Medical Image Classification Using DCNN of Breast Cancer

Project-Based Laboratory 2 (ECE413)

Bachelor of Technology

In

Electronics & Communications Engineering

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DECLARATION BY CANDIDATES

We hereby declare that the Report of the U.G. Project based Laboratory2 Work entitled **"Medical Image Classification using DCNN of Breast Cancer"** which is being submitted to the **Electronics & Communication Engineering Department, MANIT BHOPAL**, is a bonafide report of the work carried out by us. The material contained in this report has not been submitted to any University or Institution for the award of any degree.

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CERTIFICATE OF APPROVAL

It is certified that the work contained in this report titled "**Medical Image Classification using DCNN of Breast Cancer**" is the original work done by the students and has been carried out under my supervision.

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ABSTRACT

Breast cancer remains a primary cause of cancer mortality globally, making early and accurate diagnosis crucial. This report presents a **medical image classification framework** for breast cancer detection using the **ResNet50 deep learning mode**l trained on the BreakHis dataset, which includes both benign and malignant tumor images. By leveraging ResNet50's powerful feature extraction capabilities, our model achieves high classification accuracy, supporting the automated diagnosis of breast cancer. This approach allows for quick and efficient screening, which is essential in medical imaging where large datasets and nuanced visual differences can challenge manual diagnosis.

To enhance the **interpretability** of our model, we integrate **Local Interpretable Model-Agnostic Explanations (LIME)**, an explainable AI tool, which highlights specific regions of each image that influence the model's decision. LIME produces **visual explanations** by focusing on the most significant image features, allowing clinicians to better understand the factors contributing to each classification and building trust in AI-aided diagnostics. Experimental results indicate that ResNet50 combined with LIME not only achieves robust performance on breast cancer image classification but also provides transparent, interpretable insights that bridge the gap between deep learning advancements and practical healthcare applications. This research highlights the potential of **explainable AI in enhancing clinical decision-making** and fostering greater trust in **AI-based diagnostic systems**.

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TABLE OF CONTENTS

LIST OF FIGURES AND TABLES

1. INTRODUCTION

Breast cancer is one of the most common and life-threatening cancers affecting women worldwide. Early and accurate detection of breast cancer is essential for improving patient outcomes and survival rates. Traditional diagnostic methods, which include manual examination of histopathology slides by pathologists, can be time-consuming, prone to human error, and often require considerable expertise. These challenges drive the need for automated solutions that can assist clinicians in making faster, more accurate diagnoses. Recent advances in artificial intelligence, particularly in deep learning, have shown great potential in the field of medical imaging, enabling automated classification of complex patterns in images with high precision.

This project focuses on developing a **deep learning-based breast cancer classification model** using the **ResNet50 architecture** and the **BreakHis dataset**. ResNet50, a 50-layer convolutional neural network, has demonstrated outstanding performance in image classification tasks by capturing both global and local features within an image. By leveraging ResNet50, our model aims to classify histopathology images as benign or malignant, contributing to early cancer detection and supporting clinical decision-making. A key aspect of this project is integrating **Local Interpretable Model-Agnostic Explanations (LIME)** to provide visual insights into the model's decision-making process. Explainable AI tools like LIME allow us to highlight critical regions within images that contribute most to the model's predictions, addressing the need for transparency and interpretability in AI-driven healthcare applications.

The objective of this project is to develop an accurate and interpretable model for breast cancer detection that can assist healthcare providers in diagnostic workflows. This report details the dataset selection process, model design, and implementation methodology, along with performance evaluation and potential applications. We also discuss future directions for this work, emphasizing the role of AI in transforming healthcare diagnostics and improving patient care.

2. LITERATURE REVIEW

Advancements in artificial intelligence (AI) and the increasing availability of structured and unstructured healthcare data have driven significant research into AI applications for medical diagnostics, particularly in breast cancer detection. Despite promising results, a major challenge in implementing AI in clinical settings is ensuring transparency and interpretability of model predictions.

Asha et al. in [1] address the critical need for early breast cancer detection, emphasizing the impact of limited awareness on mortality rates. In their study, they utilize machine learning techniques—including DNN, CNN, and ANN architectures—with Recursive Feature Elimination (RFE) for feature selection. This automated classification system is designed to distinguish between malignant and benign breast cancer cases. The results demonstrate that the DNN model achieved the highest accuracy of 97%, outperforming other models on the dataset, highlighting its effectiveness for reliable breast cancer classification.

Building on these findings, Khater et al. in [2] address the critical need for interpretability in AI-driven diagnostics. In their study, they employ Local Interpretable Model-Agnostic Explanations (LIME) to interpret predictions of machine learning models classifying breast cancer cases as benign or malignant. The authors emphasize the significant roles of features such as "Bare Nuclei" and "Clump Thickness" in malignant classifications, and "Normal Nucleoli" and "Marginal Adhesion" in benign predictions. By providing a detailed feature-level explanation, their work demonstrates how LIME can increase transparency in medical AI applications, potentially improving trust and acceptance of AI-based diagnostic tools in clinical settings.

These studies provide a foundational basis for our project, which aims to combine the high classification performance along with the interpretability framework. By integrating LIME into a ResNet-50-based framework, we seek to develop a diagnostic tool that is both accurate and interpretable, addressing a vital need in AI-driven breast cancer detection.

3. METHODOLOGY

The methodology for this project is designed to develop an accurate and interpretable deep learning-based breast cancer detection model using histopathology images. The approach combines the power of **ResNet50,** a convolutional neural network (CNN), with **LIME** (Local Interpretable Model-Agnostic Explanations) to provide both classification accuracy and model transparency.

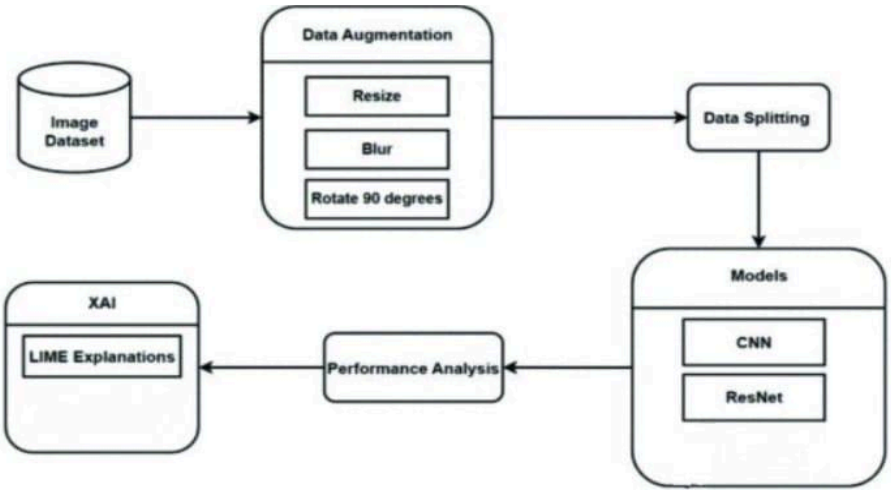

Figure: 3.1: Flowchart

As can be seen from figure 3.1, the image dataset in our case histopathology images are sent for data augmentation like resizing, blurring, and rotation to create new samples of the same image and increase accuracy which are then split into 2 halves 80% goes to training and 20% to the testing phase. The training dataset is then used to train the model. Further, the model's performance is analyzed through various parameters like confusion matrix, graph for losses, accuracy, precision, and recall.

The next section explains the various stages involved in the methodology, including dataset preparation, model selection, implementation details, and integration of the explainability technique.

3.1 Dataset Selection and Preparation

The BreakHis dataset was chosen for this project as it is a widely used benchmark in the field of breast cancer detection. The dataset consists of 7,909 microscopic images of breast tissue samples, categorized into two main classes: benign and malignant. The images are captured at multiple magnifications: 40x, 100x, 200x, and 400x, allowing the model to learn from different levels of detail.

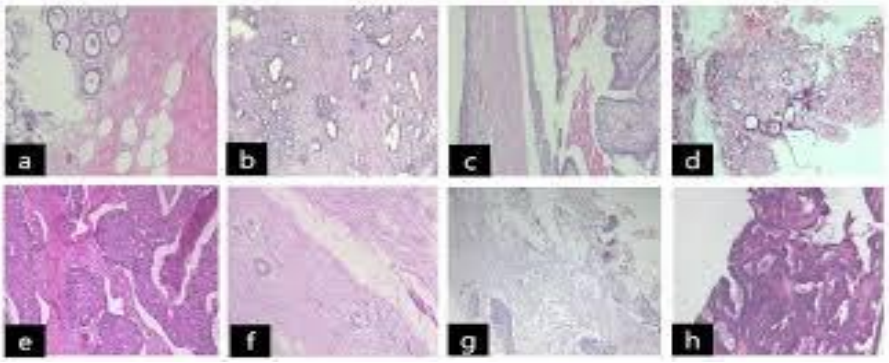

Figure: 3.2: Datset Histopatheic Images

The data is divided into the following steps:

3.1.1 Data Preprocessing:

The images are first resized to a consistent size to ensure that the model processes them uniformly. Additionally, normalization is applied to scale pixel values into a specific range (e.g., 0-1) to improve model convergence during training.

3.1.2 Data Augmentation:

Although not the primary focus of this report, basic augmentation techniques such as flipping, rotation, and zooming can be applied to enhance model robustness by introducing variability in the training data.

3.1.3 Dataset Splitting:

The dataset is split into training, validation, and test sets. Typically, 70% of the data is used for training, 15% for validation, and 15% for testing. This ensures that the model is trained on a diverse set of images while leaving unseen data for performance evaluation.

3.2 Convolutional Neural Network (CNN) Model: ResNet50

A Convolutional Neural Network (CNN) is a type of deep learning model specifically designed for processing grid-like data such as images. CNNs are well-suited for image classification tasks because they are capable of learning hierarchical patterns, starting from low-level features (edges and textures) to more complex features (shapes and objects).

The core building block of a CNN is the **convolutional layer**, which applies a series of

filters (kernels) to the input image to detect various patterns. The convolution operation slides these filters across the image, producing feature maps that highlight relevant patterns. Other layers, such as **max-pooling layers**, downsample the feature maps to reduce dimensionality and focus on the most significant features.

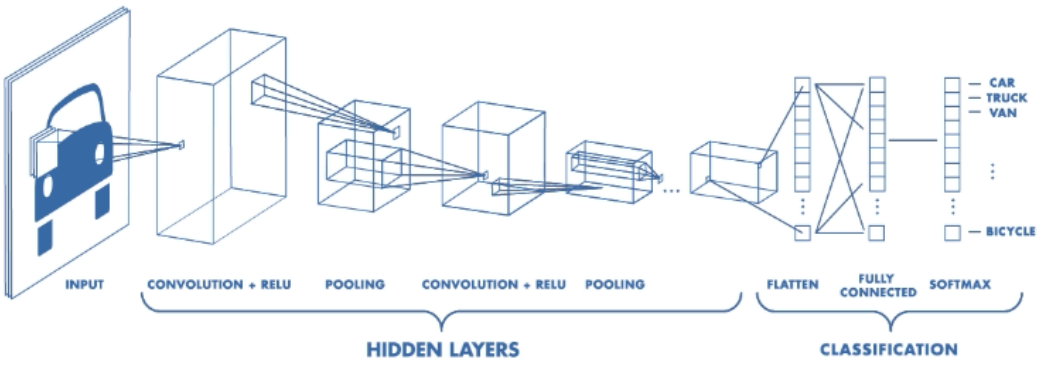

Figure: 3.3: Convolution Neural Networks Architecture

In this project, we leverage **ResNet50**, a deep CNN architecture with 50 layers. ResNet (Residual Networks) introduces a novel architecture by using **residual blocks** that allow the network to skip certain layers, helping to mitigate the problem of vanishing gradients in deep networks. This skip connection or identity mapping ensures that the model can learn deeper representations without the degradation of accuracy, even with an increased number of layers.

3.2.1 ResNet50 Architecture:

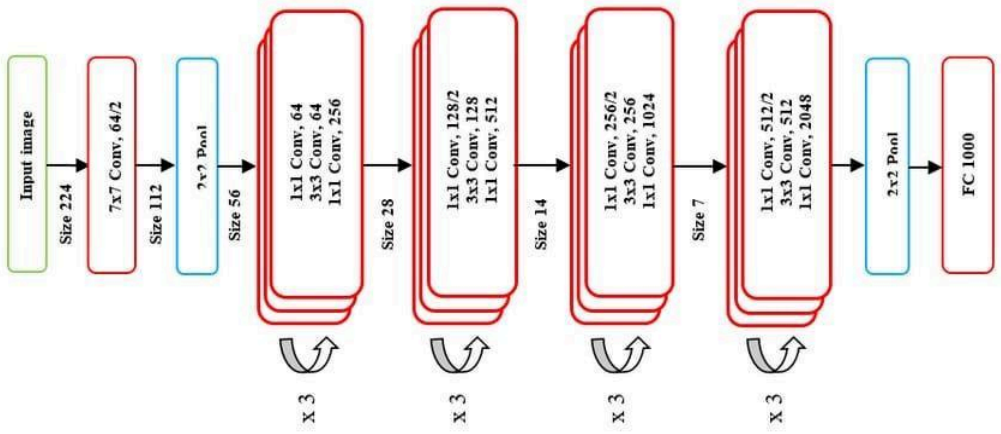

Figure 3.4: Resnet 50 Model Architecture

ResNet 50 model usually contains the following -

- **Input Layer:** Takes the preprocessed histopathology image as input.
- **Convolutional Layers**: These layers apply filters to the input image and learn hierarchical features.
- **Residual Blocks**: A key component of ResNet, where layers are skipped to facilitate learning of deeper representations.
- **Fully Connected (Dense) Layers**: The final layers are dense layers that interpret the features learned by the convolutional layers and produce the final output, in this case, a classification of the image as benign or malignant.
- **Output Layer**: A softmax or sigmoid activation function outputs a probability score for each class.

3.2.2 Model Selection

ResNet50 was selected due to its proven effectiveness in medical image classification tasks, offering high accuracy and robustness when dealing with complex patterns in histopathology images. The architecture is fine-tuned on the BreakHis dataset to optimize performance for breast cancer classification.

3.3 Implementation Details

The ResNet50 model, pre-trained on the ImageNet dataset, is chosen for its strong feature extraction capabilities, which are particularly useful for image classification tasks. In this project, we fine-tune ResNet50 for the BreakHis dataset by unfreezing the last 10 layers of the model. This approach enables these layers to learn more specialized features, adapting to the unique characteristics of benign and malignant cancer images:

3.3.1 Model Training:

The ResNet50 model is pre-trained on the ImageNet dataset (a large-scale image classification dataset), and the weights are fine-tuned for the BreakHis dataset.

3.3.2 Regularization Techniques:

We incorporate L2 regularization and Dropout layers within the model architecture to prevent overfitting and improve generalization. L2 regularization is applied to the dense layers with a regularization factor of 0.01. In contrast, Dropout layers are added with a rate of 0.5 to reduce dependency on individual neurons and improve robustness.

3.3.3 Optimizer and Loss Function:

The model training is conducted using the **Adam optimizer**, set with an initial learning rate of `1e-4`. Adam is chosen for its adaptive learning rate, which enhances convergence speed and stability. Additionally, **categorical cross-entropy** is used as the loss function, as it is suitable for this multi-class classification task.

3.3.4 Epochs and Batch Size:

The training process is carried out over multiple epochs 150 with a batch size of 32, depending on the available computational resources.

3.3.5 Evaluation Metrics:

Key metrics such as accuracy, precision, recall, F1 score, and the confusion matrix are used to evaluate model performance.

3.4 Explainability with LIME

One of the challenges of deep learning models is their **black-box nature**, which makes it difficult to understand how the model makes predictions. In medical applications, this lack of interpretability is a critical issue, as clinicians must trust and understand the reasoning behind AI-driven decisions.

To address this, we integrate **LIME (Local Interpretable Model-Agnostic Explanations)**, an explainability technique that provides insight into individual predictions made by the model. LIME works by approximating the complex, black-box model with a simpler, interpretable model (such as a linear regression) in the local vicinity of the prediction. This helps explain why the model made a specific decision for a particular image.

3.4.1 LIME Workflow:

- A given image is input into the trained ResNet50 model.
- LIME perturbs the image and generates a set of interpretable features that are relevant to the model's decision.
- LIME then builds a local surrogate model that can explain the contribution of each feature to the final prediction, providing a heatmap or visualization that highlights the most critical areas in the image that influenced the model's decision.

By using LIME, we can better understand and visualize the areas of the histopathology images that the ResNet50 model deems important for classifying the tumor as benign or malignant. This not only increases model transparency but also helps pathologists in validating the model's predictions, making the tool more reliable in clinical settings.

3.5 Performance Evaluation and Model Optimization

The performance of the model is evaluated on the test set using various metrics such as accuracy, precision, recall, and F1 score. Hyperparameter tuning, including adjusting the learning rate and optimizer settings, is performed to enhance model performance. The model's generalization capability is also tested by evaluating it on unseen data, and overfitting is mitigated using techniques like **early stopping** and **dropout**.

3.6 Integration and Deployment Considerations

Once the model achieves satisfactory performance, it can be integrated into clinical decision support systems (CDSS) for real-time breast cancer detection. Additionally, the integration of LIME will ensure that the model's predictions are interpretable, providing value to clinicians who require transparent decision-making tools.

4. EXPERIMENTAL SETUP

4.1 Software and Tools Used

- **Python 3. x**: Python served as the primary programming language for implementing the machine learning pipeline.
- **TensorFlow and Keras**: TensorFlow was used as the backend deep learning framework, while Keras (a high-level API in TensorFlow) facilitated model building, training, and evaluation. The model's architecture, training, and inference processes were built using TensorFlow's ResNet50 model.
- **LIME (Local Interpretable Model-agnostic Explanations)**: The LIME library was used to improve the interpretability of the ResNet50 model's predictions, helping to visualize feature relevance in medical images.
- **Other Libraries**: Additional libraries like Matplotlib and Seaborn were employed for data visualization, while NumPy and Pandas were used for data handling and metric calculations.

The entire code was developed and executed in **Google Colab** to leverage its GPU/TPU acceleration capabilities, optimizing training speed. The setup also enabled easy access to storage and ensured the reproducibility of results.

4.2 Hardware Specifications

- **TPU (Tensor Processing Unit)**: Google Colab's TPU was utilized to accelerate model training. This setup provides high computational power, specifically optimized for deep learning workloads.
- **Local Machine**: Testing and initial model setup were conducted on a personal laptop, an HP model with a 64-bit architecture.

4.3 Dataset Splitting Strategy:

Training Dataset: The dataset was split into training, validation, and test sets for accurate model evaluation.

- The **training dataset** consisted of breast cancer images with various labels to represent benign and malignant cases, prepared in a directory structure that Keras

could infer for classification tasks.

Validation Dataset: Used to tune the model and monitor its performance, especially with callbacks like early stopping and learning rate reduction.

The image_dataset_from_directory utility from TensorFlow was used to load and preprocess the dataset, ensuring that images were resized to (150,150) for consistency with the ResNet50 input requirements.

4.4 Model Architecture

ResNet50 Convolutional Base: We used a pre-trained ResNet50 model, excluding its top (fully connected) layers, as a feature extractor for our image classification task.

- The final 10 layers of ResNet50 were set to trainable for fine-tuning.

Fully Connected Layers: Custom fully connected layers with dropout were added to enhance classification performance. These layers progressively reduced dimensionality and implemented dropout to mitigate overfitting.

4.5 Training Configuration

- **Optimizer**: Adam optimizer was chosen with a learning rate of 1e-4.
- **Loss Function**: Sparse categorical cross-entropy loss was used due to the two-class (benign and malignant) classification problem.
- **Callbacks**: Early stopping (with patience set to 10) and learning rate reduction (with a reduction factor of 0.2) were employed to prevent overfitting and optimize model convergence.

4.6 Evaluation Metrics and Visualization

- **Confusion Matrix and Classification Report**: To assess performance, a confusion matrix and classification report were generated. These metrics provided insight into class-wise accuracy and errors.
- **LIME Explanations**: LIME was used to create visual explanations of the model's predictions, enhancing interpretability by highlighting image regions relevant to the classification.

5. RESULTS AND DISCUSSION

5.1. Training and Validation Accuracy and Losses Graphs

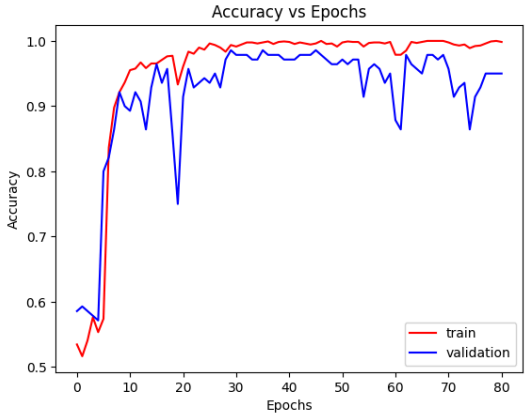

Figure: 5.1.1: Accuracy VS Epoch

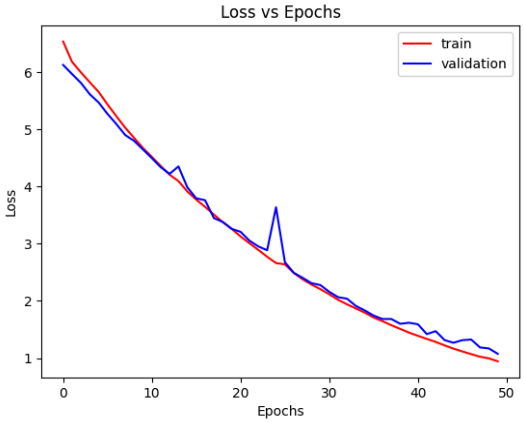

Figure: 5.1.2 : Loss VS Epoch

The first graph (Figure 5.1.1) shows the training and validation accuracy versus epochs, highlighting the model's performance improvement over time. The second graph (Figure 5.1.2) illustrates the training and validation loss versus epochs, showing a consistent decrease, indicating effective model learning and convergence.

5.2. Confusion Matrix

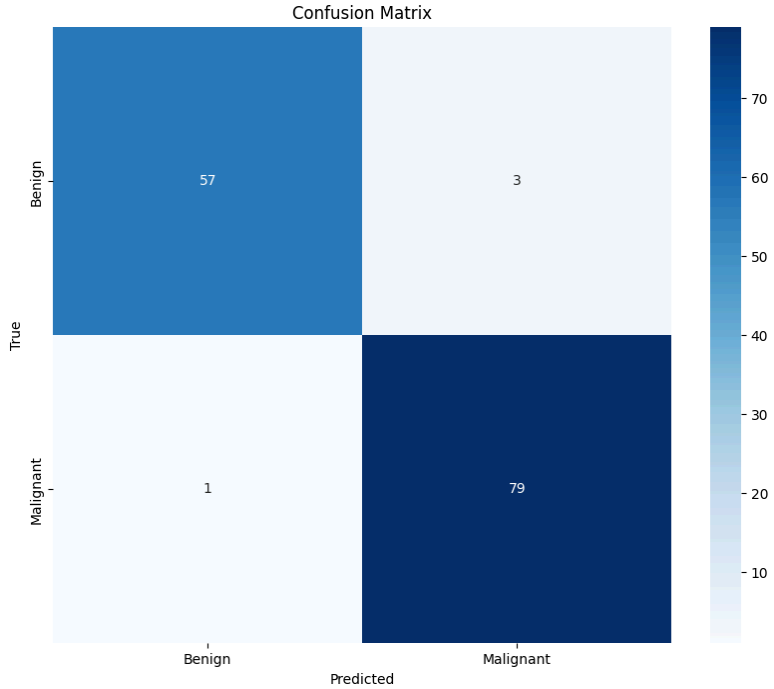

Figure: 5.2: Confusion Matrix

The confusion matrix displays the classification performance of the model. It shows 57 true positives (benign correctly classified), 79 true negatives (malignant correctly classified), 3 false positives (benign misclassified as malignant), and 1 false negative (malignant misclassified as benign), reflecting high overall accuracy.

5.3. Classification report

Table: 5.3: Classification Report

	Precision	Recall	f1-score	Support
Benign	0.98	0.95	0.97	60
Malignant	0.96	0.99	0.98	80
Accuracy			0.97	140
Macro avg	0.97	0.97	0.97	140
Weighted avg	0.97	0.97	0.97	140

The classification report provides performance metrics:
Benign: Precision: 0.98, Recall: 0.95, F1-score: 0.97.
Malignant: Precision: 0.96, Recall: 0.99, F1-score: 0.98.
Overall accuracy: **0.97**, with macro and weighted averages of precision, recall, and F1-score at 0.97.

5.4. Evaluation Metrics

Table: 5.4: Evaluation Metrics

Binary Class	Class	True Positive	True Negative	False Positive	False Negative
0	Benign	57	79	1	3
1	Malignant	79	57	3	1

This table summarizes binary classification results:

Benign: 57 True Positives, 79 True Negatives, 1 False Positive, 3 False Negatives.

Malignant: 79 True Positives, 57 True Negatives, 3 False Positives, 1 False Negative.

5.5. Lime AI Explanation

➔ Benign Image

The left side shows a benign tissue sample labeled as "True Class: 0," representing normal cells. The right side illustrates the predicted class, also labeled "0," with yellow regions indicating areas classified as benign, while black areas are non-relevant.

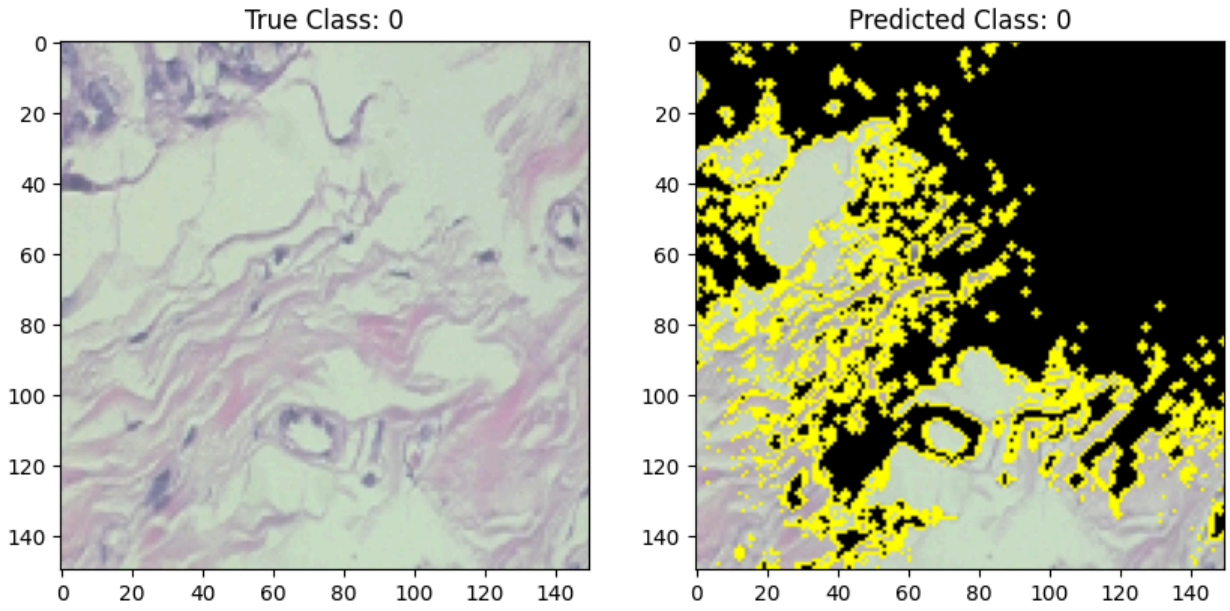

Figure: 5.5.1 : Benign Image

➔ Malignant Image

The left side displays a malignant tissue sample labeled as "True Class: 1," representing cancerous cells. The right side shows the predicted class, "1," where yellow regions represent areas predicted as malignant, contrasting with black regions that are non-relevant.

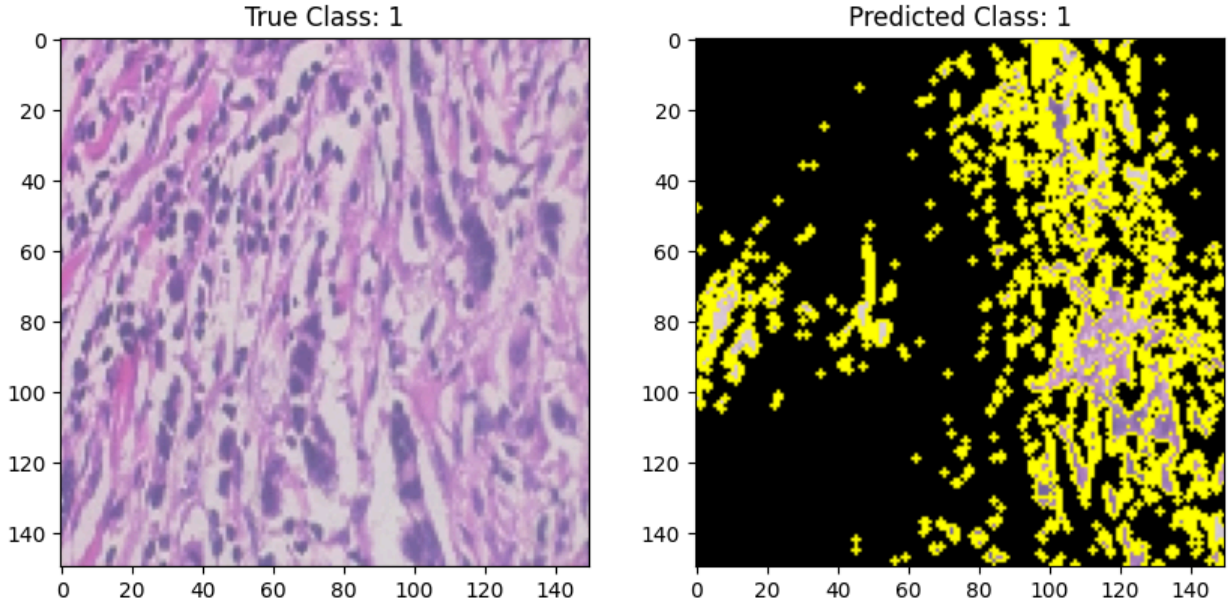

Figure: 5.5.2 : Malignant Image

The ResNet50-based model achieved strong results, with a 97% overall accuracy in classifying breast cancer images. The precision and recall values for both benign and malignant categories were high, indicating reliable performance in distinguishing between these classes. With a precision of 98% for benign and 96% for malignant cases, the model effectively minimizes misdiagnoses in a clinical context.

Using LIME (Local Interpretable Model-agnostic Explanations) added interpretability by highlighting key image areas that influenced the model's predictions. This helped ensure that predictions aligned with visually relevant tumor regions, building transparency and trust. LIME explanations can also assist in error analysis, allowing practitioners to assess misclassified cases and gain insights into the model's behavior, which could guide future model improvements.

In summary, the model's high accuracy and interpretability through LIME make it a promising tool for aiding breast cancer diagnosis in real-world applications.

6. APPLICATION

1. **Clinical Decision Support:** This model can serve as a valuable tool for pathologists by assisting in the rapid classification of breast tissue samples as benign or malignant. By automating the initial screening process, clinicians can prioritize the cases that require immediate attention, enhancing the efficiency and effectiveness of cancer diagnosis in hospitals and clinics.

2. **Telemedicine and Remote Diagnostics:** In areas with limited access to specialized healthcare professionals, this model could be deployed as part of a telemedicine solution. Remote clinics could send histopathology images to a central system that uses the model for preliminary diagnostics, facilitating early cancer detection in underserved regions.

3. **Cancer Research and Drug Development**: The model could support researchers in studying large datasets of histopathology images, and identifying trends and correlations in tissue samples across various cancer subtypes. This capability could accelerate research in cancer biology and aid in the development of targeted therapies by identifying specific characteristics associated with different tumor types.

4. **Pathology Lab Automation**: This model could be integrated into digital pathology workflows to assist lab technicians in processing and analyzing large volumes of histopathology slides. By pre-classifying images, would streamline lab operations, reduce manual workload, and help standardize diagnostic quality across pathology labs.

5. **Medical Education and Training**: The model, along with its explainable AI component (LIME), can be used in training programs for medical students and radiology residents. By showing how the model reaches its predictions, educators can use it to teach students about the visual characteristics of benign versus malignant tissues, improving their diagnostic skills and understanding of AI in healthcare.

6. **Health Data Analytics and Population Studies**: The model can be used for large-scale epidemiological studies by analyzing anonymized histopathology image datasets across populations. Insights gained from these analyses can inform public health policies, identify risk factors, and contribute to preventive healthcare measures on a broader scale.

7. CONCLUSION

This project demonstrates the potential of deep learning in enhancing breast cancer diagnosis through the classification of histopathological images. By utilizing the **ResNet50 architecture**, we achieved high accuracy in distinguishing between benign and malignant tumors in the BreakHis dataset, underscoring the capability of advanced convolutional neural networks to handle complex medical image data. Furthermore, the integration of **Local Interpretable Model-Agnostic Explanations (LIME)** provided critical transparency into the model's decision-making process, allowing medical professionals to interpret the basis of each prediction. This explainability is essential for fostering trust in AI-driven diagnostic tools, especially in high-stakes areas like cancer diagnosis.

The findings of this project highlight the importance of combining accuracy with interpretability in medical applications. By bridging the gap between artificial intelligence and practical healthcare needs, this approach shows promise for improving diagnostic efficiency, reducing human error, and ultimately supporting clinicians in making more informed decisions. Future advancements, such as integrating multi-modal data and developing real-time deployment solutions, could further expand the model's applicability, bringing us closer to reliable and accessible AI-assisted diagnostics in clinical environments.

8. FUTURE SCOPE

1. **Multi-Modal Data Integration**: Combine histopathology images with other relevant data (e.g., patient demographics, genetic profiles, medical histories) to create a more comprehensive and accurate diagnostic model.
2. **Real-Time Clinical Deployment: Develop** a user-friendly application or software system for easy integration into hospital workflows, enabling clinicians to use the model in real-time diagnostic settings.
3. **Transfer Learning with Broader Medical Datasets**: Utilize pre-trained models from extensive medical datasets to improve performance, especially in scenarios with limited labeled data.
4. **Application to Other Cancer Types**: The model can be extended to classify other cancer types or related pathologies, making it a versatile diagnostic tool in oncology.
5. **Model Optimization for Hardware Constraints**: Optimize the model for deployment on various hardware, including low-power devices in remote or resource-limited settings, to improve accessibility.
6. **Automated Feedback Loop for Model Improvement**: Integrate a feedback mechanism for continuous model improvement by collecting and incorporating real-time data from clinical use cases. This ensures adaptability and accuracy over time.
7. **Enhancement with Advanced Preprocessing Techniques**: Implement advanced image preprocessing techniques, such as noise reduction and contrast enhancement, to improve image quality and potentially boost classification accuracy.
8. **Integration with Cloud-Based Services**: Explore cloud-based deployment options to enable scalability, remote access, and collaborative diagnostic processes across different healthcare institutions.
9. **Incorporation of Federated Learning**: Federated learning can be used to train the model on distributed datasets from multiple hospitals without compromising patient data privacy, enabling a more generalized model across diverse populations.
10. **Longitudinal Analysis for Prognosis Prediction**: Extend the model to predict patient prognosis by analyzing temporal data across multiple histopathology samples, aiding in long-term patient monitoring and treatment planning.

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