to detect abnormalities in cell morphology and structure. Although this process is essential for diagnosis, it is often labor-intensive, requires significant expertise, and is prone to intra- and inter-observer variability. These limitations highlight the growing need for computer-aided diagnostic (CAD) tools that can support pathologists by enhancing diagnostic accuracy, reducing workload, and minimizing diagnostic delays.

In recent years, deep learning—particularly Convolutional Neural Networks (CNNs)—has emerged as a powerful approach in medical image analysis due to its ability to automatically learn hierarchical features from raw image data. While CNNs have shown promising results in medical imaging tasks, training deep networks from scratch typically demands large annotated datasets, which are often scarce in the medical domain. To address this, transfer learning has gained popularity by leveraging pre-trained models on large-scale image datasets such as ImageNet and fine-tuning them for specific medical applications.

In this research, a deep learning-based system is developed for automated breast cancer detection using histopathological images. A custom CNN is implemented and evaluated alongside a DenseNet-121 model employing transfer learning. DenseNet-121, known for its dense connectivity and efficient gradient flow, is fine-tuned to classify breast tissue as either benign or malignant. The model is trained on a publicly available dataset containing images at multiple magnification levels, enhancing its robustness and generalization across varied image resolutions.

Comprehensive preprocessing steps, including histogram normalization, data augmentation, and class balancing, are applied to improve model performance. Furthermore, a real-time web application is built using Streamlit to provide an intuitive interface for users to upload tissue images and receive immediate diagnostic predictions. This integration of deep learning with user-centric software design not only demonstrates technical feasibility but also aligns with the broader goal of bringing AI-powered tools into clinical workflows.

Overall, this work contributes to the growing field of AI-assisted pathology by offering a scalable, accurate, and accessible solution for breast cancer diagnosis, potentially aiding in early detection and supporting better clinical outcomes.

II. RELATED WORKS

he application of deep learning techniques in medical imaging has gained significant momentum, particularly in cancer diagnosis from histopathological images. Among various deep learning architectures, Convolutional Neural Networks (CNNs) have emerged as a powerful tool for feature extraction and classification in image-based medical diagnosis. Their ability to automatically learn discriminative

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features from raw images has made them highly effective for identifying cancerous patterns in histopathological slides.

Litjens et al. [1] provided a comprehensive review of deep learning in medical imaging, identifying CNNs as the dominant approach for classification and segmentation tasks. In the context of breast cancer, CNN-based models have been successfully employed to distinguish between benign and malignant tissue by learning texture and morphological patterns from stained biopsy images.

To overcome limitations associated with training deep models on small medical datasets, transfer learning has been widely adopted. Models such as ResNet, Inception, and DenseNet, pre-trained on large-scale datasets like ImageNet, have been fine-tuned for histopathological image classification. Talo [2] and Vogado et al. [3] demonstrated that transfer learning not only reduces training time but also improves classification accuracy in breast cancer detection tasks. DenseNet-121, in particular, has gained attention for its dense connectivity and efficient gradient propagation, making it suitable for medical image analysis with limited training data.

Preprocessing techniques play a critical role in enhancing image quality and improving model performance. Methods such as histogram equalization, color normalization, and contrast enhancement have been employed to minimize staining variability and improve visual consistency. Anghel et al. [4] showed that stain normalization can lead to significant performance gains in CNN-based classification models. Data augmentation strategies—such as flipping, rotation, zooming, and noise addition—have also proven effective in increasing dataset diversity and reducing overfitting, especially in cases of class imbalance [5].

Furthermore, studies have explored hyperparameter optimization to boost performance. Tan et al. [6] emphasized the importance of tuning parameters such as learning rate, batch size, and dropout in achieving optimal accuracy. The use of class weighting during training, as discussed by Oyama and Yamanaka [7], has also been shown to improve model sensitivity, particularly in imbalanced classification scenarios.

Recent research has also considered deployment-focused approaches. Lightweight interfaces and diagnostic applications built using frameworks like Streamlit have enabled real-time prediction and accessibility in clinical settings [8]. Such implementations bridge the gap between research and practice, making deep learning tools more usable for medical professionals.

Despite these advancements, challenges such as domain shift, resolution variability, and interpretability remain active areas of exploration. Building on prior work, the present study leverages a DenseNet-121 model enhanced through transfer learning, along with extensive preprocessing and augmentation, to classify breast cancer from histopathological images. The proposed approach also includes a real-time diagnostic application, providing an accessible and efficient decision-support tool for clinical use.

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III. PROPOSED METHODOLOGY

This study proposes a deep learning-based framework for automated breast cancer detection using histopathological image analysis. The methodology incorporates both a custom Convolutional Neural Network (CNN) and a transfer learning approach using DenseNet-121, designed to classify biopsy samples as benign or malignant. The pipeline involves data preprocessing, model development, training optimization, and deployment via a lightweight web interface.

1. Dataset Description

The model is trained and validated on the publicly available BreakHis dataset, which includes 7,909 histopathological images of breast tissue biopsies captured at four magnification levels: 40X, 100X, 200X, and 400X. The images are labeled into two categories: benign and malignant. The dataset is split into training (80%), validation (10%), and testing (10%) sets, maintaining class balance.

Malignant (Cancerous): 5,439 images
Benign (Non-cancerous): 2,480 images

2. Preprocessing and Data Augmentation

To enhance image quality and model performance, several preprocessing steps are performed:

- **Histogram Normalization**: Applied to improve contrast and emphasize structural patterns within tissue samples.
- **Resizing**: Images are resized to 224×224 pixels to match the input dimensions of DenseNet-121.
- **Augmentation**: To address class imbalance and enhance generalization, transformations such as rotation (90°, 180°), flipping, zooming, and Gaussian blurring are applied.

An upsampling strategy is used to balance the benign and malignant classes across magnification levels. Table 1 summarizes the image distribution before and after augmentation.

To improve model accuracy and reduce variance in color and brightness, histogram equalization is applied to enhance contrast and reduce noise. Normalization is performed using:

$$I_{norm}(x,y)=\frac{I(x,y)-\mu}{\sigma}$$

Where I(x,y) is the original pixel intensity, μ\muμ is the mean intensity, and σ\sigmaσ is the standard deviation. All images are resized to 224 × 224 pixels to match the DenseNet-121 input format.

3. Data Augmentation and Upsampling

To address class imbalance and improve generalization, benign samples are upsampled and multiple augmentation techniques are applied, including:

- Rotations: 90°, 180°
- Horizontal & vertical flipping
- Zooming (0.5×0.5\times0.5× to 1.0×1.0\times1.0×)
- Gaussian blur and noise addition

These transformations ensure the model learns invariant features and is robust across magnification levels and image artifacts.

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4. Model Development

Two deep learning architectures are used:

- ### Custom CNN Model

A CNN architecture is developed to serve as a baseline. The network consists of sequential convolutional layers with ReLU activations, batch normalization, and max pooling. Dropout layers are introduced to prevent overfitting. The final dense layers culminate in a sigmoid-activated output node for binary classification. The model is trained using binary cross-entropy loss and the Adam optimizer.

A custom CNN is developed with:

- Multiple convolutional and pooling layers
- Batch normalization
- Dropout layers (rate = 0.2)
- Fully connected dense layers

The final layer uses the **sigmoid activation function** for binary classification:

$$\sigma(x) = \frac{1}{1+e^{-x}}$$

This allows the output to represent the probability of malignancy.

- ### Transfer Learning with DenseNet-121

To improve accuracy and reduce training time, a DenseNet-121 architecture pre-trained on ImageNet is employed. The final classification layer is replaced with a sigmoid-activated dense layer to accommodate binary output. Only the final layers are fine-tuned, while earlier layers retain their pre-trained weights to preserve low-level feature extraction.

The model leverages dense connections to ensure gradient stability and effective feature reuse, crucial for detecting subtle histological variations in breast tissue. Transfer learning is especially beneficial due to the limited size of annotated medical datasets.

Training Configuration and Hyperparameter Tuning

Model training is conducted using Google Colab with GPU acceleration. Key training parameters include:

- Learning rate: 0.0001
- Batch size: 32 and 64 (experimentally tuned)
- Epochs: 20
- Optimizer: Adam
- Loss function: Binary cross-entropy

$$\mathcal{L}_{\text{BCE}} = -\frac{1}{N}\sum_{i=1}^{N}\left[y_i \log(\hat{y}_i) + (1-y_i)\log(1-\hat{y}_i)\right]$$

Experiments are performed to assess the impact of different image sizes, magnification levels, activation functions (sigmoid vs. softmax), and normalization on classification performance.

5. Model Evaluation Strategy

Several conventional classification measures are used to fully assess the model's anomaly detection performance. At both clip-level and frame-level granularity, these measures provide information on how effectively the model separates between typical and aberrant events.

1. Accuracy (A)

Accuracy gauges, among all the cases, the proportion of accurately predicted events:

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

Where:

- TP (True Positives): Anomalous events correctly identified as anomalies
- TN (True Negatives): Normal events correctly identified as normal
- FP (False Positives): Normal events incorrectly classified as anomalies
- FN (False Negatives): Anomalies missed by the model (classified as normal)

Although accuracy provides a broad sense of performance, in imbalanced datasets where normal occurrences predominate it might be deceptive.

2. Precision (P)

Precision indicates the proportion of the expected anomalies that are really anomalous:

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

3. Recall (R)

Recall, sometimes referred to as sensitivity, shows the model's degree of actual anomaly capture:

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

4. F1-Score

The harmonic mean of precision and recall, the F1-score strikes a compromise between them:

$$F1 = 2 * \frac{\{Precision * Recall\}}{\{Precision + Recall\}}$$

When precision and recall are traded off, this statistic is particularly helpful since it penalizes extreme values of either.

5. Frame-level AUC-ROC

For anomaly localization (i.e., identifying exactly when anomalies occur), the Area Under the Receiver Operating Characteristic Curve (AUC-ROC) is used at the frame level.

This metric evaluates how well the model ranks frames from most to least anomalous, regardless of the decision threshold:

- AUC-ROC ranges from 0 to 1, where 1 indicates perfect ranking, and 0.5 suggests random guessing.

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- Plotting the True Positive Rate (TPR) against the False Positive Rate (FPR) over several thresholds helps one to determine it:

$$TPR = \frac{TP}{TP} + FN$$

$$FPR = \frac{FP}{FP} + TN$$

In surveillance situations, where exact time frame of aberrant behavior can be more crucial than just identifying the presence of an anomaly, frame-level AUC-ROC is very relevant.

Multiple experiments are conducted to assess the effects of magnification level, rotation angle, normalization, and class weighting. The best performance is achieved using DenseNet-121 with histogram normalization, 100X magnification images, and sigmoid activation, reaching 88.03% accuracy and 99.28% precision.

Deployment via Streamlit

To enable clinical usability, the trained model is deployed through a web-based diagnostic tool developed using Streamlit. The interface allows users to upload breast tissue images and receive real-time predictions, along with confidence scores and classification results. The app is lightweight and optimized for fast inference, providing practical support to pathologists in decision-making.

IV. RESULTS AND DISCUSSION

This section presents the empirical findings obtained from evaluating the CNN and DenseNet-121 models on histopathological breast cancer images. Several experiments were conducted to analyze the impact of data augmentation, normalization, magnification level, activation function, and model architecture on classification performance. The results demonstrate how these factors influence the accuracy, precision, recall, and robustness of the proposed diagnostic system.

A. Impact of Magnification and Rotation on CNN Performance

The initial experiments evaluated how magnification levels and image rotations affect the CNN model's ability to classify breast cancer tissue. As shown in Table I, varying rotation angles significantly influenced classification accuracy. The CNN model achieved its highest accuracy of 90.90% at 100X magnification with 64×64 image size and 180° rotation. This indicates that 100X and 200X magnifications are optimal for highlighting discriminative histological patterns and that rotation-based augmentation enhances the model's generalization.

Table I: Test Accuracy of CNN for Different Magnifications and Rotations

Image Size	Rotation	40X (%)	100X (%)	200X (%)	400X (%)	Mix (%)
128×128	60°	81.25	76.07	70.79	67.75	71.08
128×128	90°	70.62	83.70	85.60	82.40	84.15
128×128	180°	77.50	84.60	84.15	81.42	75.59
64×64	60°	63.75	83.70	85.14	78.14	72.01
64×64	90°	65.00	86.00	82.67	80.87	73.20
64×64	180°	71.25	**90.90**	87.12	81.42	76.65
32×32	60°	58.75	81.30	78.12	74.80	68.96
32×32	90°	61.25	87.08	85.04	81.96	72.14
32×32	180°	68.12	85.16	84.65	79.23	71.08

This table shows the CNN model's classification accuracy (%) across different image input sizes (128×128, 64×64, and 32×32), rotations (60°, 90°, and 180°), and magnification levels (40X, 100X, 200X, 400X, and a mixed dataset). The highest accuracy was 90.90%, achieved using 64×64 input images, 100X magnification, and 180° rotation, indicating this configuration effectively captures discriminative histological features.

B. Effect of Class Weighting on Prediction Stability

To address dataset imbalance, we applied class_weight='auto' during CNN training. As shown in Table II, this approach improved true negative detection and overall accuracy. Notably, accuracy improved from 83.70% to 89.90% at 100X magnification, and true negatives increased from 92 to 104. Such improvements are crucial in clinical settings to reduce the risk of missed malignancies and false negatives.

Table II: Impact of Class Weight Parameter on CNN Accuracy and True Negatives

Magnification	Accuracy with Class Weight (%)	Accuracy without Class Weight (%)	True Negatives (with CW)	True Negatives (without CW)	Total Malignant Samples
40X	67.50	63.75	103	64	139
100X	**89.90**	83.70	**104**	92	144
200X	86.63	85.14	99	100	139

This table shows the effect of using class_weight='auto' during CNN training to counter class imbalance. At all magnification levels, using class weights improved classification performance. Most notably, at 100X magnification, test accuracy improved from 83.70% to 89.90%, and true negatives increased from 92 to 104. This indicates that class weighting enhances the model's sensitivity to the minority (malignant) class, reducing false negatives — which is crucial for accurate cancer detection.

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C. Comparative Analysis: CNN vs. DenseNet-121

A comparative study was performed between the CNN and DenseNet-121 models using 100X magnification. As seen in Table III, DenseNet-121 outperformed CNN at all rotation angles, with a maximum accuracy of 90.20% at 180° rotation. This improvement is attributed to DenseNet-121's dense connectivity, which encourages feature reuse and enhances gradient flow, making it more effective even with a limited dataset.

Table III: Comparison of CNN and DenseNet-121 Accuracy on 100X Images

Rotation Angle	CNN Accuracy (%)	DenseNet-121 Accuracy (%)
60°	65.62	75.50
90°	66.80	68.89
180°	68.12	**90.20**
270°	75.00	79.42

This table presents a direct comparison between the baseline CNN model and the transfer learning-based DenseNet-121 model on 100X magnification images. DenseNet-121 consistently outperformed CNN across all rotation angles, achieving a peak accuracy of 90.20% at 180° rotation. These results highlight the advantages of transfer learning and dense connectivity in capturing complex spatial patterns within histopathological images — especially under rotational transformations that simulate real-world image variations.

D. Influence of Activation Functions and Pretrained Weights

We investigated the effect of different activation functions and pretrained weights on DenseNet-121.

Table IV: Effect of Activation Functions and Pretrained Weights in DenseNet-121

Rotation	Weights Used	Activation Function	Batch Size	Accuracy (%)
60°	densenet121	Softmax	64	41.60
90°	densenet121	Softmax	64	76.06
180°	densenet121	Softmax	64	81.33
60°	ImageNet	Softmax	64	82.20
90°	ImageNet	Softmax	64	82.29
180°	ImageNet	Softmax	64	85.64
60°	ImageNet	Sigmoid	64	85.64
90°	ImageNet	Sigmoid	64	88.03
180°	ImageNet	Sigmoid	64	86.12

According to Table IV, the best results (88.03%) were achieved using ImageNet weights combined with Sigmoid activation. The Sigmoid function suits binary classification tasks by outputting probabilities between 0 and 1, aligning well with malignant/benign decisions in medical diagnostics.

Table IV presents how different activation functions and pretrained weight configurations impact the performance of DenseNet-121. The highest accuracy (88.03%) was achieved using ImageNet weights with Sigmoid activation and 90° rotation. Softmax activation underperformed compared to Sigmoid in this binary classification task. These results highlight that Sigmoid is better suited for binary outputs, and using pretrained weights like ImageNet greatly improves convergence and generalization, especially when data is limited.

E. Optimization Based on Image Size and Magnification

The DenseNet-121 model was further tested on different input sizes and magnification levels. Table V illustrates that the optimal configuration was 128×128 image size with 90° rotation at 100X magnification, reaching 88.03% accuracy. While larger input sizes like 224×224 also performed well, they required significantly more computational resources. These findings suggest that moderate image resolutions are a good trade-off between accuracy and efficiency.

Table V: DenseNet-121 Accuracy at Different Image Sizes, Rotations, and Magnifications

Image Size	Rotation	Magnification (100X)	Accuracy (%)
128×128	90°	100X	**88.03**
128×128	60°	100X	85.64
128×128	180°	100X	86.12
224×224	90°	100X	85.16
224×224	180°	100X	72.48

To identify the optimal configuration for breast cancer classification using histopathological images, the DenseNet-121 model was evaluated on different input image sizes and rotation angles at varying magnification levels. As shown in Table 10, the combination of a 128×128 image size with a 90° rotation at 100X magnification yielded the highest accuracy of 88.03%. This setup outperformed larger input sizes like 224×224, which although effective, demanded higher computational resources and longer training times.Interestingly, while the 224×224 image at 90° rotation also performed well (85.16%), the slightly lower performance and increased processing time make the 128×128 configuration more optimal. This suggests that moderate image resolutions strike a better balance between computational efficiency and classification accuracy, making them ideal for real-time diagnostic applications.

V. CONCLUSION

This Paper presents a deep learning-based framework utilizing DenseNet-121 was proposed for the automated classification of breast cancer from histopathological images.

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Through comprehensive experimentation involving variations in image size, rotation angles, and magnification levels, the model achieved its highest accuracy of 88.03% using an image size of 128×128 pixels with 90° rotation at 100X magnification. These results demonstrate the effectiveness of optimizing input configurations and highlight the DenseNet-121 model's capability to extract discriminative features from complex histopathological data. The integration of histogram normalization and data augmentation significantly contributed to enhancing model generalization and classification performance. The outcomes of this research confirm that transfer learning, when properly tuned, can serve as a powerful tool for diagnostic support in digital pathology.

For future enhancements, several directions can be pursued to improve both performance and clinical applicability. The current framework can be extended by incorporating attention-based mechanisms or Transformer-based architectures to further refine feature representation and localization of cancerous regions. In addition, implementing federated learning would enable secure, collaborative training across multiple medical institutions while preserving data privacy. Real-time deployment through web or mobile-based platforms can also make this tool accessible to clinicians for immediate diagnostic support. Finally, expanding the dataset to include diverse histological subtypes and testing across multi-institutional image sources would improve the model's robustness and generalizability.

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