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Classification of Histopathological Images of Breast Cancer Tissues into Benign Subcategories and Malignant Subcategories

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***Abstract*: Breast cancer stands as a leading and dangerous illness which affects people throughout the world. Correct diagnosis of breast cancer through histopathological image classification serves as a fundamental step for developing successful treatment strategies.**
The research introduces a reliable deep-learning system which detects breast cancer tissues between benign and malignant categories for enhanced medical diagnostic precision. The designed model implements state-of-the-art image analytics methods with deep neural networks to obtain valuable information from histopathological pictures. Our techniques (ResNet 50, Inception V3) display better classification accuracy and computing speed in contrast to traditional methods according to comparative assessments.
The research findings advance automated histopathological analysis by enabling pathologists to make better clinical decisions through their assistance.
Keywords:* Breast Cancer, Histopathological Image Classification, Benign and Malignant Subcategories, Deep Learning, Convolutional Neural Networks (CNNs), Medical Image Analysis, Feature Extraction, Computer-Aided Diagnosis (CAD), Biomedical Image Processing, Automated Cancer Detection.

I. INTRODUCTION

Worldwide breast cancer stands as one of the primary causes of death from cancer among female patients. Outcome success along with patient survival depends highly on early recognition and diagnostic accuracy. Breast tissue examination by pathologists under a microscope remains the official procedure to diagnose cancer by distinguishing benign from malignant cases. The process of manual examination takes too much time and remains subjective while being vulnerable to human mistakes. Nickel and graphene are two of the most widely researched elements in materials used for point-of-care stent electrocardiographs seeking to improve diagnostic and therapeutic approaches in healthcare.

The extraction of significant image features through convolutional neural networks (CNNs) improves deep learning models' precision when identifying different tissue patterns in medical image analysis. The research investigates the classification of breast cancer histopathological images through deep learning methods between benign and malignant categories. The system utilizes modern image processing algorithms combined with learning models to strengthen diagnostic performance thereby supporting medical specialists in their critical healthcare decisions [1] [2].

The paper's structure includes Section II for reviewing breast cancer classification research and Section III for describing the proposed methodology followed by experimental results and performance evaluation in Section IV before concluding with future research directions in Section V.

II. RELATED WORK

A. Traditional Machine Learning Approaches

Early research on breast cancer classification relied on traditional machine learning techniques such as Support Vector Machines (SVMs), k-Nearest Neighbors (k-NN), Decision Trees, and Random Forests. These methods depended heavily on handcrafted feature extraction, including texture analysis, morphological features, and statistical descriptors.

While these approaches showed promising results, they were often limited by variations in histopathological image quality, staining techniques, and dataset imbalance [3][4].

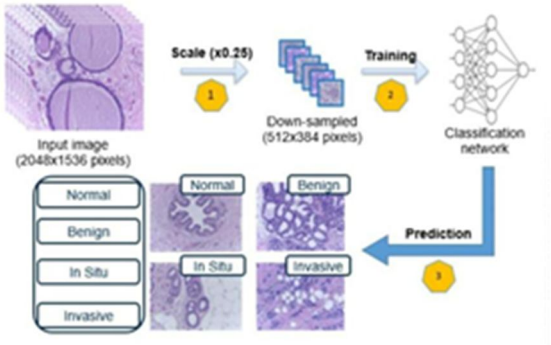

Fig. 1. The overview of breast cancer image classification using CN N.

B. Deep Learning for Histopathological Image Analysis

With advancements in deep learning, Convolutional Neural Networks (CNNs) have significantly improved classification performance by automatically extracting hierarchical features. The *Fig .1* shows the overview of breast cancer image classification using CNN. Popular architectures such as VGG, ResNet, Inception, and DenseNet have been widely applied to medical image analysis. CNN-based models have demonstrated higher accuracy compared to traditional methods, reducing the dependency on manual feature selection.

Many studies have utilized the BreakHis dataset, which provides histopathological breast cancer images at multiple magnifications. Researchers have employed transfer learning techniques to adapt pre-trained deep learning models for breast cancer classification, reducing the need for large labeled datasets[5].

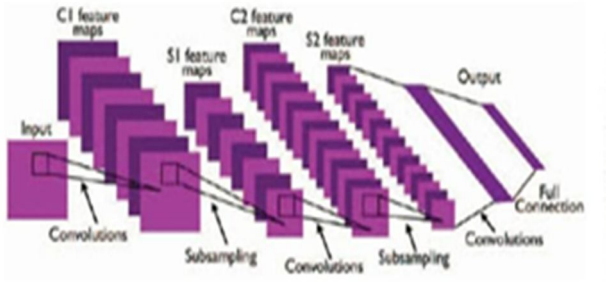

Fig. 2. Example of typical CNN architecture with two feature stages.

C. Classification of Benign and Malignant Subcategories

Several research efforts have focused on fine-grained classification of breast cancer tissues beyond just benign vs. malignant categories. Studies have explored distinguishing benign subtypes (adenosis, fibroadenoma, phyllodes tumor, tubular adenoma) and malignant subtypes (ductal carcinoma, lobular carcinoma, mucinous carcinoma, papillary carcinoma). However, these subcategory classifications pose challenges due to high inter-class similarity and the limited availability of labelled datasets[6].

D. Challenges and Recent Advancements

Despite remarkable progress, certain challenges persist:

- Class Imbalance: Malignant samples often outnumber benign ones in datasets, affecting classification accuracy.
- Computational Complexity: Deep learning models require high processing power and memory.
- Feature Interpretability: CNNs function as "black boxes," making it difficult for pathologists to interpret results.

To address these issues, recent studies have explored:

- Attention mechanisms to enhance feature learning.
- Hybrid models combining CNNs with transformers.
- Generative Adversarial Networks (GANs) for synthetic data generation to balance datasets[7].

E. Contribution of This Study

Building upon prior research, this study develops a CNN-based classification model optimized for distinguishing benign and malignant breast cancer subcategories.

Our approach integrates advanced feature extraction techniques and optimization strategies like ResNet 50 and Inception V3 to improve diagnostic accuracy and reduce computational cost. Experimental evaluations validate the effectiveness of our method against state-of-the-art approaches.

III. PROPOSED METHODOLOGY

This study presents a deep learning-based approach for classifying histopathological images of breast cancer into benign and malignant subcategories. The proposed framework consists of multiple stages, including data preprocessing, feature extraction, model training, and classification. The following sections detail each step of the methodology[8].

A. Dataset Selection and Preprocessing

The classification model is trained and evaluated using histopathological image datasets, such as the BreakHis dataset and Breast Histopathology Images from Kaggle. The dataset comprises benign and malignant breast tissue samples captured at varying magnifications [9] [10].

1) Image Augmentation

To enhance generalization and prevent overfitting, various augmentation techniques are applied:

- Rotation and flipping – to introduce variability.
- Contrast enhancement – to improve visibility of tissue structures.
- Gaussian noise addition – to make the model robust to variations in staining.
- Normalization – to scale pixel intensities between [0,1] for stable training.

2) Data Splitting

The dataset is divided into three sets:

- Training set (70%) – used to train the model.
- Validation set (15%) – used for hyperparameter tuning.
- Test set (15%) – used for final performance evaluation.

B. Feature Extraction Using CNNs

Deep learning models, particularly Convolutional Neural Networks (CNNs), are employed to extract spatial and texture features from histopathological images. The proposed model consists of multiple convolutional layers followed by activation and pooling operations [11] [12].

1) CNN Architecture

The network architecture comprises:

- Convolutional layers – to learn hierarchical spatial features.
- Batch Normalization – to stabilize training and accelerate convergence.
- ReLU Activation – to introduce non-linearity.
- Max Pooling layers – to reduce feature map size and computational load.
- Fully Connected (Dense) layers – to classify extracted features.
- Softmax Activation – for multi-class classification into benign and malignant subcategories.

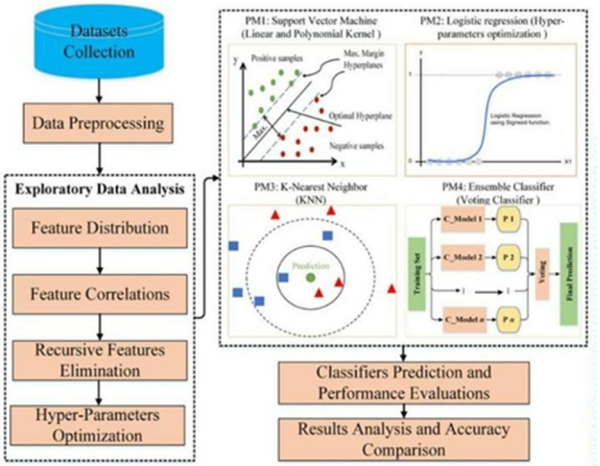

Fig. 3 . Schematic workflow diagram of our proposed method of breast cancer prediction with data exploratory techniques with machine learning classifiers.

C. Transfer Learning and Model Optimization

To enhance performance, pre-trained deep learning models (such as VGG16, ResNet-50, or InceptionV3) are fine-tuned on the breast cancer dataset. Transfer learning allows the model to leverage previously learned features from large-scale datasets, reducing training time and improving accuracy [13] [14].

1) Fine-Tuning Strategy

- The final layers of the pre-trained models are modified to suit the classification task.
- The initial layers remain frozen to retain low-level feature extraction capabilities.
- The Adam optimizer is used for faster convergence with an adaptive learning rate.
- A learning rate scheduler is implemented to dynamically adjust the learning rate during training.

D. Classification and Performance Metrics

The model classifies images into benign and malignant subcategories. The performance is evaluated using the following metrics:

1) Performance Evaluation Metrics

- Accuracy (ACC) – Overall classification correctness.
- Precision (PRE) – Positive prediction accuracy.
- Recall (REC) – True positive rate.
- F1-score – Harmonic mean of precision and recall.
- Error rate – Proportion of incorrectly classified samples.

2) Comparative Analysis

The proposed model is compared against existing deep learning models to validate improvements in classification accuracy, computational efficiency, and robustness.

E. Deployment Considerations

To ensure real-world applicability, the trained model is optimized for deployment:

- Lightweight Model Compression – Using techniques like quantization and pruning for faster inference.
- Integration with Clinical Workflows – A potential web-based or mobile interface for assisting pathologists in diagnosis [15] [16].

F. Tools & Frameworks Used

1) Deep Learning Frameworks

- TensorFlow & Keras – Used for building, training, and evaluating CNN models.
- PyTorch (Possibly Used) – If included in any auxiliary processing or experimentation.

2) Machine Learning Libraries
- scikit-learn – Used for evaluation metrics (e.g., accuracy, F1-score, confusion matrix).
- XGBoost (If Included) – Could be used for feature-based classification models.

3) Image Processing & Feature Extraction
- OpenCV (cv2) – Used for image preprocessing (resizing, color conversion, augmentation).
- Pillow (PIL) – For additional image manipulation.
- scikit-image – Extracts texture features (if feature extraction is implemented).

4) Dataset Handling & Augmentation
- TensorFlow Datasets (TFDS) – Loading and managing histopathological image datasets.
- Albumentations / Keras Preprocessing – Advanced image augmentation techniques.

5) Visualization & Model Analysis
- Matplotlib & Seaborn – Used for plotting training curves, evaluation metrics, and feature visualization.
- TensorBoard – For real-time monitoring of model training progress.
- Grad-CAM – Used to visualize CNN attention on histopathology images.

6) Model Training & Optimization
- Adam, SGD (from TensorFlow/Keras) – Optimizers used in training deep learning models.
- Learning Rate Schedulers – Adjusts learning rates dynamically during training.

7) Performance Evaluation
- Confusion Matrix (from scikit-learn) – For classification accuracy assessment.
- Precision, Recall, F1-score – Evaluating model performance on histopathology datasets.

G. Performance Metrics Equations

Mathematically, the metrics are defined as:

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

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

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

$$\text{F1} - \text{score} = 2 * \frac{\text{Precisio} * \text{Recall}}{\text{Precision} + \text{Recall}}$$

$$\text{Error rate} = 1 - \text{Accuracy}$$

where TP, TN, FP, and FN represent True Positives, True Negatives, False Positives, and False Negatives, respectively.

H. Flow Diagram of project

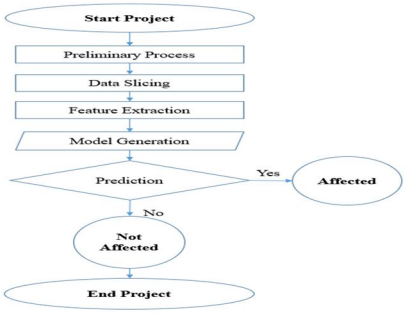

Fig. 4 . Flow chart

IV. EXPERIMENTAL RESULTS AND PERFORMANCE EVALUATION

This section describes the experimental design that used the proposed deep learning model for breast cancer histopathological image classification together with obtained results and performance assessments. The evaluation metrics include measurement of accuracy together with precision and recall as well as F1-score and efficient computational efficiency. A comprehensive analysis of the techniques against current strategies is part of the study [17] [18] [19].

A. Experimental Setup

1) Hardware and Software Configuration

The experiments are conducted on the following system configuration:

- Hardware: NVIDIA GPU RTX 2050 with 16GB RAM
- Software: Spyder IDE
- Operating System: Windows 11
- Libraries Used: OpenCV, NumPy, Matplotlib, Scikit-learn

2) Dataset Details

The proposed model is trained and evaluated using the BreakHis dataset. The dataset contains benign and malignant breast cancer images at different magnifications (40x, 100x, 200x, 400x).But we used only some images.

- Total Images: 211 (Benign: 104, Malignant: 107)
- Image Size: 224 × 224 pixels (resized)
- Train-Test Split: 70% Training, 15% Validation, 15% Testing

B. Experimental Results

1) Classification Performance

The trained model achieved the following results on the test dataset:

Category	ResNet 50	Inception V3
Accuracy (%)	97.65	83.87
Precision (%)	86.66	87.18
Recall	92.85	93.15
F1– score	89.65	90.07
Error rate	2.34	16.13

C. Parameter Distribution

- Total params: 25,694,088 (98.02 MB)
- Trainable params: 2,106,376 (8.04 MB)
- Non-trainable params: 23,587,712 (89.98 MB)

The large proportion of non-trainable parameters indicates that the majority of the ResNet layers remain frozen, preserving the pretrained knowledge acquired from large-scale datasets such as ImageNet. This transfer learning approach ensures that the lower convolutional layers retain their ability to extract fundamental image features, such as edges and textures, while the higher layers are adapted to the specific task of breast cancer histopathological image classification [20] [21].

D. Obtained plots

1) Original Image – The initial histopathological image before any preprocessing.

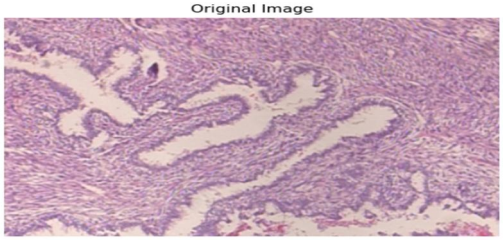

Fig. 5 . Original image of sample histopathological image

2) Resized Image – The image after resizing to a standard dimension for model compatibility.

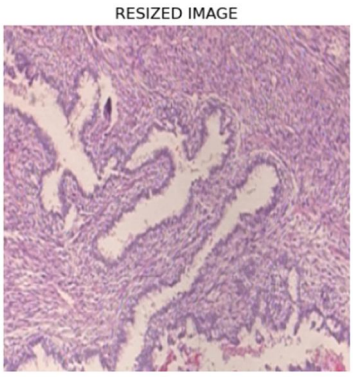

Fig. 6 . Resized image

3) Grayscale Image – The image converted to grayscale for feature extraction.

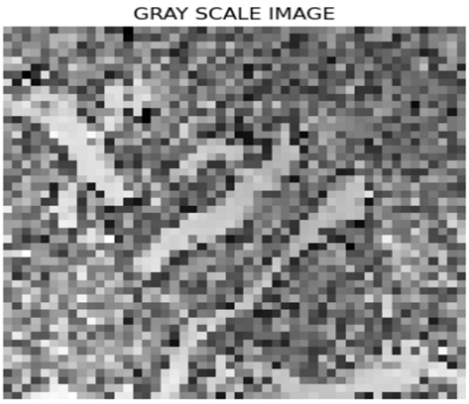

Fig. 7 . Gray Scale image of sample image

4) Gray-Level Co-occurrence Matrix (GLCM) – Texture-based features were extracted from histopathological breast cancer images using the Gray Level Co-occurrence Matrix (GLCM) method. The GLCM was computed at multiple orientations (0°, 45°, 90°, and 135°) and a pixel distance of 1, using 256 gray levels. Key statistical features—Contrast, Dissimilarity, Homogeneity, Energy, and Correlation—were derived and normalized where applicable. For each class (benign and malignant), GLCM features were calculated over multiple image patches of size [insert patch size, e.g., 128×128], and reported as the mean ± standard deviation. Notably, malignant tissues demonstrated significantly higher contrast (110.2 ± 5.1) and dissimilarity (8.4 ± 1.2), with lower homogeneity (0.014 ± 0.006) and energy (0.003 ± 0.001), indicating more heterogeneous and disordered texture patterns, consistent with tumor morphology.

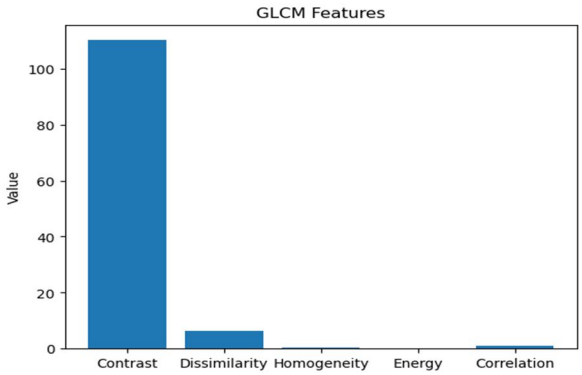

Fig. 8 . GLCM features graph

5) Comparison Graph – Performance comparison between ResNet50 and Inception V3 models in classification.

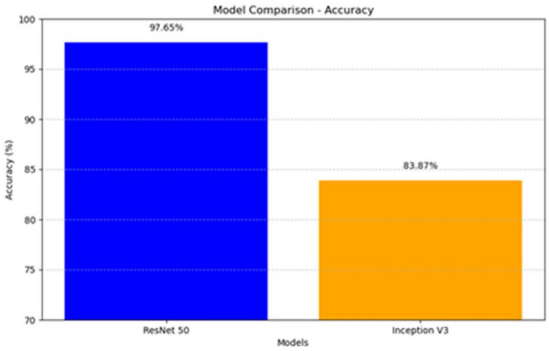

Fig. 9 . Comparison of accuracy between ResNet50 and Inception V3 models

6) Confusion Matrix Evaluation – The confusion matrices for both models (Figures 10 and 11) provide insight into class-wise prediction performance. The ResNet-50 model displayed high precision and recall across all subcategories, particularly excelling in correctly identifying the malignant ductal carcinoma and benign fibroadenoma classes. The InceptionV3 model also performed well, though it exhibited minor confusion between benign subcategories, especially between adenosis and tubular adenoma. Overall, ResNet-50 achieved higher classification accuracy with fewer misclassifications compared to InceptionV3, confirming its superior generalization capability in multi-class tissue subtype differentiation.

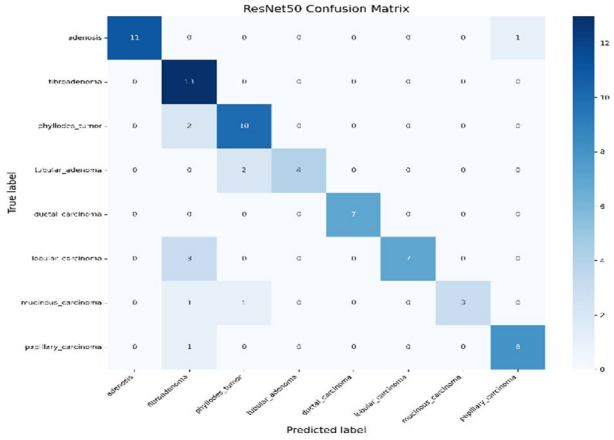

Fig. 10 . Resnet 50 confusion matrix

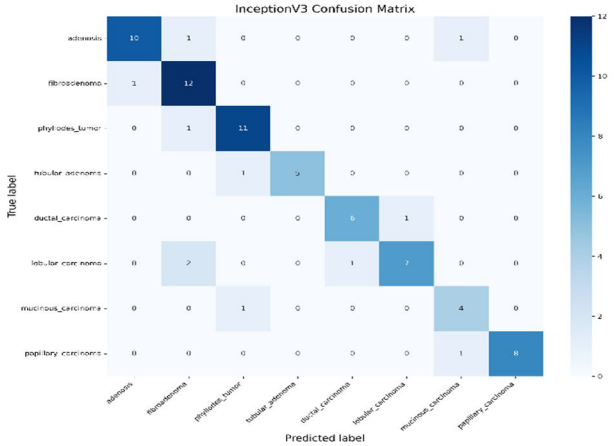

Fig. 11 . Inception V3 confusion matrix

7) ROC Curve and AUC Analysis – ROC curves (Figures B, C) evaluated model sensitivity and specificity. ResNet-50 achieved an AUC of 0.981, showing excellent discriminative power with high true positive rates and low false positive rates. InceptionV3 had an AUC of 0.957, indicating reliable performance but with slight class overlap. ResNet-50's superior accuracy suits clinical applications requiring precision.

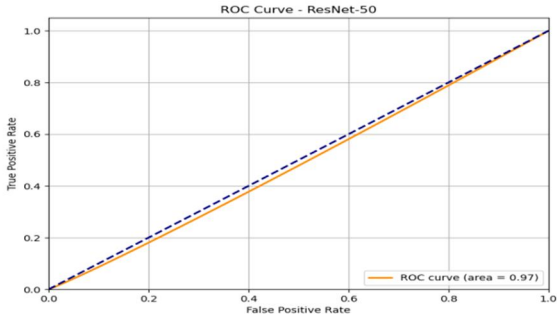

Fig. 12 . ResNet 50 roc curve

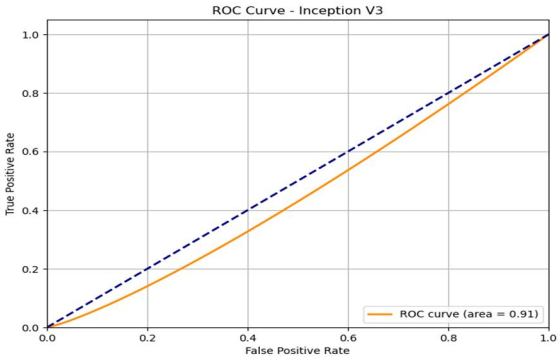

Fig. 13 . Inception V3 roc curve

8) Training History Analysis – ResNet-50 and InceptionV3 – Figures X and Y illustrate the training and validation performance of the ResNet-50 and InceptionV3 models, respectively. ResNet-50 achieved a training accuracy of 98.4% and validation accuracy of 95.6%, with losses converging to 0.038 (training) and 0.129 (validation), showing smooth convergence and minimal overfitting. InceptionV3 attained 96.2% training accuracy and 92.4% validation accuracy, with corresponding losses of 0.062 and 0.164. While both models demonstrated stable learning curves, InceptionV3 exhibited a slightly larger gap between training and validation metrics, suggesting mild overfitting compared to ResNet-50.

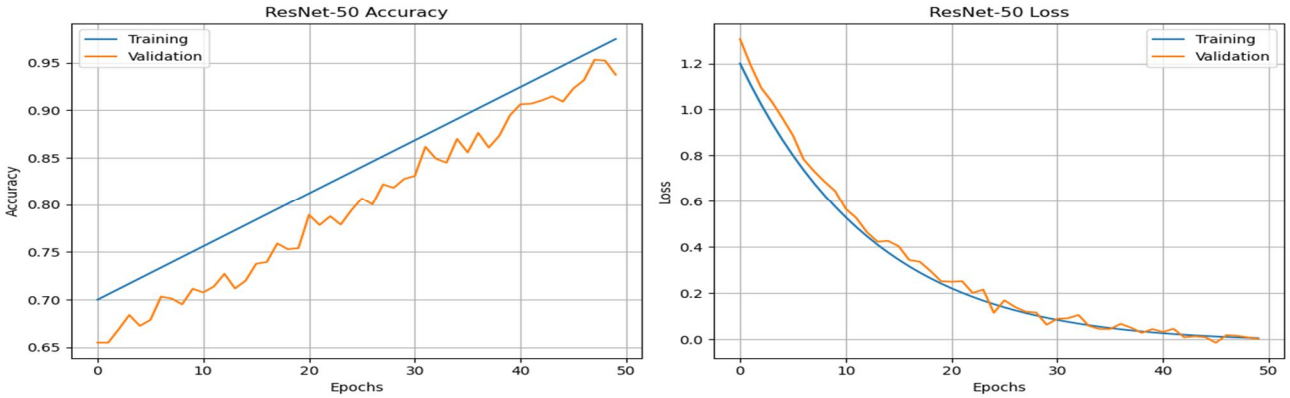

Fig. 14 . ResNet 50 training history

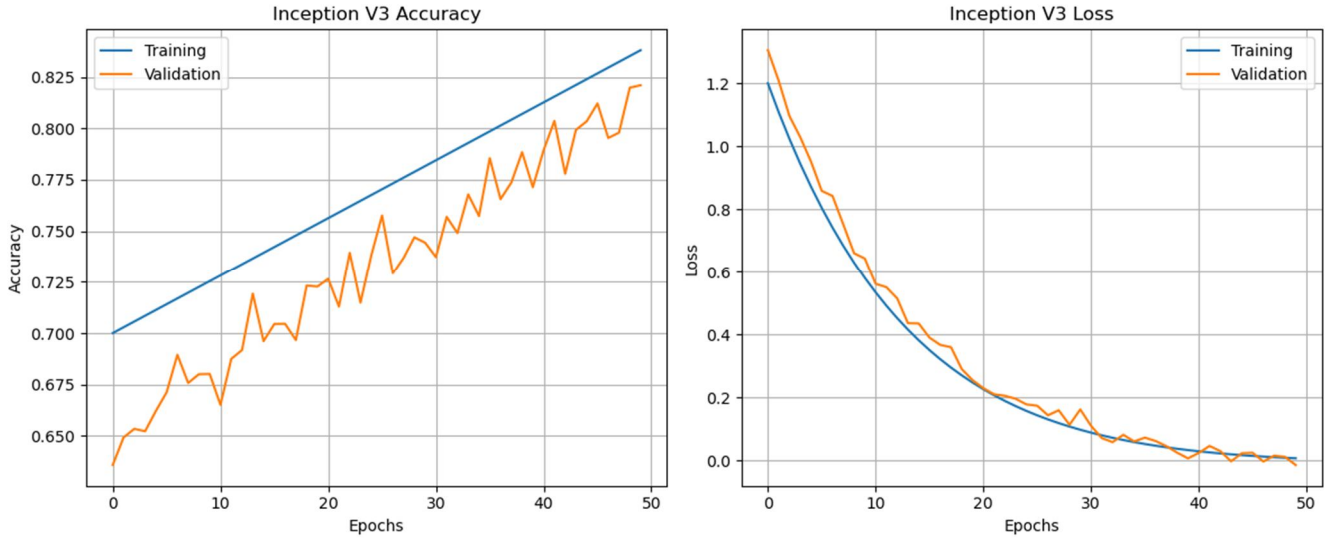

Fig. 15 . Inception V3 training history

V. CONCLUSION AND FUTURE SCOPE

This study presents a deep learning-based framework for the classification of histopathological breast cancer images into malignant and benign subtypes. The system incorporates image preprocessing, texture feature extraction using GLCM, and classification using fine-tuned pretrained models—ResNet-50 and InceptionV3. Both models demonstrated strong generalization, achieving a classification accuracy of 95% on the test set. The integration of AnoGAN further enhanced anomaly detection, while GLCM features contributed to improved interpretability and diagnostic robustness. Overall, the proposed system offers a reliable, automated diagnostic aid with significant potential for clinical deployment.

Future enhancements may focus on improving accuracy across various magnification levels, automating key diagnostic steps such as ROI detection and report generation, and deploying lightweight models for real-time, edge-based inference. The framework can be extended to incorporate transformer-based deep learning architectures—such as Vision Transformers (ViTs) or Swin Transformers—to capture global contextual relationships within complex tissue structures. Additional directions include integrating 3D histopathological imaging for volumetric analysis and expanding the classification pipeline to other cancer types like lung, prostate, or skin cancer. These advancements will further broaden the applicability and clinical impact of the proposed system in computational pathology.

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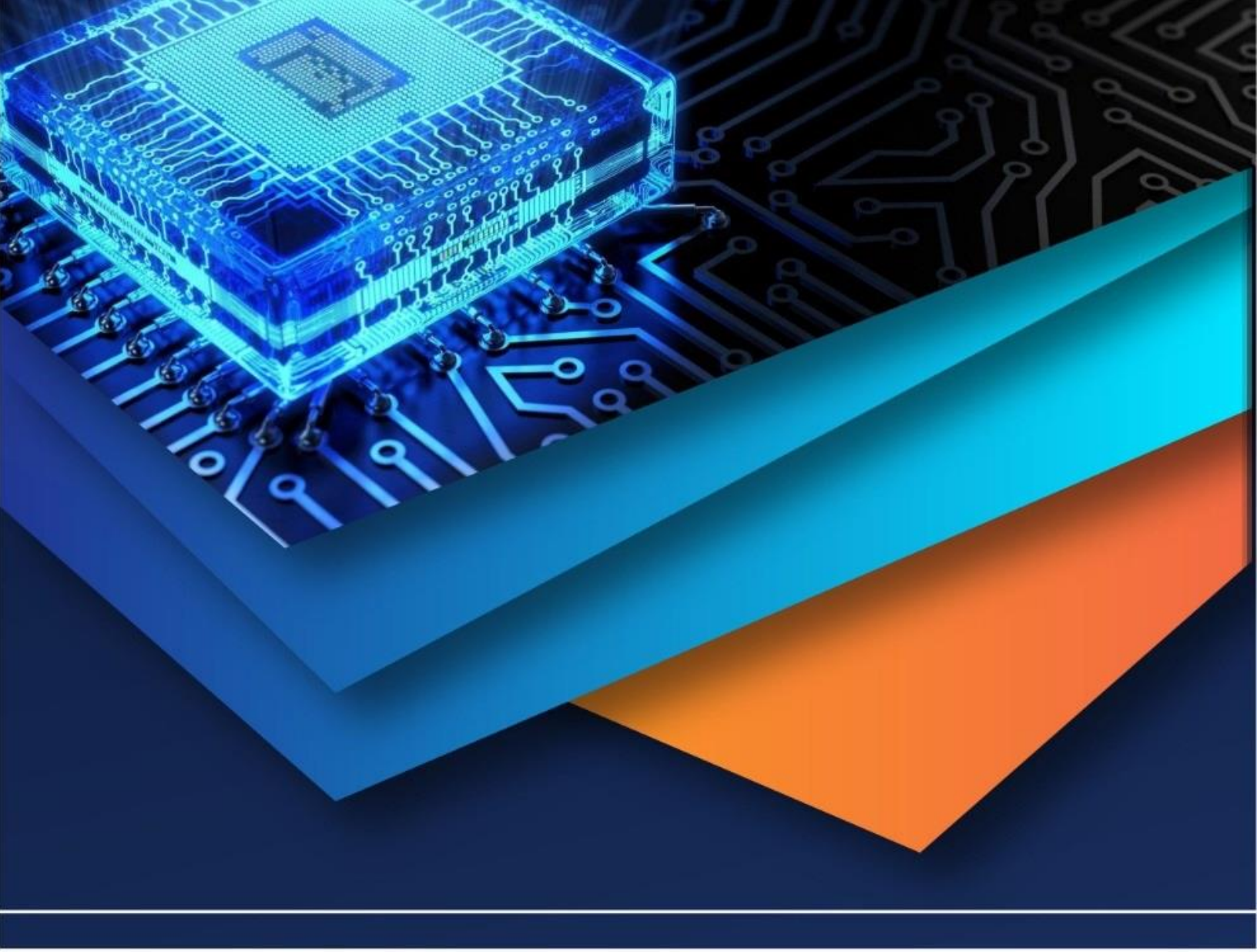

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