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MULTI-STAGE BREAST CANCER CLASSIFICATION FROM HISTOPATHOLOGICAL IMAGES USING XCEPTIONNET

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Abstract

Breast cancer is one of the leading causes of mortality among women worldwide, where early and accurate diagnosis plays a critical role in improving patient survival. In this study, a deep learning-based framework is proposed for the automated classification of breast cancer histopathological images. The proposed approach utilizes transfer learning with the XceptionNet architecture to perform both binary classification (benign vs. malignant) and multi-class classification of tumor subtypes. The model is trained and evaluated on the BreakHis dataset, which contains microscopic images at multiple magnification levels. Comprehensive preprocessing techniques, including image resizing, normalization, and data augmentation, are applied to improve model generalization. The dataset is divided into training, validation, and testing sets, and 5-fold cross-validation is employed to ensure robustness and reproducibility. The proposed model achieves superior performance with an accuracy of 98.57% for binary classification, while achieving competitive results of 95.4% and 93.82% for benign and malignant multi-class classification, respectively. In addition to accuracy, other evaluation metrics such as precision, recall, and F1-score are used to validate the effectiveness of the model. Experimental results demonstrate that the proposed framework outperforms several existing approaches in terms of classification accuracy and reliability. This study highlights the potential of deep learning and transfer learning techniques in assisting medical professionals for accurate and efficient breast cancer diagnosis.

1. Introduction

Breast cancer is one of the most prevalent and life-threatening diseases among women worldwide, representing a major global health concern. According to recent cancer statistics, breast cancer remains the most frequently diagnosed cancer and a leading cause of cancer-related mortality among women [1]. Global health reports further indicate a continuously rising incidence rate, emphasizing the urgent need for early detection and accurate diagnostic strategies [2].

Medical imaging techniques such as mammography, ultrasound, and magnetic resonance imaging (MRI) play a crucial role in breast cancer detection and diagnosis. However, these techniques often suffer from limitations such as inter-observer variability, noise, and subtle variations in tumor appearance, which make accurate diagnosis challenging. To address these issues, computational approaches such as radiomics have been introduced to enhance the detection and classification of breast abnormalities [3]. Furthermore, deep learning-based models, including multi-view mammogram classification frameworks, have demonstrated improved performance by leveraging contextual and spatial information from medical images [4]. Recent advancements in artificial intelligence have led to the development of various deep learning-based frameworks for breast cancer diagnosis. Evidential deep learning approaches have been proposed to improve prediction reliability and interpretability in mammography analysis [5], while contrastive learning and cross-view learning techniques have enhanced model generalization across diverse imaging conditions [6]. Earlier computer-aided diagnosis systems also aimed to support radiologists by improving classification accuracy and reducing diagnostic errors [7].

In addition, modern deep learning architectures, including convolutional neural networks (CNNs), transformer-based models, and hybrid frameworks, have significantly improved performance in medical image analysis tasks. For instance, advanced architectures such as ConvNeXt-based models and U-Net variants have shown promising results in medical image segmentation [8]. Transformer-based approaches and knowledge distillation techniques have further enhanced classification performance in breast ultrasound imaging [9], while hybrid CNN-transformer models have demonstrated the ability to capture both local and global features effectively [10]. Moreover, transfer learning using pre-trained models such as VGG and Inception has been widely adopted for breast cancer classification, yielding competitive performance across various datasets [11]. Hybrid deep learning frameworks and attention-based models have also been proposed to further improve classification accuracy and feature representation [12]–[14].

Despite these advancements, several limitations remain in existing studies. Most approaches focus on a single classification task, particularly binary classification (benign vs. malignant), and fail to address the complexity of multi-class subtype classification. Additionally, many models are evaluated on limited datasets or lack robust validation strategies, which restricts their generalization capability. Although few-shot learning and meta-learning techniques have been explored to overcome data limitations, challenges related to variability and scalability still persist [15]. Furthermore, while deep learning applications in histopathological imaging have shown promising results, issues related to interpretability, robustness, and computational efficiency remain open research problems [16]. Similarly, different studies have used a range of CNNs for skin and colorectal cancer [17]-

[19]. Recent studies integrating deep learning with data balancing strategies and optimized architectures have demonstrated improved performance in mammogram classification tasks [20]. Automated deep learning-based systems have further enhanced abnormality detection and diagnostic accuracy in medical imaging [21], while ongoing advancements continue to highlight the importance of developing efficient and reliable early detection systems [22].

Global health organizations continue to emphasize the increasing burden of breast cancer and the necessity for improved diagnostic solutions [23]–[25]. Although conventional imaging modalities such as mammography remain essential in clinical practice, their effectiveness can be significantly enhanced through artificial intelligence-based approaches [26], [27]. Recent global cancer reports further reinforce the urgent need for advanced computational frameworks for early detection and accurate diagnosis [28]–[30]. To address these challenges, this study proposes a deep learning-based framework for breast cancer classification using histopathological images. Unlike existing approaches that primarily focus on single-task classification, the proposed method introduces a unified multi-level classification framework that simultaneously performs binary classification (benign vs. malignant) and multi-class subtype classification. The proposed approach leverages transfer learning with the XceptionNet architecture to effectively extract discriminative features from histopathological images. Furthermore, comprehensive preprocessing techniques, robust validation using cross-validation, and multiple evaluation metrics are employed to ensure reliability and reproducibility. The main contributions of this study are:

1. the development of a unified framework for multi-level breast cancer classification
2. the effective utilization of transfer learning for improved feature extraction and classification performance, and extensive experimental validation demonstrating superior performance and robustness compared to existing methods.

2. Related Work

Breast cancer diagnosis has been thoroughly investigated owing to its significant global incidence and clinical intricacy. Recent statistical and clinical studies underscore the significance of early detection and precise classification in enhancing patient survival rates [31], [32]. The diverse characteristics of breast cancer, encompassing various subtypes and tumor traits, complicates its diagnosis, necessitating sophisticated computational methodologies [33].

A. Conventional and Imaging-Based Approaches:

Ultrasound, magnetic resonance imaging (MRI), and positron emission tomography (PET) are all traditional diagnostic methods that have been very helpful in finding breast cancer. Ultrasound imaging is especially good at finding things early on, especially in places with few resources. However, it often depends on the operator and doesn't show many features [35]. Likewise, MRI and PET-based imaging methods give detailed information about structure and function, but they need to be interpreted by experts and are expensive to run and use [36]. These limitations make it hard for them to grow and show that automated diagnostic solutions are needed.

B. Deep Learning-Based Classification Approaches:

As artificial intelligence has progressed, deep learning models, especially convolutional neural networks (CNNs), have shown to be better at analyzing medical images. Comprehensive reviews demonstrate that CNN-based methodologies substantially enhance classification accuracy by autonomously extracting hierarchical features from medical images [38], [39]. Nevertheless, despite their efficacy, CNN models frequently fail to encapsulate global contextual information, which is essential for precise classification in intricate histopathological images.

To overcome these constraints, numerous studies have suggested sophisticated and alternative architectures. Quantum-inspired models and optimization-based techniques have been developed to improve classification performance; however, these methods frequently entail greater computational complexity and reduced interpretability [40], [51]. Likewise, object detection frameworks like YOLO and transformer-based detection models have demonstrated encouraging outcomes in pinpointing tumor regions in mammographic images; however, their efficacy is significantly reliant on extensive annotated datasets [41].

C. Hybrid and Transformer-Based Models:

Recent research trends have moved toward hybrid architectures that use both CNNs and transformer-based models to take advantage of both local and global feature representations. Hybrid CNN-transformer frameworks and feature fusion strategies have shown better results in tasks like segmentation and classification [50], [42]. Transformer-based models, such as vision transformers and Swin-based architectures, have demonstrated exceptional efficacy in capturing long-range dependencies in medical images [43], [68]. Even though these methods have some benefits, they usually need big datasets and a lot of computing power, which makes them less useful in real-world clinical settings. To fix these problems, people have suggested using lightweight transformer models. However, these models often trade performance for efficiency [37]. This balance between accuracy and computational cost is still a big problem in current research.

D. Transfer Learning and Feature Optimization Techniques:

Transfer learning has become a strong way to make models work better, especially when there isn't much labeled data to work with. DenseNet, EfficientNet, and AlexNet are examples of pre-trained architectures that have been used successfully to classify breast cancer, getting good accuracy [53], [57], and [58]. These models use what they learn from big datasets to make feature extraction and generalization better.

But when used on medical datasets with different characteristics, transfer learning-based methods may have problems with overfitting and domain adaptation. Recent research has endeavored to mitigate these constraints via hybrid transfer learning frameworks and feature optimization methodologies [66]. These methods make the model work better, but they also make it more complicated and require careful tuning.

E. Advanced Learning Strategies and Explainability

To improve the model's robustness and adaptability even more, researchers have looked into advanced learning techniques like meta-learning, few-shot learning, and multimodal learning [47], [45]. The goal of these methods is to make generalization better across different datasets and less reliant on large amounts of labeled data. There are also explainable artificial intelligence (XAI) techniques that have been developed to make models more transparent and easier to understand. These are important for clinical use [44], [62]. While these methods enhance trust and usability, they frequently add computational overhead and complexity, rendering them impractical for real-time clinical applications.

F. Specialized Models and Dataset Challenges:

Numerous studies have suggested specialized architectures for the classification and segmentation of breast cancer, encompassing attention-based networks, multi-task learning frameworks, and lightweight segmentation models [48], [49], [71]. Moreover, spectral imaging and CNN-based techniques have been investigated for expedited subtype classification [52]. Even with these improvements, a big problem with most studies is that they don't test their results on a wide range of datasets. Commonly used public datasets include INbreast, TCGA-BRCA, and Breast Cancer Wisconsin. However, models that are trained on these datasets often don't work well on new data distributions [63]–[65]. Recent studies underscore the necessity for cross-dataset validation and standardized evaluation protocols to guarantee dependable model performance [67], [68].

3. Proposed Method

The methodology of this study presents a structured framework for the automated classification of breast cancer histopathological images using deep learning techniques. The proposed approach is designed to ensure high classification accuracy, robustness, and reproducibility by integrating data preprocessing, transfer learning, and multi-level classification strategies. The overall workflow of the proposed system consists of dataset preparation, preprocessing, model development, training, and performance evaluation.

3.1. Dataset Description:

In this study, the publicly available BreakHis dataset is utilized for the classification of breast cancer histopathological images. The BreakHis dataset is widely used in medical imaging research due to its diversity and high-quality microscopic images. It consists of a total of 7,909 breast tumor images, which are categorized into two primary classes: benign and malignant. The benign category includes four subtypes: adenosis, fibroadenoma, phyllodes tumor, and tubular adenoma. Similarly, the malignant category is divided into four subtypes: ductal carcinoma, lobular carcinoma, mucinous carcinoma, and papillary carcinoma. This hierarchical structure allows for both binary and multi-class classification tasks. One of the key characteristics of the dataset is the variation in magnification factors. The images are captured at four different magnification levels: 40×, 100×, 200×, and 400×. This variation introduces additional complexity, as the visual features of tumor tissues differ significantly across magnification levels. Consequently, the dataset provides a realistic scenario for evaluating the robustness and generalization capability of deep learning models. The diversity in image resolution, texture, and tumor morphology makes the BreakHis dataset particularly suitable for developing and evaluating automated breast cancer classification systems.

3.2. Data preprocessing:

Data preprocessing plays a crucial role in improving the performance and generalization capability of deep learning models. In this study, several preprocessing steps are applied to the BreakHis histopathological image dataset to ensure data consistency and enhance model learning. First, all images are resized to a fixed dimension to match the input size required by the XceptionNet architecture. This step ensures uniformity across the dataset and allows efficient batch processing during training. Next, pixel intensity normalization is performed by scaling the values to the range of 0 to 1. This normalization helps stabilize the learning process, improves convergence speed, and prevents the model from being biased toward higher intensity values.

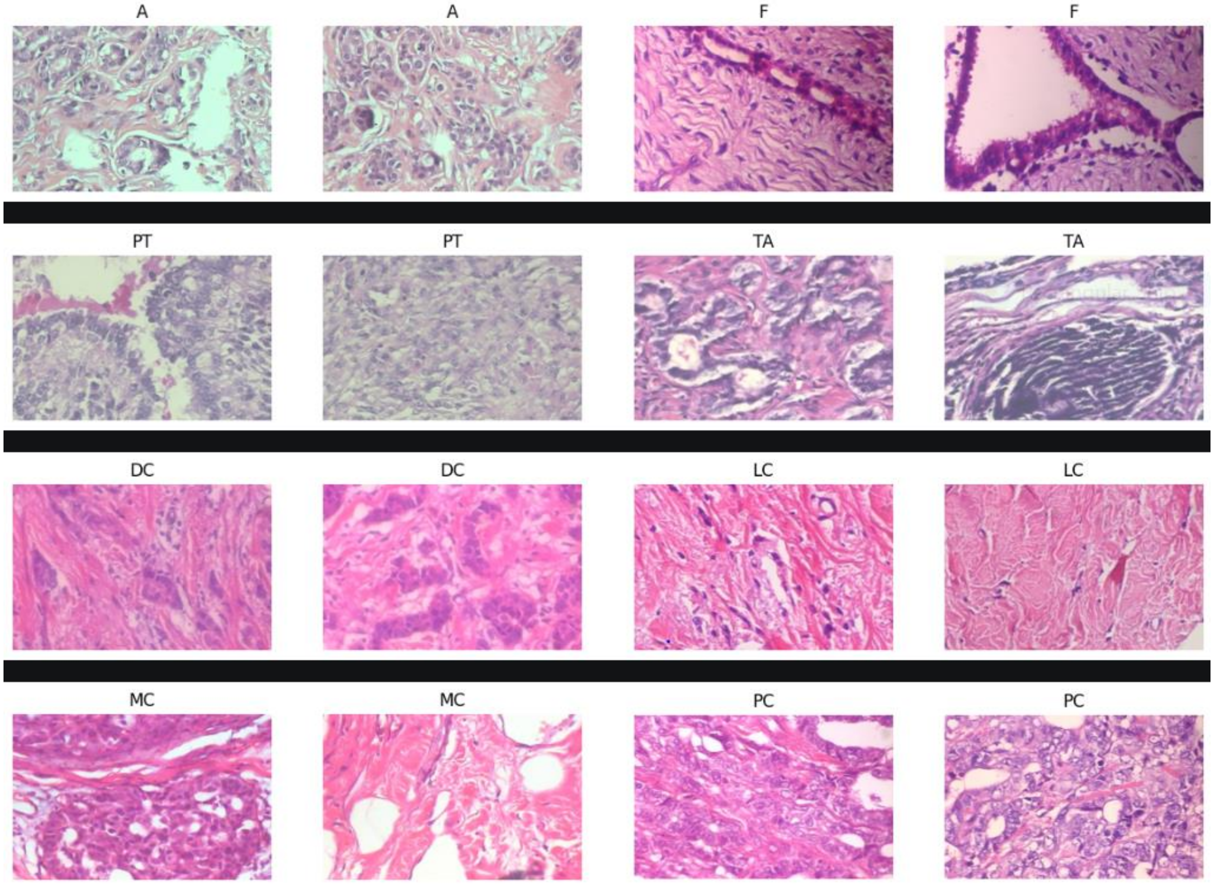

Figure 3.1: Sample Histopathological Images from BreakHis Dataset

To address the issues of limited data and class imbalance, data augmentation techniques are applied to the training dataset. These techniques include random rotation, horizontal and vertical flipping, zooming, shifting, and brightness adjustments. Instead of generating and storing augmented images, real-time data augmentation is used, where transformations are applied dynamically during training. This approach reduces memory usage and improves the model's ability to generalize to unseen data.

Furthermore, the dataset is divided into three subsets: training (60%), validation (20%), and testing (20%). This split ensures that the model is trained on sufficient data, while validation and testing sets are used to evaluate its performance on unseen samples. Overall, these preprocessing steps enhance the quality of the dataset, reduce overfitting, and enable the model to learn more robust and discriminative features for accurate breast cancer classification.

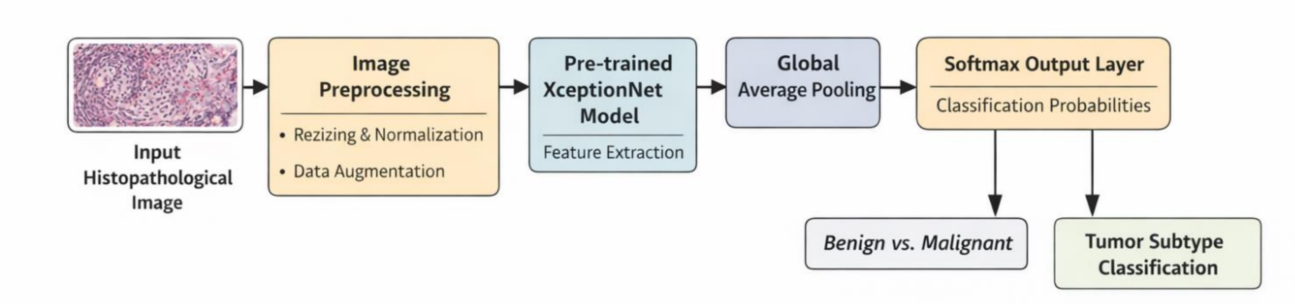

Figure 3.2: Model Architecture Flow

3.3 Proposed Framework:

The proposed framework is based on a deep learning approach using the XceptionNet architecture for breast cancer classification. XceptionNet is a convolutional neural network that utilizes depthwise separable convolutions, enabling efficient feature extraction from histopathological images while reducing computational complexity. This makes it highly suitable for capturing fine-grained patterns in medical images. In this study, a transfer learning strategy is adopted, where the pre-trained XceptionNet model is used as a feature extractor. The lower layers of the network capture generic visual features, while the upper layers are fine-tuned for the specific task of breast cancer classification. Additional fully connected layers are integrated with the base model, followed by a Softmax activation function to generate final predictions. The proposed framework processes input histopathological images through a sequence of preprocessing steps, followed by feature extraction using XceptionNet, and finally classification into different categories.

3.4 Classification Methodologies:

To evaluate the performance of the proposed framework, three different classification methodologies are implemented. These methodologies are designed to analyze the model at different levels, including general cancer detection and fine-grained subtype classification.

3.4.1 Binary Classification (Benign vs Malignant):

In this approach, the model classifies histopathological images into two categories: benign and malignant. This is the primary classification task, which determines whether the tissue is cancerous or non-cancerous. The output layer consists of two neurons with a Softmax activation function to generate classification probabilities. This methodology provides an overall evaluation of the model's ability to distinguish between healthy and cancerous tissues.

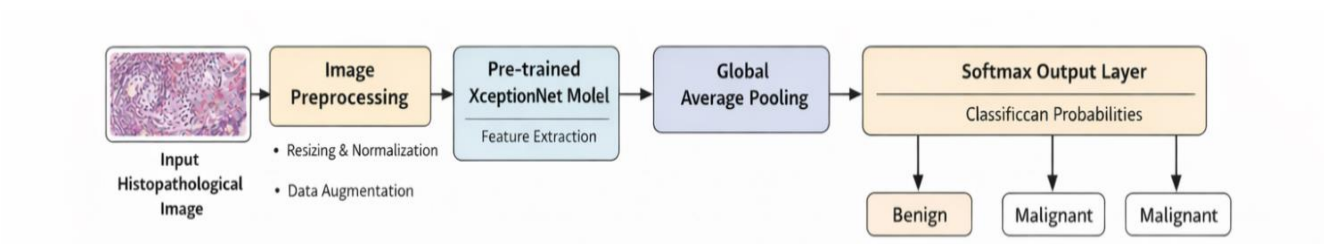

Figure 3.3: Methodology 1 Binary Classification Architecture Flow

3.4.2 Benign Subtype Classification:

In this methodology, the model focuses on the classification of benign tumor subtypes. The input images are classified into four categories: adenosis, fibroadenoma, phyllodes tumor, and tubular adenoma. This multi-class classification task requires the model to identify subtle differences among benign tissue structures. The output layer is modified to include four neurons corresponding to the benign classes, followed by a Softmax activation function.

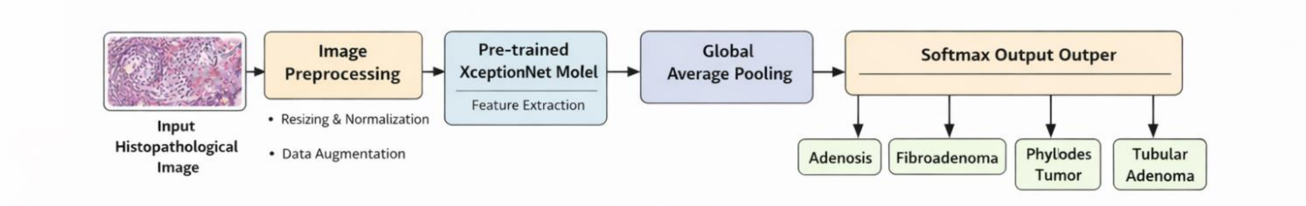

Figure 3.4: Benign Subtype Classification Architecture Flow

3.4.3 Malignant Subtype Classification:

In this methodology, the model classifies malignant tumor images into four subtypes: ductal carcinoma, lobular carcinoma, mucinous carcinoma, and papillary carcinoma. This task is more challenging due to the similarity among malignant patterns. Similar to the benign classification, the output layer contains four neurons with Softmax activation. This allows the model to predict the probability of each malignant subtype.

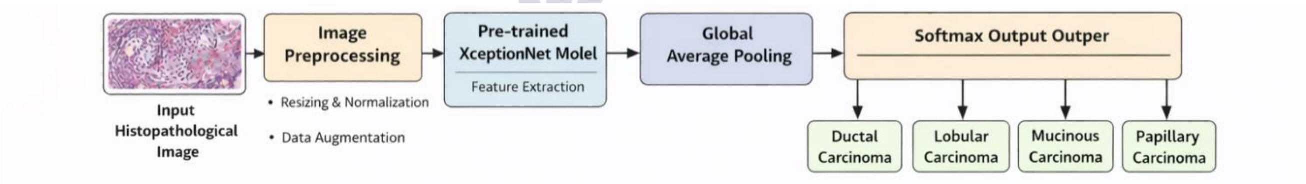

Figure 3.5: Malignant Subtype Classification Architecture Flow

4. Results and Discussion:

This chapter presents the experimental results obtained from the proposed XceptionNet-based framework for breast cancer classification. The model is evaluated on the BreakHis dataset using three classification methodologies, including binary classification and multi-class classification for benign and malignant subtypes. The performance of the model is analyzed using standard evaluation metrics to assess its effectiveness and reliability.

4.1 Binary Classification Results

The performance of the proposed XceptionNet model for binary classification (benign vs. malignant) is presented in this section. The model achieved a high classification accuracy, demonstrating its strong capability to distinguish between cancerous and non-cancerous breast tissue images. The experimental results show that the model obtained an accuracy of **98.57**%, with a precision of **98.57**%, recall of **98.88**%, and an F1-score of **98.72**%. These results indicate that the model performs exceptionally well in identifying malignant cases while maintaining a low rate of false predictions

Table 4.1: Binary Classification Performance

Metric	Value
Accuracy	98.57%
Precision	98.57%
Recall	98.88%
F1-Score	98.72%

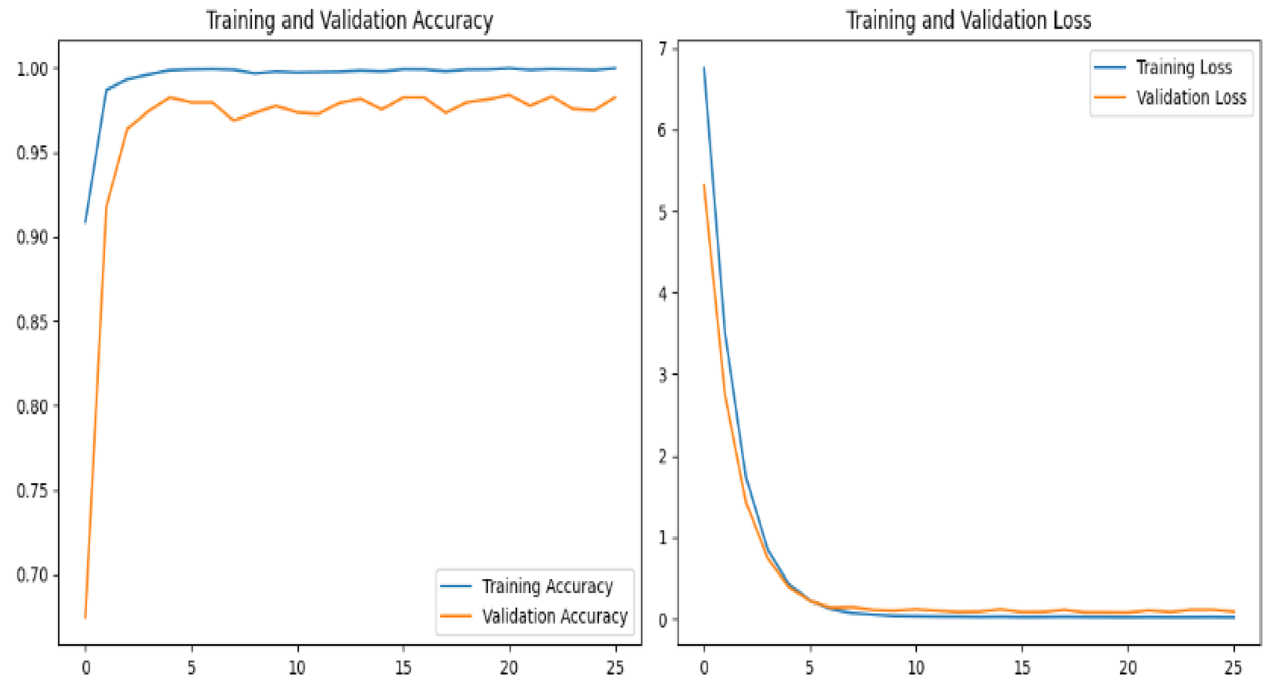

Figure 4.1: Training and Validation Accuracy and Loss Graphs of Binary Model

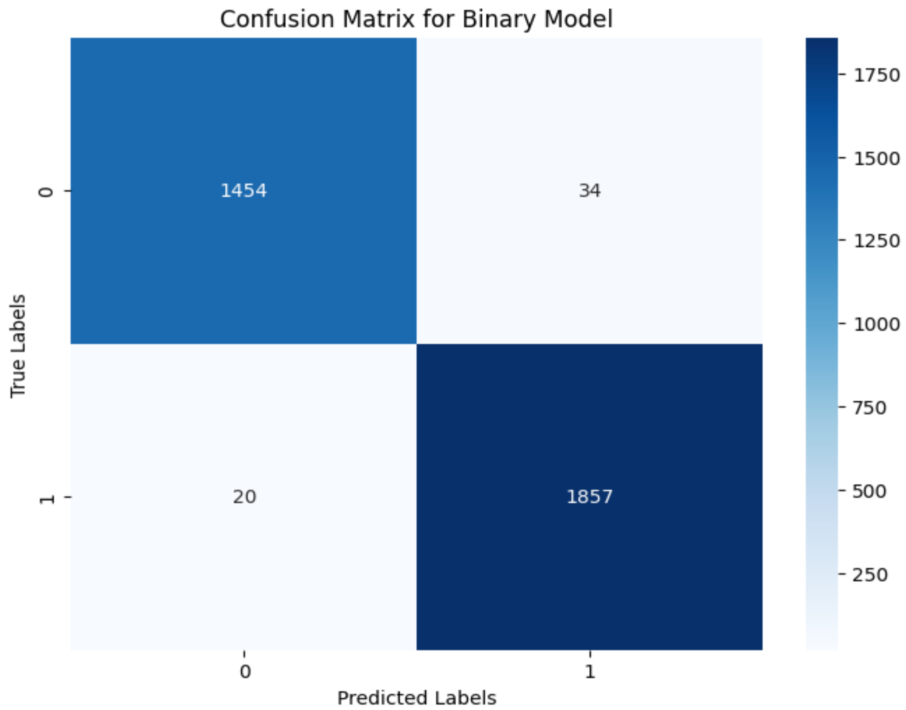

Figure 4.2: Confusion matrix for Binary Model

4.2 Benign Subtype Classification Results

This section presents the performance of the proposed XceptionNet model for benign subtype classification. In this task, the model classifies histopathological images into four benign categories, including adenosis, fibroadenoma, phyllodes tumor, and tubular adenoma. Compared to binary classification, this task is more challenging due to the similarity among benign tissue patterns. The experimental results show that the model achieved an accuracy of **95.40%**, with a precision of **95.95%**, recall of **94.04%**, and an F1-score of **94.89%**. These results indicate that the model is capable of learning subtle differences among benign subtypes and performing accurate multi-class classification.

Table 4.2: Benign Subtype Classification Performance

Metric	Value
Accuracy	95.40%
Precision	95.95%
Recall	94.04%
F1-Score	94.89%

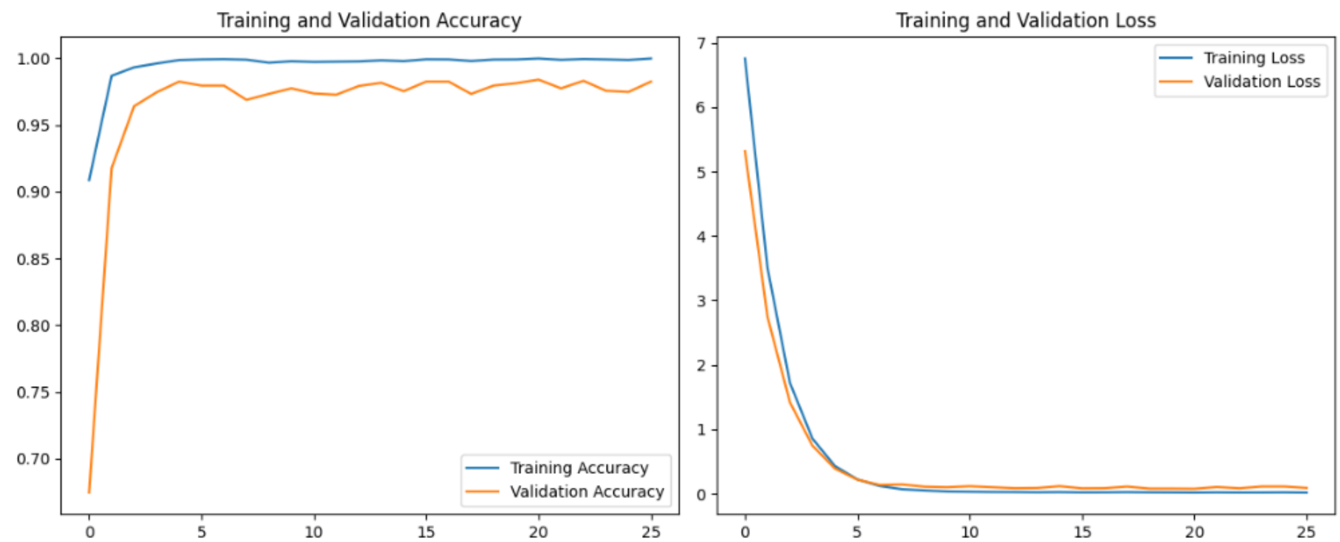

Figure 4.3 : Training and Validation Accuracy and Loss Graphs of Benign Model

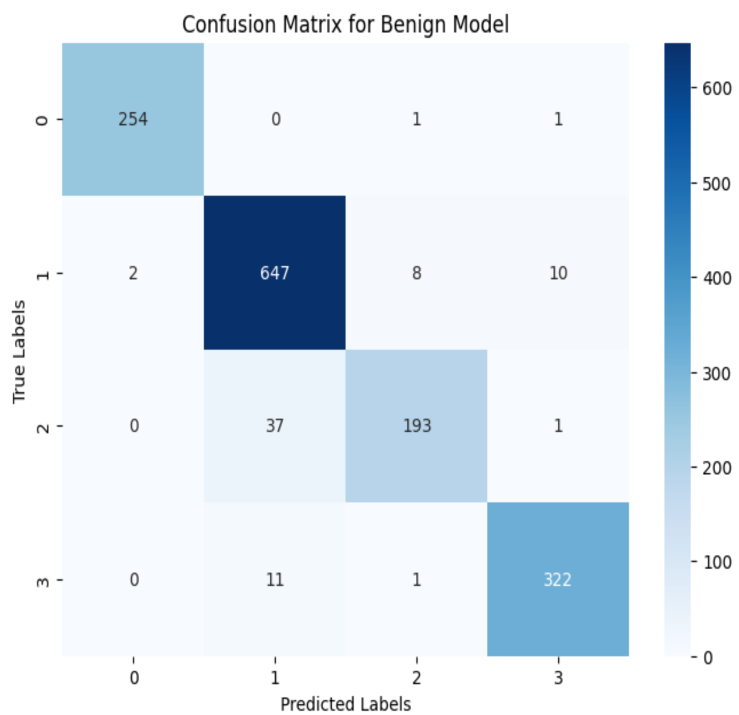

Figure 4.4: Confusion matrix for Benign Model

4.3 Malignant Subtype Classification Results

This section presents the performance of the proposed XceptionNet model for malignant subtype classification. In this task, the model classifies histopathological images into four malignant categories, including ductal carcinoma, lobular carcinoma, mucinous carcinoma, and papillary carcinoma. This classification is more complex due to the high similarity among malignant tissue patterns. The experimental results show that the model achieved an accuracy of **93.82%**, with a precision of **93.87%**, recall of **93.93%**, and an F1-score of **93.87%**. These results indicate that the model is capable of effectively distinguishing between different malignant subtypes, although the performance is slightly lower compared to binary classification due to increased complexity.

Table 4.3: Malignant Subtype Classification Performance

Metric	Value
Accuracy	93.82%
Precision	93.87%
Recall	93.93%
F1-Score	93.87%

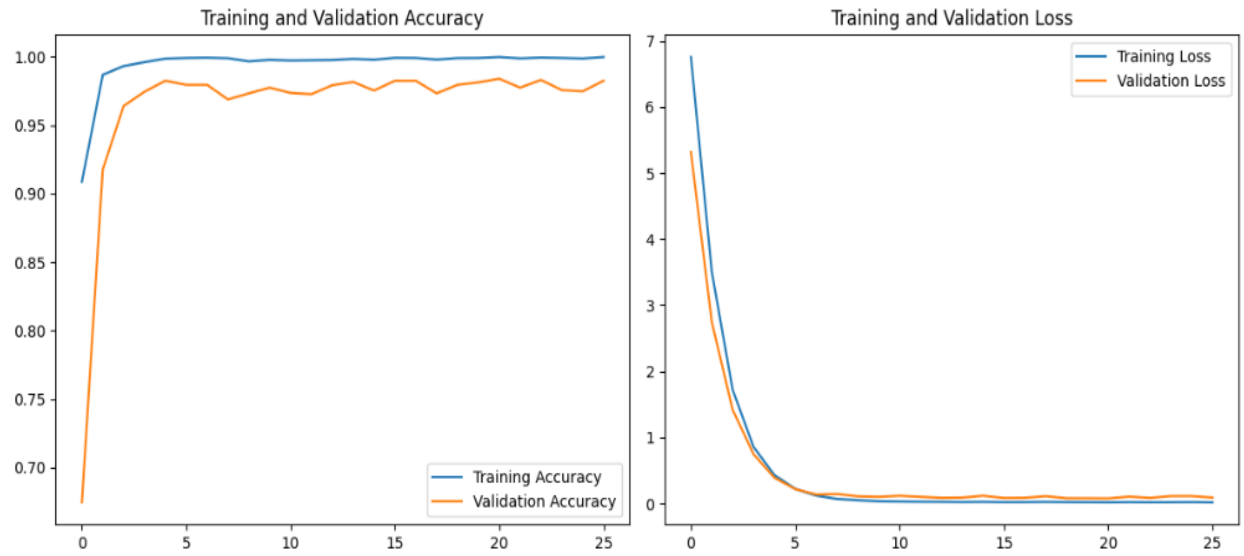

Figure 4.5: Training and Validation Accuracy and Loss Graphs of Malignant Model

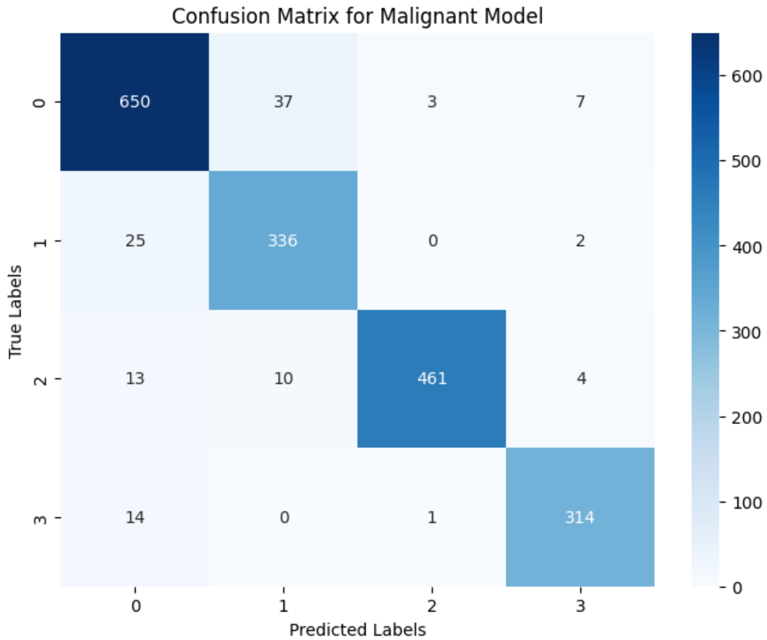

Figure 4.6: Confusion Metrix for Malignant Model

5. Conclusion

This study presented a deep learning-based framework for breast cancer classification using histopathological images from the BreakHis dataset. The proposed approach utilized the XceptionNet architecture with a transfer learning strategy to effectively extract discriminative features from breast tissue images. Comprehensive preprocessing techniques, including resizing, normalization, and data augmentation, were applied to enhance dataset quality and improve model generalization. To thoroughly evaluate the proposed model, three classification methodologies were implemented, including binary classification (benign vs. malignant) and multi-class classification for both benign and malignant subtypes. The experimental results demonstrated that the model achieved high performance across all tasks, with the highest accuracy observed in binary classification. Although multi-class classification presented additional challenges due to the similarity among tissue patterns, the model maintained strong and reliable performance. Overall, the findings confirm that the proposed XceptionNet-based framework is an effective and robust solution for automated breast cancer classification. The model shows strong potential to assist medical professionals in early detection and diagnosis, improving accuracy and reducing diagnostic time.

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