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## Breast Cancer Detection

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This work is dedicated to every patient striving to receive the medical care they deserve. We hope that our efforts can, in some small way, contribute to making their journey toward better health a little easier.

Thank you all for helping turn this vision into reality.

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# Chapter 1: Introduction

## 1.1) Overview

Breast cancer remains one of the most prevalent and life-threatening cancers among women globally, accounting for a significant portion of cancer-related morbidity and mortality. Early detection is vital in improving treatment success rates and overall survival. Advances in artificial intelligence (AI) and deep learning have opened new possibilities in medical diagnostics, particularly in the analysis of medical imaging.

This project introduces an AI-powered mobile application specifically designed to aid in the early detection and monitoring of breast cancer through the analysis of mammogram images. The solution integrates two deep learning models: one based on the **Xception** architecture for binary classification (cancerous or non-cancerous), and another model for generating detailed diagnostic reports. Both models are trained using the publicly available CBIS-DDSM dataset, known for its rich collection of annotated mammographic images.

To ensure accessibility and usability, the trained models were deployed within a mobile application developed using Flutter. The app provides several key features, including mammogram analysis, a chatbot assistant for user inquiries, and a medication reminder system. This integration of AI with mobile technology is aimed at empowering users and healthcare providers with timely, accurate, and actionable insights.

## **1.2) Problem Statement**

Despite the advancements in breast cancer treatment, late diagnosis remains a primary reason for high mortality rates. Many regions, especially in low-resource settings, lack access to expert radiologists and diagnostic tools. Traditional methods of breast cancer screening are time-consuming, expensive, and not always readily available. There is a pressing need for an accessible, cost-effective, and accurate tool that supports early detection, patient education, and follow-up care. This project addresses this gap by developing an AI-based mobile platform capable of assisting in the early detection and monitoring of breast cancer through mammogram image analysis.

## **1.3) Scope and Objectives**

### **1.3.1) Scope:**

This project focuses on the development and integration of deep learning models into a mobile platform for breast cancer detection. The models are trained solely on the CBIS-DDSM dataset and deployed within a Flutter-based mobile app. The solution is designed for use by both healthcare professionals and patients for preliminary assessment and support.

### **1.3.2) Objectives:**

- To develop a deep learning model using the Xception architecture for classifying mammogram images.
- To implement a secondary model for generating diagnostic reports based on detected abnormalities.
- To build a mobile application that incorporates these models and offers user-centric features such as:
  - Mammogram image upload and analysis.
  - AI-based chat assistant for breast cancer-related queries.
  - Medication alarm system for treatment adherence.

## **1.4) Report Organization**

This report is organized into the following chapters:

- **Chapter 1: Introduction** – Provides an overview of the project, defines the problem statement, outlines the scope and objectives, describes the work methodology, and presents the work plan.
- **Chapter 2: Medical Overview** – Offers a detailed medical background of breast cancer, its common signs and symptoms, and the importance of early screening. This chapter also explores the growing role of artificial intelligence (AI) in the medical field, especially in disease detection and diagnostic support.
- **Chapter 3: Literature Review** – Reviews existing research on the application of AI in clinical oncology, cancer screening and detection, and computer-aided diagnosis (CAD) systems. It also examines the deep learning model architectures commonly used in disease diagnosis and discusses current advancements in deep learning for mammography.
- **Chapter 4: Proposed Model** – Describes the architecture and functionality of the deep learning models developed in this project, including their training processes and the CBIS-DDSM dataset used. This chapter explains the classification and diagnostic reporting capabilities of the models.
- **Chapter 5: System Requirements and Design** – Outlines the functional and non-functional requirements of the system and presents the overall design, including the integration of AI models with the mobile platform.
- **Chapter 6: Mobile Application** – Focuses on the development of the Flutter-based mobile application, detailing its core features such as image upload and analysis, the AI chat assistant, and the medication reminder system.

- **Chapter 7: Future Work** – Discusses potential improvements and extensions to the current system, such as incorporating additional imaging modalities, improving model accuracy, and expanding accessibility.
- **Chapter 8: References** – Lists all the academic papers, datasets, tools, and other sources cited throughout the report.

## 1.5) Work Methodology

The methodology followed in this project consists of several critical phases that led to the development and deployment of an AI-powered mobile application for breast cancer detection:

### 1. Data Collection and Preprocessing

Two mammogram image datasets were used in this project to ensure a more diverse and representative training base:

- **Mammogram Mastery Dataset – A Robust Dataset:** This dataset contains a wide range of labeled mammogram images and provides detailed annotations that support effective training of deep learning models for breast cancer detection.
- **CBIS-DDSM (Curated Breast Imaging Subset of the Digital Database for Screening Mammography):** A well-established and widely used public dataset containing annotated mammographic images, specifically curated for research in computer-aided detection and diagnosis.

Images from both datasets underwent preprocessing steps including normalization, resizing to a consistent resolution, and augmentation techniques such as rotation and flipping to increase dataset diversity and reduce overfitting.

## **2. Model Development**

Several state-of-the-art convolutional neural network (CNN) architectures were initially explored, including: **ResNet50**, **InceptionV3**, **DenseNet** and **Xception**.

After comparative evaluation, the **Xception** architecture was selected as the primary model for both classification and diagnostic purposes due to its superior accuracy and performance in distinguishing between normal and abnormal mammogram images.

Two main models were developed:

- **Classification Model:** A deep learning model based on the Xception architecture, trained to classify mammogram images into cancerous and non-cancerous categories.
- **Diagnostic Report Generator:** A secondary model designed to provide more granular diagnostic output by identifying patterns and abnormalities in the image that support clinical interpretation.

## **3. Model Training and Evaluation**

The models were trained and validated on a combined dataset derived from the Mammogram Mastery and CBIS-DDSM sources. Performance metrics such as accuracy, sensitivity, specificity, and confusion matrices were used to evaluate the effectiveness of each model during and after training.

## **4. Mobile Application Development**

A mobile application was developed using **Flutter** to integrate the trained models into a user-friendly platform. The app supports mammogram image uploads, runs inference using the embedded AI models, and presents results to users in an interpretable format.

## **5. System Integration and Testing**

The AI models were deployed within the mobile app environment and tested on multiple devices to ensure compatibility and stability. User experience was also evaluated to verify that the system met its intended functionality.

### **1.6) Work Plan**

This project adopted an **Agile development methodology**, enabling iterative progress, continuous testing, and adaptability to evolving requirements. The architecture was designed to function **entirely on-device**, eliminating the need for a backend server or cloud storage. All processing, prediction, and data caching were performed locally using **Flutter** with **shared memory (device storage)** to ensure performance, privacy, and offline accessibility. The work was structured into eight sprints:

#### **Sprint 1: Project Initiation and Requirements Gathering (Week 1–2)**

- Defined the project's objectives, core functionality, and target user personas.
- Conducted a literature review on breast cancer detection and mobile AI applications.
- Identified necessary components: image processing, AI-based diagnosis, local data storage.
- Outlined system specifications and UI/UX requirements.

#### **Sprint 2: Dataset Acquisition and Preprocessing (Week 3–4)**

- Collected mammographic datasets including:
  - CBIS-DDSM Dataset
  - Mammogram Mastery Dataset

- Performed preprocessing using Python: resizing, normalization, class encoding, and data cleaning.
- Stored preprocessed data in serialized format for on-device use (e.g., .tflite or .pkl files).
- Split data into training, validation, and test sets.

### **Sprint 3: Model Training and Selection (Week 5–6)**

- Trained and evaluated three deep learning models:
  - **DenseNet**
  - **InceptionV3**
  - **Xception**
  - **ResNet**
- Compared models using accuracy, precision, recall, and F1-score on multiple target labels.
- Selected **Xception** for its superior performance in classifying mammographic abnormalities.

### **Sprint 4: On-Device Inference & Model Conversion (Week 7–8)**

- Converted the final Xception model to **TensorFlow Lite (.tflite)** format for mobile deployment.
- Integrated multi-output support for simultaneous prediction of:
  - Pathology
  - Mass shape and margins
  - Calcification attributes
  - Breast density, etc.

- Ensured optimized performance by quantizing the model for mobile efficiency.
- Validated inference results within a local Python testing environment.

### **Sprint 5: Flutter App Development – Core Features (Week 9–10)**

- Designed and implemented the **Flutter front-end** with an emphasis on:
  - User onboarding and image upload
  - Real-time AI inference using the embedded TFLite model
  - Visual display of diagnostic predictions
- Implemented **shared memory caching** to locally store:
  - Diagnostic history
  - Image metadata
  - Generated text reports
- Ensured data persistence between sessions without relying on cloud services.

### **Sprint 6: Report Generation and Local Storage (Week 11–12)**

- Developed a module to automatically generate **diagnostic reports** from model predictions.
- Saved reports locally using shared memory (e.g., SharedPreferences).
- Enabled in-app viewing and export (e.g., to PDF or image format).
- Implemented filtering and search features to allow users to retrieve previous reports efficiently.

## **Sprint 7: Testing, Optimization, and Error Handling (Week 13–14)**

- Conducted extensive **unit and integration testing** of app features and inference pipeline.
- Tested the application across different Android devices to ensure cross-platform compatibility.
- Optimized memory usage and loading time for image processing and model execution.
- Implemented graceful error handling for missing data, invalid image uploads, and I/O issues.

## **Sprint 8: Finalization, Review, and Documentation (Week 15)**

- Compiled complete project documentation, including technical references and user manual.
- Conducted a final user review and usability testing.
- Delivered a final demonstration of the offline, AI-driven diagnostic app.
- Outlined future work such as:
  - Multi-language support
  - Integration of multi-modal data inputs

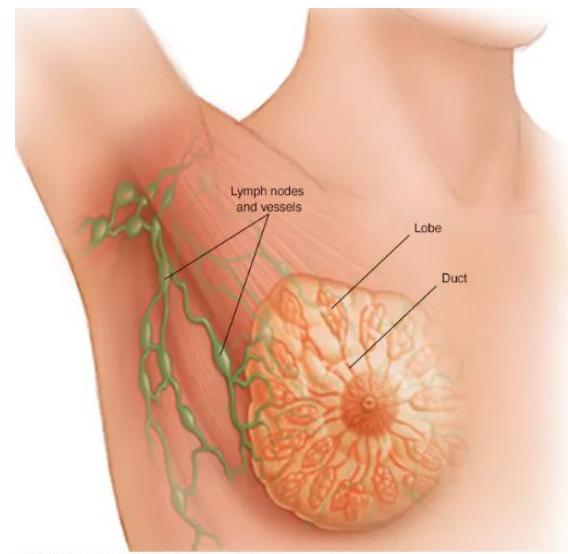
# Chapter 2: Medical background of the disease

## 2.1) Introduction

This chapter offers a brief yet comprehensive look at breast cancer, covering its causes, symptoms, types, and stages. It also explores screening methods like mammography, available treatments, and ways to reduce risk. Lastly, it highlights the growing role of AI and robotics in improving breast cancer diagnosis and care.

## 2.2) Breast Cancer Definition

Breast cancer most commonly develops in cells from the lining of milk ducts and the lobules that supply these ducts with milk. Cancers developing from the ducts are known as ductal carcinomas, while those developing from lobules are known as lobular carcinomas. There are more than 18 other sub-types of breast cancer. Some, such as ductal carcinoma in situ, develop from pre-invasive lesions. The diagnosis of breast cancer is confirmed by taking a biopsy of the concerning tissue. Once the diagnosis is made, further tests are carried out to determine if the cancer has spread beyond the breast and which treatments are most likely to be effective [1].



Each breast contains 15 to 20 lobes of glandular tissue, arranged like the petals of a daisy. The lobes are further divided into smaller lobules that produce milk for breastfeeding. Small tubes, called ducts, conduct the milk to a reservoir that lies just beneath the nipple [2].

## **2.3) Causes of breast cancer**

Healthcare professionals know that breast cancer starts when something changes the DNA inside cells in the breast tissue. A cell's DNA holds the instructions that tell a cell what to do. In healthy cells, the DNA gives instructions to grow and multiply at a set rate. The instructions tell the cells to die at a set time. In cancer cells, the DNA changes give different instructions. The changes tell the cancer cells to make many more cells quickly. Cancer cells can keep living when healthy cells would die. This causes too many cells [3].

The cancer cells might form a mass called a tumor. The tumor can grow to invade and destroy healthy body tissue. In time, cancer cells can break away and spread to other parts of the body. When cancer spreads, it's called metastatic cancer [3].

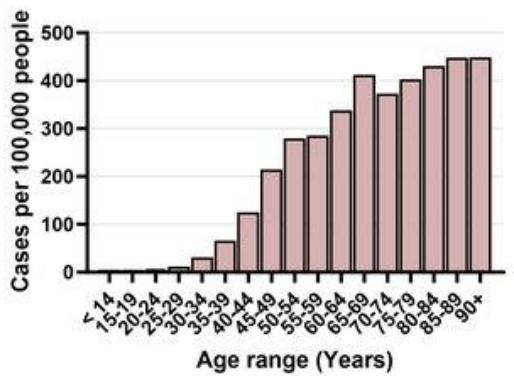
## **2.4) The prevalence of breast cancer in the world**

Statistics show that in 2022, 2.3 million women were diagnosed with breast cancer and 670,000 died worldwide. Breast cancer occurs in every country in the world in women of any age after puberty but with increasing rates later in life [4].

Global estimates reveal stark inequalities in the burden of breast cancer according to human development. For example, in countries with a very high Human Development Index (HDI), 1 in 12 women will be diagnosed with breast cancer in their lifetime and 1 in 71 will die from it [4].

In contrast, in countries with a low HDI, while only 1 in 27 women will be diagnosed with breast cancer in their lifetime, 1 in 48 will die from it [4].

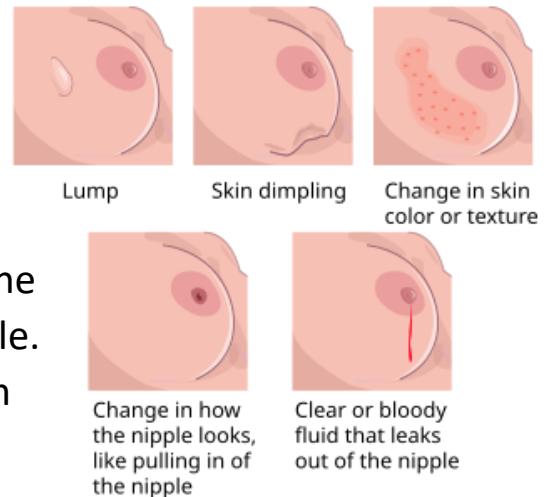
Female gender is the strongest breast cancer risk factor. Approximately 99% of breast cancers occur in women and 0.5–1% of breast cancers



occur in men. The treatment of breast cancer in men follows the same principles of management as for women [4].

## 2.5) Signs and symptoms

Most people with breast cancer have no symptoms at the time of diagnosis; their tumor is detected by a breast cancer screening test. For those who do have symptoms, a new lump in the breast is most common. Most breast lumps are not cancer, though lumps that are painless, hard, and with irregular edges are more likely to be cancerous. Other symptoms include swelling or pain in the breast; dimpling, thickening, redness, or dryness of the breast skin; and pain, or inversion of the nipple. Some may experience unusual discharge from the breasts, or swelling of the lymph nodes under the arms or along the collar bone [1].



EARLY SIGNS OF BREAST CANCER

Some less common forms of breast cancer cause distinctive symptoms. Up to 5% of people with breast cancer have inflammatory breast cancer, where cancer cells block the lymph vessels of one breast, causing the breast to substantially swell and redden over three to six months. Up to 3% of people with breast cancer have Paget's disease of the breast, with eczema-like red, scaly irritation on the nipple and areola [1].

Advanced tumors can spread (metastasize) beyond the breast, most commonly to the bones, liver, lungs, and brain. Bone metastases can cause swelling, progressive bone pain, and weakening of the bones that leads to fractures. Liver metastases can cause abdominal pain, nausea, vomiting, and skin problems – rash, itchy skin, or yellowing of the skin (jaundice). Those with lung metastases experience chest pain, shortness of breath, and regular coughing. Metastases in the brain can cause

persistent headache, seizures, nausea, vomiting, and disruptions to the affected person's speech, vision, memory, and regular behavior [1].

## **2.6) Breast cancer types**

Healthcare providers determine cancer types and subtypes so they can tailor treatment to be as effective as possible with the fewest possible side effects. Common types of breast cancer include: [5]

- Invasive (infiltrating) ductal carcinoma (IDC): This cancer starts in your milk ducts and spreads to nearby breast tissue. It's the most common type of breast cancer in the United States.
- Lobular breast cancer: This breast cancer starts in the milk-producing glands (lobules) in your breast and often spreads to nearby breast tissue. It's the second most common breast cancer in the United States.
- Ductal carcinoma in situ (DCIS): Like IDC, this breast cancer starts in your milk ducts. The difference is DCIS doesn't spread beyond your milk ducts.

Less common breast cancer types include: [5]

- Triple-negative breast cancer (TNBC): This invasive cancer is aggressive and spreads more quickly than other breast cancers.
- Inflammatory breast cancer (IBC): This rare, fast-growing cancer looks like a rash on your breast. IBC is rare in the United States.
- Paget's disease of the breast: This rare cancer affects the skin of your nipple and may look like a rash. Less than 4% of all breast cancers are Paget's disease of the breast.

### **2.6.1) Breast cancer subtypes**

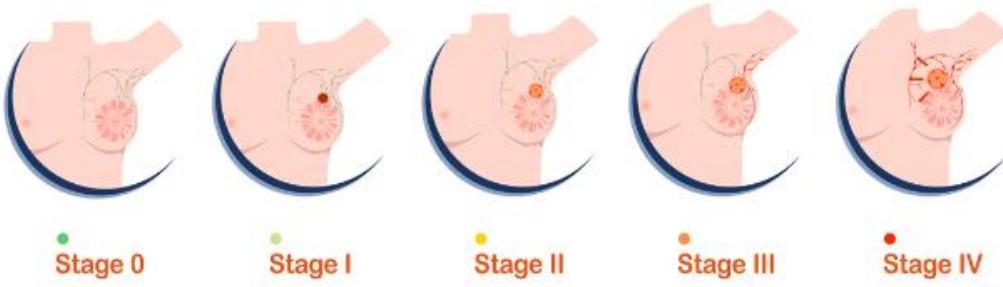
Healthcare providers classify breast cancer subtypes by receptor cell status. Receptors are protein molecules in or on cells' surfaces. They can attract or attach to certain substances in your blood, including hormones like estrogen and progesterone. Estrogen and progesterone

help cancerous cells to grow. Finding out if cancerous cells have estrogen or progesterone receptors helps healthcare providers plan breast cancer treatment [5].

Subtypes include: [5]

- ER-positive (ER+) breast cancers have estrogen receptors.
- PR-positive (PR+) breast cancers have progesterone receptors.
- HR-positive (HR+) breast cancers have estrogen and progesterone receptors.
- HR-negative (HR-) breast cancers don't have estrogen or progesterone receptors.
- HER2-positive (HER2+) breast cancers, which have higher than normal levels of the HER2 protein. This protein helps cancer cells to grow. About 15% to 20% of all breast cancers are HER2-positive.

## 2.7) Stages of breast cancer



[6]

Stage 0: The disease is noninvasive, meaning it hasn't spread from your breast ducts to other parts of your breast [5].

Stage I: There are cancerous cells in nearby breast tissue [5].

Stage II: The cancerous cells have formed a tumor or tumors. The tumor is either smaller than 2 centimeters across and has spread to underarm lymph nodes or larger than 5 centimeters across but hasn't spread to underarm lymph nodes. Tumors at this stage can measure anywhere

between 2 and 5 centimeters across, and may or may not affect the nearby lymph nodes [5].

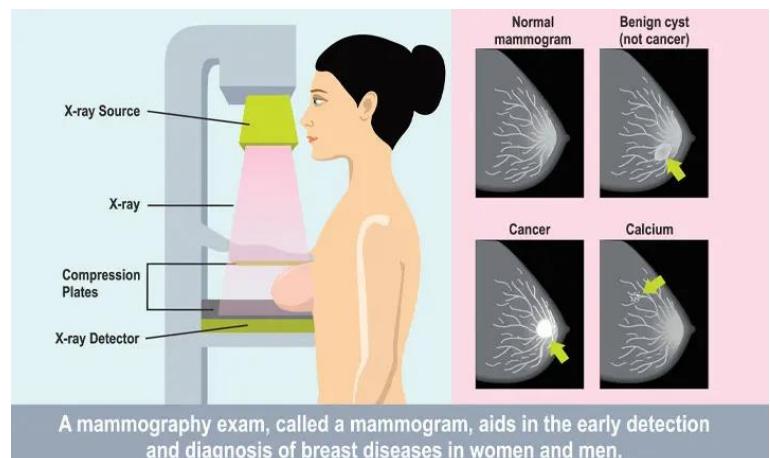
Stage III: There's breast cancer in nearby tissue and lymph nodes. Stage III is usually referred to as locally advanced breast cancer [5].

Stage IV: Cancer has spread from your breast to areas like your bones, liver, lungs or brain [5].

## 2.8) Screening of breast cancer

The most common screening test for breast cancer is low-dose X-ray imaging of the breast, called mammography. Each breast is pressed between two plates and imaged. Tumors can appear unusually dense within the breast, distort the shape of surrounding tissue, or cause small dense flecks called microcalcifications. Radiologists generally report mammogram results on a standardized scale – the six-point Breast Imaging-Reporting and Data System (BI-RADS) is the most common globally – where a higher number corresponds to a greater risk of a cancerous tumor [1].

A mammogram also reveals breast density; dense breast tissue appears opaque on a mammogram and can obscure tumors. BI-RADS categorizes breast density into four categories. Mammography can detect around 90% of breast tumors in the least dense breasts (called "fatty" breasts), but just 60% in the most dense breasts (called "extremely dense"). Women with particularly dense breasts can instead be screened by ultrasound, magnetic resonance imaging (MRI), or tomosynthesis, all of which more sensitively detect breast tumors [1] [7].



A mammography exam, called a mammogram, aids in the early detection and diagnosis of breast diseases in women and men.

## **2.9) What are the different types of mammograms?**

There are two main types of mammograms:

- Digital mammography in 2D.
- Digital mammography in 3D (digital breast tomosynthesis).

### **2D mammograms**

2D mammography involves taking pictures of each breast at two different angles — typically from top to bottom and side to side [8].



### **3D mammograms**

3D mammography is a newer type of mammogram in which each breast is compressed once and a machine takes several X-rays as it moves in an arc over your breast. A computer then puts the images together in “slices,” which allows healthcare providers to see your breast tissues in 3D [8].

## **2.10) Advantages, disadvantages and limitations of mammography screening**

### **Advantages [9]**

- Better chances of cure: Because screening generally detects cancers at an early stage, they can be treated more effectively, thereby reducing the number of deaths due to breast cancer among participants.
- Lower risk of dying from breast cancer: The number of deaths due to breast cancer is lower among participants in the screening program than non-participants.

- Less chemotherapy: Because screening generally detects cancers at an early stage, they can be treated without using chemotherapy.

### Disadvantages [9]

- Waiting and worry when additional tests are needed: Having to undergo additional tests and wait for the results often leads to worry and anxiety. However, in 95% of cases, the results of these tests are normal and do not reveal a cancer.
- Complications: Complications may occur after additional tests (e.g., biopsy).
- Disruption of daily routine: Additional tests may disrupt daily activities (e.g., absence from work).
- Risk of overdiagnosis: Since screening can detect cancers in the early stages of development, some of them may be cases of overdiagnosis. This means these cancers would not have had consequences on the person's life, because they would have remained inoffensive or would have developed very slowly.

### Limitations [9]

- Mammography does not detect all cancers. Some are invisible on the mammogram or may develop between two mammograms.
- Having a screening mammogram does not guarantee that you will survive a breast cancer.
- Treatment does not always lead to survival, even when a cancer is detected at an early stage.
- Screening mammography does not prevent breast cancer from developing.

## **2.11) What type of results do you get from a screening mammogram?**

You'll receive a result letter that gives basic information about the result and should be easy to understand. The letter may inform you of normal results or the need to return for additional imaging. Your mammogram report will also include information about your breast density, which is how much fibrous and glandular tissue you have in your breasts as compared to fatty tissue [8].

### **2.11.1) Breast Imaging Reporting and Data System (BI-RADS)**

Radiologists and healthcare providers use a standard system in medical reporting to describe screening and diagnostic mammogram findings called the Breast Imaging Reporting and Data System (BI-RADS). This system sorts the results into categories numbered 0 through 6 [8].

#### **Incomplete (BI-RADS 0)**

This result means the radiologist may have seen a possible abnormal area, but they need specialized images to evaluate it, like a diagnostic mammogram or an ultrasound. It may also mean that the radiologist wants to compare your most recent mammogram with older ones to see if there have been changes in the area over time [8].

#### **Negative (BI-RADS 1)**

This result means the radiologist didn't find a significant abnormality to report. Your breast(s) don't have any masses, distorted structures or suspicious calcifications. In this case, negative means there are no abnormal areas or findings [8].

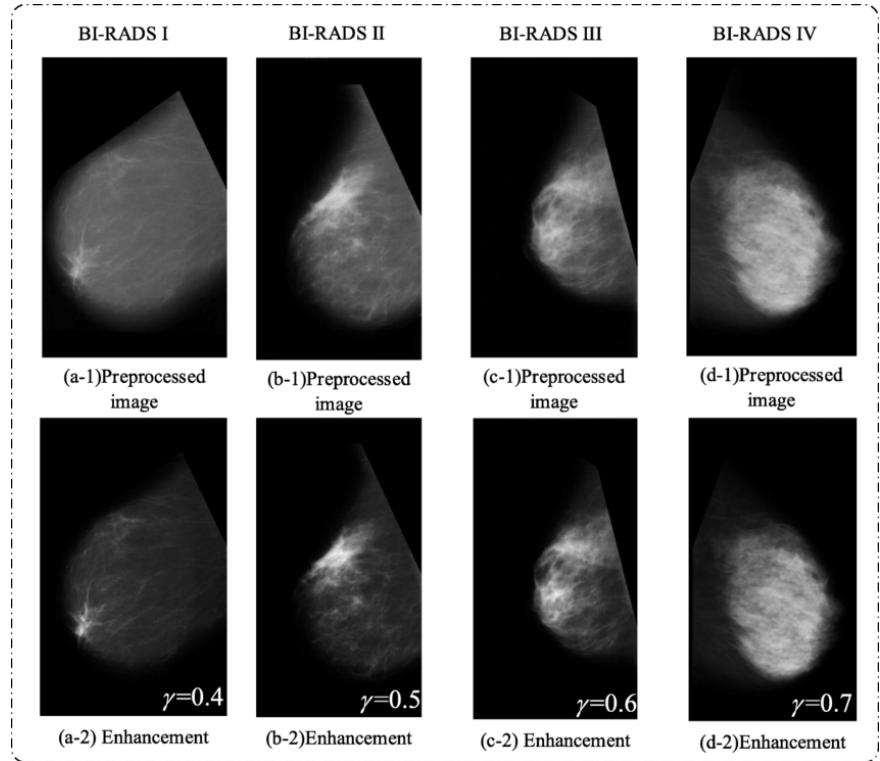
#### **Benign (noncancerous) finding (BI-RADS 2)**

This result means that the radiologist found a benign (noncancerous) structure in your breast, such as benign calcifications, cysts, lymph

nodes or fibroadenomas. The radiologist records this finding to help when comparing it to future mammograms [8].

### Probably benign finding (BI-RADS 3)

This result is only given after a diagnostic mammogram. The findings in this category have a > 98% chance of being benign (noncancerous). But since it's not proven to be benign, the radiologist wants to monitor it to be sure it doesn't change over time. You'll likely need another mammogram in six months [8].[10]



### Suspicious abnormality (BI-RADS 4)

This result is only given after a diagnostic mammogram. It means the finding(s) could be cancer but the radiologist recommends a breast biopsy for more information. The findings in this category can have a wide range of suspicion levels, and it's sometimes divided into further categories, including: [8].

- 4A: Low likelihood of being cancer (> 2% but < 10%).
- 4B: Moderate likelihood of being cancer (> 10% but < 50%).
- 4C: High likelihood of being cancer (> 50% but < 95%).

## **Highly suggestive of malignancy (BI-RADS 5)**

This result is only given after a diagnostic mammogram. The term "malignancy" refers to the presence of cancerous cells. This result means the findings look like cancer and have at least a 95% chance of being cancer. The radiologist strongly recommends a breast biopsy [8].

## **Known biopsy-proven malignancy (BI-RADS 6)**

Radiologists only use this result for findings on a mammogram that have previously been diagnosed as cancer by a biopsy. Healthcare providers use mammograms in this way to see how well the cancer is responding to treatment [8].

## **2.12) What if I have abnormal mammogram results?**

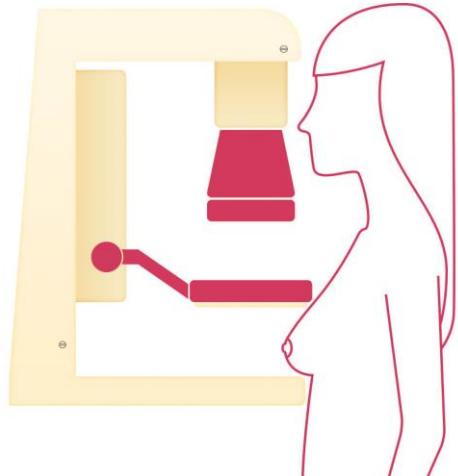
If you have an abnormal mammogram, the follow-up tests you will have depend on the recommendations of the radiologist [7].

You are likely to have a:

### **1. Diagnostic mammogram**

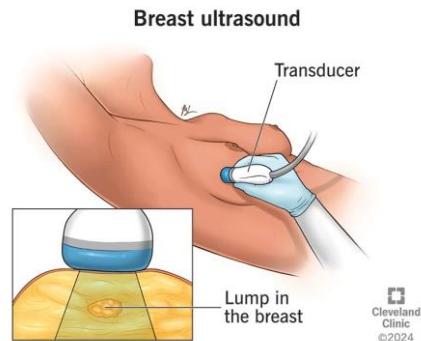
A second mammogram that focuses on specific areas of the breast – this is so that any particular areas of concern can be carefully studied [7].

A diagnostic mammogram is provided when women present with any breast symptoms or concerns, such as a breast mass, palpable lump, nipple discharge, unusual breast pain, or skin changes, and will require a referral from your health care provider. It is also used when a breast irregularity is seen on a screening mammography exam [14].



## 2. Ultrasound

An imaging test that uses sound waves to create a picture of your breast. You will lie on a table while a radiographer applies some gel and places a small instrument called a transducer on your skin. The test is painless and does not expose you to any radiation [7] [12].



## 3. Magnetic resonance imaging (MRI)

Using a powerful magnet linked to a computer, an MRI makes detailed pictures of breast tissue. Your doctor can view these pictures on a monitor or print them on film. MRI may be used along with a mammogram.

For a breast MRI, you will lie face down inside a narrow tube for up to an hour while sensors capture information used to create a more detailed image of the tissues inside your breasts. The test is painless, but can be uncomfortable for people who don't like enclosed spaces [7] [13].



## 4. Biopsy

A test in which fluid or tissue is removed from your breast to help find out if there is cancer. Your doctor may refer you to a surgeon or to a doctor who is an expert in breast disease for a biopsy [1] [7].

There are several different types of biopsies – most use a needle, but some use an incision. The type you have depends on things like how suspicious the tumour looks, how big it is, where it is in the breast, how many tumours there are, other medical problems you might have, and your personal preferences [7].

A specialist will look at the tissue sample with a microscope. It will likely take a few days to a week for you to find out the results [7].

If the results are negative or benign, that means no cancer was found. Ask the doctor whether you need any additional follow-up, and when you should have your next screening mammogram [7].



### 2.13) How is breast cancer treated?

Surgery is the primary breast cancer treatment, but healthcare providers may use other treatments. Breast cancer surgeries include: [5]

- Mastectomy.
- Lumpectomy.
- Breast reconstruction.

Providers may combine surgery with one or more of the following treatments: [5]

- Chemotherapy.
- Radiation therapy, including intraoperative radiation therapy (IORT).

- Immunotherapy.
- Hormone therapy, including selective estrogen receptor modulator (SERM) therapy.
- Targeted therapy.

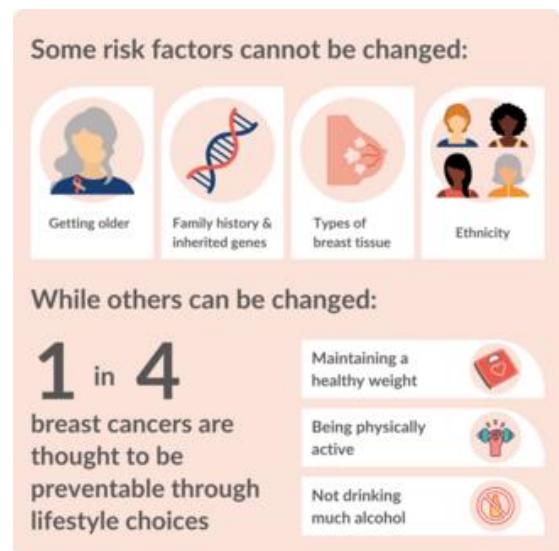
## 2.14) What are treatment side effects?

Common chemotherapy and radiation therapy side effects include fatigue, nausea and vomiting. Targeted therapy, immunotherapy and hormone therapy have similar side effects, including gastrointestinal issues like constipation and diarrhea [5].

## 2.15) How can I lower my risk?

There's no sure way to reduce breast cancer risk [1], but the American Cancer Society (ACS) has the following advice for all females:

- **Get to and stay at a healthy weight:** This is a weight that's right for you. Ask a healthcare provider for information on setting up healthy weight management [5].
- **Eat a healthy diet:** Some studies show a diet that includes vegetables, fruit, calcium-rich dairy foods and lean protein may reduce your risk of breast cancer. Avoiding red meat and processed meat may also reduce your risk [5].
- **Get moving:** Studies show that regular physical activity lowers breast cancer risk [5].
- **Avoid beverages containing alcohol:** Research shows a link between breast cancer and alcohol. The American Medical Association recommends women limit alcohol to one drink a day [5].



- **Get screened:** Mammograms often detect tumors when they're too small to be felt [5].
- **Do regular self-exams:** Examining your breasts regularly helps to maintain breast health and may allow you to find breast cancer tumors [5].

Some women have an increased risk for breast cancer because family members have it or they inherited a genetic mutation. If that's your situation [5], you may want to consider the following:

- Genetic screening for breast cancer genes [5].
- Medication that may lower breast cancer risk like tamoxifen, raloxifene or aromatase inhibitors [5].
- Prophylactic (preventive) mastectomy [5].
- Frequent breast cancer screenings and physical examinations. If you have an increased risk for breast cancer, ask your provider if you should have additional tests to detect breast cancer, particularly if you're under age 40 and have increased risk [5].

## **2.16) AI and Robotics in Breast Cancer Diagnosis and Treatment**

The integration of artificial intelligence in breast cancer diagnosis and management has the potential to improve healthcare practices and enhance patient care. With the adoption of advanced technologies like surgical robots, healthcare providers are able to achieve greater accuracy and efficiency in surgeries related to breast diseases [1].

These AI-driven robots use algorithms to provide real-time guidance, analyze imaging data, and execute procedures with precision, ultimately leading to improved surgical outcomes for people with breast cancer. Moreover, AI has the potential to transform the methods of monitoring and personalized treatment, using remote monitoring systems to facilitate continuous observation of a person's health status, assist early

detection of disease progression, and enable individualized treatment options. The overall impact of these technological advancements enhances quality of care, promoting more interactive and personalized healthcare solutions [1].

### **How AI may improve breast cancer detection?**

There are many different ways radiologists can use AI when reading mammograms, including checking their reading against the computer's reading, or turning to the computer for mammograms to prioritize first based on "likely suspicious" results. Research is ongoing in countries where there is more use of AI to check for signs of cancer, but the studies done so far suggest that AI could improve breast cancer detection in several ways: [15] [16]



### **Identifying cancer earlier**

According to the National Cancer Institute, screening mammograms miss about 20% of breast cancers. AI systems appear to have the ability to pick up very subtle signs of an early cancer that the human eye might miss [15].

A study published in *The Lancet Oncology* describes how researchers used AI to help screen mammograms of more than 80,000 women in Sweden. Half of these women had their mammogram read by AI before it was looked at by a radiologist, while the other half had theirs read by two radiologists. The study revealed that the AI group had 20% more cancers detected than the radiologist-only group [15].

## **Reducing false alarms**

A false positive result occurs when the radiologist detects an abnormal finding on a mammogram that doesn't ultimately prove to be a cancer. Before cancer can be ruled out, however, doctors may need to order multiple follow-up tests, such as additional mammogram images, ultrasound and/or a biopsy, which can be emotionally and financially draining [15].

A study of more than 91,000 mammograms from women in the U.S. and the U.K. found that the use of an AI system lowered the rate of false positives by almost 6% in the U.S. and by 1.2% in the U.K. The findings appeared in *Nature* in 2020 [15].

## **Preventing unnecessary biopsies**

"About 80% of biopsies performed on areas of concern turn out to be benign [non-cancerous]," says Dr. Patel. AI systems may be able to reduce the number of unnecessary biopsies [15].

For instance, an AI tool called iBRISK (intelligent-augmented breast cancer risk calculator) could accurately predict whether abnormal tissue flagged by doctors was more likely to be benign or cancerous, according to a study in *Radiology: Artificial Intelligence* [15].

## **Predicting cancer risk**

AI may also lead to improvements in doctors' ability to predict those people at greatest risk of developing breast cancer [15].

A study published in June 2023 found that AI was more accurate in predicting breast cancer risk than the Breast Cancer Surveillance Consortium (BCSC) risk model. The Breast Cancer Surveillance Consortium Risk Calculator estimates a woman's 5-year risk of developing invasive breast cancer based on such factors as a woman's

age, her family history of the disease, race/ethnicity, breast density, and any history of benign breast biopsies [15].

Using screening images collected from 13,600 women who had normal mammograms, five AI systems generated risk scores for developing cancer over that five-year period. AI was more accurate than the BCSC model in predicting breast cancer; the best results were achieved when AI and the BCSC model were used together. The findings appeared in Radiology [15].

## **2.17) Future Directions in Breast Cancer Diagnosis with AI**

The integration of AI in breast cancer diagnosis and therapy offers great promise for healthcare. Through advanced algorithms and machine learning, AI can enhance the accuracy and efficiency of early breast cancer detection. This can result in prompt treatment, improving patient outcomes and survival rates. Furthermore, AI can aid in personalized treatment planning by analyzing extensive data to suggest effective therapies tailored to each patient's genetic profile and disease traits. In conclusion, artificial intelligence shows potential in transforming breast cancer diagnosis and therapy. AI can also assist in monitoring treatment response and detecting any signs of cancer recurrence, allowing for timely intervention. Additionally, the integration of AI can help streamline healthcare processes, reduce healthcare costs, and alleviate the burden on healthcare professionals. Overall, the future looks promising with the incorporation of AI in breast cancer diagnosis and therapy [20].

# Chapter 3: Literature review

## 3.1) Introduction

This chapter explores the growing role of artificial intelligence in clinical oncology, focusing on its applications in cancer screening, detection, and diagnosis. It also examines the structure of deep learning models, their use in computer-aided diagnosis (CAD), and their specific impact on mammography, while addressing the challenges and limitations of AI integration in clinical settings.

## 3.2) AI in Clinical Oncology

The origins of AI can be traced back to the 1950s, aiming to create machines capable of human-like thinking and reasoning. Initially, AI in clinical medicine utilized fuzzy logic, expert systems, and artificial neural networks. Progress led to advancements in support vector machines, feature engineering, and natural language processing [20].

The rise of deep learning, convolutional neural networks, and recurrent neural networks has significantly advanced AI in medicine [20].

AI can amalgamate and analyze various data types like patient history, tumor pathology, genomics, and imaging data [20].

## 3.3) Challenges and Limitations of AI Integration in Clinical Oncology

AI applications in clinical oncology face numerous challenges and constraints. A critical issue is the lack of standardized cancer health data, impeding AI integration into clinical practice. Another hurdle is the complexity of testing, validating, certifying, and auditing AI algorithms and systems, posing significant barriers to widespread adoption. The time and resources required for data collection, model development, and translation can also impact the future clinical acceptance of AI.

methods. Moreover, carrying out prospective, multi-center, and large sample studies to validate the accuracy and generalizability of AI models is vital for comprehensive and standardized clinical application. Addressing these challenges and limitations is essential for the sustainable integration of AI in clinical oncology and for improving patient outcomes [20].

Establishing standardized protocols for data collection, curation, and sharing will facilitate the creation of robust, diverse datasets that support the development and validation of AI algorithms [20].

Streamlining testing, certification, and auditing processes for AI systems will expedite their integration into clinical workflows [20].

Investments in infrastructure for data management, computational resources, and AI development expertise will be key in translating research findings into practical clinical applications. Promoting a culture of transparency and reproducibility in AI research will enhance the credibility and trustworthiness of AI models, fostering their acceptance in clinical settings [20].

### **3.4) Cancer screening and cancer detection**

Cancer screening has been a highly active area of AI research. AI algorithms have been tested in diseases with active screening programs such as lung cancer and breast cancer. In breast cancer, some studies have shown that AI algorithms can equal the performance of expert readers, be used as a second reader for screening mammographic reviews, provide triaging for prioritizing image reading and have been found to be acceptable to women undergoing mammographic screening. However, real-world evidence is still insufficient to recommend the wide adoption of AI-based tools for breast screening. In addition to systematic screening, opportunistic screening (the detection of abnormalities in exams obtained for other purposes) [22].

### **3.5) AI-Based Computer-Aided Diagnosis (CAD)**

AI-based computer-aided diagnosis (CAD) systems have shown potential in identifying breast cancer. These systems utilize deep learning models and convolutional neural networks (CNNs) to improve the detection and interpretation of mammograms [20].

By using AI, CAD systems can provide faster, more precise, and unbiased interpretations of mammograms, aiding radiologists in making accurate decisions. Integrating AI models into CAD systems holds the promise of improving the early diagnosis of breast cancer, leading to better survival rates and reduced mortality [20].

In traditional computer vision tasks, there are many large-scale and well-annotated datasets, such as ImageNet (over 14 million labeled images from 20,000 categories) and COCO (with more than 200,000 annotated images across 80 categories). In contrast, publicly available medical datasets tend to be much smaller. For example, among the datasets for different tasks, only ChestX-ray14 and DeepLesion contain more than 100,000 labeled medical images, while most datasets have only a few thousand or even just hundreds of images [19].

The lack of medical datasets is represented in three aspects:

- **Small Number of Medical Images:**

The number of medical images in datasets is usually small. This problem is mainly due to the high cost associated with the data collection. Medical images are collected from computerized tomography (CT), ultrasonic imaging (US), magnetic resonance imaging (MRI) scans, and positron emission tomography (PET), all of which are expensive and labor-intensive [19].

- **Limited Annotations:**

Only a small portion of medical images are annotated. These annotations, including classification labels (e.g., benign or malignant), and the segmentation annotations of lesion areas, require efforts from experienced doctors [19].

- **Difficulty in Collecting Positive Cases for Rare Diseases:**

It is difficult to collect enough positive cases for some rare diseases to obtain balanced datasets. This scarcity limits the ability of deep learning models to generalize well across diverse medical conditions, hindering their full potential in CAD applications [19].

### 3.6) General Structures of Deep Learning Models Used for Disease Diagnosis

In the last decades, deep learning techniques, especially CNNs, have achieved great success in disease diagnosis. Fig. 4 shows the structure of a typical CNN that is used for disease diagnosis in chest X-ray images. The CNN employs alternating convolutional and pooling layers, and contains trainable filter banks per layer. Each individual filter in a filter bank is able to generate a feature map. This process is alternated, and the CNN can learn increasingly more and more abstract features that

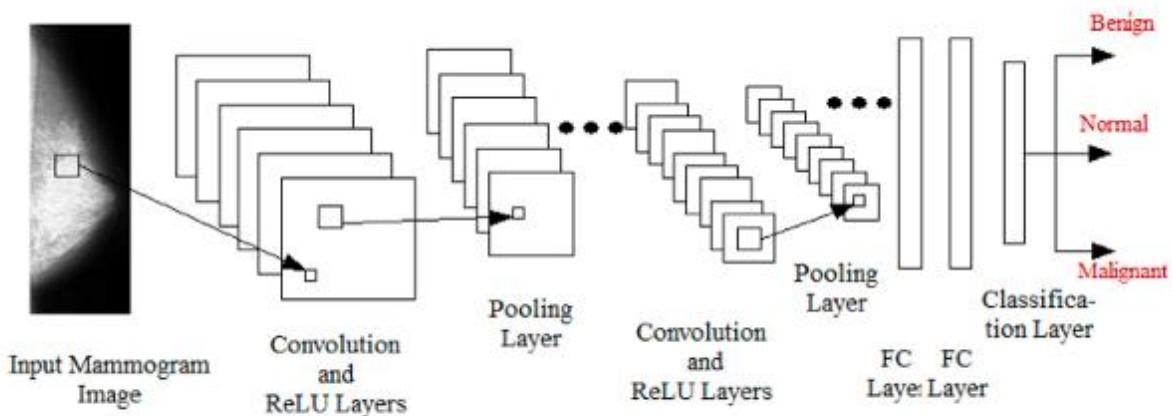
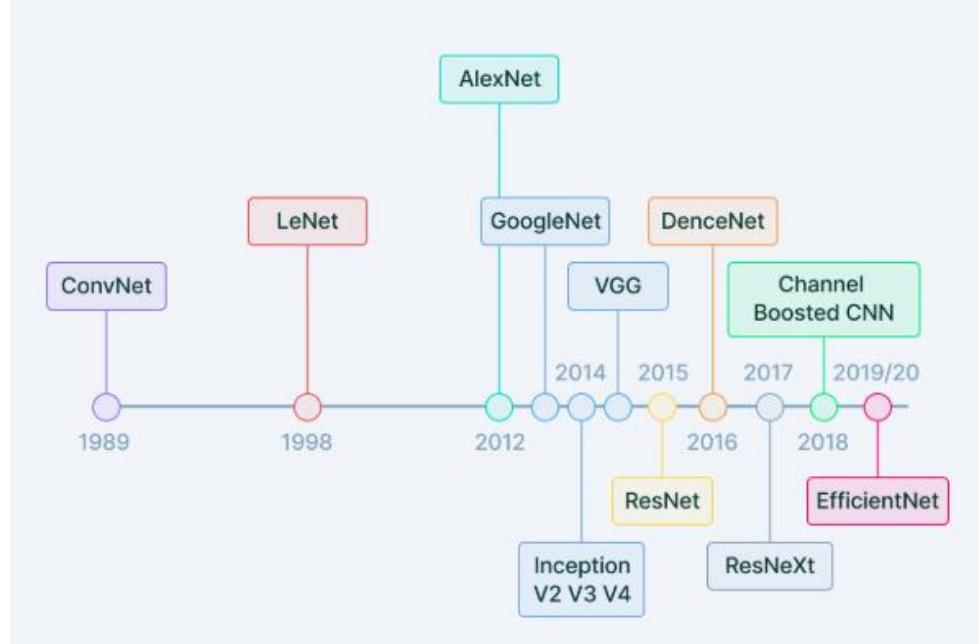


Fig. 8. Classical CNN architecture.

will later be used by the fully connected layers to accomplish the classification task [19].

However, the above works generally directly apply CNNs to medical image analysis or slightly modified CNNs (e.g., by modifying the number of kernels, the number of channels, or the size of filters), and no medical knowledge is incorporated. In addition, these methods generally require large medical datasets to achieve satisfactory performance [19].

Nowadays, transfer learning is preferred over classical DL techniques as it yields better performance in the presence of small datasets, unlike standard CNN techniques. It is first trained using a source domain dataset (a large dataset) to generate a pre-trained model. Then, it reuses the pre-trained model on a small dataset (medical dataset), which may not be related to the target work, to fine-tune the pre-trained model. Hence, it improves the classification performance.



Several transfer learning models: AlexNet, VGGNet, ResNet , GoogLeNet, MobileNet, and MobileNetV2 [21] [17].

Li et al. have presented DenseNet-II for breast cancer classification and compared its performance with AlexNet, VGGNet, GoogleNet, and DenseNet [21].

### **3.7) Deep learning for Mammography**

The section presents the recent literature on ML and DL for four discernible Mammography tasks: breast density classification, calcification detection and classification, breast asymmetry detection and classification, mass detection and classification. A tremendous number of Mammogram datasets are available, that can be used to analyze the hidden new patterns for the early detection of diseases [27].

The Digital Database for Screening Mammography (DDSM) is the largest available Mammogram database used for Mammographic image analysis. This database is the synergetic effort of “Massachusetts General Hospital”, “Sandia National Laboratories” and the “University of South Florida Computer Science and Engineering”. The Mammograms were acquired from “Massachusetts General Hospital” (MGH), “Wake Forest University School of Medicine” (WFU), “Sacred Heart” (SH) Hospital, and “Washington University” (WU) of St. Louis School of Medicine. DDSM dataset contains 2620 examples, with two images of each breast [27].

# Chapter 4: Proposed Models

## 4.1) Introduction

This chapter presents a detailed analysis of two major breast cancer imaging datasets—Mammogram Mastery and CBIS-DDSM. It outlines key dataset statistics, model evaluation strategies, and performance metrics. Deep learning models including ResNet50, Xception, DenseNet, and InceptionV3 are evaluated and compared. The chapter also provides a breakdown of dataset files and offers detailed performance reports for each model tested.

## 4.2) Summary of the Mammogram Mastery A Robust Dataset: Breast Cancer

Dataset link:

<https://www.kaggle.com/datasets/abdulrazakadekunle/mammogram-mastery-a-robust-dataset-breast-cancer/data>

This dataset consists exclusively of mammography images in **JPG format**, categorized to represent cases of **breast cancer** and **non-cancer**.

4.2.1) Key Dataset Statistics	
Number of Images	10,430
Modality	MG (Mammography)
It is divided into:	
Original Dataset	Cancer: 125 Images Non-Cancer: 620 Images
Augmented Dataset	Cancer: 1625 Images Non-Cancer: 8060 Images

#### **4.2.2) Model Evaluation Strategy**

four deep learning models—**InceptionV3**, **ResNet50**, **Xception**, and **DenseNet**—were applied to the dataset for breast cancer classification. Each model was trained and evaluated using key performance metrics, such as accuracy, precision, recall, and F1-score. A comprehensive comparative analysis was conducted to assess the effectiveness of each model.

Transfer learning was applied uniformly across all models using pre-trained weights from the **ImageNet** dataset.

All models were trained and evaluated on an **Augmented dataset** of the *Mammogram Mastery: A Robust Dataset*.

The input images were resized to **100 × 100 pixels** with **3 RGB channels**. The model was trained for **100 epochs** with a **batch size of 32**. The custom classification head included fully connected layers with **ReLU activations**, **dropout** for regularization, and **batch normalization** to improve training stability. The final output layer used **softmax activation** to perform multi-class classification based on the number of target classes which are cancer or non-cancer.

### 4.2.3) Performance metrics

Performance metrics are quantitative measures used to evaluate the effectiveness of a model, algorithm, or system. Common metrics include: [23]

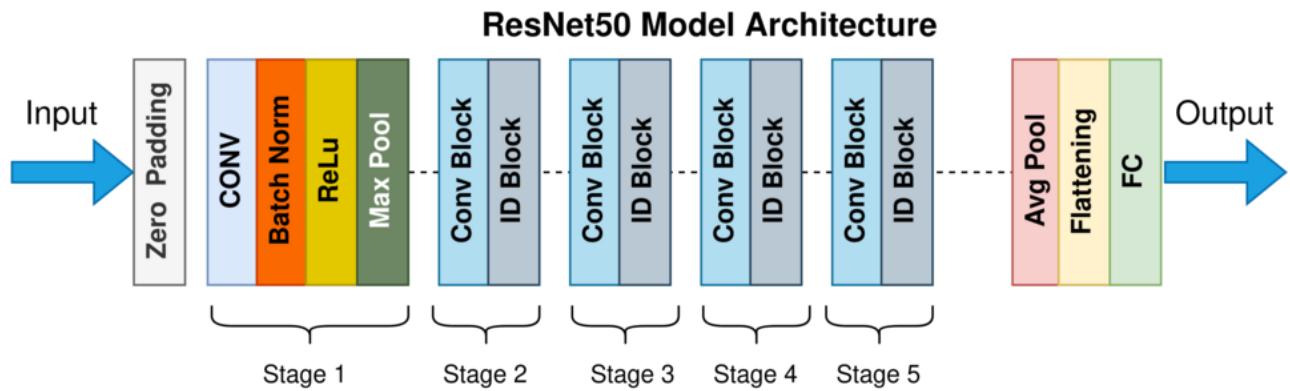
$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN}$$

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

$$F1-score = \frac{TP}{TP + \frac{1}{2}(FP + FN)}$$

- **Accuracy:** Proportion of correctly predicted instances.
- **Recall (Sensitivity):** Proportion of true positives among all actual positives.
- **F1-Score:** Harmonic mean of precision and recall, useful for imbalanced datasets.
- **Confusion Matrix:** A table summarizing correct and incorrect predictions.
- **ROC-AUC:** Measures the ability of a classifier to distinguish between classes.
- **Precision:** Proportion of true positives among all predicted positives.

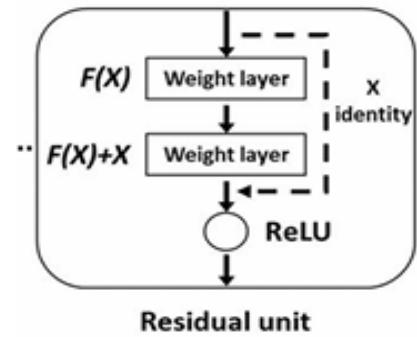
## 4.2.4) Model-1: ResNet50



ResNet50 is a 50 layers CNN model<sup>25</sup> with residual blocks that contain multiple convolutional layers along with connections, allowing for easier training of deeper networks [23].

In ResNet50, skip connections are significant components, which are crucial for addressing the challenges associated with training very deep neural networks. Skip connections, or residual connections, allow the network to focus on learning residual mappings rather than the complete desired mapping. This is achieved by introducing shortcut connections that bypass one or more layers, directly adding the input of a block to its output [23].

The mathematical representation of a residual block's output is  $F(x)+x$ , where  $F(x)$  denotes the transformational output of the convolutional layers and  $x$  is the input [23].



## Model Architecture

Layer (type)	Output Shape	Param #
resnet50 (Functional)	(None, 4, 4, 2048)	23,587,712
global_average_pooling2d_1 (GlobalAveragePooling2D)	(None, 2048)	0
dense_3 (Dense)	(None, 256)	524,544
dropout_2 (Dropout)	(None, 256)	0
batch_normalization_96 (BatchNormalization)	(None, 256)	1,024
dense_4 (Dense)	(None, 128)	32,896
dropout_3 (Dropout)	(None, 128)	0
batch_normalization_97 (BatchNormalization)	(None, 128)	512
dense_5 (Dense)	(None, 2)	258

Total params: 24,146,946 (92.11 MB)

Trainable params: 558,466 (2.13 MB)

Non-trainable params: 23,588,480 (89.98 MB)

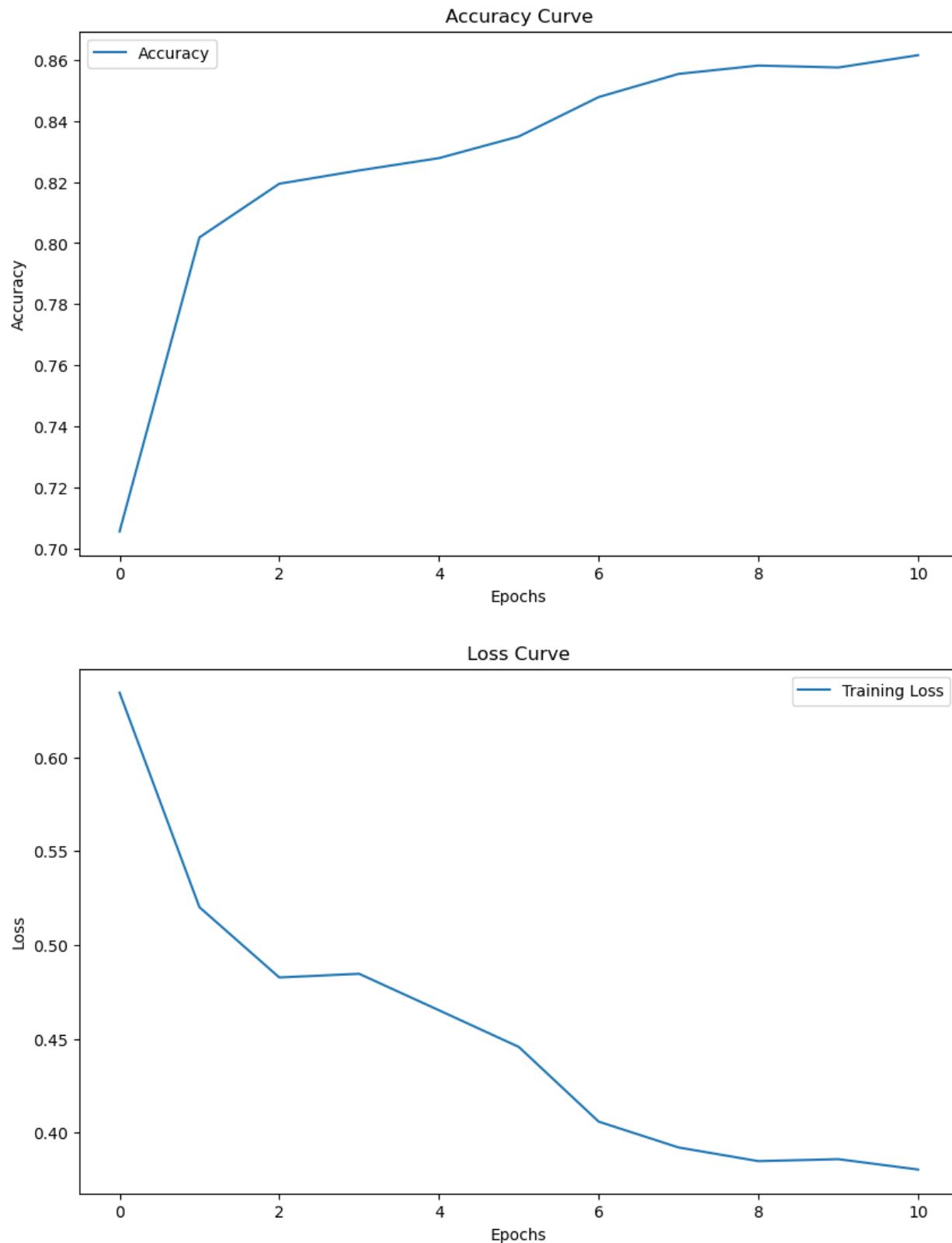
## Model Accuracy

```
Epoch 1/100
194/194 177s 777ms/step - accuracy: 0.6279 - loss: 0.7457 - val_accuracy: 0.8381 - val_loss: 0.4465
Epoch 2/100
194/194 140s 725ms/step - accuracy: 0.7950 - loss: 0.5354 - val_accuracy: 0.8381 - val_loss: 0.4715
Epoch 3/100
194/194 139s 718ms/step - accuracy: 0.8204 - loss: 0.4777 - val_accuracy: 0.8381 - val_loss: 0.5532
Epoch 4/100
194/194 152s 786ms/step - accuracy: 0.8199 - loss: 0.4907 - val_accuracy: 0.8381 - val_loss: 0.5024
Epoch 5/100
194/194 127s 655ms/step - accuracy: 0.8277 - loss: 0.4624 - val_accuracy: 0.8381 - val_loss: 0.5166
Epoch 6/100
194/194 141s 729ms/step - accuracy: 0.8282 - loss: 0.4618 - val_accuracy: 0.8381 - val_loss: 0.5295
Epoch 7/100
194/194 140s 721ms/step - accuracy: 0.8433 - loss: 0.4189 - val_accuracy: 0.8381 - val_loss: 0.5780
Epoch 8/100
194/194 166s 859ms/step - accuracy: 0.8529 - loss: 0.3968 - val_accuracy: 0.8406 - val_loss: 0.5203
Epoch 9/100
194/194 161s 831ms/step - accuracy: 0.8525 - loss: 0.4000 - val_accuracy: 0.8381 - val_loss: 0.5441
Epoch 10/100
194/194 142s 733ms/step - accuracy: 0.8494 - loss: 0.4051 - val_accuracy: 0.8387 - val_loss: 0.5779
Epoch 11/100
194/194 137s 708ms/step - accuracy: 0.8696 - loss: 0.3661 - val_accuracy: 0.8381 - val_loss: 0.5749
```

Test Accuracy: 0.8425400257110596

```
61/61 34s 560ms/step - accuracy: 0.8289 - loss: 0.4651
```

## Accuracy and Loss Diagrams

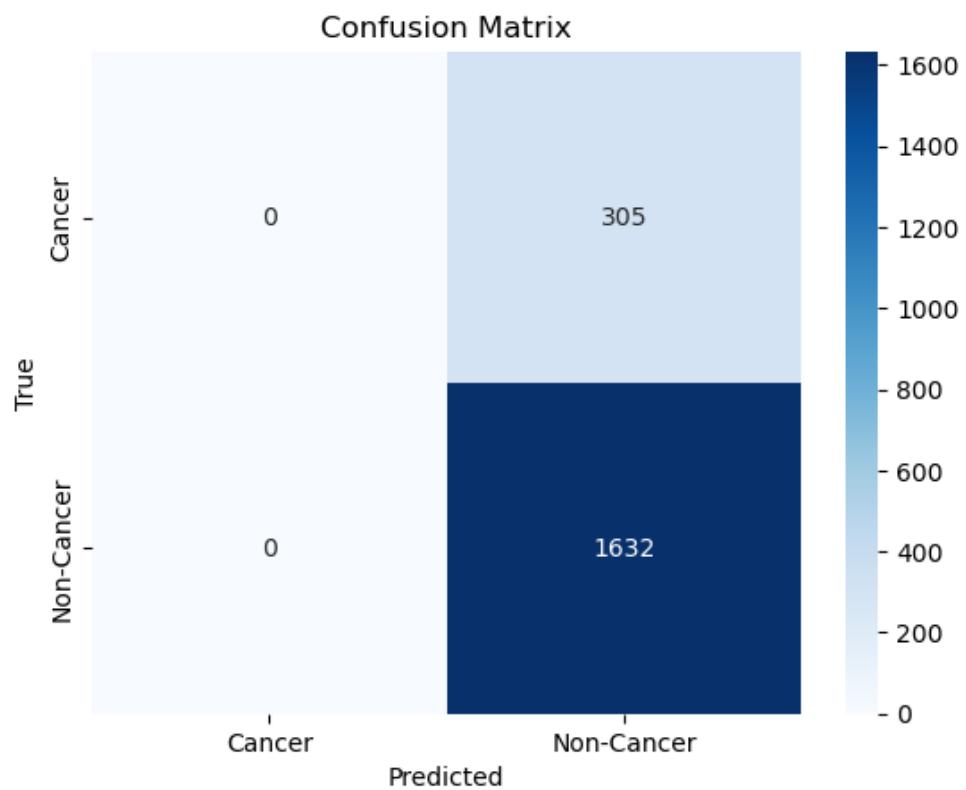


## Classification Report

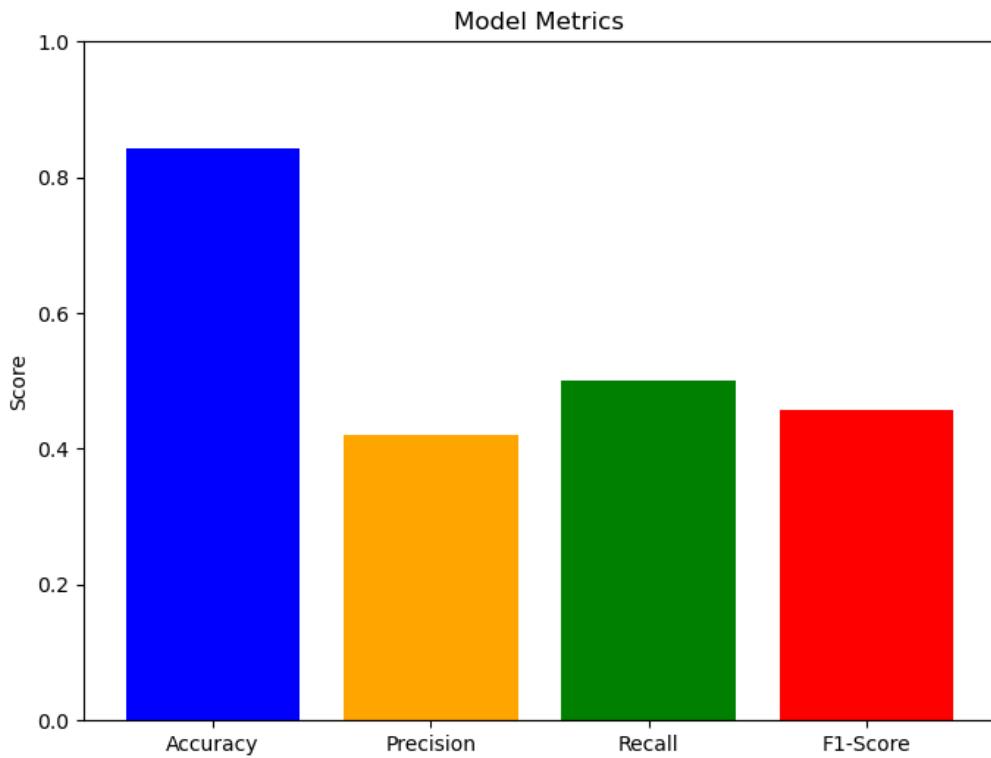
```
Classification Report:  
precision    recall   f1-score   support  
  
Cancer        0.00     0.00      0.00      305  
Non-Cancer    0.84     1.00      0.91     1632  
  
accuracy          0.84  
macro avg       0.42     0.50      0.46     1937  
weighted avg    0.71     0.84      0.77     1937  
  
Accuracy: 0.84  
Precision: 0.42  
Recall: 0.50  
F1-Score: 0.46
```

---

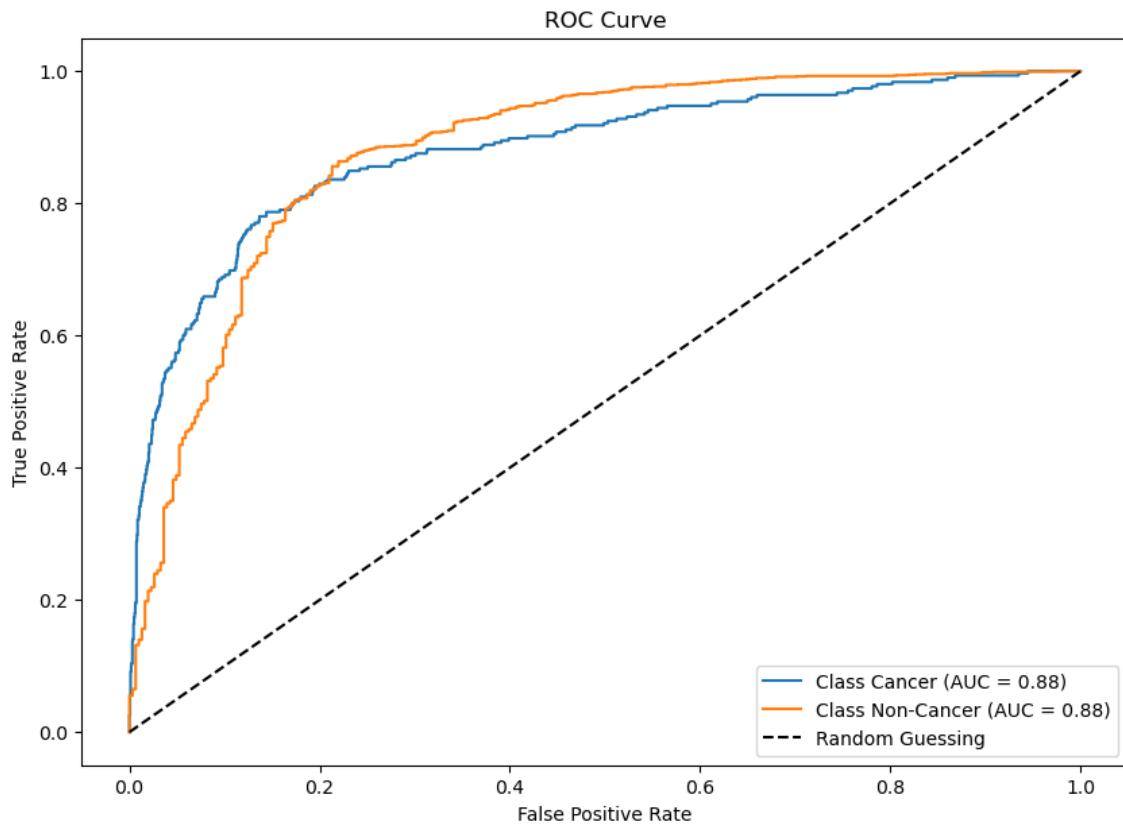
## Confusion Matrix



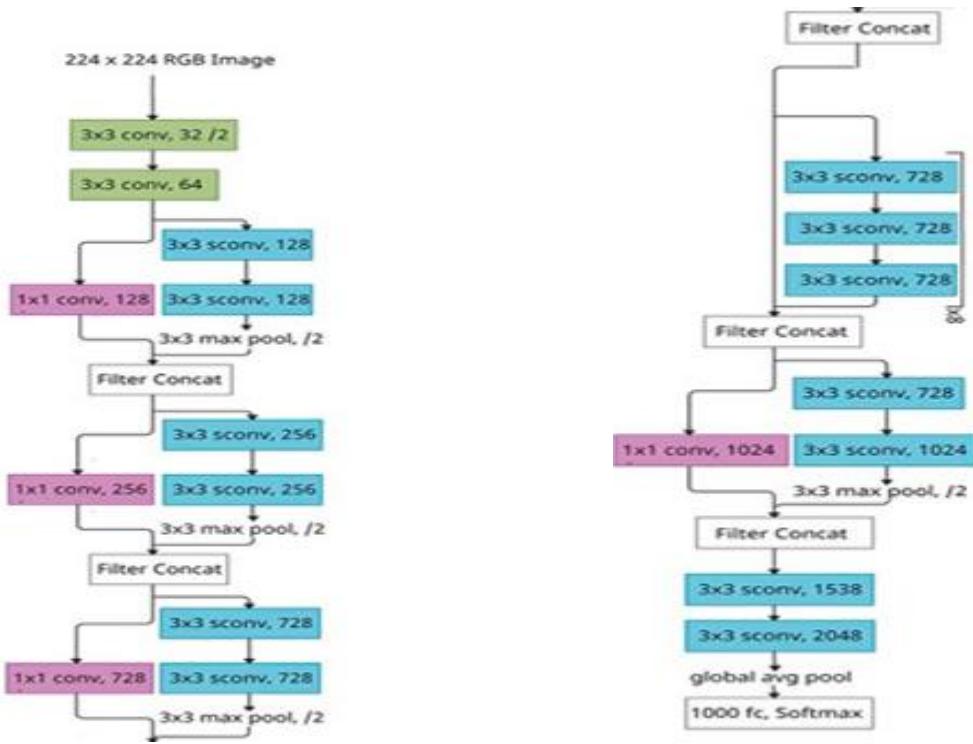
## Model Metrics



## ROC Curve



#### 4.2.5) Model-2: Xception



Xception was “proposed by François Chollet, the creator and chief maintainer of the Keras library” (Bovik, 2005). The architecture Xception contains 36 Convnet layers making the feature abstraction base of the network. Except for the first and last modules, “the 36 convolutional layers are divided into 14 modules, all of which contain linear residual connections around them” (Metwally et al., 2018). Xception was recommended by François Chollet, the Keras library’s founder and major maintainer (Miao and Miao, 2018) [24].

## Model Architecture

Layer (type)	Output Shape	Param #
xception (Functional)	(None, 3, 3, 2048)	20,861,480
global_average_pooling2d (GlobalAveragePooling2D)	(None, 2048)	0
dense (Dense)	(None, 256)	524,544
dropout (Dropout)	(None, 256)	0
batch_normalization_4 (BatchNormalization)	(None, 256)	1,024
dense_1 (Dense)	(None, 128)	32,896
dropout_1 (Dropout)	(None, 128)	0
batch_normalization_5 (BatchNormalization)	(None, 128)	512
dense_2 (Dense)	(None, 2)	258

Total params: 21,420,714 (81.71 MB)

Trainable params: 558,466 (2.13 MB)

Non-trainable params: 20,862,248 (79.58 MB)

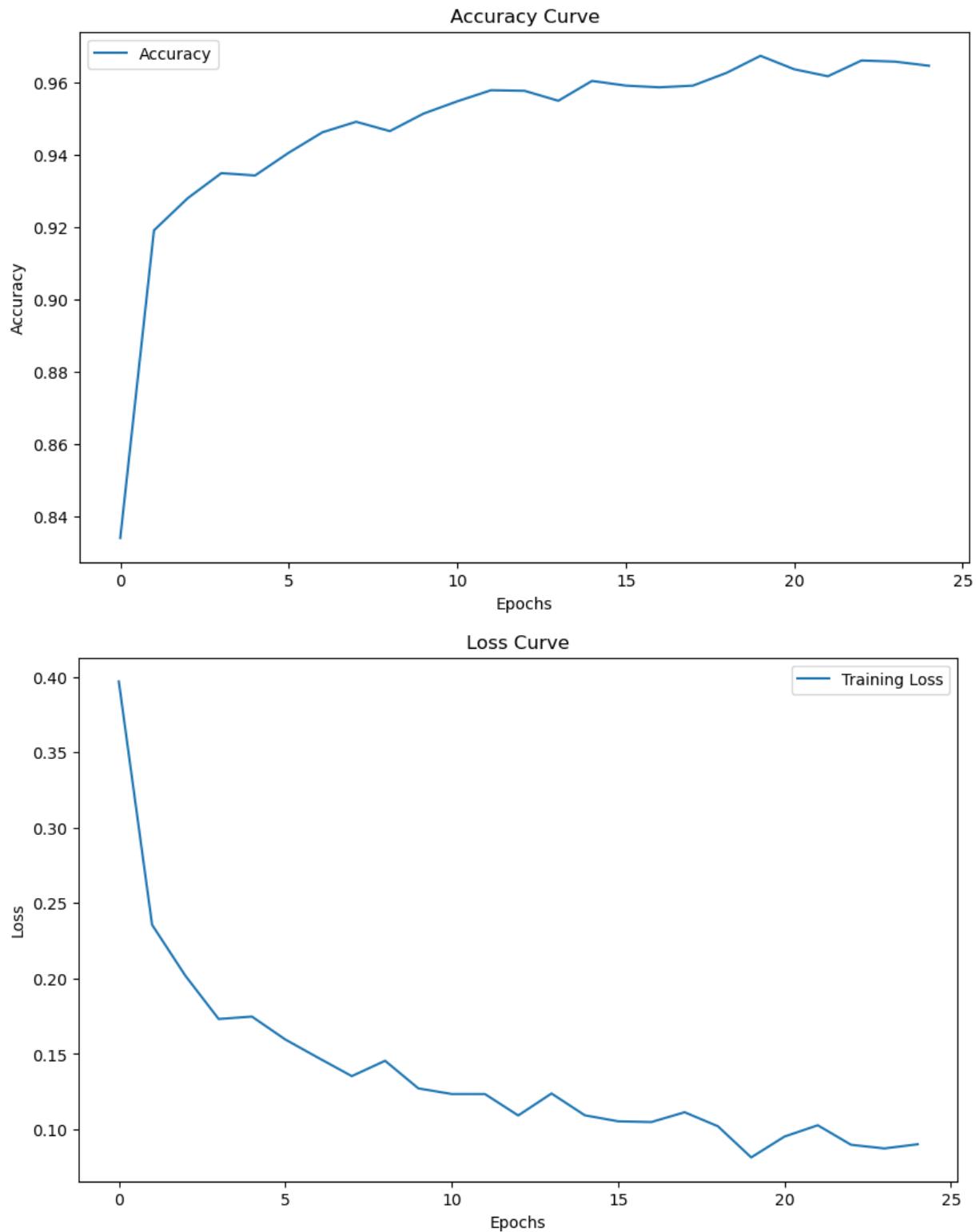
## Model Accuracy

Epoch 1/100  
194/194 210s 879ms/step - accuracy: 0.7462 - loss: 0.5533 - val\_accuracy: 0.9181 - val\_loss: 0.2309  
Epoch 2/100  
194/194 162s 837ms/step - accuracy: 0.9100 - loss: 0.2524 - val\_accuracy: 0.9277 - val\_loss: 0.1998  
Epoch 3/100  
194/194 160s 823ms/step - accuracy: 0.9271 - loss: 0.2052 - val\_accuracy: 0.9277 - val\_loss: 0.2036  
Epoch 4/100  
194/194 162s 837ms/step - accuracy: 0.9376 - loss: 0.1708 - val\_accuracy: 0.9374 - val\_loss: 0.1692  
Epoch 5/100  
194/194 162s 835ms/step - accuracy: 0.9332 - loss: 0.1778 - val\_accuracy: 0.9445 - val\_loss: 0.1629  
Epoch 6/100  
194/194 160s 827ms/step - accuracy: 0.9333 - loss: 0.1727 - val\_accuracy: 0.9413 - val\_loss: 0.1641  
Epoch 7/100  
194/194 161s 830ms/step - accuracy: 0.9493 - loss: 0.1541 - val\_accuracy: 0.9458 - val\_loss: 0.1600  
Epoch 8/100  
194/194 156s 807ms/step - accuracy: 0.9474 - loss: 0.1344 - val\_accuracy: 0.9484 - val\_loss: 0.1608  
Epoch 9/100  
194/194 159s 822ms/step - accuracy: 0.9504 - loss: 0.1406 - val\_accuracy: 0.9503 - val\_loss: 0.1437  
Epoch 10/100  
194/194 151s 777ms/step - accuracy: 0.9488 - loss: 0.1356 - val\_accuracy: 0.9548 - val\_loss: 0.1276  
Epoch 11/100  
194/194 161s 829ms/step - accuracy: 0.9579 - loss: 0.1148 - val\_accuracy: 0.9503 - val\_loss: 0.1414  
Epoch 12/100  
194/194 159s 819ms/step - accuracy: 0.9628 - loss: 0.1173 - val\_accuracy: 0.9490 - val\_loss: 0.1570  
Epoch 13/100  
194/194 158s 817ms/step - accuracy: 0.9579 - loss: 0.1099 - val\_accuracy: 0.9535 - val\_loss: 0.1447  
Epoch 14/100  
194/194 186s 731ms/step - accuracy: 0.9569 - loss: 0.1207 - val\_accuracy: 0.9523 - val\_loss: 0.1387  
Epoch 15/100  
194/194 147s 758ms/step - accuracy: 0.9630 - loss: 0.1024 - val\_accuracy: 0.9574 - val\_loss: 0.1248  
  
Epoch 16/100  
194/194 144s 744ms/step - accuracy: 0.9611 - loss: 0.1034 - val\_accuracy: 0.9600 - val\_loss: 0.1293  
Epoch 17/100  
194/194 152s 784ms/step - accuracy: 0.9582 - loss: 0.1040 - val\_accuracy: 0.9568 - val\_loss: 0.1375  
Epoch 18/100  
194/194 134s 688ms/step - accuracy: 0.9575 - loss: 0.1102 - val\_accuracy: 0.9606 - val\_loss: 0.1272  
Epoch 19/100  
194/194 131s 677ms/step - accuracy: 0.9647 - loss: 0.0982 - val\_accuracy: 0.9581 - val\_loss: 0.1321  
Epoch 20/100  
194/194 139s 720ms/step - accuracy: 0.9679 - loss: 0.0798 - val\_accuracy: 0.9587 - val\_loss: 0.1333  
Epoch 21/100  
194/194 141s 725ms/step - accuracy: 0.9624 - loss: 0.0991 - val\_accuracy: 0.9561 - val\_loss: 0.1577  
Epoch 22/100  
194/194 133s 686ms/step - accuracy: 0.9645 - loss: 0.0890 - val\_accuracy: 0.9600 - val\_loss: 0.1293  
Epoch 23/100  
194/194 132s 682ms/step - accuracy: 0.9665 - loss: 0.0914 - val\_accuracy: 0.9606 - val\_loss: 0.1386  
Epoch 24/100  
194/194 125s 644ms/step - accuracy: 0.9650 - loss: 0.0916 - val\_accuracy: 0.9568 - val\_loss: 0.1419  
Epoch 25/100  
194/194 155s 801ms/step - accuracy: 0.9643 - loss: 0.0915 - val\_accuracy: 0.9594 - val\_loss: 0.1388

Test Accuracy: 0.9628291130065918

61/61 37s 600ms/step - accuracy: 0.9620 - loss: 0.1222

## Accuracy and Loss Diagrams



## Classification Report

Classification Report:

	precision	recall	f1-score	support
Cancer	0.93	0.85	0.89	336
Non-Cancer	0.97	0.99	0.98	1601
accuracy			0.96	1937
macro avg	0.95	0.92	0.93	1937
weighted avg	0.96	0.96	0.96	1937

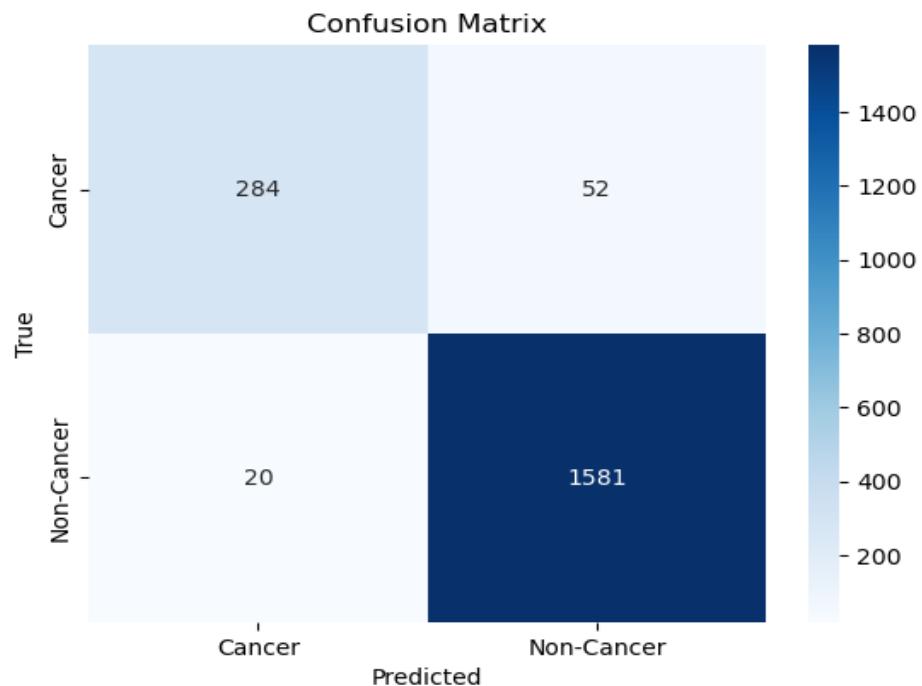
Accuracy: 0.96

Precision: 0.95

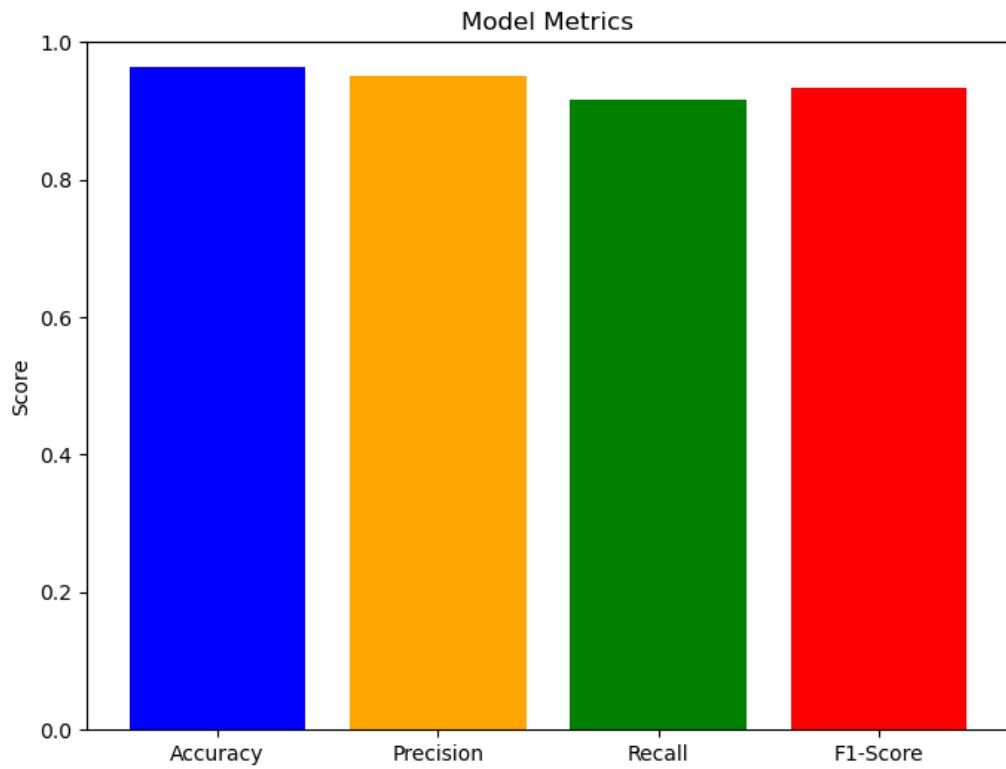
Recall: 0.92

F1-Score: 0.93

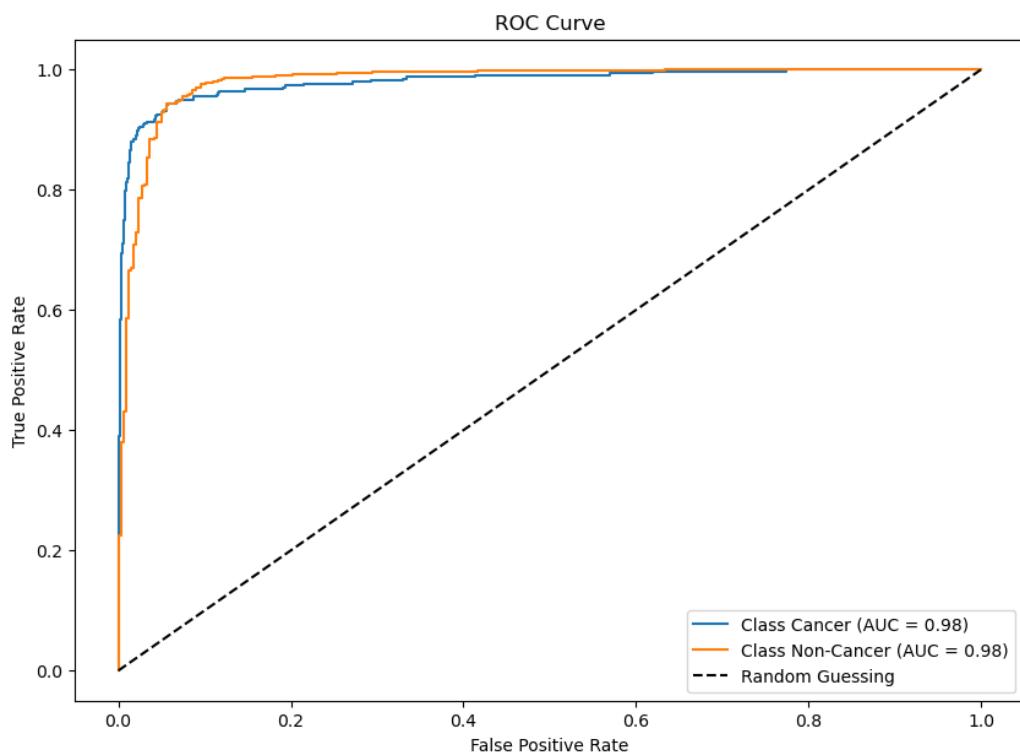
## Confusion Matrix



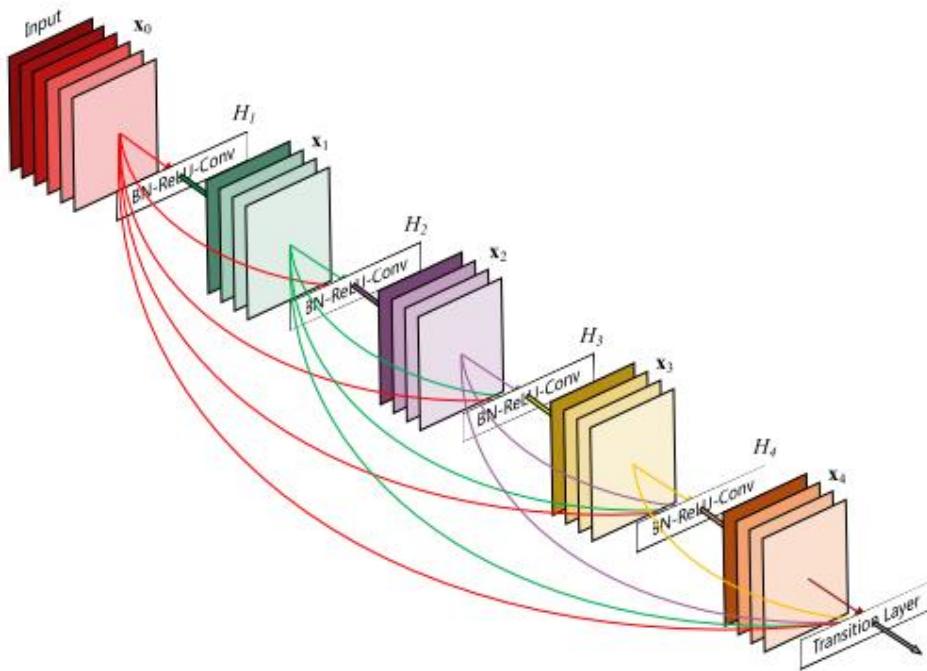
## Model Metrics



## ROC Curve



#### 4.2.6) Model-3: DenseNet121



DenseNet (Densely Connected Convolutional Networks) is a CNN architecture designed to improve feature reuse and gradient flow through dense connectivity between layers. Unlike traditional CNNs, where each layer is connected only to adjacent layers, DenseNet establishes direct connections between all layers within a dense block, enhancing training efficiency and mitigating the vanishing gradient problem [25].

For  $L$  layers, there are  $L(L+1)/2$  direct connections. For each layer, the feature maps of all the preceding layers are used as inputs, and its own feature maps are used as input for each subsequent layers.

## Model Architecture

Layer (type)	Output Shape	Param #
densenet121 (Functional)	(None, 3, 3, 1024)	7,037,504
global_average_pooling2d (GlobalAveragePooling2D)	(None, 1024)	0
dense (Dense)	(None, 256)	262,400
dropout (Dropout)	(None, 256)	0
batch_normalization (BatchNormalization)	(None, 256)	1,024
dense_1 (Dense)	(None, 128)	32,896
dropout_1 (Dropout)	(None, 128)	0
batch_normalization_1 (BatchNormalization)	(None, 128)	512
dense_2 (Dense)	(None, 2)	258

Total params: 7,334,594 (27.98 MB)

Trainable params: 296,322 (1.13 MB)

Non-trainable params: 7,038,272 (26.85 MB)

## Model Accuracy

Epoch 1/100  
194/194 131s 550ms/step - accuracy: 0.7759 - loss: 0.5246 - val\_accuracy: 0.9419 - val\_loss: 0.1693  
Epoch 2/100  
194/194 98s 505ms/step - accuracy: 0.8982 - loss: 0.2668 - val\_accuracy: 0.9497 - val\_loss: 0.1666  
Epoch 3/100  
194/194 95s 488ms/step - accuracy: 0.9155 - loss: 0.2395 - val\_accuracy: 0.9561 - val\_loss: 0.1501  
Epoch 4/100  
194/194 95s 491ms/step - accuracy: 0.9264 - loss: 0.2051 - val\_accuracy: 0.9439 - val\_loss: 0.1553  
Epoch 5/100  
194/194 89s 458ms/step - accuracy: 0.9209 - loss: 0.2072 - val\_accuracy: 0.9542 - val\_loss: 0.1357  
Epoch 6/100  
194/194 95s 490ms/step - accuracy: 0.9365 - loss: 0.1858 - val\_accuracy: 0.9548 - val\_loss: 0.1332  
Epoch 7/100  
194/194 90s 462ms/step - accuracy: 0.9311 - loss: 0.1919 - val\_accuracy: 0.9574 - val\_loss: 0.1289  
Epoch 8/100  
194/194 92s 472ms/step - accuracy: 0.9210 - loss: 0.2097 - val\_accuracy: 0.9568 - val\_loss: 0.1218  
Epoch 9/100  
194/194 91s 467ms/step - accuracy: 0.9287 - loss: 0.1926 - val\_accuracy: 0.9490 - val\_loss: 0.1383  
Epoch 10/100  
194/194 90s 462ms/step - accuracy: 0.9413 - loss: 0.1731 - val\_accuracy: 0.9555 - val\_loss: 0.1141  
Epoch 11/100  
194/194 90s 466ms/step - accuracy: 0.9326 - loss: 0.1815 - val\_accuracy: 0.9568 - val\_loss: 0.1378  
Epoch 12/100  
194/194 98s 506ms/step - accuracy: 0.9345 - loss: 0.1729 - val\_accuracy: 0.9361 - val\_loss: 0.1614  
Epoch 13/100  
194/194 95s 489ms/step - accuracy: 0.9313 - loss: 0.1804 - val\_accuracy: 0.9587 - val\_loss: 0.1126  
Epoch 14/100  
194/194 96s 493ms/step - accuracy: 0.9363 - loss: 0.1743 - val\_accuracy: 0.9626 - val\_loss: 0.1195

```

Epoch 15/100
194/194 102s 525ms/step - accuracy: 0.9381 - loss: 0.1577 - val_accuracy: 0.9516 - val_loss: 0.1245
Epoch 16/100
194/194 94s 486ms/step - accuracy: 0.9337 - loss: 0.1740 - val_accuracy: 0.9529 - val_loss: 0.1212
Epoch 17/100
194/194 88s 454ms/step - accuracy: 0.9438 - loss: 0.1608 - val_accuracy: 0.9632 - val_loss: 0.1118
Epoch 18/100
194/194 80s 414ms/step - accuracy: 0.9430 - loss: 0.1481 - val_accuracy: 0.9555 - val_loss: 0.1198
Epoch 19/100
194/194 86s 445ms/step - accuracy: 0.9397 - loss: 0.1575 - val_accuracy: 0.9335 - val_loss: 0.1757
Epoch 20/100
194/194 86s 446ms/step - accuracy: 0.9404 - loss: 0.1506 - val_accuracy: 0.9626 - val_loss: 0.1154
Epoch 21/100
194/194 102s 525ms/step - accuracy: 0.9438 - loss: 0.1472 - val_accuracy: 0.9645 - val_loss: 0.0968
Epoch 22/100
194/194 102s 527ms/step - accuracy: 0.9438 - loss: 0.1402 - val_accuracy: 0.9587 - val_loss: 0.1094
Epoch 23/100
194/194 99s 511ms/step - accuracy: 0.9510 - loss: 0.1282 - val_accuracy: 0.9671 - val_loss: 0.1158
Epoch 24/100
194/194 100s 517ms/step - accuracy: 0.9519 - loss: 0.1367 - val_accuracy: 0.9671 - val_loss: 0.0969
Epoch 25/100
194/194 100s 515ms/step - accuracy: 0.9532 - loss: 0.1217 - val_accuracy: 0.9632 - val_loss: 0.1007
Epoch 26/100
194/194 142s 515ms/step - accuracy: 0.9483 - loss: 0.1318 - val_accuracy: 0.9645 - val_loss: 0.1028
Epoch 27/100
194/194 167s 646ms/step - accuracy: 0.9519 - loss: 0.1270 - val_accuracy: 0.9613 - val_loss: 0.1164
Epoch 28/100
194/194 175s 900ms/step - accuracy: 0.9461 - loss: 0.1425 - val_accuracy: 0.9652 - val_loss: 0.0989
Epoch 29/100
194/194 182s 941ms/step - accuracy: 0.9475 - loss: 0.1373 - val_accuracy: 0.9729 - val_loss: 0.1031
Epoch 30/100
194/194 184s 947ms/step - accuracy: 0.9501 - loss: 0.1289 - val_accuracy: 0.9716 - val_loss: 0.0965

Epoch 31/100
194/194 189s 975ms/step - accuracy: 0.9507 - loss: 0.1215 - val_accuracy: 0.9652 - val_loss: 0.1067
Epoch 32/100
194/194 186s 959ms/step - accuracy: 0.9505 - loss: 0.1278 - val_accuracy: 0.9529 - val_loss: 0.1147
Epoch 33/100
194/194 187s 966ms/step - accuracy: 0.9494 - loss: 0.1386 - val_accuracy: 0.9671 - val_loss: 0.1048
Epoch 34/100
194/194 185s 952ms/step - accuracy: 0.9498 - loss: 0.1259 - val_accuracy: 0.9606 - val_loss: 0.1297
Epoch 35/100
194/194 185s 955ms/step - accuracy: 0.9582 - loss: 0.1121 - val_accuracy: 0.9671 - val_loss: 0.1068
Epoch 36/100
194/194 202s 953ms/step - accuracy: 0.9550 - loss: 0.1224 - val_accuracy: 0.9639 - val_loss: 0.1073
Epoch 37/100
194/194 183s 945ms/step - accuracy: 0.9614 - loss: 0.1131 - val_accuracy: 0.9690 - val_loss: 0.1248
Epoch 38/100
194/194 173s 893ms/step - accuracy: 0.9575 - loss: 0.1174 - val_accuracy: 0.9690 - val_loss: 0.0966
Epoch 39/100
194/194 146s 753ms/step - accuracy: 0.9553 - loss: 0.1221 - val_accuracy: 0.9555 - val_loss: 0.1379
Epoch 40/100
194/194 237s 934ms/step - accuracy: 0.9611 - loss: 0.1118 - val_accuracy: 0.9594 - val_loss: 0.1278

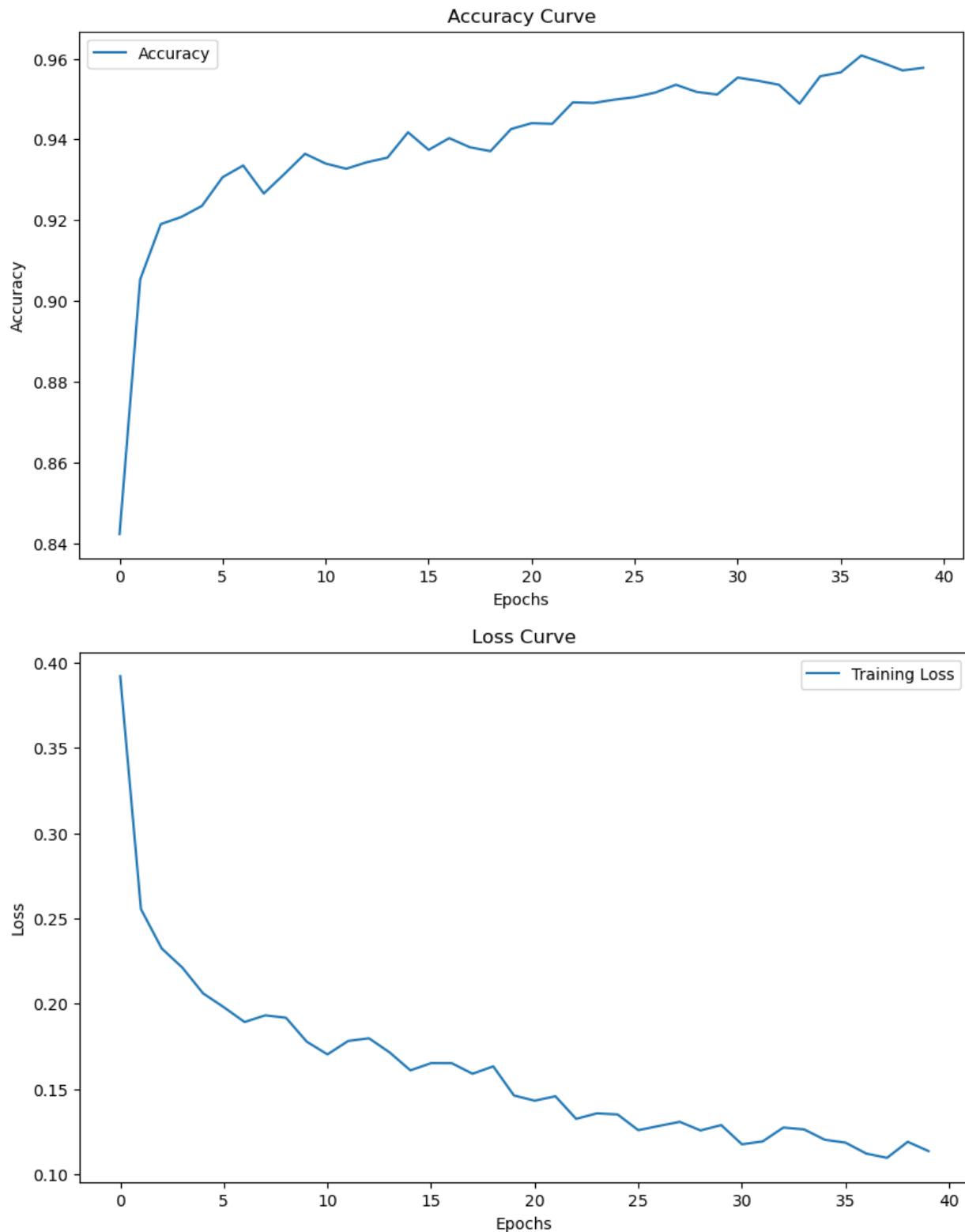
```

Test Accuracy: 0.9638616442680359

---

61/61 45s 741ms/step - accuracy: 0.9636 - loss: 0.1155

## Accuracy and Loss Diagrams

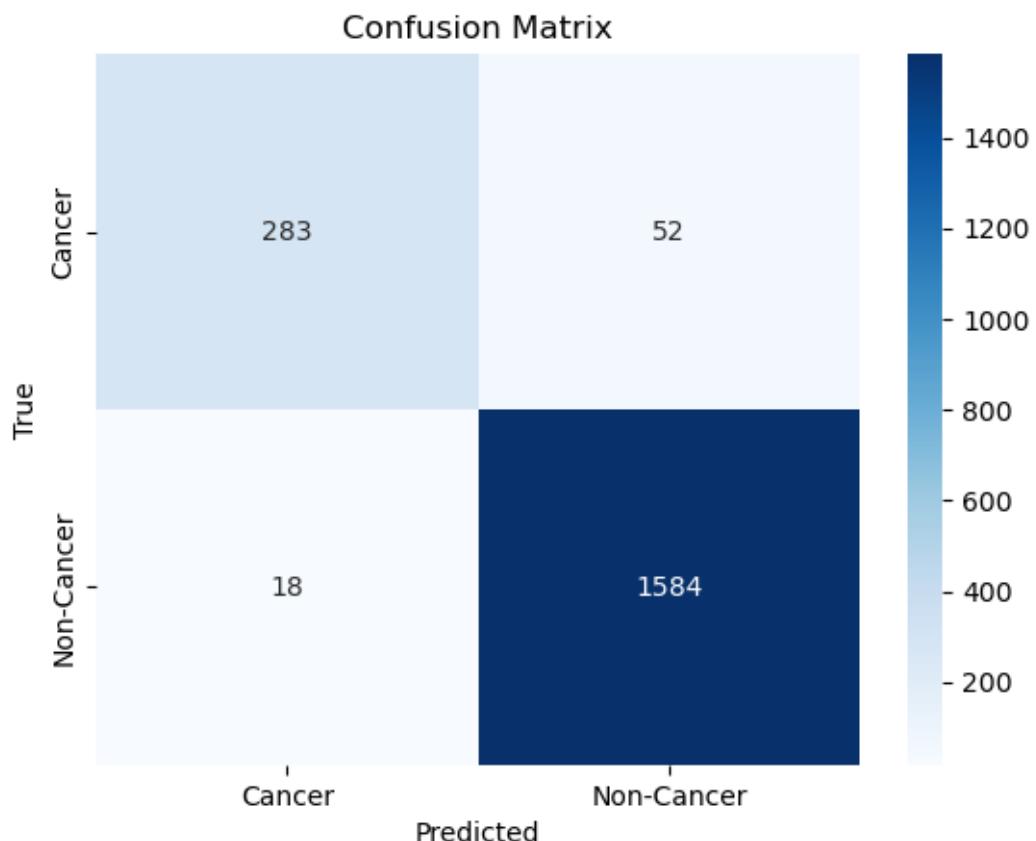


## Classification Report

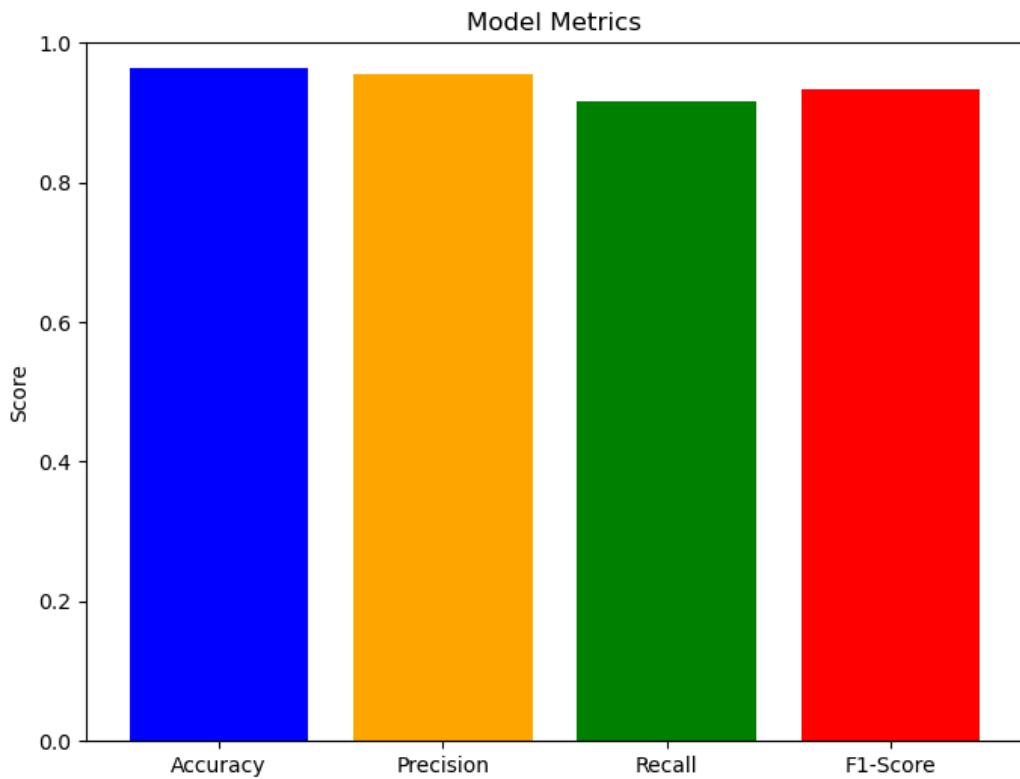
Classification Report:				
	precision	recall	f1-score	support
Cancer	0.94	0.84	0.89	335
Non-Cancer	0.97	0.99	0.98	1602
accuracy			0.96	1937
macro avg	0.95	0.92	0.93	1937
weighted avg	0.96	0.96	0.96	1937

Accuracy: 0.96  
Precision: 0.95  
Recall: 0.92  
F1-Score: 0.93

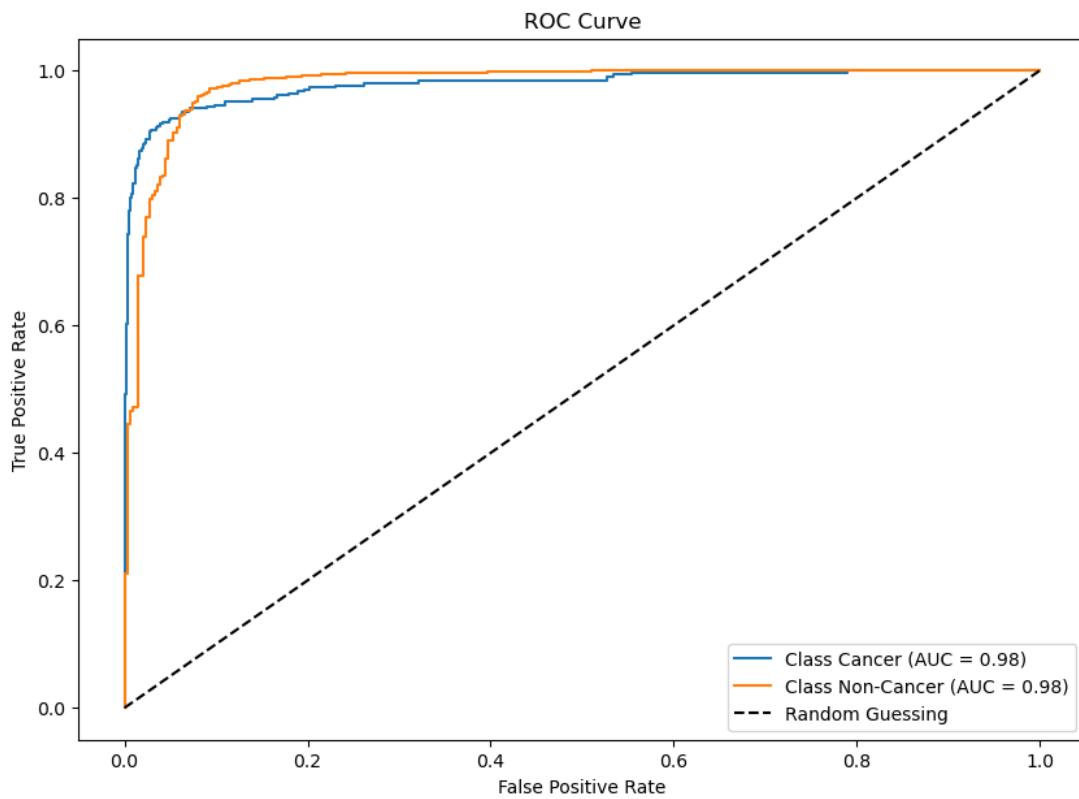
## Confusion Matrix



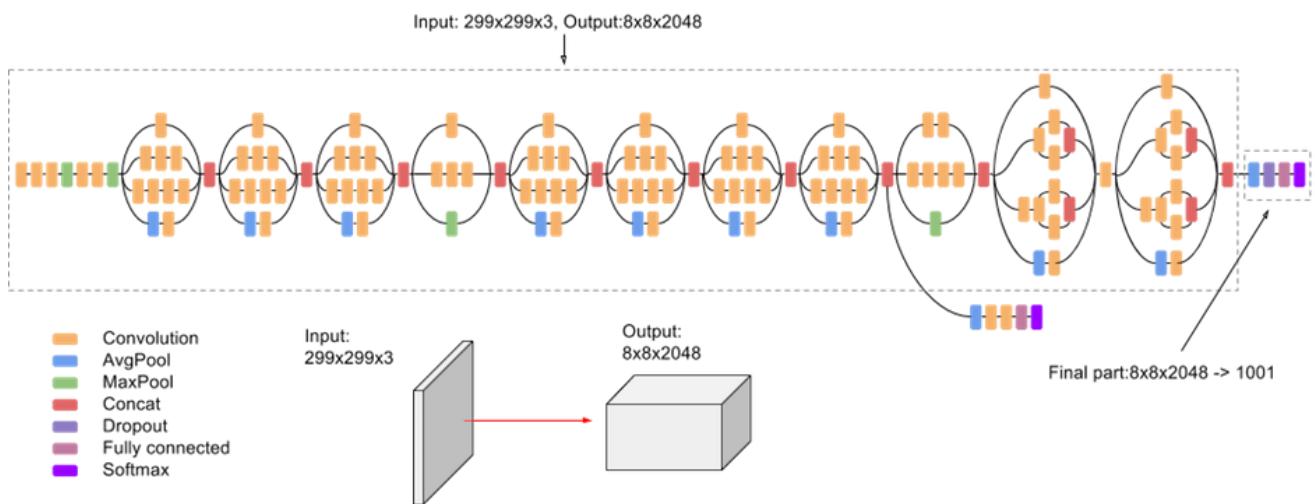
## Model Metrics



## ROC Curve



#### 4.2.7) Model-4: InceptionV3



InceptionV3 on the ImageNet dataset, is “a widely used image recognition model that has been found to achieve higher than 78.1 percent accuracy” (Alkronz et al., 2019). It has 42 layers and can categorize images to 1000 different object categories: Devices, laptops, pens, and a variety of animals are among the items. it has built a library of rich feature demonstrations for an extensive variety of images. The input image size is 299 by 299 pixels. Convolutions, average pooling, max pooling, concats, dropouts, and fully linked layers are among the symmetric and asymmetric building components in the model. Batch normalization is applied to activation inputs and is used extensively throughout the model. Loss is calculated using Softmax” (Muntas and Yusuf, 2019). [24]

## Model Architecture

Layer (type)	Output Shape	Param #
inception_v3 (Functional)	(None, 1, 1, 2048)	21,802,784
global_average_pooling2d (GlobalAveragePooling2D)	(None, 2048)	0
dense (Dense)	(None, 256)	524,544
dropout (Dropout)	(None, 256)	0
batch_normalization_94 (BatchNormalization)	(None, 256)	1,024
dense_1 (Dense)	(None, 128)	32,896
dropout_1 (Dropout)	(None, 128)	0
batch_normalization_95 (BatchNormalization)	(None, 128)	512
dense_2 (Dense)	(None, 2)	258

Total params: 22,362,018 (85.30 MB)

Trainable params: 558,466 (2.13 MB)

Non-trainable params: 21,803,552 (83.17 MB)

## Model Accuracy

```
Epoch 1/100
194/194 125s 344ms/step - accuracy: 0.7671 - loss: 0.5372 - val_accuracy: 0.9252 - val_loss: 0.2158
Epoch 2/100
194/194 54s 278ms/step - accuracy: 0.9152 - loss: 0.2463 - val_accuracy: 0.9258 - val_loss: 0.2017
Epoch 3/100
194/194 55s 285ms/step - accuracy: 0.9243 - loss: 0.2153 - val_accuracy: 0.9316 - val_loss: 0.2026
Epoch 4/100
194/194 64s 328ms/step - accuracy: 0.9351 - loss: 0.1928 - val_accuracy: 0.9387 - val_loss: 0.1713
Epoch 5/100
194/194 79s 403ms/step - accuracy: 0.9345 - loss: 0.1723 - val_accuracy: 0.9368 - val_loss: 0.1834
Epoch 6/100
194/194 52s 267ms/step - accuracy: 0.9391 - loss: 0.1707 - val_accuracy: 0.9284 - val_loss: 0.1856
Epoch 7/100
194/194 59s 306ms/step - accuracy: 0.9400 - loss: 0.1673 - val_accuracy: 0.9413 - val_loss: 0.1707
Epoch 8/100
194/194 56s 290ms/step - accuracy: 0.9522 - loss: 0.1412 - val_accuracy: 0.9465 - val_loss: 0.1698
Epoch 9/100
194/194 57s 294ms/step - accuracy: 0.9547 - loss: 0.1310 - val_accuracy: 0.9413 - val_loss: 0.1658
Epoch 10/100
194/194 55s 281ms/step - accuracy: 0.9453 - loss: 0.1437 - val_accuracy: 0.9477 - val_loss: 0.1641
Epoch 11/100
194/194 52s 269ms/step - accuracy: 0.9503 - loss: 0.1402 - val_accuracy: 0.9381 - val_loss: 0.1818
Epoch 12/100
194/194 52s 267ms/step - accuracy: 0.9505 - loss: 0.1344 - val_accuracy: 0.9413 - val_loss: 0.1525
Epoch 13/100
194/194 52s 269ms/step - accuracy: 0.9474 - loss: 0.1377 - val_accuracy: 0.9490 - val_loss: 0.1673
Epoch 14/100
194/194 54s 276ms/step - accuracy: 0.9518 - loss: 0.1403 - val_accuracy: 0.9510 - val_loss: 0.1798
Epoch 15/100
194/194 54s 280ms/step - accuracy: 0.9548 - loss: 0.1137 - val_accuracy: 0.9477 - val_loss: 0.1809
Epoch 16/100
194/194 58s 297ms/step - accuracy: 0.9606 - loss: 0.1103 - val_accuracy: 0.9523 - val_loss: 0.1559
```

```
Epoch 17/100  
194/194 66s 342ms/step - accuracy: 0.9602 - loss: 0.1169 - val_accuracy: 0.9471 - val_loss: 0.1622  
Epoch 18/100  
194/194 59s 306ms/step - accuracy: 0.9607 - loss: 0.1067 - val_accuracy: 0.9439 - val_loss: 0.2005  
Epoch 19/100  
194/194 56s 291ms/step - accuracy: 0.9595 - loss: 0.1145 - val_accuracy: 0.9497 - val_loss: 0.1592  
Epoch 20/100  
194/194 65s 333ms/step - accuracy: 0.9594 - loss: 0.1053 - val_accuracy: 0.9432 - val_loss: 0.1711  
Epoch 21/100  
194/194 78s 400ms/step - accuracy: 0.9578 - loss: 0.1201 - val_accuracy: 0.9452 - val_loss: 0.1574  
Epoch 22/100  
194/194 58s 298ms/step - accuracy: 0.9643 - loss: 0.1027 - val_accuracy: 0.9535 - val_loss: 0.1521  
Epoch 23/100  
194/194 57s 295ms/step - accuracy: 0.9602 - loss: 0.1042 - val_accuracy: 0.9497 - val_loss: 0.1929  
Epoch 24/100  
194/194 59s 304ms/step - accuracy: 0.9617 - loss: 0.1037 - val_accuracy: 0.9497 - val_loss: 0.1728  
Epoch 25/100  
194/194 64s 329ms/step - accuracy: 0.9688 - loss: 0.0854 - val_accuracy: 0.9465 - val_loss: 0.1830  
Epoch 26/100  
194/194 63s 327ms/step - accuracy: 0.9544 - loss: 0.1224 - val_accuracy: 0.9490 - val_loss: 0.1691  
Epoch 27/100  
194/194 58s 301ms/step - accuracy: 0.9676 - loss: 0.0933 - val_accuracy: 0.9452 - val_loss: 0.1769  
Epoch 28/100  
194/194 58s 298ms/step - accuracy: 0.9661 - loss: 0.1013 - val_accuracy: 0.9548 - val_loss: 0.1720  
Epoch 29/100  
194/194 58s 300ms/step - accuracy: 0.9672 - loss: 0.0882 - val_accuracy: 0.9490 - val_loss: 0.1790  
Epoch 30/100  
194/194 61s 316ms/step - accuracy: 0.9725 - loss: 0.0822 - val_accuracy: 0.9484 - val_loss: 0.1807  
Epoch 31/100  
194/194 59s 304ms/step - accuracy: 0.9630 - loss: 0.1070 - val_accuracy: 0.9503 - val_loss: 0.1629  
Epoch 32/100  
194/194 58s 300ms/step - accuracy: 0.9596 - loss: 0.1034 - val_accuracy: 0.9523 - val_loss: 0.1558
```

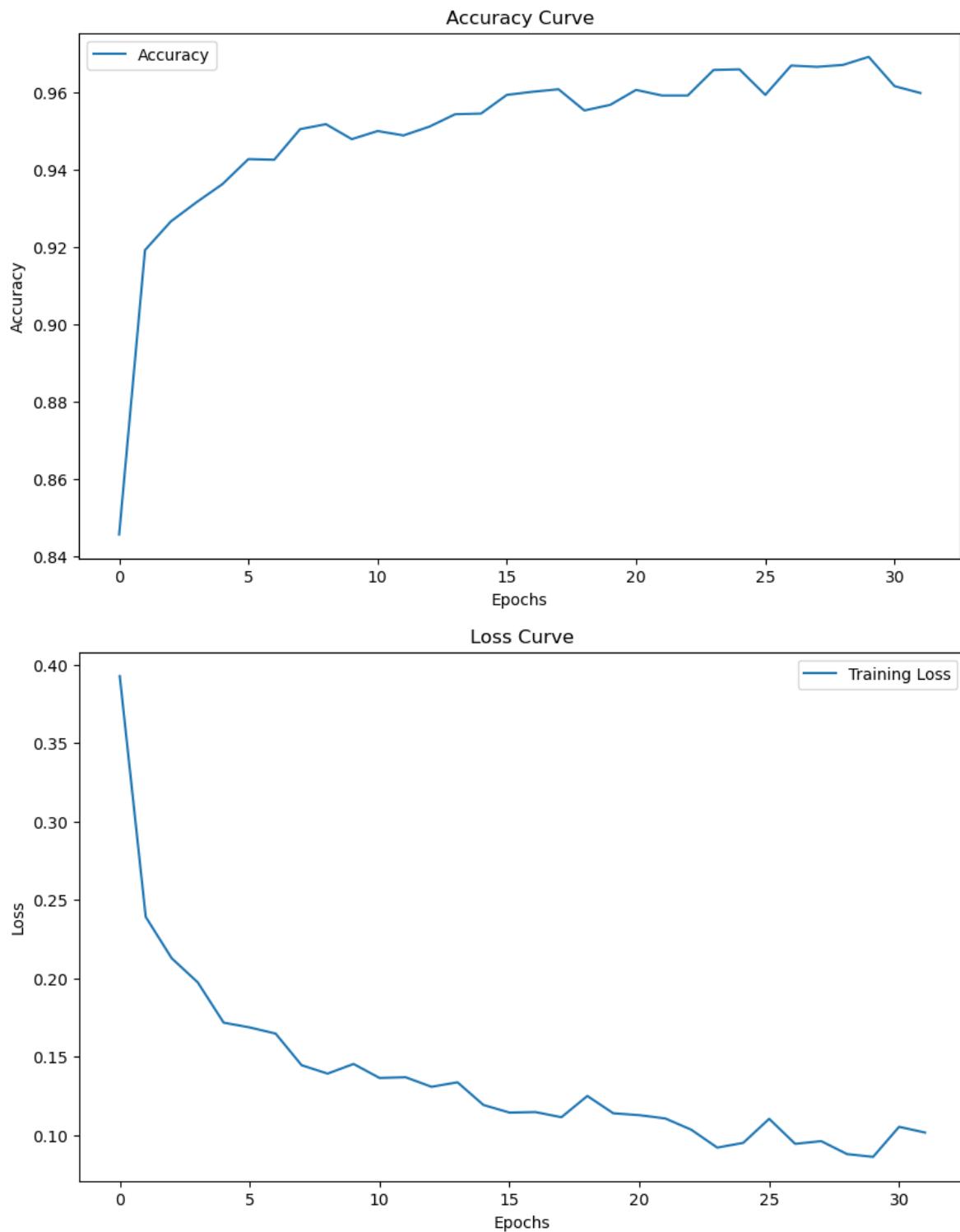
---

Test Accuracy: 0.9623128771781921

---

61/61 14s 237ms/step - accuracy: 0.9681 - loss: 0.1019

## Accuracy and Loss Diagrams

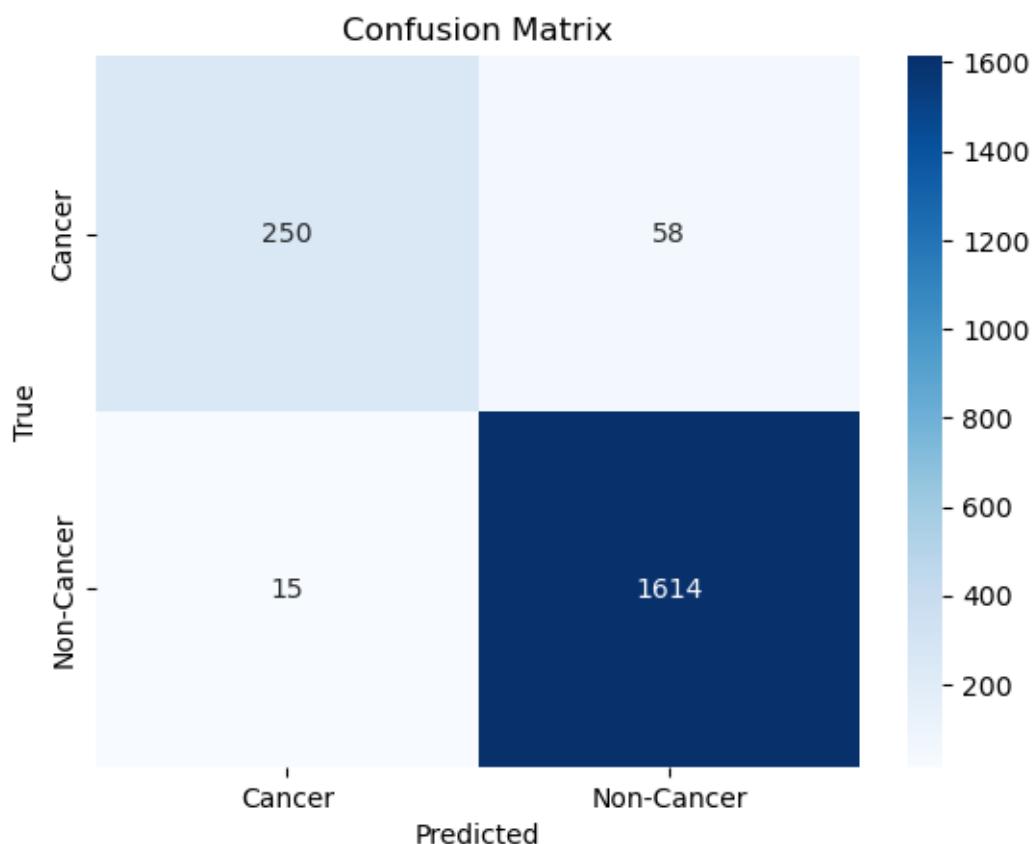


## Classification Report

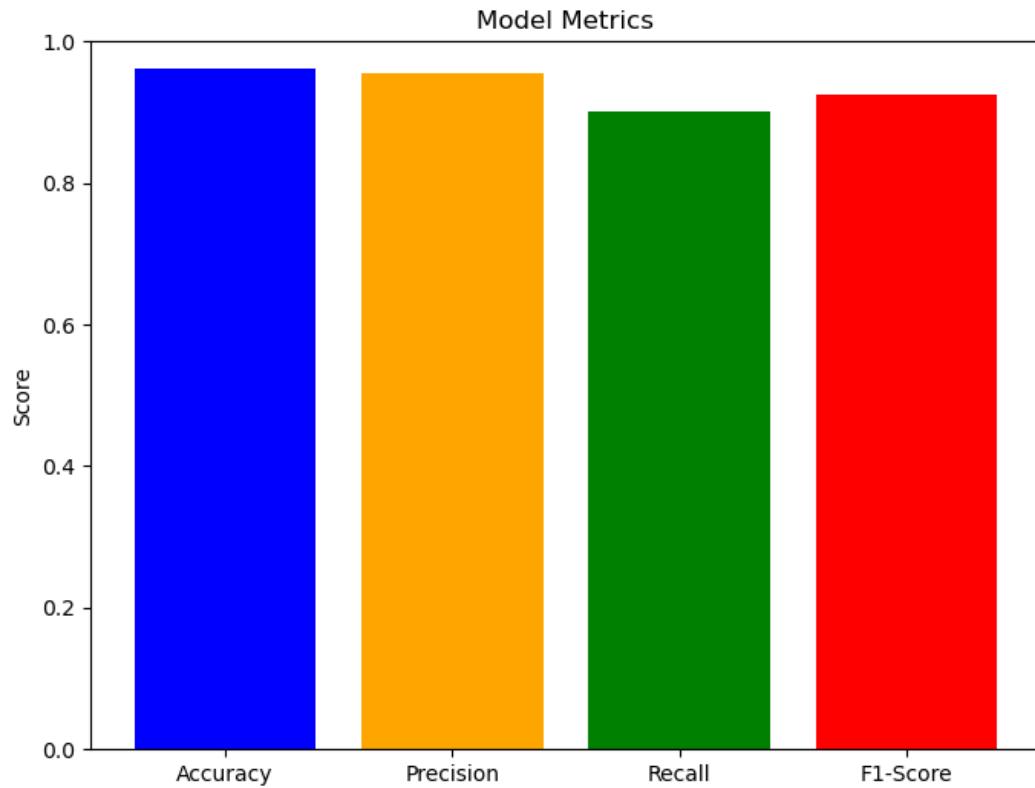
Classification Report:					
	precision	recall	f1-score	support	
Cancer	0.94	0.81	0.87	308	
Non-Cancer	0.97	0.99	0.98	1629	
accuracy			0.96	1937	
macro avg	0.95	0.90	0.93	1937	
weighted avg	0.96	0.96	0.96	1937	

Accuracy: 0.96  
Precision: 0.95  
Recall: 0.90  
F1-Score: 0.93

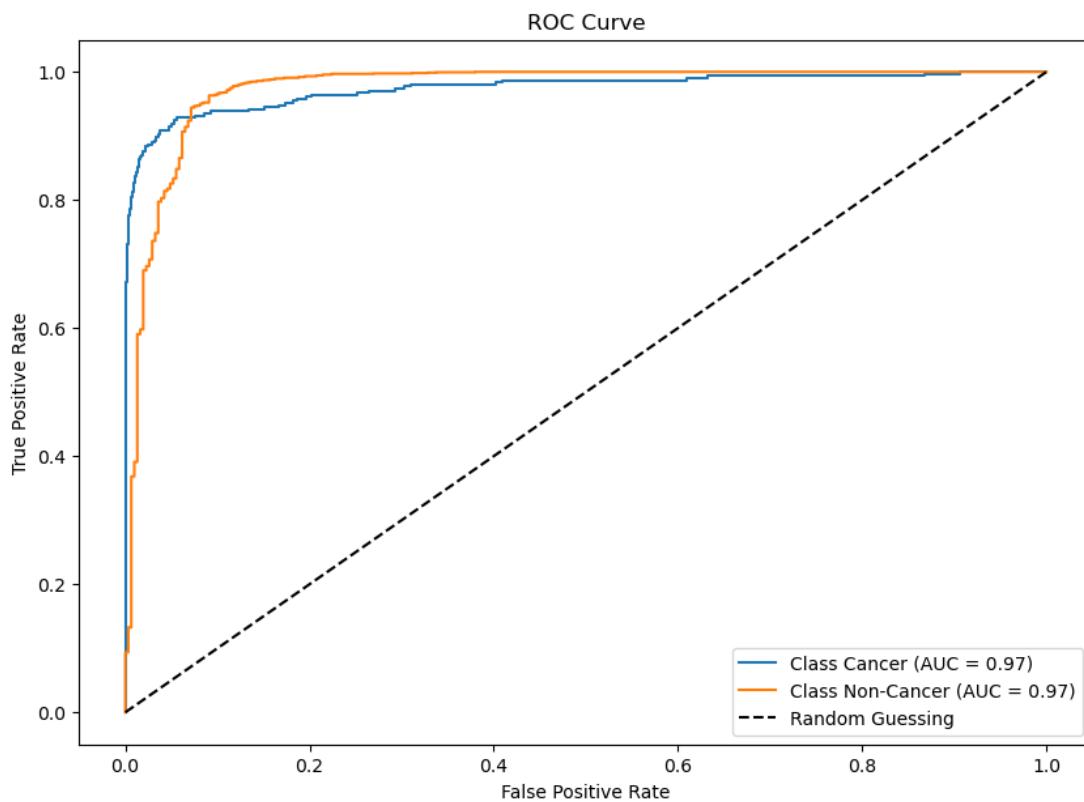
## Confusion Matrix



## Model Metrics



## ROC Curve



## 4.3) Comparison between Models

Model	Accuracy	Precision	Recall	F1-score	Training Speed
ResNet-50	0.84	0.42	0.50	0.46	Fast (11epoch)
Xception	0.96	0.95	0.92	0.93	Moderate (25epoch)
InceptionV3	0.96	0.95	0.90	0.93	Slow (32epoch)
Densenet121	0.96	0.95	0.92	0.93	Very slow (40epoch)

Following the comparison, we employed all models across various classification methods for breast cancer detection. Among these, the **Xception model** was selected due to its superior accuracy. Notably, our results demonstrated higher accuracy compared to those reported in a study that utilized the same dataset, as well as additional datasets such as MIAS and CBIS-DDSM [26].

The study demonstrated the effectiveness of a fused CNN model for breast cancer segmentation and classification tasks. The model, which combined the best attributes of EfficientNetB5 and Xception, achieved a classification accuracy of 96% [26].

Table 2: Performance evaluation various CNN models and the Fused model applied to the database

Model	Accuracy	Loss	Sensitivity	Specificity	Precision	Recall	F1-Score
Densenet201	93.75%	0.2080	89.96%	100.00%	94.64%	93.75%	94.19%
Resnet50V2	92.45%	0.2433	99.58%	80.69%	93.13%	92.45%	92.79%
Xception	96.88%	0.1061	99.16%	93.10%	96.93%	96.88%	96.90%
MobileNetV2	62.24%	0.6669	100.00%	0.00%	38.74%	62.24%	47.75%
EfficientNetB5	99.48%	0.0178	100.00%	98.62%	99.48%	99.48%	99.48%
Proposed Fused model	98.99%	0.0523	99.33%	97.24%	98.91%	97.88%	98.89%

## 4.4) Summary of the CBIS-DDSM Dataset

### Description:

Dataset link: <https://www.kaggle.com/datasets/awsaf49/cbis-ddsm-breast-cancer-image-dataset/data>

The CBIS-DDSM (Curated Breast Imaging Subset of DDSM) dataset is a collection of medical images in JPEG format, derived from the original dataset which was 163GB in size. The resolution of the images in the CBIS-DDSM dataset has been maintained to match that of the original dataset. This dataset is primarily focused on breast imaging for mammography [18].

#### 4.4.1) Key Dataset Statistics

Number of Studies	6,775
Number of Images	10,239
Modality	MG (Mammography)
Image Size	6 GB in JPEG format
Number of Participants	1,566 (Note: The dataset's structure results in multiple patient IDs per participant, making it appear as if there are 6,671 patients according to DICOM metadata, but there are actually 1,566 distinct participants.)
3 Types of Images	Cropped images --> 3859 ROI mask images --> 3340 Full mammogram images --> 3038

#### 4.4.2) Dataset Description:

The CBIS-DDSM dataset is an updated and standardized version of the Digital Database for Screening Mammography (DDSM). The DDSM originally consisted of 2,620 scanned film mammography studies, encompassing normal, benign, and malignant cases with verified

pathology information. The dataset's large scale and comprehensive ground truth data make it valuable for developing and testing decision support systems in mammography [18].

The CBIS-DDSM collection is a carefully selected subset of the DDSM data, curated by a trained mammographer. The images have been decompressed and converted to DICOM format, and the dataset includes updated ROI (Region of Interest) segmentation and bounding boxes, as well as pathologic diagnosis information for training data [18].

Researchers and practitioners in the field of mammography have faced challenges in replicating research results due to the lack of a standardized evaluation dataset. Most computer-aided diagnosis (CADx) and detection (CADe) algorithms for breast cancer in mammography rely on private datasets or unspecified subsets of public databases. The CBIS-DDSM dataset addresses this challenge by providing a well-curated, publicly accessible, and standardized version of the DDSM for future CAD research in mammography [18].

It is important to note that the dataset's structure assigns multiple patient IDs to each participant, which can be misleading. For instance, a participant may have 10 separate patient IDs, each containing information about different scans. Despite this, there are only 1,566 actual participants in the cohort [18].

It includes decompressed images, data selection and curation by trained mammographers, updated mass segmentation and bounding boxes, and pathologic diagnosis for training data, formatted similarly to modern computer vision data sets. The data set contains **753 calcification cases and 891 mass cases**, providing a data-set size capable of analyzing decision support systems in mammography [18].

Metadata for each abnormality is included as an associated CSV file containing the following: [18]

- Patient ID: the first 7 characters of images in the case file
- Density category
- Breast: Left or Right
- View: CC or MLO
- Number of abnormality for the image (This is necessary as there are some cases containing multiple abnormalities.
- Mass shape (when applicable)
- Mass margin (when applicable)
- Calcification type (when applicable)
- Calcification distribution (when applicable)
- BI-RADS assessment
- Pathology: Benign, Benign without call-back, or Malignant
- Subtlety rating: Radiologists' rating of difficulty in viewing the abnormality in the image
- Path to image files

There are individual files for mass and calcification training and test sets: [18]

- mass\_case\_description\_train\_set.csv
- mass\_case\_description\_test\_set.csv
- calc\_case\_description\_train\_set.csv
- calc\_case\_description\_test\_set.csv

	Benign Cases	Malignant Cases
Calcification Training Set	329 cases (552 abnormalities)	273 cases (304 abnormalities)
Calcification Test Set	85 cases (112 abnormalities)	66 cases (77 abnormalities)
Mass Training Set	355 cases (387 abnormalities)	336 cases (361 abnormalities)
Mass Test Set	117 cases (135 abnormalities)	83 cases (87 abnormalities)

## 4.4.3) Tables of dataset

### 4.4.3.1) First [calc\_case\_description\_train\_set.csv]:

Col-1: paitent\_id

Col-2: breast density { from 1 to 4 }

Col-3: left or right breast { LEFT--> 53% , RIGHT -->47% }

Col-4: image view { MLO --> 52% “medio-lateral-oblique” , CC -->48% “cranio-cauda ”}

Col-5: abnormality id { from 1 to 7 }

Col-6: abnormality type { calcification }

Col-7: calc type

0	PLEOMORPHIC	664
1	AMORPHOUS	139
2	PUNCTATE	106
3	LUCENT_CENTER	93
4	VASCULAR	82
5	FINE_LINEAR_BRANCHING	77
6	COARSE	35
7	ROUND_AND_REGULAR-LUCENT_CENTER	33
8	PLEOMORPHIC-FINE_LINEAR_BRANCHING	28
9	ROUND_AND_REGULAR-LUCENT_CENTER-PUNCTATE	24
10	ROUND_AND_REGULAR-EGGSHELL	23
11	PUNCTATE-PLEOMORPHIC	21
12	DYSTROPHIC	20
13	LUCENT_CENTERED	19
14	ROUND_AND_REGULAR-LUCENT_CENTER-DYSTROPHIC	18
15	ROUND_AND_REGULAR	17
16	ROUND_AND_REGULAR-LUCENT_CENTERED	14
17	AMORPHOUS-PLEOMORPHIC	12

18	LARGE_RODLIKE-ROUND_AND_REGULAR	11
19	PUNCTATE-AMORPHOUS	10
20	COARSE-ROUND_AND_REGULAR-LUCENT_CENTER	10
21	VASCULAR-COARSE-LUENT_CENTERED	8
22	LUENT_CENTER-PUNCTATE	8
23	ROUND_AND_REGULAR-PLEOMORPHIC	7
24	EGGSHELL	7
25	PUNCTATE-FINE_LINEAR_BRANCHING	6
26	VASCULAR-COARSE	6
27	ROUND_AND_REGULAR-PUNCTATE	5
28	SKIN-PUNCTATE-ROUND_AND_REGULAR	4
29	SKIN-PUNCTATE	4
30	COARSE-ROUND_AND_REGULAR-LUENT_CENTERED	4
31	PUNCTATE-ROUND_AND_REGULAR	4
32	LARGE_RODLIKE	4
33	AMORPHOUS-ROUND_AND_REGULAR	3
34	PUNCTATE-LUENT_CENTER	3
35	SKIN	2
36	VASCULAR-COARSE-LUENT_CENTER-ROUND_AND_REGULA...	2
37	COARSE-PLEOMORPHIC	2
38	ROUND_AND_REGULAR-PUNCTATE-AMORPHOUS	2
39	COARSE-LUENT_CENTER	2
40	MILK_OF_CALCIUM	2
41	COARSE-ROUND_AND_REGULAR	2
42	SKIN-COARSE-ROUND_AND_REGULAR	1
43	ROUND_AND_REGULAR-AMORPHOUS	1
44	PLEOMORPHIC-PLEOMORPHIC	1

Calcification cancer has 45 types, the majority of which are PLEOMORPHIC.

Col-8 : calc distribution

0	CLUSTERED	740
1	SEGMENTAL	168
2	REGIONAL	99
3	LINEAR	90
4	DIFFUSELY_SCATTERED	37
5	CLUSTERED-LINEAR	25
6	CLUSTERED-SEGMENTAL	5
7	LINEAR-SEGMENTAL	5
8	REGIONAL-REGIONAL	1

Col-9 : assessment { from 0 to 5 “BI-RADS-SCORE” }

Col-10 : pathology

0	MALIGNANT	544
1	BENIGN	528
2	BENIGN_WITHOUT_CALLBACK	474

#### **4.4.3.2) Second [calc\_case\_description\_test\_set.csv]:**

Col-1 : patient\_id

Col-2 : breast density { from 0 to 4 }

Col-3 : left or right breast { LEFT--> 56% , RIGHT -->44% }

Col-4 : image view { MLO --> 54% “medio-lateral-oblique” , CC -->46% “cranio-cauda ”}

Col-5 : abnormality id { from 1 to 5 }

Col-6 : abnormality type { calcification }

Col-7 : calc type

0	PLEOMORPHIC	149
1	AMORPHOUS	43
2	PUNCTATE	26

3	FINE_LINEAR_BRANCHING	25
4	LUCENT_CENTER	17
5	ROUND_AND_REGULAR	10
6	PUNCTATE-PLEOMORPHIC	9
7	VASCULAR	8
8	EGGSHELL	6
9	AMORPHOUS-PLEOMORPHIC	4
10	PUNCTATE-AMORPHOUS-PLEOMORPHIC	4
11	COARSE	4
12	COARSE-LUCENT_CENTER	4
13	PLEOMORPHIC-FINE_LINEAR_BRANCHING	3
14	PUNCTATE-AMORPHOUS	2
15	COARSE-ROUND_AND_REGULAR	2
16	COARSE-PLEOMORPHIC	2
17	SKIN	2
18	ROUND_AND_REGULAR-PLEOMORPHIC	1
19	PLEOMORPHIC-AMORPHOUS	1

Col-8 : calc distribution

0	CLUSTERED	195
1	SEGMENTAL	34
2	LINEAR	22
3	DIFFUSELY_SCATTERED	3
4	CLUSTERED-LINEAR	4
5	REGIONAL	3
6	LINEAR-SEGMENTAL	2

Col-9 : assessment { from 0 to 5 “BI-RADS-SCORE” }

Col-10 : pathology

0	MALIGNANT	130
1	BENIGN	129
2	BENIGN_WITHOUT_CALLBACK	67

#### **4.4.3.3) Third [mass\_case\_description\_train\_set.csv]:**

Col-1 : patient\_id

Col-2 : breast density { from 1 to 4 }

Col-3 : left or right breast { LEFT--> 52% , RIGHT -->48% }

Col-4 : image view { MLO --> 54% “medio-lateral-oblique” , CC -->46% “cranio-cauda ”}

Col-5 : abnormality id { from 1 to 6 }

Col-6 : abnormality type { mass }

Col-7 : mass shape

0	IRREGULAR	351
1	OVAL	321
2	LOBULATED	305
3	ROUND	123
4	ARCHITECTURAL_DISTORTION	80
5	LYMPH_NODE	26
6	IRREGULAR-ARCHITECTURAL_DISTORTION	45
7	FOCAL_ASYMMETRIC_DENSITY	19
8	ASYMMETRIC_BREAST_TISSUE	20
9	OVAL-LOBULATED	1
10	IRREGULAR-FOCAL_ASYMMETRIC_DENSITY	2
11	LOBULATED-LYMPH_NODE	3
12	LOBULATED-ARCHITECTURAL_DISTORTION	2
13	OVAL-LYMPH_NODE	6
14	LOBULATED-IRREGULAR	5
15	ROUND-OVAL	3
16	ROUND-IRREGULAR- ARCHITECTURAL_DISTORTION	1
17	ROUND-LOBULATED	1

Col-8 : mass margin

0	CIRCUMSCRIBED	305
1	SPICULATED	281
2	ILL_DEFINED	278
3	OBSCURED	197
4	CIRCUMSCRIBED-ILL_DEFINED	27
5	MICROLOBULATED	108
6	ILL_DEFINED-SPICULATED	25
7	OBSCURED-ILL_DEFINED	19
8	CIRCUMSCRIBED-OBSCURED	19
9	OBSCURED-SPICULATED	4
10	OBSCURED-ILL_DEFINED-SPICULATED	4
11	MICROLOBULATED-ILL_DEFINED	3
12	MICROLOBULATED-ILL_DEFINED-SPICULATED	2
13	MICROLOBULATED-SPICULATED	2
14	CIRCUMSCRIBED-MICROLOBULATED	1

Col-9 : assessment { from 0 to 5 “BI-RADS-SCORE” }

Col-10 : pathology

0	MALIGNANT	637
1	BENIGN	577
2	BENIGN_WITHOUT_CALLBACK	104

#### 4.4.3.4) Fourth [mass\_case\_description\_test\_set.csv]:

Col-1 : patient\_id

Col-2 : breast density { from 1 to 4 }

Col-3 : left or right breast { LEFT--> 51% , RIGHT -->49% }

Col-4 : image view { MLO --> 53% “medio-lateral-oblique” , CC -->47% “cranio-cauda ”}

Col-5 : abnormality id { from 1 to 4 }

Col-6 : abnormality type { mass }

Col-7 : mass shape { IRREGULAR-->30%,OVAL-->24%,Other (174)-->46% }

0	IRREGULAR	113
1	OVAL	91
2	LOBULATED	79
3	ROUND	41
4	ARCHITECTURAL_DISTORTION	23
5	LYMPH_NODE	9
6	IRREGULAR-ARCHITECTURAL_DISTORTION	7
7	FOCAL_ASYMMETRIC_DENSITY	6
8	ASYMMETRIC_BREAST_TISSUE	5
9	OVAL-LOBULATED	1
10	IRREGULAR-ASYMMETRIC_BREAST_TISSUE	1
11	LOBULATED-LYMPH_NODE	1
12	LOBULATED-IRREGULAR	1

Col-8 : mass margin { ILL\_DEFINED-->24%,CIRCUMSCRIBED-->23%,Other (199)-->53% }

0	CIRCUMSCRIBED	87
1	SPICULATED	82
2	ILL_DEFINED	92
3	OBSCURED	50
4	MICROLOBULATED	21
5	ILL_DEFINED-SPICULATED	5
6	OBSCURED-ILL_DEFINED	5
7	CIRCUMSCRIBED-OBSCURED-ILL_DEFINED	4
8	CIRCUMSCRIBED-OBSCURED	3
9	CIRCUMSCRIBED-MICROLOBULATED-ILL_DEFINED	3
10	OBSCURED-CIRCUMSCRIBED	2
11	CIRCUMSCRIBED-ILL_DEFINED	2
12	MICROLOBULATED-ILL_DEFINED	2
13	CIRCUMSCRIBED-SPICULATED	1
14	OBSCURED-ILL_DEFINED-SPICULATED	1
15	CIRCUMSCRIBED-MICROLOBULATED	1

Col-9 : assessment { from 0 to 5 “BI-RADS-SCORE” }

## Col-10 : pathology

0	MALIGNANT	194
1	BENIGN	147
2	BENIGN_WITHOUT_CALLBACK	37

### 4.4.3.5) Fifth [dicom\_info.csv ]:

This table have 38 columns

```
Data columns (total 38 columns):
 #   Column           Non-Null Count Dtype  
 ---  -- 
 0   file_path        10237 non-null  object  
 1   image_path       10237 non-null  object  
 2   AccessionNumber 0 non-null      float64 
 3   BitsAllocated   10237 non-null  int64  
 4   BitsStored      10237 non-null  int64  
 5   BodyPartExamined 10237 non-null  object  
 6   Columns          10237 non-null  int64  
 7   ContentDate     10237 non-null  int64  
 8   ContentTime      10237 non-null  float64 
 9   ConversionType   10237 non-null  object  
 10  HighBit         10237 non-null  int64  
 11  InstanceNumber  10237 non-null  int64  
 12  LargestImagePixelValue 10237 non-null  int64  
 13  Laterality       9671 non-null  object  
 14  Modality         10237 non-null  object  
 15  PatientBirthDate 0 non-null      float64 
 16  PatientID        10237 non-null  object  
 17  PatientName      10237 non-null  object  
 18  PatientOrientation 10237 non-null  object  
 19  PatientSex        0 non-null      float64 
 20  PhotometricInterpretation 10237 non-null  object  
 21  PixelRepresentation 10237 non-null  int64  
 22  ReferringPhysicianName 0 non-null      float64 
 23  Rows              10237 non-null  int64  
 24  SOPClassUID       10237 non-null  object  
 25  SOPInstanceUID    10237 non-null  object  
 26  SamplesPerPixel   10237 non-null  int64  
 27  SecondaryCaptureDeviceManufacturer 10237 non-null  object  
 28  SecondaryCaptureDeviceManufacturerModelName 10237 non-null  object  
 29  SeriesDescription  9671 non-null  object  
 30  SeriesInstanceUID  10237 non-null  object  
 31  SeriesNumber       10237 non-null  int64  
 32  SmallestImagePixelValue 10237 non-null  int64  
 33  SpecificCharacterSet 10237 non-null  object  
 34  StudyDate         9671 non-null  float64 
 35  StudyID           10237 non-null  object  
 36  StudyInstanceUID  10237 non-null  object  
 37  StudyTime         9671 non-null  float64 

dtypes: float64(7), int64(12), object(19)
```

## 4.4.4) Detailed Model Report

### 4.4.4.1) Dataset Preprocessing Phase I: dicom\_info.csv Table

#### 1) Column Removal:

The following columns were dropped from the dataset due to irrelevance to the diagnostic task or lack of informative value:

- PatientBirthDate
- AccessionNumber
- PatientSex
- ReferringPhysicianName

#### 2) Handling Missing Values:

Columns with null values were identified and processed using backward fill (bfill) to maintain data integrity. The imputation was applied along the row axis (axis=0) for the following columns:

- SeriesDescription
- Laterality
- StudyDate
- StudyTime

```
dicom_data.drop(['PatientBirthDate','AccessionNumber','PatientSex','ReferringPhysicianName'],axis =1, inplace=True)

dicom_data['SeriesDescription'].fillna(method = 'bfill', axis = 0, inplace=True)
dicom_data['Laterality'].fillna(method = 'bfill', axis = 0, inplace=True)
dicom_data['StudyDate'].fillna(method = 'bfill', axis = 0, inplace=True)
dicom_data['StudyTime'].fillna(method = 'bfill', axis = 0, inplace=True)
```

#### 3) Image Path Adjustment:

Image paths in the dataset were updated to reflect new directory structures, ensuring compatibility with the training process.

Adjustments were made for the following image types:

- Mammogram images

- Region of Interest (ROI) images
- Cropped images

#### **4.4.4.2) Dataset Preprocessing Phase II:**

***calc\_case\_description\_train.csv & calc\_case\_description\_test.csv Table***

##### **1) Categorical Data Conversion:**

Several columns containing categorical data were explicitly converted to the category data type to optimize memory usage and facilitate subsequent analysis. This conversion was applied to the following columns in both training and testing datasets:

- pathology
- calc type
- calc distribution
- abnormality type
- image view
- left or right breast

```
calc_case_train['pathology'] = calc_case_train['pathology'].astype('category')
calc_case_train['calc type'] = calc_case_train['calc type'].astype('category')
calc_case_train['calc distribution'] = calc_case_train['calc distribution'].astype('category')
calc_case_train['abnormality type'] = calc_case_train['abnormality type'].astype('category')
calc_case_train['image view'] = calc_case_train['image view'].astype('category')
calc_case_train['left or right breast'] = calc_case_train['left or right breast'].astype('category')

calc_case_test['pathology'] = calc_case_test['pathology'].astype('category')
calc_case_test['calc type'] = calc_case_test['calc type'].astype('category')
calc_case_test['calc distribution'] = calc_case_test['calc distribution'].astype('category')
calc_case_test['abnormality type'] = calc_case_test['abnormality type'].astype('category')
calc_case_test['image view'] = calc_case_test['image view'].astype('category')
calc_case_test['left or right breast'] = calc_case_test['left or right breast'].astype('category')
```

##### **2) Handling Missing Values:**

Among the columns with missing data, the backward fill (bfill) method was applied specifically to the **calc type** and **calc distribution** columns along the row axis to impute null values. This

targeted imputation helps maintain data continuity while preserving the integrity of the other features.

```
calc_case_train['calc type'].fillna(method = 'bfill', axis = 0, inplace=True)
calc_case_train['calc distribution'].fillna(method = 'bfill', axis = 0, inplace=True)

calc_case_test['calc type'].fillna(method = 'bfill', axis = 0, inplace=True)
calc_case_test['calc distribution'].fillna(method = 'bfill', axis = 0, inplace=True)
```

#### 4.4.4.3) Dataset Preprocessing – Phase III: *mass\_case\_description\_train.csv & mass\_case\_description\_test.csv* Tables

##### 1) Categorical Data Conversion:

we preprocess the mass\_case\_train and mass\_case\_test datasets by converting selected columns to categorical data types.

The columns converted to the category type in both datasets include:

- left or right breast
- image view
- mass margins
- mass shape
- abnormality type

```
mass_case_train['left or right breast'] = mass_case_train['left or right breast'].astype('category')
mass_case_train['image view'] = mass_case_train['image view'].astype('category')
mass_case_train['mass margins'] = mass_case_train['mass margins'].astype('category')
mass_case_train['mass shape'] = mass_case_train['mass shape'].astype('category')
mass_case_train['abnormality type'] = mass_case_train['abnormality type'].astype('category')

mass_case_test['left or right breast'] = mass_case_test['left or right breast'].astype('category')
mass_case_test['image view'] = mass_case_test['image view'].astype('category')
mass_case_test['mass margins'] = mass_case_test['mass margins'].astype('category')
mass_case_test['mass shape'] = mass_case_test['mass shape'].astype('category')
mass_case_test['abnormality type'] = mass_case_test['abnormality type'].astype('category')
```

##### 2) Handling Missing Values:

Among the columns with missing data, the backward fill (bfill) method was applied specifically to the **mass type** and **mass distribution** columns along the row axis to impute null values.

```
mass_case_train['mass shape'].fillna(method = 'bfill', axis = 0, inplace=True)
mass_case_train['mass margins'].fillna(method = 'bfill', axis = 0, inplace=True)
```

```
mass_case_test['mass margins'].fillna(method = 'bfill', axis = 0, inplace=True)
```

#### 4.4.4.4) Final Phase of Dataset Preprocessing: Image Conversion and Multi-Label Encoding

After completing the preprocessing of individual tables, the following steps were undertaken to finalize the dataset for model training:

##### 1) Dataset Consolidation:

All four preprocessed tables were concatenated into a single unified dataset. This consolidation was performed column-wise to ensure a consistent schema across all image records.

```
full_dataset = pd.concat([calc_case_train, calc_case_test,mass_case_train,mass_case_test], axis=0)
```

##### 2) Image Path Mapping:

For each image entry, the corresponding file path was updated to reflect its new location within the project directory structure. This step was crucial to enable seamless data access during model training.

```
def fix_image_path(data):
    for indx, image in enumerate(data.values):
        img_name = image[11].split('/')[2]
        if img_name in full_mammo_dict:
            data.iloc[indx, 11] = full_mammo_dict[img_name]
        else:
            data.iloc[indx, 11] = None
        img_name = image[12].split('/')[2]
        if img_name in cropped_images_dict:
            data.iloc[indx, 12] = cropped_images_dict[img_name]
        else:
            data.iloc[indx, 11] = None
        img_name = image[13].split('/')[2]
        if img_name in roi_img_dict:
            data.iloc[indx, 13] = roi_img_dict[img_name]
        else:
            data.iloc[indx, 13] = None
```

```
fix_image_path(full_dataset)
```

### 3) Missing Value Imputation:

Any remaining missing values in the combined dataset were addressed using a combination of **backward fill (bfill)** and **forward fill (ffill)** methods:

- **Backward Fill (bfill)** replaces missing values using the next valid observation in the same column.
- **Forward Fill (ffill)** replaces missing values using the previous valid observation in the same column.

```
full_dataset['image file path'].fillna(method = 'bfill', axis = 0, inplace=True)
full_dataset['breast density'].fillna(method = 'ffill', axis = 0, inplace=True)
full_dataset['calc type'].fillna(method = 'ffill', axis = 0, inplace=True)
full_dataset['calc distribution'].fillna(method = 'ffill', axis = 0, inplace=True)
full_dataset['ROI mask file path'].fillna(method = 'ffill', axis = 0, inplace=True)
full_dataset['breast_density'].fillna(method = 'bfill', axis = 0, inplace=True)
full_dataset['mass shape'].fillna(method = 'bfill', axis = 0, inplace=True)
full_dataset['mass margins'].fillna(method = 'bfill', axis = 0, inplace=True)
```

### 4) Label Harmonization:

To standardize the pathology column, the label **BENIGN WITHOUT CALLBACK** was replaced with **BENIGN**

```
full_dataset['pathology']=full_dataset['pathology'].replace('BENIGN WITHOUT CALLBACK', 'BENIGN')
```

### 5) Image Preprocessing

Each image in the dataset was processed using a custom function to prepare it for model training. The key operations included:

- Absolute Path Resolution: Ensured correct image file access.
- Image Loading and RGB Conversion: Loaded the image and converted it to RGB format.
- Resizing and Normalization: Resized all images to a fixed size of **224×224×3** and normalized pixel values to the [0, 1] range.
- Invalid Image Removal: Entries with missing or unreadable images were removed from the dataset.

## 6) Feature and Label Encoding

the processed image data and associated labels were prepared for model training:

- **Feature Matrix Creation:**

The full\_image column, containing the processed image arrays, was converted into a NumPy array X\_full, serving as the input feature matrix.

- **Label Encoding:**

Categorical target variables were one-hot encoded using pandas.get\_dummies() to convert them into binary format suitable for multi-class classification. The encoded label arrays include:

- y\_mass\_shape
- y\_mass\_margins
- y\_calc\_type
- y\_calc\_distribution
- y\_pathology
- y\_breast\_density
- y\_left\_or\_right\_breast
- y\_image\_view
- y\_abnormality\_id
- y\_abnormality\_type

This transformation ensures that all target variables are in a machine-readable format for model training and evaluation.

#### **4.4.5) Model Evaluation Strategy**

Three deep learning models—**InceptionV3**, **Xception**, and **DenseNet** were employed to support the detailed diagnostic reporting of mammographic images for breast cancer analysis. Each model was trained and evaluated using key performance metrics, including accuracy, precision, recall, and F1-score. A comprehensive comparative analysis was carried out to assess the effectiveness of each model in classifying abnormalities and aiding in diagnosis. This evaluation facilitated the identification of the most suitable model for enhancing diagnostic accuracy and reliability in the context of mammogram-based breast cancer detection.

The input images were resized to **224 × 224 pixels with three RGB channels** to ensure compatibility with all three selected models: **DenseNet201**, **InceptionV3**, and **Xception**. Each model was initialized with **ImageNet pre-trained weights** and used as a **frozen base** for feature extraction, preserving their learned representations.

A consistent **custom classification head** was appended to each base model, comprising:

- **Global Average Pooling** to reduce spatial dimensions,
- Fully connected **Dense layers** with **ReLU activations**,
- **Dropout layers** (with rates of 0.5 and 0.3) for regularization,
- And **Batch Normalization** layers to enhance training stability.

Each model was designed to perform **multi-task classification**, predicting multiple diagnostic attributes simultaneously. To achieve this, the shared feature representation from the classification head was passed to **ten distinct output layers**, each corresponding to a specific diagnostic label. These outputs included:

- **Mass Shape**
- **Mass Margins**
- **Calcification Type**
- **Calcification Distribution**
- **Pathology**
- **Breast Density**
- **Left or Right Breast**
- **Image View**
- **Abnormality ID**
- **Abnormality Type**

Each output layer used a **Dense layer** with a **softmax activation function**, allowing for multi-class classification across the respective label categories. This architecture enabled the models to jointly learn from shared features and provide comprehensive diagnostic predictions, enhancing the interpretability and clinical relevance of the model outputs.

## 4.4.6) Model-1: DenseNet201

### Model Architecture

Layer (type)	Output Shape	Param #	Connected to
input_layer (InputLayer)	(None, 128, 128, 3)	0	-
densenet201_full (Functional)	(None, 4, 4, 1920)	18,321,984	input_layer[0][0]
global_average_poo... (GlobalAveragePool...)	(None, 1920)	0	densenet201_full...
dense (Dense)	(None, 256)	491,776	global_average_p...
dropout (Dropout)	(None, 256)	0	dense[0][0]
batch_normalization (BatchNormalizatio...)	(None, 256)	1,024	dropout[0][0]
dense_1 (Dense)	(None, 128)	32,896	batch_normalizat...
dropout_1 (Dropout)	(None, 128)	0	dense_1[0][0]
batch_normalizatio... (BatchNormalizatio...)	(None, 128)	512	dropout_1[0][0]
mass_shape (Dense)	(None, 20)	2,580	batch_normalizat...
mass_margins (Dense)	(None, 19)	2,451	batch_normalizat...
calc_type (Dense)	(None, 47)	6,063	batch_normalizat...
calc_distribution (Dense)	(None, 9)	1,161	batch_normalizat...
pathology (Dense)	(None, 2)	258	batch_normalizat...
breast_density (Dense)	(None, 5)	645	batch_normalizat...
left_or_right_brea... (Dense)	(None, 2)	258	batch_normalizat...
image_view (Dense)	(None, 2)	258	batch_normalizat...
abnormality_id (Dense)	(None, 7)	903	batch_normalizat...
abnormality_type (Dense)	(None, 2)	258	batch_normalizat...

Total params: 18,863,027 (71.96 MB)

Trainable params: 540,275 (2.06 MB)

Non-trainable params: 18,322,752 (69.90 MB)

## Model Accuracy

abnormality\_id\_accuracy: 0.8499 - abnormality\_id\_loss: 0.4913 -  
abnormality\_type\_accuracy: 0.5659 - abnormality\_type\_loss: 0.6983 -  
breast\_density\_accuracy: 0.6610 - breast\_density\_loss: 0.8867 -  
calc\_distribution\_accuracy: 0.8046 - calc\_distribution\_loss: 0.7651 -  
calc\_type\_accuracy: 0.6724 - calc\_type\_loss: 1.5468 -  
image\_view\_accuracy: 0.9444 - image\_view\_loss: 0.1916 -  
left\_or\_right\_breast\_accuracy: 0.6560 - left\_or\_right\_breast\_loss:  
0.6504 - loss: 8.4984 - mass\_margins\_accuracy: 0.6605 -  
mass\_margins\_loss: 1.2134 - mass\_shape\_accuracy: 0.5373 -  
mass\_shape\_loss: 1.4442 - pathology\_accuracy: 0.6814 -  
pathology\_loss: 0.6108

```
23/23 ━━━━━━━━ 26s 1s/step - abnormality_id_accuracy: 0.8499 - abnormality_id_loss: 0.4913 - abnormality_type_accuracy: 0.5659 - abnormality_type_loss: 0.6983 - breast_density_accuracy: 0.6610 - breast_density_loss: 0.8867 - calc_distribution_accuracy: 0.8046 - calc_distribution_loss: 0.7651 - calc_type_accuracy: 0.6724 - calc_type_loss: 1.5468 - image_view_accuracy: 0.9444 - image_view_loss: 0.1916 - left_or_right_breast_accuracy: 0.6560 - left_or_right_breast_loss: 0.6504 - loss: 8.4984 - mass_margins_accuracy: 0.6605 - mass_margins_loss: 1.2134 - mass_shape_accuracy: 0.5373 - mass_shape_loss: 1.4442 - pathology_accuracy: 0.6814 - pathology_loss: 0.6108
```

## Testing & Evaluation

We give model image for testing and this is output

```
Output mass_shape: Predicted 'IRREGULAR-ARCHITECTURAL_DISTORTION' with probability 0.42
Output mass_margins: Predicted 'SPICULATED' with probability 0.55
Output calc_type: Predicted 'PLEOMORPHIC' with probability 0.88
Output calc_distribution: Predicted 'CLUSTERED' with probability 0.85
Output pathology: Predicted 'BENIGN' with probability 0.54
Output breast_density: Predicted '3.0' with probability 0.70
Output left_or_right_breast: Predicted 'LEFT' with probability 0.68
Output image_view: Predicted 'CC' with probability 0.99
Output abnormality_id: Predicted '1' with probability 0.97
Output abnormality_type: Predicted 'mass' with probability 0.56
```

## 4.4.7) Model-2: InceptionV3

### Model Architecture

Layer (type)	Output Shape	Param #	Connected to
input_layer_2 (InputLayer)	(None, 224, 224, 3)	0	-
InceptionV3_full (Functional)	(None, 5, 5, 2048)	21,802,784	input_layer_2[0]...
global_average_poo... (GlobalAveragePool...)	(None, 2048)	0	InceptionV3_full...
dense_2 (Dense)	(None, 256)	524,544	global_average_p...
dropout_2 (Dropout)	(None, 256)	0	dense_2[0][0]
batch_normalizatio... (BatchNormalizatio...)	(None, 256)	1,024	dropout_2[0][0]
dense_3 (Dense)	(None, 128)	32,896	batch_normalizat...
dropout_3 (Dropout)	(None, 128)	0	dense_3[0][0]
batch_normalizatio... (BatchNormalizatio...)	(None, 128)	512	dropout_3[0][0]
mass_shape (Dense)	(None, 20)	2,580	batch_normalizat...
mass_margins (Dense)	(None, 19)	2,451	batch_normalizat...
calc_type (Dense)	(None, 47)	6,063	batch_normalizat...
calc_distribution (Dense)	(None, 9)	1,161	batch_normalizat...
pathology (Dense)	(None, 2)	258	batch_normalizat...
breast_density (Dense)	(None, 5)	645	batch_normalizat...
left_or_right_brea... (Dense)	(None, 2)	258	batch_normalizat...
image_view (Dense)	(None, 2)	258	batch_normalizat...
abnormality_id (Dense)	(None, 7)	903	batch_normalizat...
abnormality_type (Dense)	(None, 2)	258	batch_normalizat...

Total params: 22,376,595 (85.36 MB)

Trainable params: 573,043 (2.19 MB)

Non-trainable params: 21,803,552 (83.17 MB)

## Model Accuracy

abnormality\_id\_accuracy: 0.8490 - abnormality\_id\_loss: 0.5352 -  
abnormality\_type\_accuracy: 0.5255 - abnormality\_type\_loss: 0.6955 -  
breast\_density\_accuracy: 0.6488 - breast\_density\_loss: 0.9867 -  
calc\_distribution\_accuracy: 0.8024 - calc\_distribution\_loss: 0.8074 -  
calc\_type\_accuracy: 0.6720 - calc\_type\_loss: 1.6361 -  
image\_view\_accuracy: 0.8923 - image\_view\_loss: 0.3212 -  
left\_or\_right\_breast\_accuracy: 0.7310 - left\_or\_right\_breast\_loss:  
0.5894 - loss: 8.8704 - mass\_margins\_accuracy: 0.6935 -  
mass\_margins\_loss: 1.1880 - mass\_shape\_accuracy: 0.5678 -  
mass\_shape\_loss: 1.4446 - pathology\_accuracy: 0.6203 -  
pathology\_loss: 0.6645

```
23/23 21s 910ms/step - abnormality_id_accuracy: 0.8490 - abnormality_id_loss: 0.5352 - abnormality_type_accuracy: 0.5255 - abnormality_type_loss: 0.6955 - breast_density_accuracy: 0.6488 - breast_density_loss: 0.9867 - calc_distribution_accuracy: 0.8024 - calc_distribution_loss: 0.8074 - calc_type_accuracy: 0.6720 - calc_type_loss: 1.6361 - image_view_accuracy: 0.8923 - image_view_loss: 0.3212 - left_or_right_breast_accuracy: 0.7310 - left_or_right_breast_loss: 0.5894 - loss: 8.8704 - mass_margins_accuracy: 0.6935 - mass_margins_loss: 1.1880 - mass_shape_accuracy: 0.5678 - mass_shape_loss: 1.4446 - pathology_accuracy: 0.6203 - pathology_loss: 0.6645
```

## Testing & Evaluation

We give model image for testing and this is output

```
Output mass_shape: Predicted 'IRREGULAR-ARCHITECTURAL_DISTORTION' with probability 0.40
Output mass_margins: Predicted 'SPICULATED' with probability 0.55
Output calc_type: Predicted 'PLEOMORPHIC' with probability 0.86
Output calc_distribution: Predicted 'CLUSTERED' with probability 0.88
Output pathology: Predicted 'MALIGNANT' with probability 0.52
Output breast_density: Predicted '3.0' with probability 0.79
Output left_or_right_breast: Predicted 'LEFT' with probability 0.61
Output image_view: Predicted 'CC' with probability 0.96
Output abnormality_id: Predicted '1' with probability 0.92
Output abnormality_type: Predicted 'mass' with probability 0.65
```

## 4.4.8) Model-3: Xception

### Model Architecture

Layer (type)	Output Shape	Param #	Connected to
input_layer_4 (InputLayer)	(None, 224, 224, 3)	0	-
Xception_full (Functional)	(None, 7, 7, 2048)	20,861,480	input_layer_4[0]...
global_average_poo... (GlobalAveragePool...)	(None, 2048)	0	Xception_full[0]...
dense_4 (Dense)	(None, 256)	524,544	global_average_p...
dropout_4 (Dropout)	(None, 256)	0	dense_4[0][0]
batch_normalizatio... (BatchNormalizatio...)	(None, 256)	1,024	dropout_4[0][0]
dense_5 (Dense)	(None, 128)	32,896	batch_normalizat...
dropout_5 (Dropout)	(None, 128)	0	dense_5[0][0]
batch_normalizatio... (BatchNormalizatio...)	(None, 128)	512	dropout_5[0][0]
mass_shape (Dense)	(None, 20)	2,580	batch_normalizat...
mass_margins (Dense)	(None, 19)	2,451	batch_normalizat...
calc_type (Dense)	(None, 47)	6,063	batch_normalizat...
calc_distribution (Dense)	(None, 9)	1,161	batch_normalizat...
pathology (Dense)	(None, 2)	258	batch_normalizat...
breast_density (Dense)	(None, 5)	645	batch_normalizat...
left_or_right_brea... (Dense)	(None, 2)	258	batch_normalizat...
image_view (Dense)	(None, 2)	258	batch_normalizat...
abnormality_id (Dense)	(None, 7)	903	batch_normalizat...
abnormality_type (Dense)	(None, 2)	258	batch_normalizat...

Total params: 21,435,291 (81.77 MB)

Trainable params: 573,043 (2.19 MB)

Non-trainable params: 20,862,248 (79.58 MB)

## Model Accuracy

abnormality\_id\_accuracy: 0.8512 - abnormality\_id\_loss: 0.5305 -  
abnormality\_type\_accuracy: 0.5984 - abnormality\_type\_loss: 0.6589 -  
breast\_density\_accuracy: 0.6397 - breast\_density\_loss: 0.9328 -  
calc\_distribution\_accuracy: 0.7998 - calc\_distribution\_loss: 0.7852 -  
calc\_type\_accuracy: 0.6701 - calc\_type\_loss: 1.5558 -  
image\_view\_accuracy: 0.9105 - image\_view\_loss: 0.2898 -  
left\_or\_right\_breast\_accuracy: 0.7974 - left\_or\_right\_breast\_loss:  
0.5062 - loss: 8.5311 - mass\_margins\_accuracy: 0.6935 -  
mass\_margins\_loss: 1.1775 - mass\_shape\_accuracy: 0.5724 -  
mass\_shape\_loss: 1.4419 - pathology\_accuracy: 0.6217 -  
pathology\_loss: 0.6494

23/23 ━━━━━━━━ 53s 2s/step - abnormality\_id\_accuracy: 0.8512 - abnormality\_id\_loss: 0.5305 - abnormality\_type\_accuracy: 0.5984 - abnormality\_type\_loss: 0.6589 - breast\_density\_accuracy: 0.6397 - breast\_density\_loss: 0.9328 - calc\_distribution\_accuracy: 0.7998 - calc\_distribution\_loss: 0.7852 - calc\_type\_accuracy: 0.6701 - calc\_type\_loss: 1.5558 - image\_view\_accuracy: 0.9105 - image\_view\_loss: 0.2898 - left\_or\_right\_breast\_accuracy: 0.7974 - left\_or\_right\_breast\_loss: 0.5062 - loss: 8.5311 - mass\_margins\_accuracy: 0.6935 - mass\_margins\_loss: 1.1775 - mass\_shape\_accuracy: 0.5724 - mass\_shape\_loss: 1.4419 - pathology\_accuracy: 0.6217 - pathology\_loss: 0.6494

## Classification Report

Classification Report for mass\_shape:

	precision	recall	f1-score	support
0	0.00	0.00	0.00	21
1	0.00	0.00	0.00	7
2	0.00	0.00	0.00	8
3	1.00	0.01	0.02	112
4	0.56	0.99	0.72	396
5	0.00	0.00	0.00	1
7	0.00	0.00	0.00	61
9	0.00	0.00	0.00	1
12	0.33	0.25	0.29	4
13	0.50	0.03	0.06	68
14	0.00	0.00	0.00	1
15	0.00	0.00	0.00	1
16	0.00	0.00	0.00	33
accuracy			0.56	714
macro avg	0.18	0.10	0.08	714
weighted avg	0.52	0.56	0.41	714

Classification Report for mass\_margins:

	precision	recall	f1-score	support
0	0.00	0.00	0.00	72
1	0.00	0.00	0.00	4
2	0.00	0.00	0.00	1
4	0.00	0.00	0.00	2
5	0.00	0.00	0.00	1
6	0.00	0.00	0.00	1
7	0.00	0.00	0.00	72
8	0.00	0.00	0.00	7
9	0.00	0.00	0.00	31
10	0.00	0.00	0.00	1
12	0.00	0.00	0.00	1
13	0.00	0.00	0.00	36
14	0.00	0.00	0.00	1
15	0.00	0.00	0.00	7
17	0.00	0.00	0.00	1
18	0.67	1.00	0.80	476
accuracy			0.67	714
macro avg	0.04	0.06	0.05	714
weighted avg	0.44	0.67	0.53	714

Classification Report for calc\_type:

	precision	recall	f1-score	support
0	0.00	0.00	0.00	40
1	0.00	0.00	0.00	4
3	0.00	0.00	0.00	7
4	0.00	0.00	0.00	1
5	0.00	0.00	0.00	1
7	0.00	0.00	0.00	1
8	0.00	0.00	0.00	1
9	0.00	0.00	0.00	5
10	0.00	0.00	0.00	2
11	0.00	0.00	0.00	23
12	0.00	0.00	0.00	2
13	0.00	0.00	0.00	3
14	0.00	0.00	0.00	21
15	0.00	0.00	0.00	4
16	0.00	0.00	0.00	9
18	0.69	0.99	0.82	494
19	0.00	0.00	0.00	1
20	0.00	0.00	0.00	7
22	0.00	0.00	0.00	33
23	0.00	0.00	0.00	2
25	0.00	0.00	0.00	1
27	0.00	0.00	0.00	5
29	0.00	0.00	0.00	6
30	0.00	0.00	0.00	1
31	0.00	0.00	0.00	3
32	0.00	0.00	0.00	7
accuracy			0.69	714
macro avg	0.05	0.06	0.05	714
weighted avg	0.48	0.69	0.57	714

Classification Report for calc\_distribution:

	precision	recall	f1-score	support
0	0.81	0.99	0.89	575
1	0.00	0.00	0.00	11
2	0.00	0.00	0.00	1
3	1.00	0.17	0.29	6
4	0.00	0.00	0.00	32
5	0.00	0.00	0.00	3
6	0.00	0.00	0.00	29
8	0.00	0.00	0.00	57
accuracy			0.80	714
macro avg	0.23	0.15	0.15	714
weighted avg	0.66	0.80	0.72	714

	precision	recall	f1-score	support
0	0.85	1.00	0.92	604
1	0.33	0.01	0.03	74
2	0.00	0.00	0.00	19
3	0.00	0.00	0.00	9
4	0.00	0.00	0.00	7
5	0.00	0.00	0.00	1
accuracy			0.85	714
macro avg	0.20	0.17	0.16	714
weighted avg	0.75	0.85	0.78	714

Classification Report for pathology:

	precision	recall	f1-score	support		precision	recall	f1-score	support	
0	0.59	0.98	0.74	401		0	0.95	0.82	0.88	324
1	0.83	0.12	0.21	313		1	0.87	0.97	0.91	390
accuracy			0.60	714	accuracy			0.90	714	
macro avg	0.71	0.55	0.47	714	macro avg	0.91	0.89	0.90	714	
weighted avg	0.69	0.60	0.51	714	weighted avg	0.91	0.90	0.90	714	

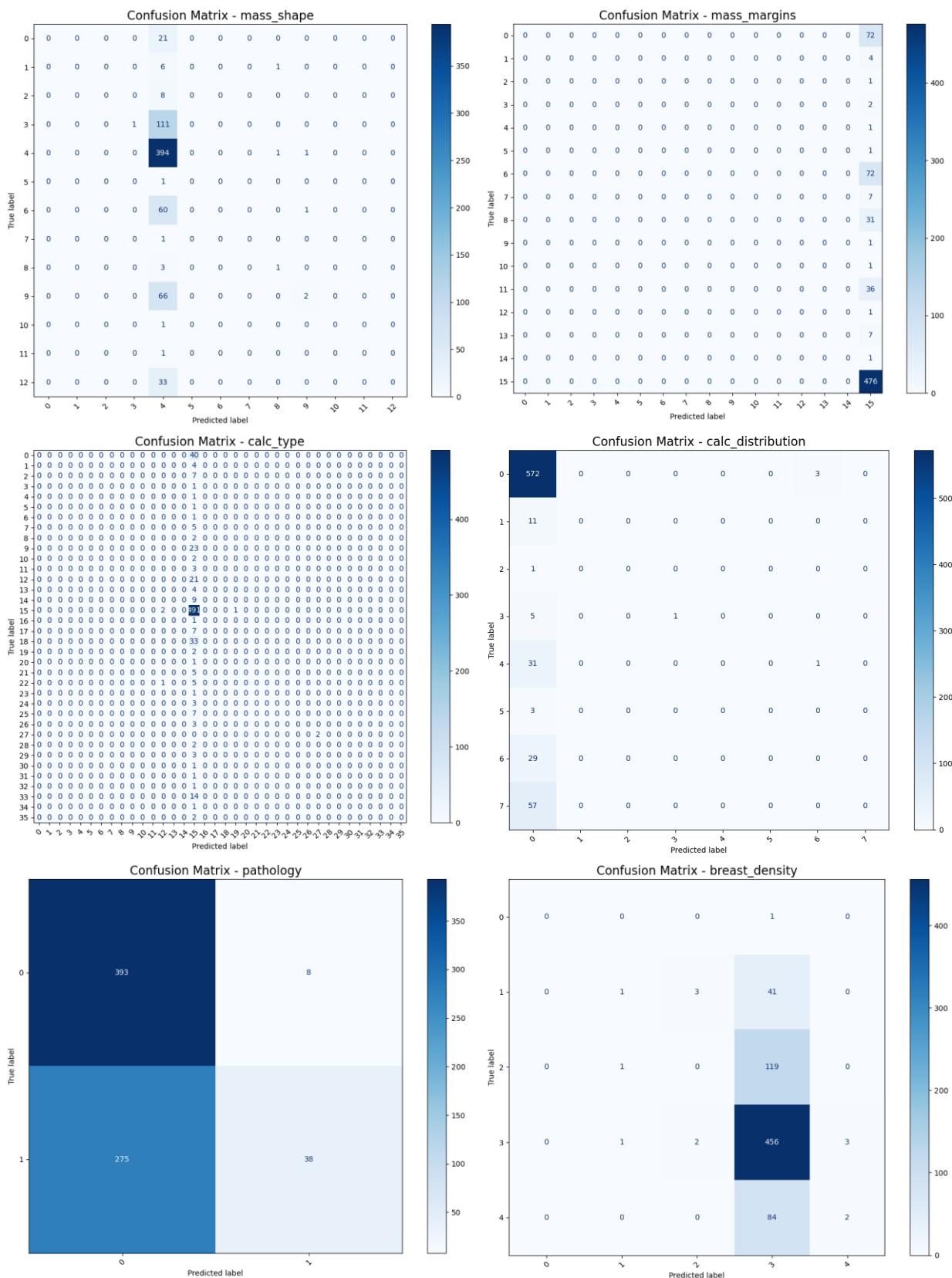
Classification Report for breast\_density:

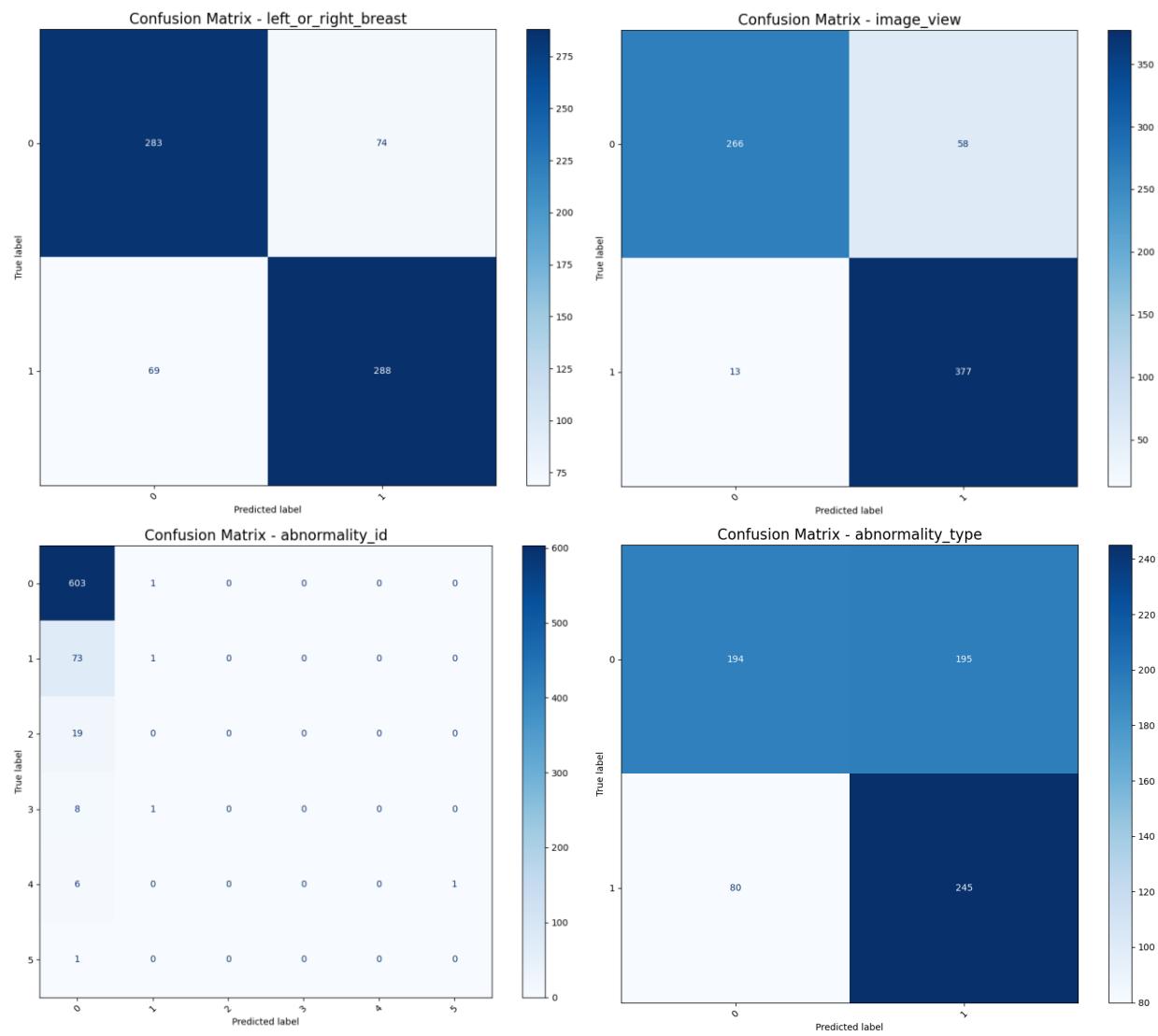
	precision	recall	f1-score	support		precision	recall	f1-score	support	
0	0.00	0.00	0.00	1		0	0.80	0.79	0.80	357
1	0.33	0.02	0.04	45		1	0.80	0.81	0.80	357
2	0.00	0.00	0.00	120						
3	0.65	0.99	0.78	462	accuracy			0.80	714	
4	0.40	0.02	0.04	86	macro avg	0.80	0.80	0.80	714	
accuracy			0.64	714	weighted avg	0.80	0.80	0.80	714	
macro avg	0.28	0.21	0.17	714						
weighted avg	0.49	0.64	0.52	714						

Classification Report for abnormality\_type:

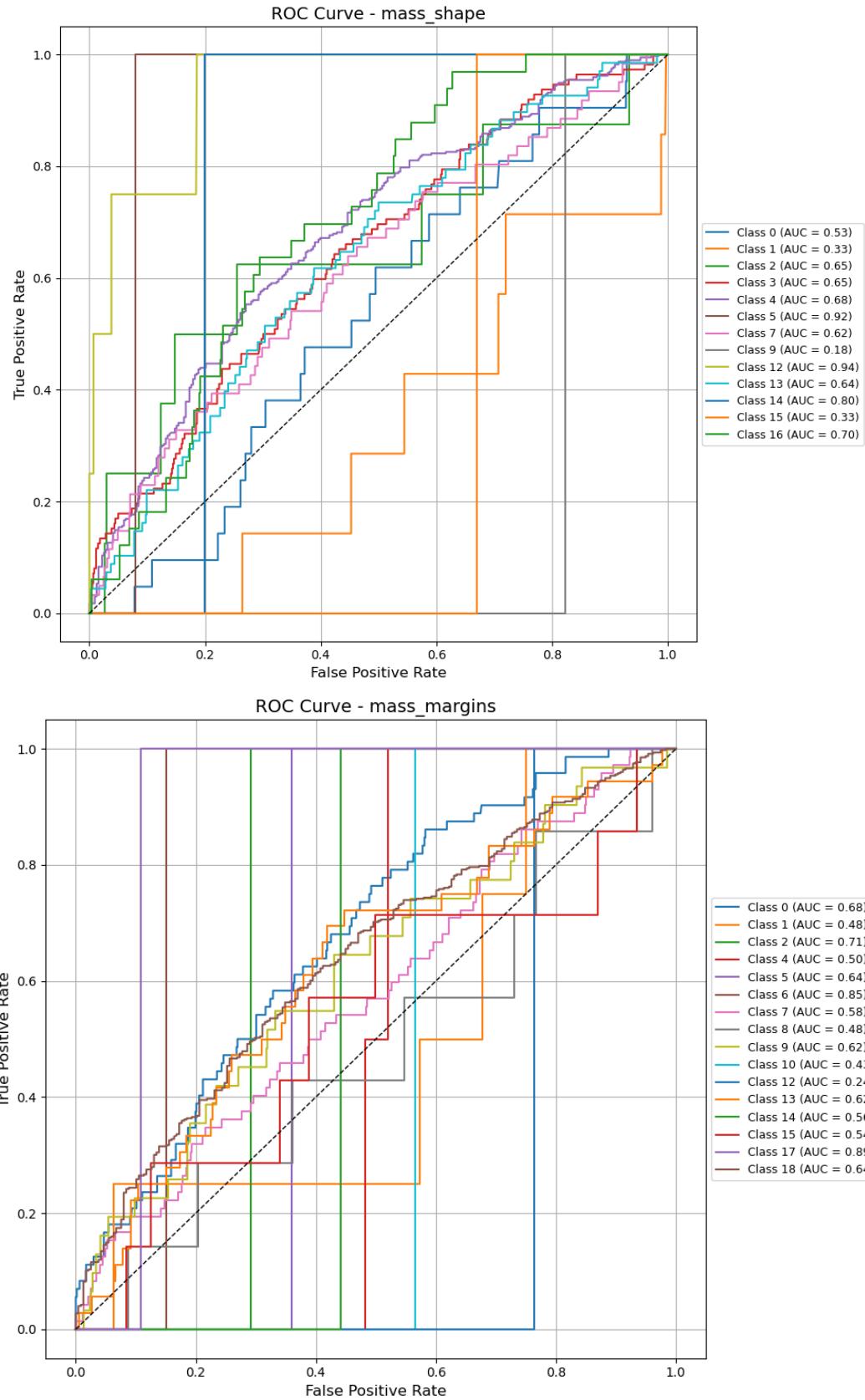
	precision	recall	f1-score	support
0	0.71	0.50	0.59	389
1	0.56	0.75	0.64	325
accuracy			0.61	714
macro avg	0.63	0.63	0.61	714
weighted avg	0.64	0.61	0.61	714

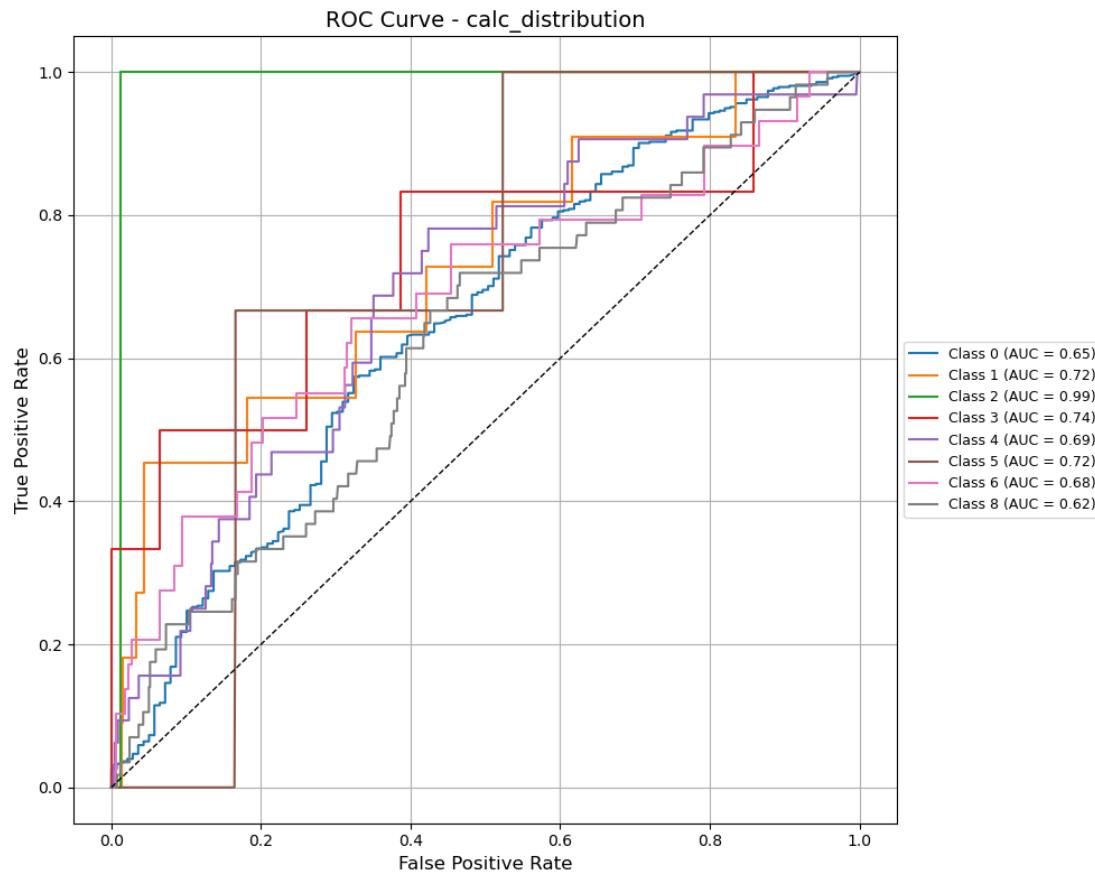
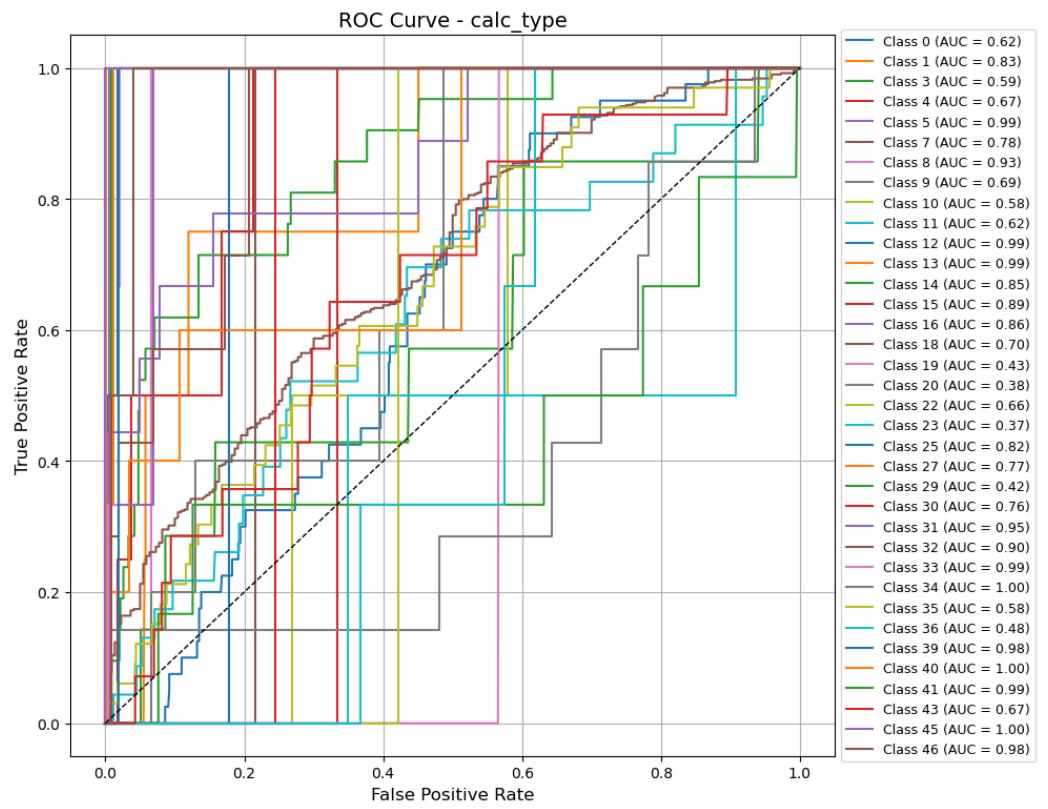
## Confusion Matrix



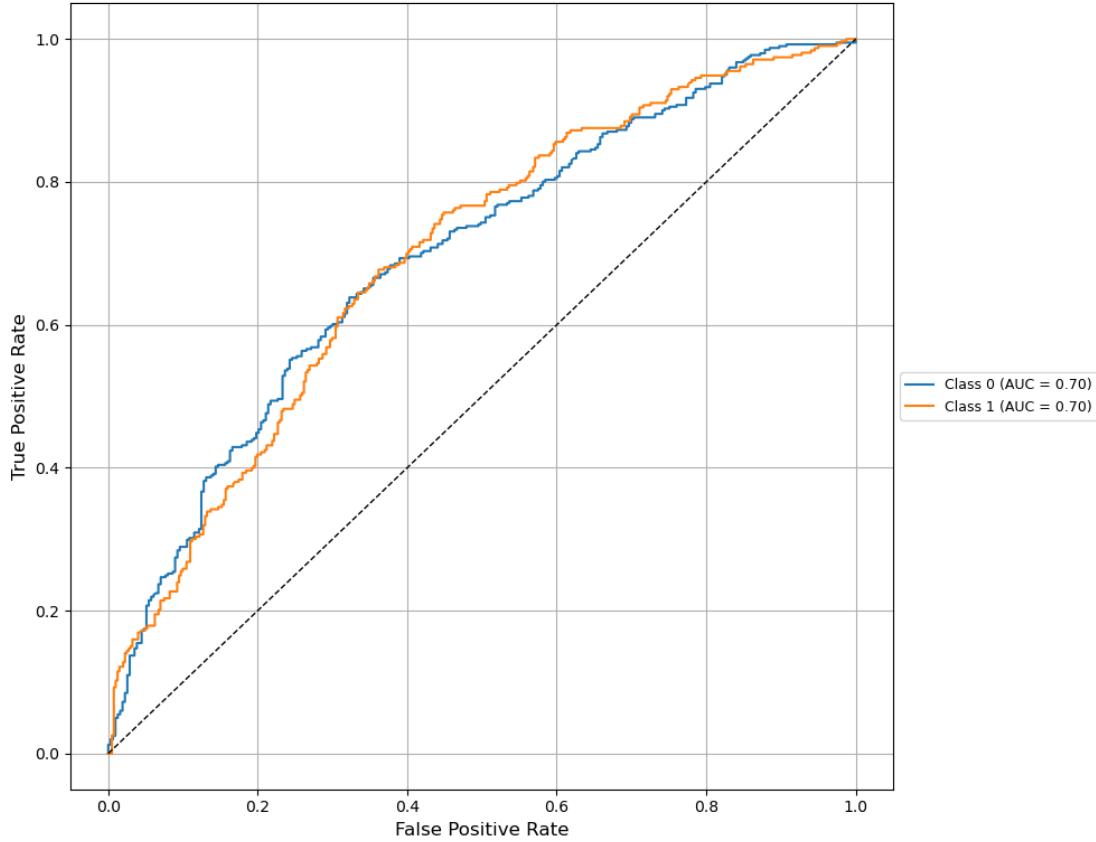


## ROC Curve

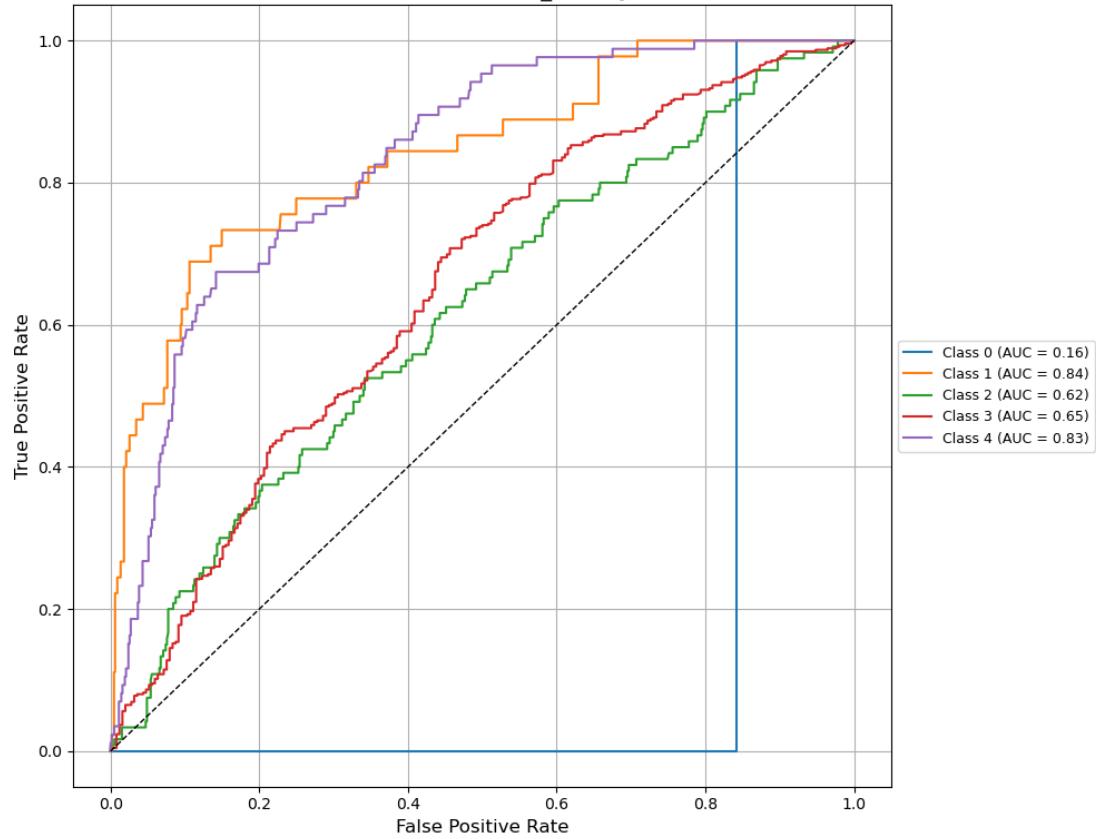




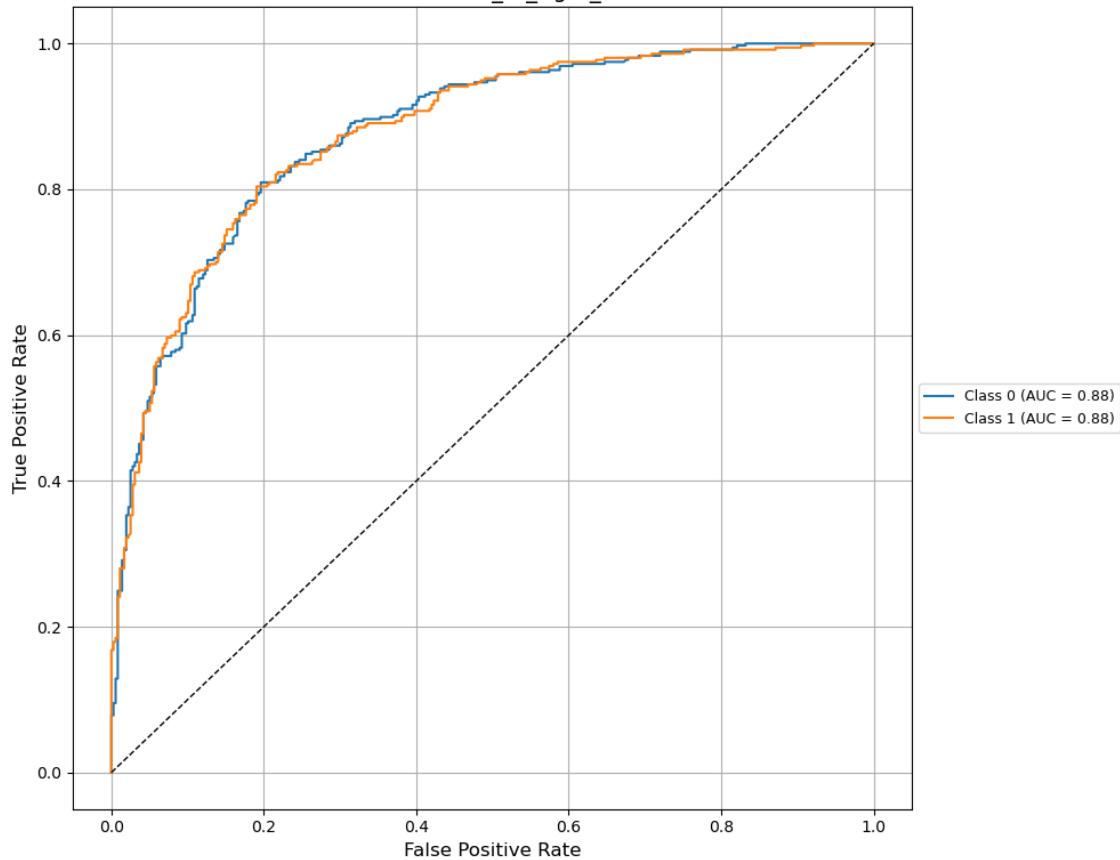
ROC Curve - pathology



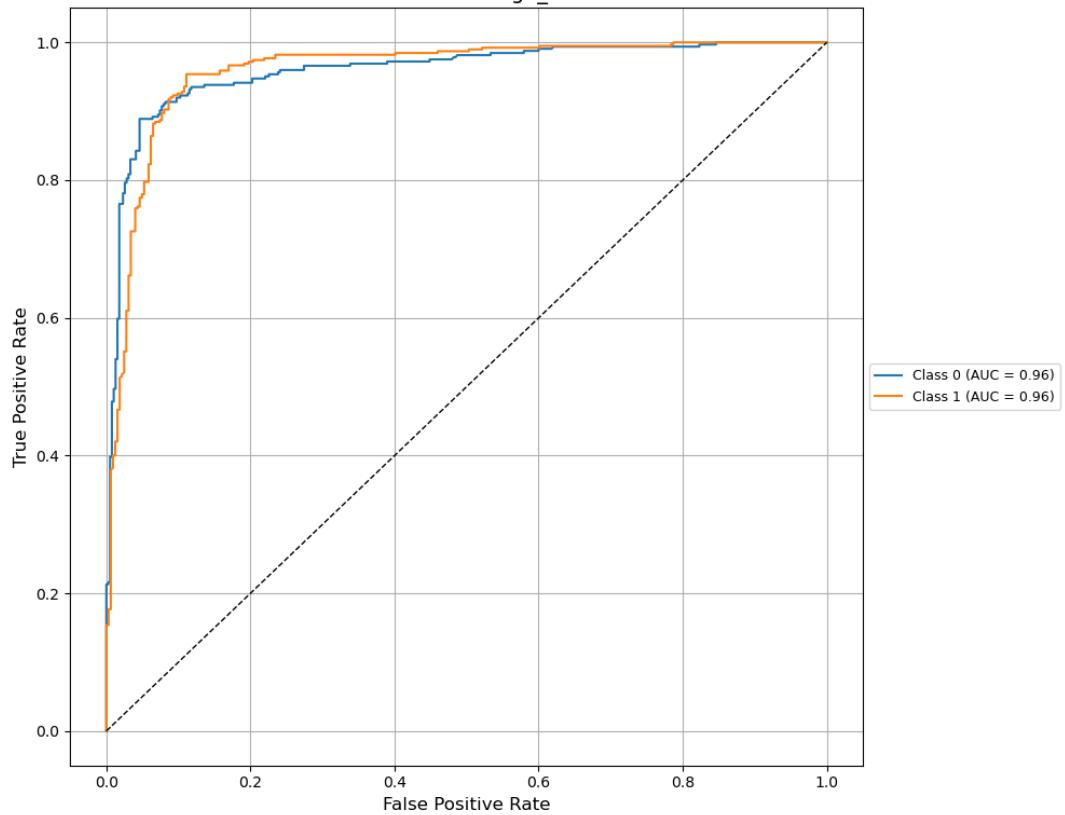
ROC Curve - breast\_density

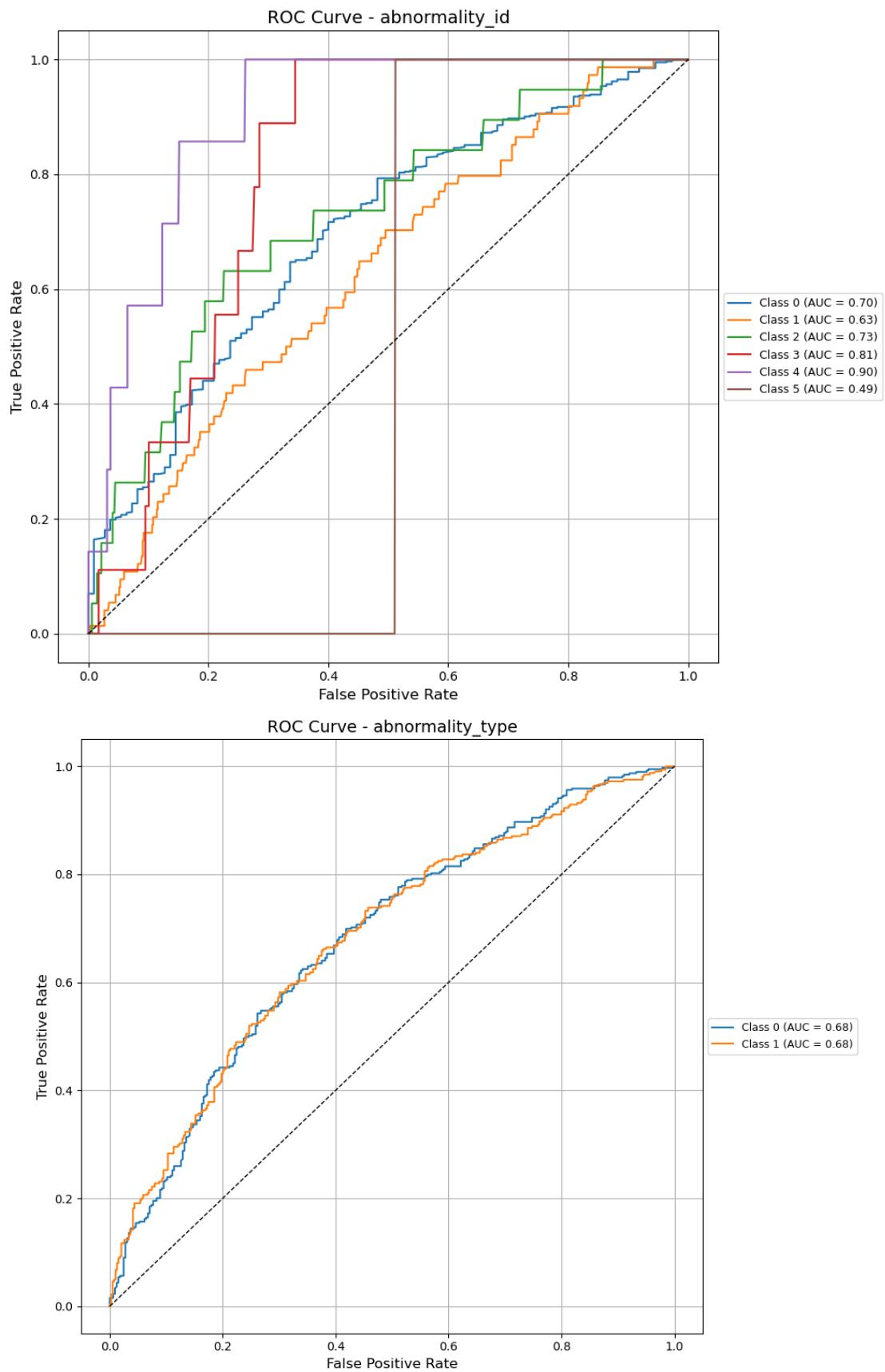


ROC Curve - left\_or\_right\_breast



ROC Curve - image\_view





## Testing & Evaluation

We give model image for testing and this is output

```
Output mass_shape: Predicted 'IRREGULAR-ARCHITECTURAL_DISTORTION' with probability 0.67
Output mass_margins: Predicted 'SPICULATED' with probability 0.74
Output calc_type: Predicted 'PLEOMORPHIC' with probability 0.72
Output calc_distribution: Predicted 'CLUSTERED' with probability 0.83
Output pathology: Predicted 'BENIGN' with probability 0.55
Output breast_density: Predicted '3.0' with probability 0.64
Output left_or_right_breast: Predicted 'LEFT' with probability 0.60
Output image_view: Predicted 'CC' with probability 0.55
Output abnormality_id: Predicted '1' with probability 0.90
Output abnormality_type: Predicted 'calcification' with probability 0.64
```

## 4.5) Comparison between Models

Among the evaluated models, **Xception** was selected as the final model due to its superior performance across all target label categories. It consistently achieved the highest accuracy, demonstrating robust predictive capability and generalization. This made Xception the most suitable choice for supporting precise diagnosis and effective training in the context of multi-label classification of mammographic images.

# Chapter 5: System Requirements and Design

## 5.1) Introduction

This section outlines the core functional and non-functional requirements of the system, followed by UML diagrams that visually represent its structure and behavior. These elements together provide a clear foundation for system design and development.

## 5.2) Functional Requirements

Functional Requirement is a summary of the function that the program will deliver. Describes the software program or its portion. Function is the input to the software system, its behavior and outputs. It can be a measurement, data processing, business method, user experience, or some other unique feature that determines what role the program is likely to execute.

### a) Log In

The system provides security features through username-password matching where only authorized user can access the system.

- **Input:** Email, Password
- **Output:** Invalid or successfully logged in

### b) Sign Up

New users create an account to use the system.

- **Input:** Name, Email Address, Number and Password.
- **Output:** Successfully Registered.

### c) AI Cancer Detection (Detailed Model)

A patient can use the AI models to classify the input image for breast cancer detection. The user can either upload an image from the gallery or take a photo using the camera. it is analyzed using AI models to detect abnormalities and classify it into different categories, including potential breast cancer.

- **Input:** Mammogram or breast tissue scan (uploaded or captured)
- **Output:** If it is a valid breast scan, the system detects abnormalities and provides a detailed report.

#### **d) AI Cancer Detection (Simple Model)**

The patient uploads a breast scan image. The AI model checks the image and tells whether it shows cancer or not, along with a confidence percentage.

- **Input:** Mammogram or breast tissue scan (uploaded or captured)
- **Output:** Result: Cancer or Non-Cancer, Confidence: e.g., 95% sure it's Cancer

#### **e) Save AI Result**

A patient can save their AI detection results. The system allows patients to upload their AI-generated detection page, which is then processed to generate a detailed report in PDF format.

- **Input:** AI Detection Page (uploaded), Result
- **Output:** Detailed report generated and downloaded as a PDF.

#### **f) History**

The history feature allows users to access and manage their previous reports. Users can view a list of all past reports for reference and easily delete any report they no longer need.

- **Input:** User action (view or delete).
- **Output:** Display of previous reports or confirmation of successful deletion.

#### **g) Medicine Alarm**

A medicine timer helps users manage their medication schedule efficiently. Simply enter the name of the medication and set a time for the alert via notifications. Users can choose to receive reminders

daily or weekly and have the flexibility to modify the schedule or cancel the medication at any time.

- **Input:** Medication name, alert time, frequency (daily/weekly), modifications or cancellations.
- **Output:** Timely notifications for medication reminders, updated schedule, or canceled alerts.

#### **h) AI-Powered Chatbot Assistant**

This system features an AI-powered chatbot designed to assist users by answering a wide range of questions. Users can interact with the chatbot through a simple chat interface, asking any question they may have. The AI processes the input and responds with accurate and relevant information.

- **Input:** User message or question (via chat).
- **Output:** AI-generated answer or response based on the user's query.

#### **i) Settings**

The settings feature allows users to customize their app experience. Users can adjust the font size for better readability and enable or disable dark mode for a more comfortable viewing experience.

- **Input:** User action (modify font size, toggle dark mode).
- **Output:** Updated font size or theme applied successfully.

### **5.3) Non-Functional Requirements**

Non-functional requirements define quality attributes like performance and usability. For example, how fast does the app load? These requirements ensure reliability and efficiency, preventing issues that could impact user experience. They also set constraints on the app's architecture for optimal functionality.

### **a) Availability**

The app is available at all times, meaning the user can access it using an application.

### **b) Reliability**

As the app provide the right tools for problem solving it is made in such a way that the app is reliable in its operations and for securing the sensitive details.

### **c) Performance**

Our App didn't take more than a few seconds if there was a good internet connection, also it is fast and responsive, with minimal latency and downtime.

### **d) Usability**

Our App is user-friendly and easy to navigate, with a clear and intuitive interface.

### **e) Data integrity**

Our App is described by accuracy, completeness, and consistency of data mean safety of data and security.

## **5.4) UML Diagrams**

The system design provides a graphical representation that illustrates how the system is structured, functions, and is utilized. It helps in understanding the overall architecture, workflow, and interaction between various components of the system.

### **1st Analysis:**

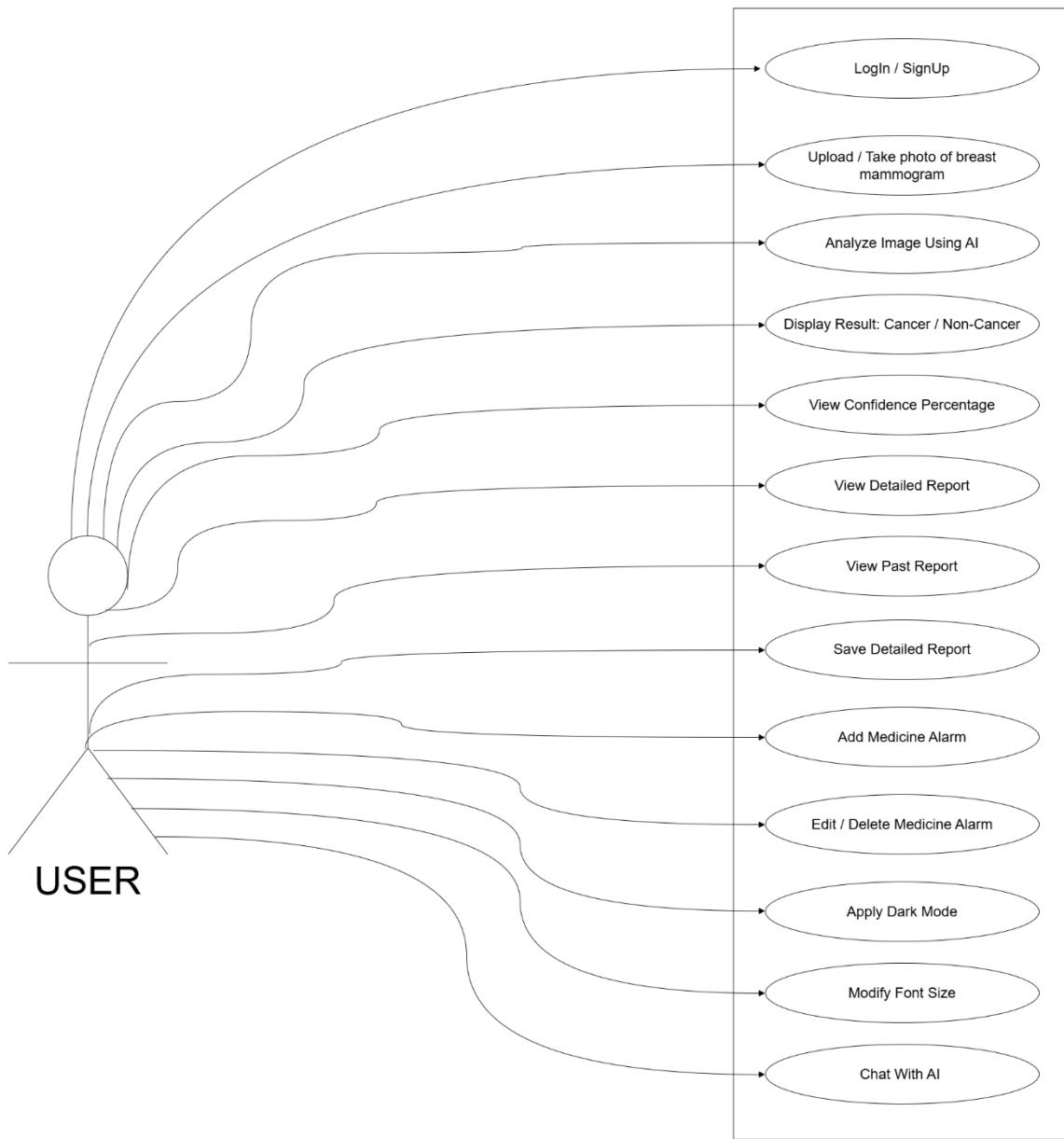
- a) Use Case Diagram

### **2nd Design:**

- a) Activity Diagram

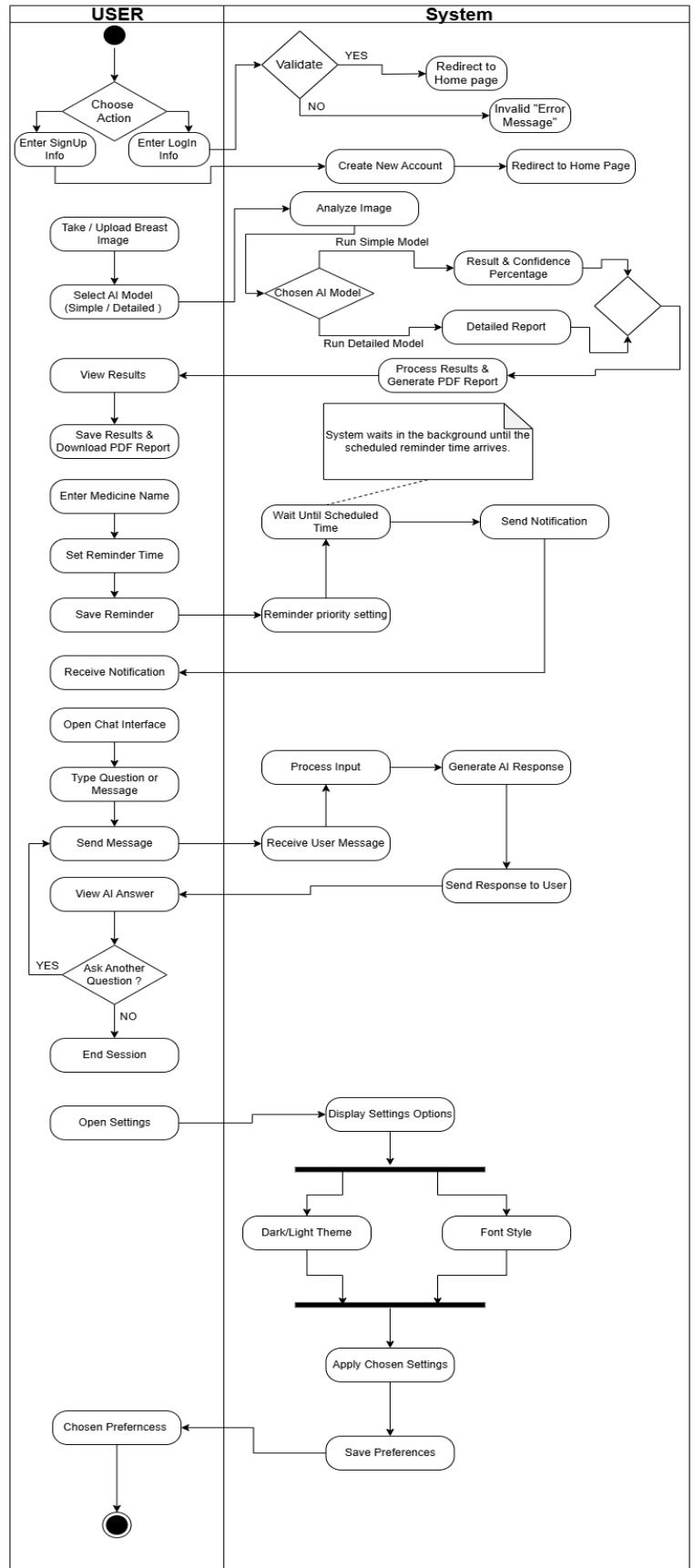
### 5.4.1) Use Case Diagram

Use case diagram shows a graphical representation of the interaction of device components with users. It helps to identify the requirements of the system and to provide clearness of understanding.



## 5.4.2) Activity Diagram

Activity diagram provides a graphical representation of the workflow or the sequence of activities within a system. It helps to visualize the flow of operations, decision points, and parallel processes, offering a clear understanding of how the system behaves from start to finish.



# Chapter 6: Application

## 6.1) Introduction

This chapter covers the integration of AI models with Flask for mobile deployment, including simple and detailed prediction endpoints and image preprocessing. It also provides an overview of the app's user interface, highlighting key features such as login, predictions, report history, medicine alarms, AI chat, and settings.

## 6.2) Integration of AI Models with Flask for Mobile Application Deployment

The following Python script demonstrates the integration of deep learning models within a Flask-based web service. This service acts as a backend API that can be consumed by mobile applications to perform real-time predictions based on medical image inputs.

### 6.2.1) Purpose

The main objective of this implementation is to expose trained AI models—specifically for cancer detection and detailed diagnostic analysis—through a **Flask RESTful API**. This enables seamless communication between the mobile application frontend and the AI models deployed on a server or local machine.

### 6.2.2) Simple Prediction Endpoint

```
@app.route("/predict/simple", methods=["POST"])
```

- Accepts an image file via POST.
- Processes the image to match input requirements.
- Predicts whether the image indicates **Cancer** or **Non-Cancer**.
- Returns the predicted class and confidence score.

### 6.2.3) Detailed Prediction Endpoint

```
@app.route("/predict/detailed", methods=["POST"])
```

- Predicts multiple attributes such as mass shape, calcification type, breast density, pathology, and more.
- Returns a structured diagnostic report including timestamp and advisory notes.

### 6.2.4) Preprocessing of Image

To prepare an input image for prediction by resizing, normalizing, and formatting it for the model.

```
def preprocess_image(img, IMG_SIZE):  
    img = img.resize((IMG_SIZE, IMG_SIZE))  
    img = np.array(img) / 255.0  
    img = np.expand_dims(img, axis=0)  
    return img
```

- **Resize** the image to the required dimensions (e.g., 100×100 or 224×224).
- **Normalize** pixel values to the range [0, 1] by dividing by 255.
- **Add batch dimension** so the model receives the input in the correct format.

### 6.2.5) Decode output

To convert a numeric prediction (e.g., 0, 1, 2) into a readable label using the dataset's column values.

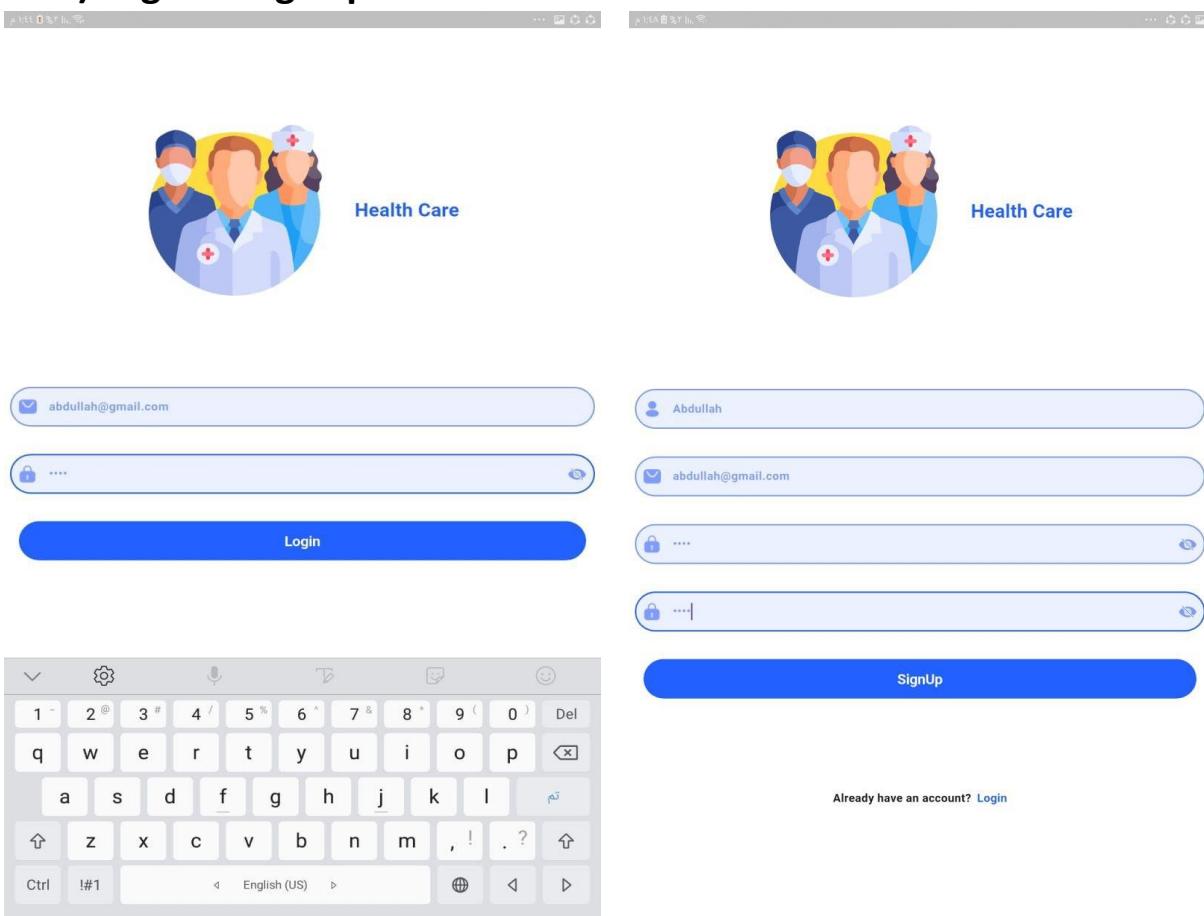
```
def decode_prediction(encoded_value, column_name):  
    unique_values = csv_data[column_name].unique()  
    return str(unique_values[int(encoded_value)])
```

- Fetch all unique labels from the specified CSV column.
- Use the predicted number (**encoded\_value**) as an index to get the corresponding label.

## 6.3) User Interface Overview: Mobile Application Tab Screenshots

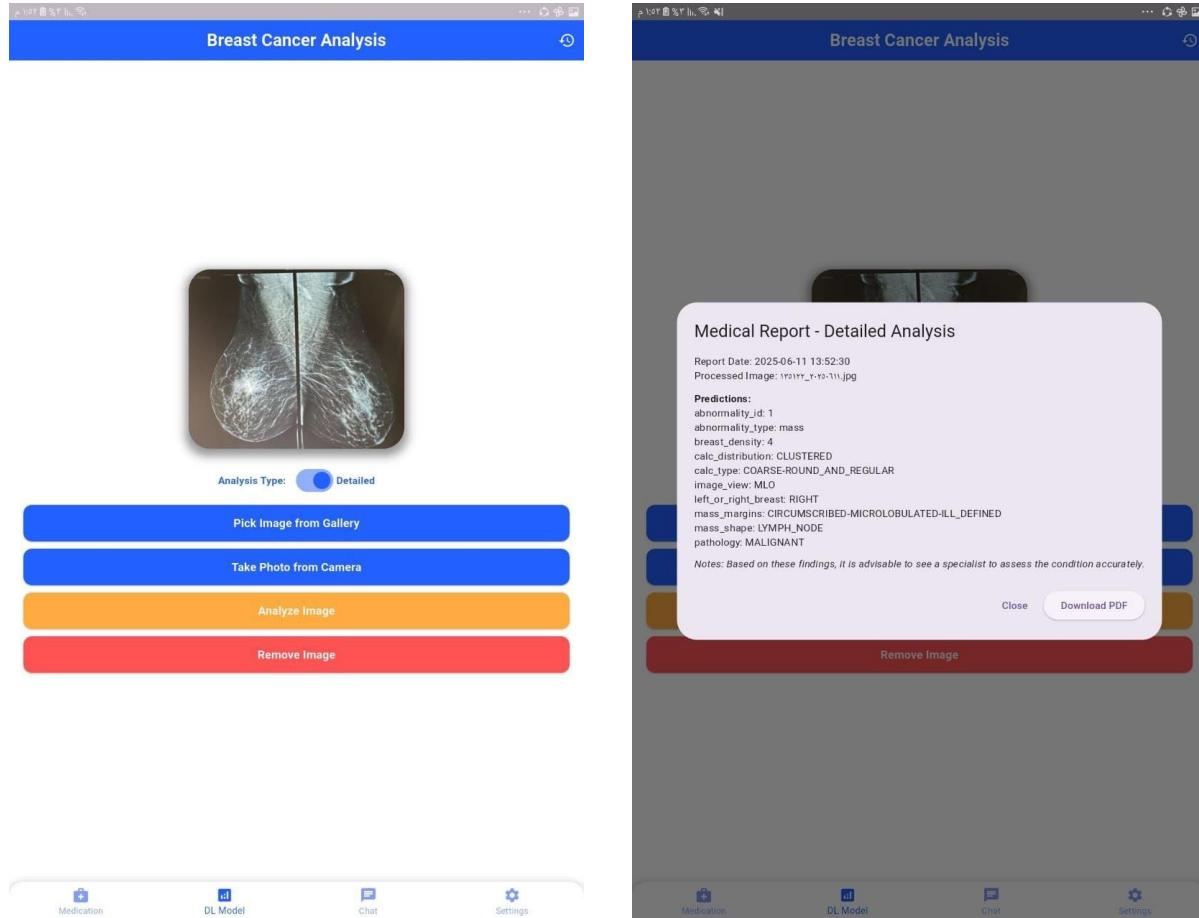
This section presents visual representations of the mobile application's main interface tabs. Each screenshot highlights a specific feature, including user authentication, prediction results, report history, reminders, AI chat, and settings. These visuals help illustrate the app's functionality and user-friendly design.

### 6.3.1) LogIn & SignUp



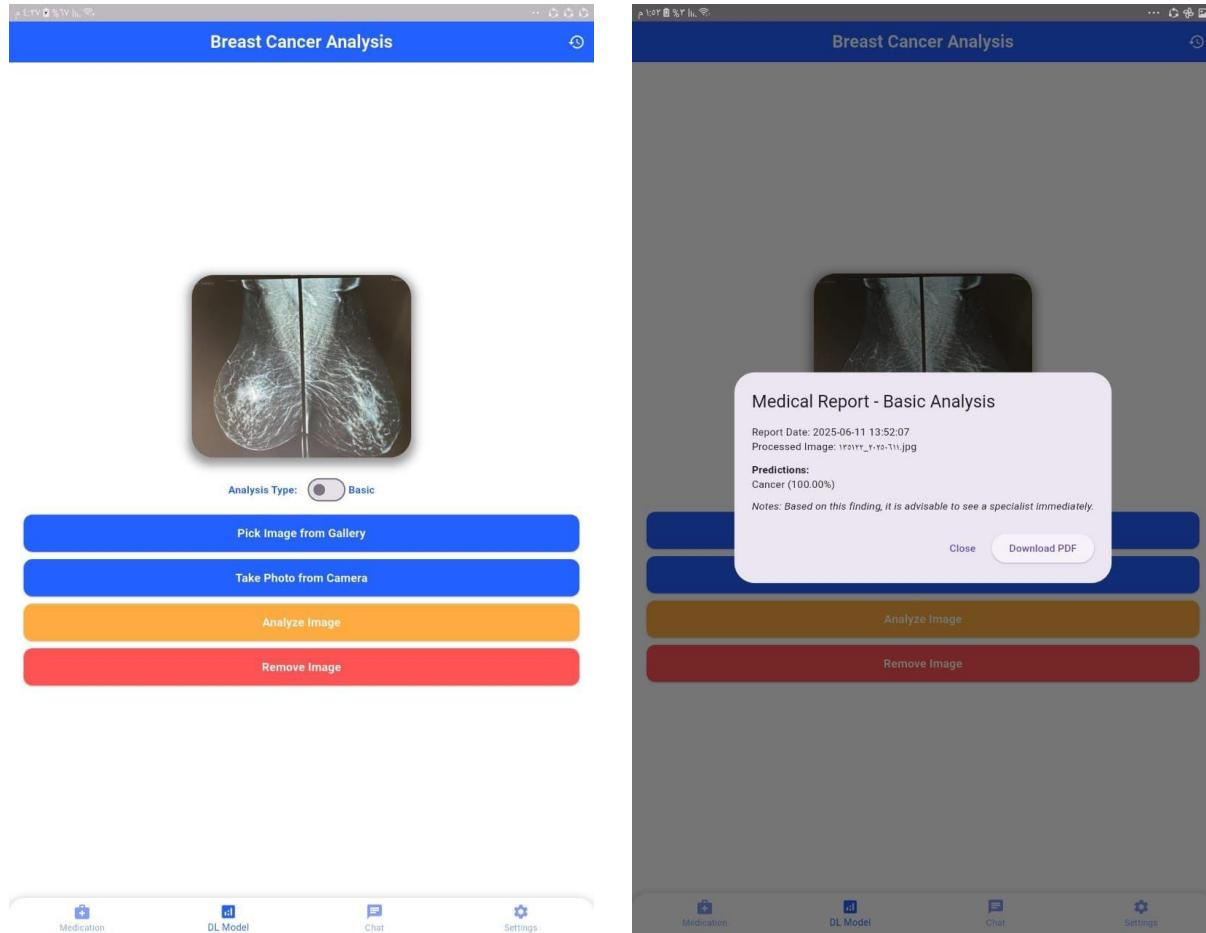
### 6.3.2 Detailed Model Prediction

The user uploads an image and selects the **Detailed Model** option. The image is processed and analyzed by the model, which predicts multiple diagnostic attributes. A detailed report is then generated, including key findings such as mass shape, margins, pathology, and more, along with the upload timestamp and image name.



### 6.3.3) Simple Model Prediction

The user uploads an image and selects the Simple Model option. The image is analyzed to determine whether it indicates Cancer or Non-Cancer. The result is returned along with a confidence percentage and the uploaded image name.



#### 6.3.4) PDF Report History

This section provides a complete log of all diagnostic PDF reports generated through the application.

Users can refer to this history to track previous analyses and access past reports at any time.

Report 1  
Date: 2025-06-11 12:56:10

Report 2  
Date: 2025-06-11 12:56:13

Report 3  
Date: 2025-06-11 13:52:07

Report 4  
Date: 2025-06-11 13:52:30

Medical Report - Detailed Analysis  
Report Date: 2025-06-11 13:52:30  
Processed Image: 20250611\_135230.jpg

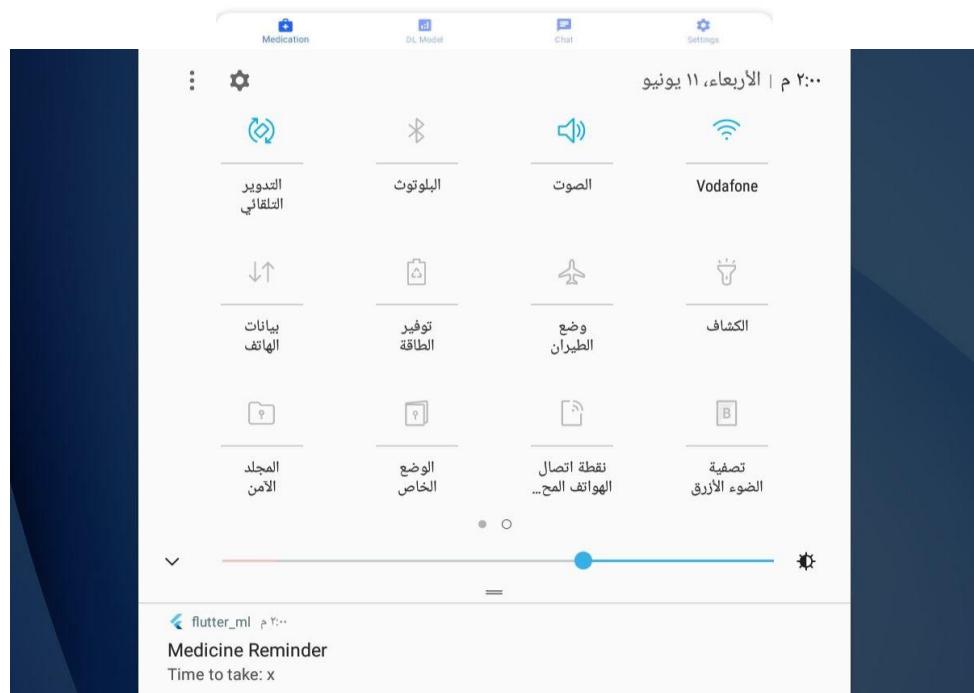
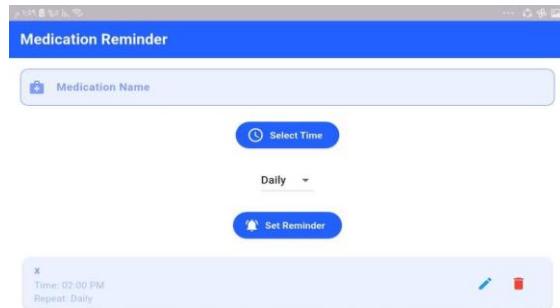
**Prediction:**

- abnormality: 1
- anomaly\_type: mass
- breast\_density: 4
- calc\_distribution: CLUSTERED
- calc\_type: COARSE-ROUND\_AND\_REGULAR
- image\_view: MLO
- left\_or\_right\_breast: RIGHT
- mass\_margins: CIRCUMSCRIBED-MICROLOBULATED-ILL\_DEFINED
- mass\_shape: LYMPH\_NODE
- pathology: MALIGNANT

*Notes: Based on these findings, it is advisable to see a specialist to assess the condition accurately.*

### 6.3.5) Medicine Alarm

Users can set reminders by entering the medicine name, dosage, and time. The app sends notifications to ensure timely intake, supporting consistent and effective medication management.



## 6.3.6) AI Chat Assistant

The AI Chat Assistant allows users to interact with an intelligent system to ask health-related questions, receive guidance, and get support in using the application.

Chat with AI

what is breast cancer??

Breast cancer is a disease in which cells in the breast grow out of control. These cells can invade surrounding tissues or spread (metastasize) to other areas of the body.

Here's a breakdown of key aspects:

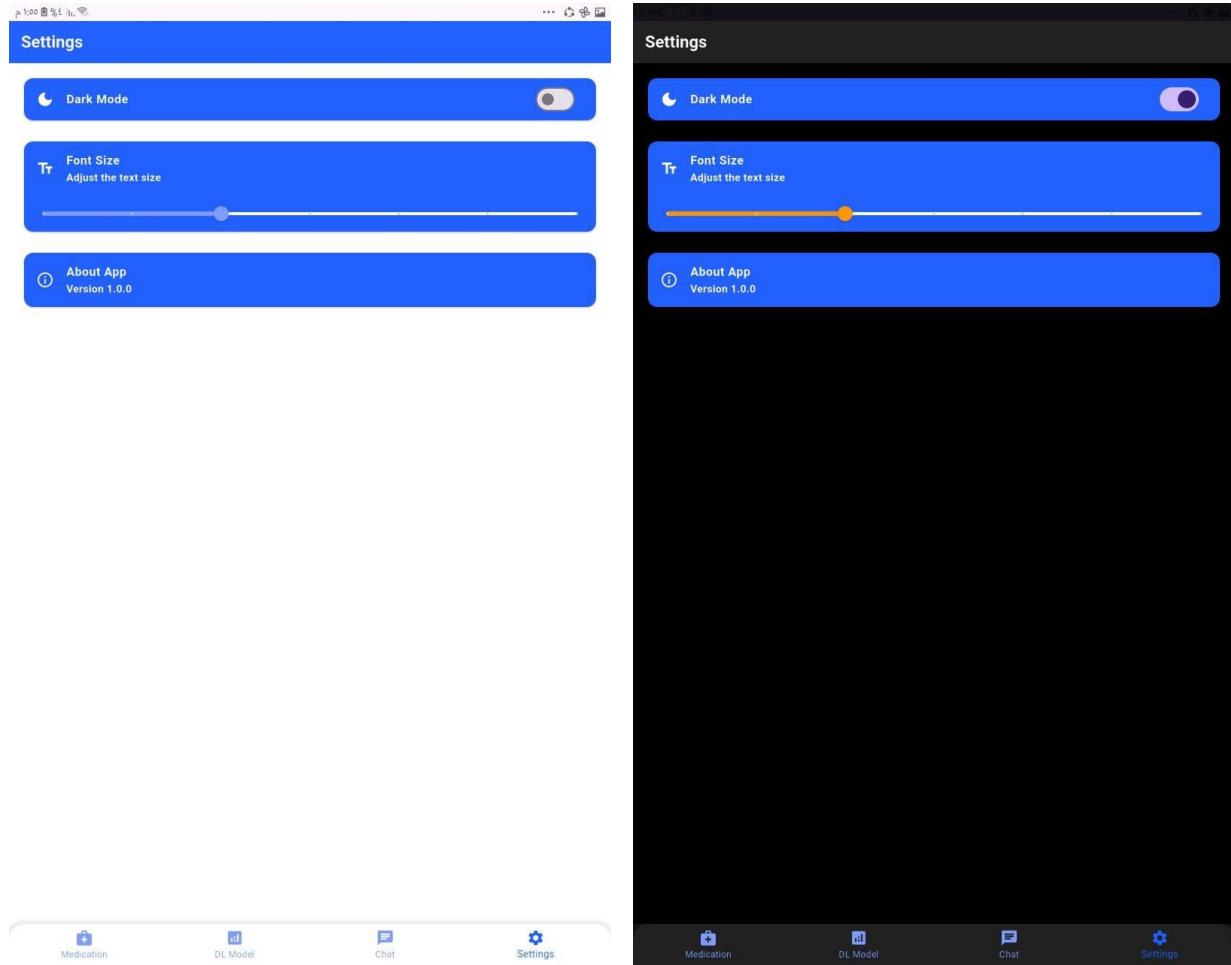
- \* **What it is:** Cancer starts when cells in the body begin to grow uncontrollably. In breast cancer, this happens in the breast tissue.
- \* **Types:** There are several types of breast cancer, depending on which cells in the breast become cancerous. The most common types are:
  - \* **Invasive Ductal Carcinoma (IDC):** Starts in the milk ducts and spreads outside of them. It's the most common type.
  - \* **Invasive Lobular Carcinoma (ILC):** Starts in the milk-producing lobules and spreads outside of them.
- There are also less common types, like inflammatory breast cancer, Paget's disease of the nipple, and triple-negative breast cancer.
- \* **How it develops:** Breast cancer develops when genetic mutations cause cells in the breast to divide and multiply abnormally. These cells form a tumor, which can be benign (non-cancerous) or malignant (cancerous).
- \* **Risk factors:** Several factors can increase the risk of breast cancer:
  - \* **Age:** The risk increases with age.
  - \* **Family history:** Having a close relative with breast cancer increases the risk.
  - \* **Genetics:** Certain gene mutations (e.g., BRCA1 and BRCA2) significantly increase the risk.
  - \* **Personal history of breast cancer:** Having had breast cancer before increases the risk of recurrence or developing it in the other breast.
  - \* **Hormonal factors:** Early menstruation, late menopause, hormone therapy, and birth control pills can slightly increase the risk.
  - \* **Lifestyle factors:** Obesity, lack of physical activity, alcohol consumption, and smoking can increase the risk.
- \* **Symptoms:** Common symptoms of breast cancer include:
  - \* A new lump or thickening in the breast or underarm area
  - \* Changes in the size or shape of the breast
  - \* Nipple discharge (other than breast milk)
  - \* Nipple retraction (turning inward)
  - \* Skin changes, such as dimpling, puckering, or redness
  - \* Pain in the breast (less common, but possible)
- \* **Diagnosis:** Breast cancer is typically diagnosed through:
  - \* **Clinical breast exam:** A physical examination by a doctor.
  - \* **Mammogram:** An X-ray of the breast.

Ask anything... >

Medication DL Model Chat Settings

### 6.3.7) App Settings

Users can customize font style, enable dark mode, and view the app's system version.



# Chapter 7: Future Work

## 7.1) Introduction

This section presents future plans to expand the application's capabilities, including multi-cancer detection using diverse imaging types and enhanced features like clinical decision support, teleconsultation, and patient record management. The goal is to develop a comprehensive digital health assistant for improved diagnosis and patient care.

## 7.2) Future Enhancements Toward a Multi-Cancer AI Diagnostic and Health Management Platform

We envision several key areas for expanding and enhancing the capabilities of our application and underlying AI models. Our primary objective is to broaden the scope of cancer detection beyond breast cancer, extending support to multiple cancer types such as lung, skin, prostate, cervical, and colorectal cancers. This will involve training and validating new models using diverse and comprehensive datasets specific to each cancer type, as well as incorporating a wider range of medical imaging modalities including CT scans, MRIs, PET scans, and ultrasound images. By doing so, we aim to build a robust multi-cancer detection framework capable of assisting in the diagnosis of various malignancies with high accuracy and reliability.

In addition to expanding the AI models, we plan to significantly enhance the functionality of the mobile application to create a more holistic and user-centric medical platform. Key features under consideration include:

- **Multi-cancer Detection Module:** An integrated system where users can upload various types of medical images for detection of different cancers, not limited to mammograms.

- **Specialized Clinic Integration:** A dedicated section within the app where users can browse and book appointments with oncology clinics and specialists based on their diagnostic reports and location preferences.
- **Report-Based Clinical Decision Support:** Enhanced visualization and interpretation of diagnostic results, including graphical summaries, recommendations for follow-up tests, and potential treatment pathways.
- **Patient History and Record Management:** A secure and personalized space for users to store, track, and manage their medical records and previous diagnostic reports.
- **Teleconsultation Features:** Integration of virtual consultation options to allow users to connect with specialists remotely, based on the AI-generated reports.
- **Smart Notifications and Reminders:** Advanced scheduling tools to remind users of upcoming appointments, medication times, and follow-up scans, improving adherence to treatment plans.

Our long-term goal is to evolve this application into a comprehensive digital health assistant that empowers patients, supports healthcare professionals, and improves early detection and monitoring of various cancers. By combining advanced deep learning technologies with user-friendly and accessible healthcare services, we aim to contribute meaningfully to cancer care and overall public health outcomes.

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