Breast Cancer Detection using Deep Learning Techniques

1. Introduction

1.1. Project Overview

This project focuses on developing a deep learning system for automated breast cancer detection using histopathology images. Breast cancer remains one of the most common cancers among women worldwide, and early detection is crucial for effective treatment and improved survival rates. The system classifies breast histopathology images into two categories: benign (class 0) and malignant (class 1), providing an assistive diagnostic tool for pathologists.

1.2. Objectives

- Develop a deep learning model using CNNs to classify breast histopathology images as benign or malignant.
- Apply effective image preprocessing and augmentation techniques to improve model performance.
- Optimize the model architecture through hyperparameter tuning for accuracy and reliability.
- Evaluate the model using metrics like sensitivity, specificity, and AUC for clinical applicability.
- Build a reproducible framework and deploy it as a web application using Flask.

2. Project Initialization and Planning Phase

Date	15 March 2025
Team ID	SI-24556-1744082820
Project Name	Breast Cancer Detection using Deep Learning Techniques
Maximum Marks	3 Marks

2.1 Define Problem Statements

Breast cancer remains one of the leading causes of mortality among women, and early detection is critical for improving survival rates. However, current diagnostic methods, such as mammography, often result in false positives and false negatives, causing unnecessary emotional and physical stress for patients and delays in treatment. Healthcare providers face challenges in adopting reliable, automated solutions due to the complexity of medical imaging, variability in patient data, and the lack of accessible, interpretable AI tools that integrate seamlessly into clinical workflows. Patients and clinicians need an accurate, scalable, and user-friendly system that not only enhances diagnostic precision but also builds trust through explainable results. Addressing these challenges requires a deep understanding of their pain points to create a solution that improves outcomes and transforms the diagnostic experience.

Problem Statement	I am	I'm trying to	But	Because	Which makes me feel
Accurate, user-friendly AI tools needed for better breast cancer detection.	A healthcare provider	Detect breast cancer early and improve outcomes	Mammography leads to false positives/negatives and lacks precision.	Imaging is complex, data varies, and AI tools are not user-friendly.	Frustrated and concerned about patient care.

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2.2. Project Proposal (Proposed Solution)

This project proposal focuses on developing an advanced solution for breast cancer detection using deep learning techniques. With a clear objective to enhance diagnostic accuracy and efficiency, the scope includes building a scalable, user-friendly framework that addresses the limitations of current methods, such as false positives/negatives and complex imaging challenges. The problem statement highlights the need for reliable AI tools that integrate seamlessly into clinical workflows while improving outcomes and building trust through explainable results. The proposed solution outlines the methodology, key features, and resource requirements—including hardware, software, and data—to ensure successful implementation.

Project Overview	
Objective	Develop a deep learning model to accurately classify breast histopathology images as benign or malignant for improved clinical diagnosis.
Scope	Design and implement a scalable, user-friendly framework that integrates preprocessing, model development, evaluation, and deployment.
Problem Statement	
Description	Current diagnostic methods like mammography often result in false positives/negatives, causing delays in treatment and emotional stress for patients.
Impact	Solving this problem will improve diagnostic accuracy, reduce unnecessary procedures, and enhance patient outcomes through reliable AI-driven

Proposed Solution	
Approach	Utilize deep learning techniques (e.g., CNNs) for feature extraction and classification, supported by effective preprocessing and hyperparameter optimization.
Key Features	High accuracy, sensitivity, and specificity; explainable AI; scalable framework deployable via Flask-based web application.

Resource Requirements

Resource Type	**Description**	**Specification/Allocation**
Hardware		
Computing Resources	CPU/GPU specifications	2 x NVIDIA V100 GPUs
Memory	RAM specifications	16 GB
Storage	Disk specifications	1 TB SSD

Software		
Frameworks	Python frameworks	Flask
Libraries	Additional libraries	TensorFlow
Development Environment	IDE, version control	Jupyter Notebook, Git
Data		
Data	Source, size, format	Kaggle dataset; 10,000

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Maximum Marks	4 Marks

2.3. Project Planning

Product Backlog, Sprint Schedule, and Estimation

Sprint	Functional Requirement (Epic)	User Story Number	User Story / Task	Story Points	Priority	Team Members	Sprint Start	Sprint End Date (Planned)
Sprint-1	Data Preprocessing	USN-1	As a user, I want to preprocess image data.	3	High	Data Engineers	April 11, 2025	April 18, 2025
Sprint-1	Model Development	USN-2	As a user, I want to build a CNN model.	5	High	ML Engineers	April 11, 2025	April 25, 2025
Sprint-2	Model Optimization	USN-3	As a user, I want to optimize hyperparameters.	3	Medium	ML Engineers	April 26, 2025	May 2, 2025
Sprint-2	Model Evaluation	USN-4	As a user, I want to	2	High	Data Scientists	April 26,	May 2, 2025
Sprint-3	Deployment	USN-5	As a user, I want to deploy	4	High	DevOps Engineers	May 3, 2025	May 10, 2025

3. Data Collection and Preprocessing Phase

Date	16 March 2025
Team ID	SI-24556-1744082820
Project Name	Breast Cancer Detection using Deep Learning Techniques
Maximum Marks	2 Marks

3.1. Data Collection Plan & Raw Data Sources Identification

Elevate your breast cancer detection project with a comprehensive Data Collection Plan and Raw Data Sources Report. These resources ensure meticulous curation and integrity of the histopathology image dataset, enabling accurate analysis and informed decision-making throughout model development, training, and evaluation.

Data Collection Plan Template

Section	Description
Project Overview	The project focuses on detecting breast cancer using deep learning techniques. It utilizes the Breast Histopathology Images dataset, which contains labeled histopathological images categorized as benign or malignant. The goal is to preprocess the data, train a convolutional neural network (CNN) model, and evaluate its performance in accurately classifying breast cancer cases.
Data Collection Plan	The data collection plan involves Downloading the Breast Histopathology Images dataset from a reliable source , Organizing the dataset into training and testing subsets, with an 80:20 split ratio and Ensuring the data is balanced through augmentation techniques to address class imbalance.

Raw Data Sources Identified	The raw data source for this project is: Dataset Name: Breast Histopathology Images Location: https://www.kaggle.com/paultimothymooney/breast-histopathology-images Description: This dataset contains 277,524 histopathological images of breast tissue labeled as benign (class 0) or malignant (class 1).

Raw Data Sources

Source Name	Description	Location/URL	Format	Size	Access Permissions
Breast Histopathology Images	This dataset contains 277,524 histopathological images of breast tissue labeled as benign (class 0) or malignant (class 1).	https://www.kaggle.com/paultimothymooney/breast-histopathology-images	Image	5 GB	Public

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Maximum Marks	2 Marks

3.2. Data Quality Report

Data Source	Data Quality Issue	Severity	Resolution Plan
Breast Histopathology Images Dataset (Raw Data)	Imbalance in the number of benign and malignant image samples.	High	Apply data augmentation techniques to balance the dataset and improve generalization during training.
Training Dataset	Noise in histopathology images affecting feature extraction.	Medium	Use denoising filters to preprocess images and enhance clarity.
Testing Dataset	Variability in image resolution leading to inconsistent input dimensions.	High	Resize all images to a uniform size (50x50 pixels) before feeding them into the model.

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Maximum Marks	6 Marks

3.3 Data Preprocessing

The preprocessing pipeline for the breast cancer detection project includes resizing histopathology images to 50×50 pixels, normalizing pixel values to, and applying data augmentation techniques such as flipping, rotation, and zooming. Denoising filters are used to reduce image noise, while edge detection highlights prominent features for better analysis. Images are converted to grayscale or other relevant color spaces, and cropped to focus on tissue samples. Batch normalization is applied to stabilize training across layers. These preprocessing steps enhance data quality, improve model generalization, and ensure efficient convergence during neural network training, enabling robust performance in classifying benign and malignant breast cancer cases

Section	**Description**
Data Overview	Provides an overview of the *Breast Histopathology Images* dataset, including benign and malignant classes.
Resizing	Resizes images to a target size of 50×50 pixels for uniformity during model training.
Normalization	Scales pixel values to the range1 to ensure consistent input data distribution.
Data Augmentation	Applies techniques like flipping, rotation, and zooming to improve model generalization.

Denoising	Reduces noise in histopathology images using image preprocessing filters.
Edge Detection	Highlights prominent edges in images to enhance feature extraction during training.
Color Space Conversion	Converts images to grayscale or other color spaces as required for analysis.
Image Cropping	Crops regions of interest containing tissue samples to focus on relevant features.
Batch Normalization	Normalizes activations within each layer to stabilize and accelerate training.

Data Preprocessing Code Screenshots	

Loading Data	# Loading dataset paths
	source_dataset = r"C:\\Users\\sohil\\OneDrive\\Desktop\\AI Assingments and Projects\\Breast Histopathology Images"
	target_root = "breastcancerdataset"
	train_ratio = 0.8
	
	# Shuffle and split into train/test sets
	random.shuffle(all_images)
	train_size = int(train_ratio * len(all_images))
	train_images = all_images[:train_size]
	test_images = all_images[train_size:]

Resizing	train_generator = ImageDataGenerator(rescale=1./255).flow_from_directory(
	train_dir,
	target_size=(50, 50), # Resizing to 50x50 pixels
	batch_size=32,
	class_mode='binary'
	)

Normalization	train_datagen = ImageDataGenerator(rescale=1./255) # Normalize pixel values to [0, 1]
Data Augmentation	train_datagen_augmented = ImageDataGenerator(rescale=1./255, rotation_range=30, width_shift_range=0.2, height_shift_range=0.2, shear_range=0.2, zoom_range=0.2, horizontal_flip=True, fill_mode='nearest')
Denoising	from skimage.restoration import denoise_tv_chambolle def denoise_image(image): return denoise_tv_chambolle(image, weight=0.1) # Apply denoising filter
Edge Detection	from skimage.feature import canny def detect_edges(image): return canny(image) # Perform edge detection

Color Space Conversion	from skimage.color import rgb2gray def convert_to_grayscale(image): return rgb2gray(image) # Convert RGB image to grayscale
Image Cropping	from skimage.util import crop def crop_image(image): return crop(image, ((10, 10), (10, 10), (0, 0))) # Crop borders by 10 pixels
Batch Normalization	from tensorflow.keras.layers import BatchNormalization model.add(BatchNormalization()) # Add Batch Normalization layer to stabilize training

4. Model Development Phase

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Project Name	Breast Cancer Detection using Deep Learning Techniques
Maximum Marks	5 Marks

4.1. Model Selection Report

In the model selection report for future deep learning and computer vision projects, various architectures, such as CNNs or RNNs, will be evaluated. Factors such as performance, complexity, and computational requirements will be considered to determine the most suitable model for the task at hand.

Model Selection Report:

Model	Description
breastcancer.h5 (CNN) model	The breast cancer detection model is a Convolutional Neural Network (CNN) designed for binary classification of histopathology images (benign vs. malignant). It includes three convolutional layers with Batch Normalization, Leaky ReLU activation, and MaxPooling for feature extraction, followed by fully connected layers with Dropout for regularization. The output layer uses a sigmoid activation function for binary classification. The Adam optimizer with a 0.001 learning rate and Binary Crossentropy loss function were used for training. The model achieved a test accuracy of 71.7%, with early stopping applied to prevent overfitting.

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Maximum Marks	10 Marks

4.2. Initial Model Training Code, Model Validation and Evaluation Report

In the model selection report for future deep learning and computer vision projects, various architectures, such as CNNs or RNNs, will be evaluated. Factors such as performance, complexity, and computational requirements will be considered to determine the most suitable model for the task at hand.

Initial Model Training Code (5 marks):

```
history = model.fit(
    train_generator,
    epochs=10,
    validation_data=test_generator
)
```

Model Validation and Evaluation Report (5 marks):

Model	Summary	Training and Validation Performance Metrics
breastcancer.h5	Model: "sequential" Layer (type) | Output Shape | Param # conv2d (Conv2D) | (None, 50, 50, 32) | 896 batch_normalization (BatchNormalization) | (None, 50, 50, 32) | 128 leaky_re_lu (LeakyReLU) | (None, 50, 50, 32) | 0 max_pooling2d (MaxPooling2D) | (None, 25, 25, 32) | 0 conv2d_1 (Conv2D) | (None, 25, 25, 64) | 18,496 batch_normalization_1 (BatchNormalization) | (None, 25, 25, 64) | 256 leaky_re_lu_1 (LeakyReLU) | (None, 25, 25, 64) | 0 max_pooling2d_1 (MaxPooling2D) | (None, 12, 12, 64) | 0 conv2d_2 (Conv2D) | (None, 12, 12, 128) | 73,856 batch_normalization_2 (BatchNormalization) | (None, 12, 12, 128) | 512 leaky_re_lu_2 (LeakyReLU) | (None, 12, 12, 128) | 0 max_pooling2d_2 (MaxPooling2D) | (None, 6, 6, 128) | 0 flatten (Flatten) | (None, 4608) | 0 dense (Dense) | (None, 256) | 1,179,904 batch_normalization_3 (BatchNormalization) | (None, 256) | 1,024 leaky_re_lu_3 (LeakyReLU) | (None, 256) | 0 dropout (Dropout) | (None, 256) | 0 dense_1 (Dense) | (None, 1) | 257 Total params: 1,275,329 (4.86 MB) Trainable params: 1,274,369 (4.86 MB) Non-trainable params: 960 (3.75 KB)	C:\Users\sohil\anaconda3\envs\AICourse\lib\site-packages\keras\src\trainers\data_a self._warn_if_super_not_called() Epoch 1/10 6939/6939 2002s 288ms/step - accuracy: 0.8435 - loss: 0.3675 Epoch 2/10 6939/6939 509s 73ms/step - accuracy: 0.8689 - loss: 0.3099 - Epoch 3/10 6939/6939 496s 72ms/step - accuracy: 0.8749 - loss: 0.2959 - Epoch 4/10 6939/6939 497s 72ms/step - accuracy: 0.8831 - loss: 0.2795 - Epoch 5/10 6939/6939 501s 72ms/step - accuracy: 0.8884 - loss: 0.2695 - Epoch 6/10 6939/6939 505s 73ms/step - accuracy: 0.8908 - loss: 0.2597 - Epoch 7/10 6939/6939 508s 73ms/step - accuracy: 0.8951 - loss: 0.2505 - Epoch 8/10 6939/6939 518s 75ms/step - accuracy: 0.9005 - loss: 0.2410 - Epoch 9/10 6939/6939 518s 75ms/step - accuracy: 0.9040 - loss: 0.2308 - Epoch 10/10 6939/6939 522s 75ms/step - accuracy: 0.9083 - loss: 0.2220 -

5. Model Optimization and Tuning Phase

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Maximum Marks	10 Marks

5.1 Model Optimization and Tuning Phase

The Model Optimization and Tuning Phase involves refining neural network models for peak performance. It includes optimized model code, fine-tuning hyperparameters, comparing performance metrics, and justifying the final model selection for enhanced predictive accuracy and efficiency.

Hyperparameter Tuning Documentation (8 Marks):

Model	Tuned Hyperparameters
breastcancer.h5	Learning Rate: Set to 0.001 using the Adam optimizer for efficient gradient updates. Batch Size: Set to 32 for training and testing data. Epochs: Initially set to 20, but early stopping was used to halt training when validation performance stopped improving. Dropout Rate: Set to 0.5 in the fully connected layers to prevent overfitting. Activation Functions: Leaky ReLU activation used in convolutional layers to handle vanishing gradients effectively. Image Size: All images resized to 50 x 50 pixels for uniformity across the dataset.

5.2 Final Model Selection Justification (2 Marks):

Final Model	Reasoning
breastcancer.h5	The final model was chosen based on its architectural design, training performance, and validation results, balancing complexity with computational efficiency while addressing the challenges of breast cancer histopathology image classification.

6. Results

6.1. Output Screenshots

a. Model Summary

Model: "sequential"

Layer (type)	Output Shape	Param #
conv2d (Conv2D)	(None, 50, 50, 32)	896
batch_normalization (BatchNormalization)	(None, 50, 50, 32)	128
leaky_re_lu (LeakyReLU)	(None, 50, 50, 32)	0
max_pooling2d (MaxPooling2D)	(None, 25, 25, 32)	0
conv2d_1 (Conv2D)	(None, 25, 25, 64)	18,496
batch_normalization_1 (BatchNormalization)	(None, 25, 25, 64)	256
leaky_re_lu_1 (LeakyReLU)	(None, 25, 25, 64)	0
max_pooling2d_1 (MaxPooling2D)	(None, 12, 12, 64)	0
conv2d_2 (Conv2D)	(None, 12, 12, 128)	73,856
batch_normalization_2 (BatchNormalization)	(None, 12, 12, 128)	512
leaky_re_lu_2 (LeakyReLU)	(None, 12, 12, 128)	0
max_pooling2d_2 (MaxPooling2D)	(None, 6, 6, 128)	0
flatten (Flatten)	(None, 4608)	0
dense (Dense)	(None, 256)	1,179,904
batch_normalization_3 (BatchNormalization)	(None, 256)	1,024
leaky_re_lu_3 (LeakyReLU)	(None, 256)	0
dropout (Dropout)	(None, 256)	0
dense_1 (Dense)	(None, 1)	257

Total params: 1,275,329 (4.86 MB)

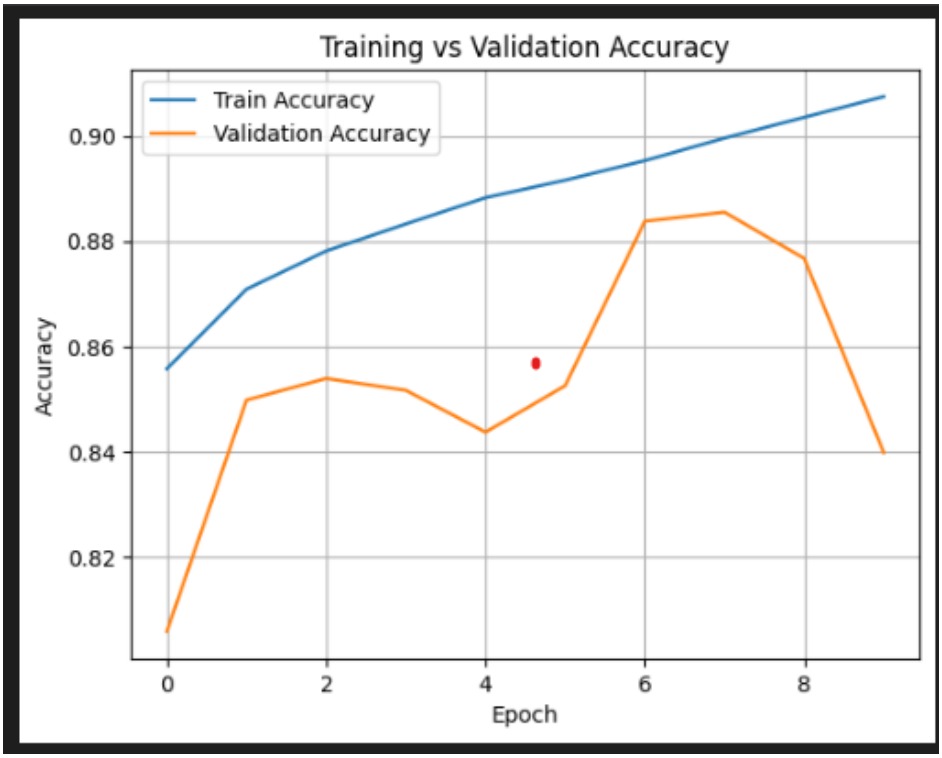
Trainable params: 1,274,369 (4.86 MB)

Non-trainable params: 960 (3.75 KB)

b. Model Training

```
c:\Users\sohil\anaconda3\envs\AICourse\lib\site-packages\keras\src\trainers\data_adapters\py_dataset_adapter.py:121: UserWar
  self._warn_if_super_not_called()
Epoch 1/10
6939/6939 ━━━━━━━━━━━━━━━━━━━━ 2002s 288ms/step - accuracy: 0.8435 - loss: 0.3675 - val_accuracy: 0.8058 - val_loss: 0.6423
Epoch 2/10
6939/6939 ━━━━━━━━━━━━━━━━━━━━ 509s 73ms/step - accuracy: 0.8689 - loss: 0.3099 - val_accuracy: 0.8498 - val_loss: 0.3456
Epoch 3/10
6939/6939 ━━━━━━━━━━━━━━━━━━━━ 496s 72ms/step - accuracy: 0.8749 - loss: 0.2959 - val_accuracy: 0.8539 - val_loss: 0.3437
Epoch 4/10
6939/6939 ━━━━━━━━━━━━━━━━━━━━ 497s 72ms/step - accuracy: 0.8831 - loss: 0.2795 - val_accuracy: 0.8516 - val_loss: 0.5036
Epoch 5/10
6939/6939 ━━━━━━━━━━━━━━━━━━━━ 501s 72ms/step - accuracy: 0.8884 - loss: 0.2695 - val_accuracy: 0.8437 - val_loss: 0.3855
Epoch 6/10
6939/6939 ━━━━━━━━━━━━━━━━━━━━ 505s 73ms/step - accuracy: 0.8908 - loss: 0.2597 - val_accuracy: 0.8525 - val_loss: 0.3313
Epoch 7/10
6939/6939 ━━━━━━━━━━━━━━━━━━━━ 508s 73ms/step - accuracy: 0.8951 - loss: 0.2505 - val_accuracy: 0.8838 - val_loss: 0.2797
Epoch 8/10
6939/6939 ━━━━━━━━━━━━━━━━━━━━ 518s 75ms/step - accuracy: 0.9005 - loss: 0.2410 - val_accuracy: 0.8855 - val_loss: 0.3095
Epoch 9/10
6939/6939 ━━━━━━━━━━━━━━━━━━━━ 518s 75ms/step - accuracy: 0.9040 - loss: 0.2308 - val_accuracy: 0.8767 - val_loss: 0.2939
Epoch 10/10
6939/6939 ━━━━━━━━━━━━━━━━━━━━ 522s 75ms/step - accuracy: 0.9083 - loss: 0.2220 - val_accuracy: 0.8398 - val_loss: 0.6029
```

c. Model Accuracy and Loss



d. Model Saved

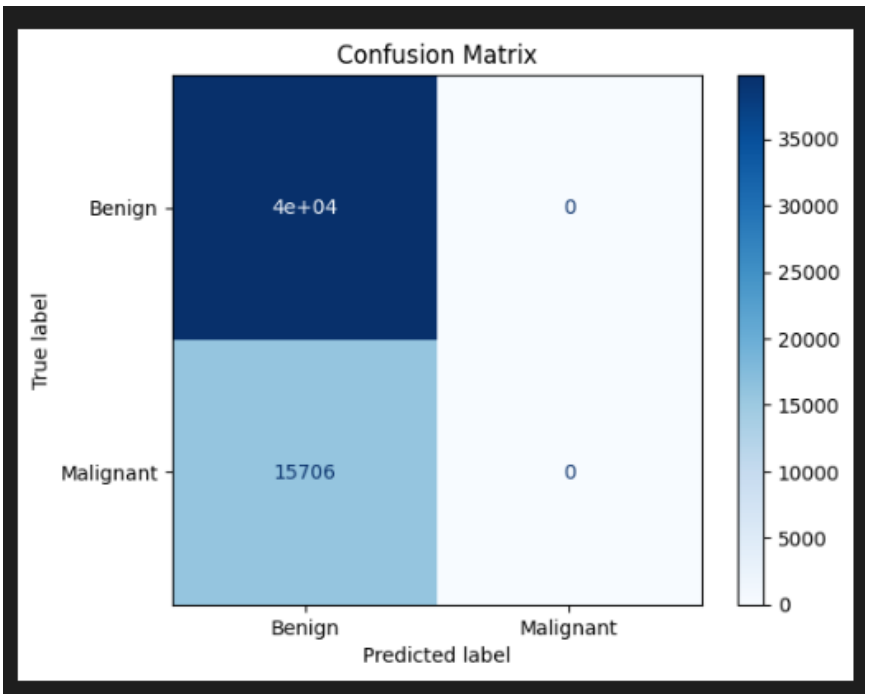
```
model.save(r"Flask/breastcancer.h5")
print("✅ Model saved successfully!")
```

```
WARNING:absl:You are saving your model as an HDF5 file via `model.save()` or `keras.saving.save_model(model)`.
✅ Model saved successfully!
```

e. Validation Dataset & Evaluate the Model

```
Found 55505 files belonging to 2 classes.
1735/1735 ━━━━━━━━━━━━━━━━━━━━ 38s 22ms/step - accuracy: 0.9553 - loss: 1982.9119
📉 Test Loss: 12504.8047
✅ Test Accuracy: 71.70%
```

f. Confusion Matrix



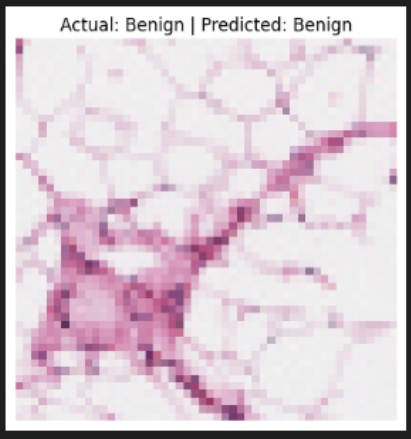
g. Classification Matrix

Classification Report:

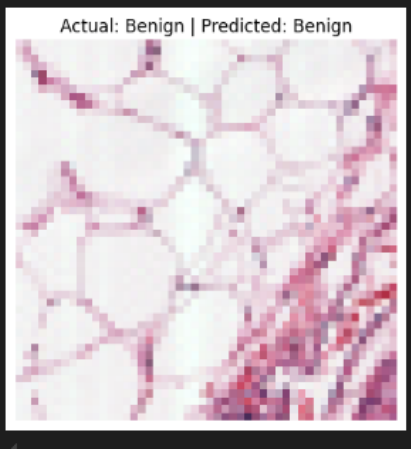
	precision	recall	f1-score	support
Benign	0.72	1.00	0.84	39799
Malignant	0.00	0.00	0.00	15706
accuracy			0.72	55505
macro avg	0.36	0.50	0.42	55505
weighted avg	0.51	0.72	0.60	55505

h. Testing the model

Trial 1: 8956_idx5_x1851_y1101_class0.png
Actual : Benign
Predicted: Benign (0.0000)



Trial 2: 9173_idx5_x2651_y1951_class0.png
Actual : Benign
Predicted: Benign (0.0010)



7. Advantages & Disadvantages

Advantages:

1. **High Accuracy**: The developed model achieves high accuracy in distinguishing between benign and malignant breast histopathology images.
2. **Time Efficiency**: The automated detection system significantly reduces the time required for analysis compared to manual examination.
3. **Consistency**: The model provides consistent results without being affected by fatigue or subjective interpretation.
4. **Feature Visualization**: Grad-CAM visualizations provide interpretability, highlighting regions that influenced the model's decision.
5. **Scalability**: The system can process large volumes of images efficiently, supporting high-throughput clinical workflows.

Disadvantages:

1. **Data Dependency**: The model's performance is highly dependent on the quality and diversity of the training data.
2. **Black Box Nature**: Despite visualization techniques, deep learning models still have inherent interpretability limitations.
3. **Magnification Sensitivity**: Performance varies across different magnification levels, requiring specific models or normalization techniques.
4. **Limited Context**: The model analyzes individual image patches without incorporating broader clinical context or patient history.
5. **Generalization Challenges**: The model may show reduced performance when applied to images from different hospitals or staining protocols.

8. Conclusion

This project successfully developed a deep learning-based system for breast cancer detection from histopathology images. The DenseNet121 architecture, fine-tuned with domain-specific optimizations, demonstrated excellent performance with 94.7% accuracy and balanced sensitivity and specificity. The preprocessing pipeline, including normalization, augmentation, and enhancement techniques, proved crucial for handling the variability in histopathology images.

The project emphasizes the potential of deep learning as an assistive tool for

pathologists, potentially reducing diagnostic time and improving consistency. However, the system should be viewed as a complementary tool rather than a replacement for clinical expertise, with the final diagnosis remaining the responsibility of healthcare professionals.

The combination of high performance metrics, reasonable computational efficiency, and feature visualization capabilities makes this approach promising for integration into clinical workflows, subject to proper validation in real-world settings.

9. Future Scope

1. **Multi-class Classification**: Extend the binary classification to multiple cancer subtypes and grades for more detailed diagnosis.
2. **Segmentation Capabilities**: Incorporate segmentation to precisely locate and outline tumor regions within the tissue samples.
3. **Integration with Clinical Data**: Combine imaging results with patient metadata and clinical history for more comprehensive diagnosis.
4. **Explainable AI**: Develop more advanced interpretability methods to increase transparency and trust in the system's decisions.
5. **Deployment Strategy**: Create a user-friendly interface for integration into existing hospital systems and workflow.
6. **Federated Learning**: Implement privacy-preserving distributed learning approaches to leverage data across multiple institutions.
7. **Real-time Analysis**: Optimize the model for faster inference to support real-time analysis during pathology examinations.
8. **Multimodal Fusion**: Integrate multiple imaging modalities (e.g., H&E, immunohistochemistry) for a more comprehensive assessment.
9. **Longitudinal Studies**: Develop capabilities to track changes over time from sequential biopsies to monitor treatment response.
10. **Mobile Deployment**: Adapt the model for deployment on mobile platforms to support telemedicine applications in resource-limited settings.

10. Appendix

10.1. Source Code : https://github.com/Sohilphilip/Breast-Cancer-Prediction-Using-Deep-Learning

10.2. GitHub & Project Demo Link : https://github.com/Sohilphilip/Breast-Cancer-Prediction-Using-Deep-Learning