

# BREAST CANCER IMAGE CLASSIFICATION USING CUSTOM CNN

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## ABSTRACT

### Background:

Breast cancer remains a primary global health concern, emphasizing the critical need for accurate diagnostic tools. This study focuses on developing a precise method for classifying breast cancer images using a specifically designed Convolutional Neural Network (CNN). The research employs the BreakHis dataset for training and evaluation, comprising high-resolution histopathological images of breast biopsy specimens stained with hematoxylin and eosin.

### Methods Used:

The unique CNN architecture incorporates convolutional layers, max-pooling layers, dropout layers, and batch normalization, tailored to capture intricate patterns distinguishing between benign and cancerous breast tissues. Comprehensive data preprocessing is implemented, involving label extraction from filenames and augmentation techniques to enhance the training set. The training of the CNN model involves using the Adam optimizer, binary cross-entropy loss, and evaluation metrics such as binary accuracy and ROC-AUC. Early halting and learning rate decrease callbacks are integrated into the training process to optimize model performance.

### Results Achieved:

The trained CNN model is assessed on a separate test dataset, and performance metrics, including ROC-AUC, accuracy, and a confusion matrix, are provided. The findings demonstrate that the custom CNN reliably categorizes breast cancer images, suggesting its potential as a valuable tool for automated breast cancer diagnosis. Notably, the study reports a high ROC-AUC value (0.98051) and satisfactory accuracy (0.93285), indicating the effectiveness of the custom CNN for breast cancer histopathology image categorization.

### Concluding Remarks:

This work underscores the significance of tailored CNN architectures in enhancing the precision of breast cancer diagnostics, contributing to the ongoing efforts to leverage machine learning in histopathological image processing. The promising outcomes of the proposed approach set the stage for further advancements in computer-aided diagnostics and medical image analysis. The reported high ROC-AUC value and accuracy affirm the efficiency of the custom CNN, supporting its potential application in real-world breast cancer diagnostic scenarios.

**Keywords:** *Breast Cancer, Global Health, Convolutional Neural Network (CNN), Diagnostic Instruments, BreakHis dataset.*

## 1. INTRODUCTION

Breast cancer is a significant global health concern, demanding modern and precise diagnostic technologies for successful identification and classification. The combination of machine learning with medical imaging has shown promise in recent years for improving the precision and effectiveness of breast cancer diagnosis. Convolutional Neural Networks (CNNs) are one of the most effective

methods for image analysis tasks. A typical methodology involving the CNN for breast cancer prediction is shown in Fig 1. This work aims to improve diagnostic processes by developing and utilizing a customized CNN for categorizing photos related to breast cancer. It is impossible to overestimate how important an accurate breast cancer diagnosis is since early identification is essential for prompt action and better patient outcomes. Conventional diagnostic techniques

frequently depend on the subjective and time-consuming histological analysis of biopsy specimens. The potential to transform diagnostic precision lies in integrating machine learning techniques and exceptionally specialized CNNs designed to handle the intricacies of image data related to breast cancer.

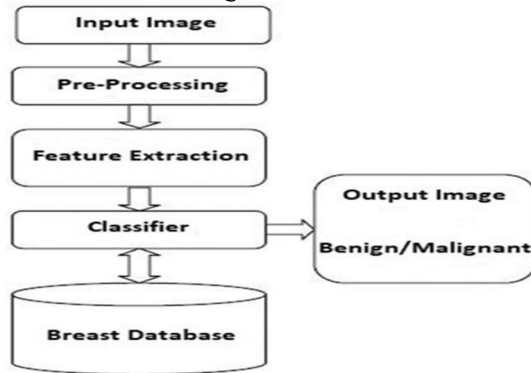


Fig 1. Different Types of Brain Tumours

Source: [9]

This research leverages the BreakHis dataset, comprised of high-resolution histopathology pictures of breast biopsy tissues stained with hematoxylin and eosin. The selection of this dataset offers a firm basis on which to train and assess the suggested custom CNN architecture. Convolutional layers, max-pooling layers, dropout layers, and batch normalization are all part of the complex CNN design precisely engineered to catch subtle patterns that suggest benign and malignant breast tissues [2]. Strict data preprocessing approaches, such as label extraction and augmentation techniques, guarantee the Model's effectiveness. The study uses the binary cross entropy loss function, the Adam optimizer, and performance measurements like binary accuracy and ROC-AUC during the training phase. Techniques like early pausing and learning rate reduction are also included to enhance CNN's performance. An analysis of a confusion matrix, accuracy, and performance metrics like ROC-AUC value is used to assess the trained Model's efficacy on a different test dataset. The promising results of this work highlight how custom CNN architectures can be used to improve and automate picture categorization for breast cancer histopathology. This study advances the field of medical image analysis while highlighting the broader implications of using cutting-edge machine learning methods in computer-aided diagnosis. The results demonstrate that the suggested custom CNN is an effective method for classifying breast cancer, as evidenced by the high ROC-AUC value and good accuracy. This suggests

that further developments in automated diagnostic approaches are possible.

#### A. Purpose of the study

The primary goal of this research is to tackle the pressing worldwide health issue of breast cancer by the introduction and application of sophisticated diagnostic technologies that capitalize on the combination of medical imaging and machine learning. Convolutional neural networks, or CNNs, are widely acknowledged as practical image-processing tools. This research aims to improve the efficacy and precision of breast cancer diagnosis by creating and utilizing a customized CNN architecture.

The study highlights the shortcomings of traditional diagnostic techniques, which frequently rely on subjective and time-consuming histological interpretation of biopsy materials, in light of the critical relevance of early breast cancer identification for better patient outcomes. Incorporating machine learning methods, namely specialized CNNs built to handle the complex complexities of breast cancer image data, can provide revolutionary improvements in diagnostic precision. The suggested custom CNN architecture is trained and assessed on the BreakHis dataset, which comprises high-resolution histopathology images of breast biopsy tissues stained with hematoxylin. The CNN's complex architecture, which includes batch normalization, max-pooling layers, dropout layers, and convolutional layers, is designed to pick up on minute patterns that indicate breast cancer and benign tissue.

The work uses strict data preparation methods, such as label extraction and augmentation procedures, to guarantee the Model's efficacy. Essential elements, including the Adam optimizer, the binary cross entropy loss function, and performance measures like binary accuracy and ROC-AUC, are used in the training phase. Techniques, including early pause and learning rate decrease, are combined to improve CNN's performance. The trained Model is thoroughly assessed using a different test dataset. This analysis includes a confusion matrix, an accuracy evaluation, and a look at performance measures such as the ROC-AUC value. In addition to advancing the field of medical image analysis, the study's encouraging findings highlight the broader implications of utilizing state-of-the-art machine learning techniques in automated diagnosis. The high ROC-AUC value and good accuracy support the study's conclusion, which indicates that the proposed custom CNN architecture is a valid and dependable approach to breast cancer classification. These results highlight the revolutionary effect of custom

CNN architectures on breast cancer histopathology picture categorization and indicate the possibility for future advancements in automated diagnostic techniques.

### B. Aim

The main aim of this project is to classify the breast cancer images, either Benign or malignant, using Custom CNN.

### C. Objectives

- Build a Convolutional Neural Network (CNN) specifically designed to accurately classify photos of breast cancer into benign and malignant categories.
- Apply robust data preparation approaches, such as label extraction and augmentation techniques, to improve the Model's ability to handle a variety of histopathological images.
- To train and assess the custom CNN architecture, use the BreakHis dataset, which consists of high-resolution breast biopsy tissues stained with hematoxylin.
- Utilise essential CNN elements such as batch normalization, max-pooling, dropout, and convolutional layers to capture complex patterns representing benign and cancerous breast tissues.
- For the CNN to function best during the training phase, use binary cross-entropy loss, the Adam optimizer, and performance measurements like binary accuracy and ROC-AUC.

### D. Research Questions

1. What architectural strategies may ensure that breast cancer images are accurately classified into benign and malignant categories using Convolutional Neural Networks (CNNs)?
2. How may robust label extraction and augmentation methods for data preparation improve the capacity of the custom CNN to process various histological pictures related to breast cancer?
3. How can the training and assessment of the suggested custom CNN architecture benefit from using the BreakHis dataset, which consists of high-resolution breast biopsy tissues stained with hematoxylin and eosin?
4. What role do crucial CNN elements like convolutional layers, max-pooling layers, dropout layers, and batch normalization play in collecting intricate patterns representing benign and cancerous breast tissues?
5. How do performance measurements like binary accuracy and ROC-AUC, binary cross-entropy

loss, and the Adam optimizer affect the CNN's optimal performance during the breast cancer picture classification training stage?

In terms of global health, the diagnosis of breast cancer is a matter of great importance and urgency. One of the most common cancers in the world and the main reason why women die from cancer is breast cancer. Since early detection greatly improves treatment outcomes and patient survival rates, there is an urgent need for accurate and timely diagnosis. Unfortunately, subjective and time-consuming histological analysis of biopsy specimens is a common component of conventional diagnostic techniques, which causes delays in diagnosis and treatment initiation. Moreover, the intricacy of breast cancer pathology presents difficulties for conventional diagnostic techniques since it necessitates expertise and is subject to interpretation variability when differentiating between benign and malignant tissues. Due to its intrinsic subjectivity, misclassifications may arise, which could lead to poor treatment choices and unfavourable patient outcomes.

Within this framework, combining machine learning with medical imaging shows promise as a way to improve the accuracy and efficiency of diagnosis. Given their impressive performance in image analysis tasks, convolutional neural networks (CNNs) may be able to address some of the difficulties associated with breast cancer diagnosis. It is possible to automate and optimise the categorization of breast cancer images by utilising sophisticated computational techniques, such as customised CNN architectures trained on massive datasets.

The introduction's research discusses the urgent need for cutting-edge diagnostic technologies that can get beyond the drawbacks of conventional approaches. The project intends to transform diagnostic procedures and enhance patient outcomes by creating and implementing a customised CNN designed especially for breast cancer image classification. The significance of this issue stems from its direct impact on people's health and well-being, underscoring the need to advance diagnostic methodologies in order to effectively combat breast cancer.

## 2. LITERATURE REVIEW

### A. Recent Studies

Breast cancer is a common type of cancer that starts in the breast cells and has the potential to be fatal. While it can also happen to men, women are far more likely to experience it. Breast cancer is characterized by an uncontrolled growth of abnormal cells in the breast tissue. If treatment is not received, the cancer may spread to neighbouring tissues and appear as a

lump or mass. Improving treatment results largely depends on early diagnosis through screening, such as mammography, and developments in diagnostic methods, such as histopathological image analysis. In this direction, [3] discusses the difficulties in histopathological cancer detection, highlighting the subjective and time-consuming nature of the manual examination. They suggest a hybrid convolutional and recurrent deep neural network to improve and automate breast cancer histopathology image classification, as shown in Fig 2. The technique preserves both the short- and long-term spatial correlations between image patches by combining the benefits of convolutional and recurrent networks. The experimental results perform better than the state-of-the-art techniques, with an average accuracy of 91.3% in a four-class classification problem. Additionally, the authors provide a significant dataset of 3771 histological pictures of breast cancer, highlighting the diversity of the disease across age groups and subtypes and offering a priceless resource to the scientific community.

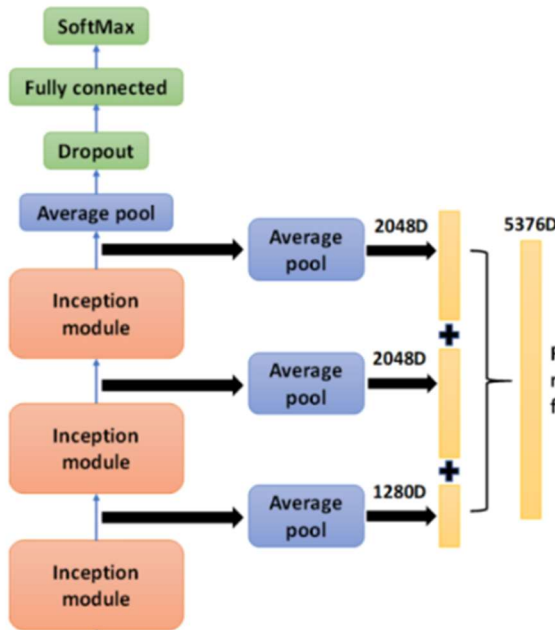


Fig 2. Proposed Method Source: [3]

Similarly, In the Same Direction [4] highlights the difficulties in the histological analysis of breast cancer and the time-consuming, subjective nature of the manual diagnosis. For the final classification of breast cancer histopathology photos showing carcinoma and non-carcinoma, the authors suggest using an ensemble deep learning technique. Based on previously trained VGG16 and VGG19 architectures, four models are trained, and an ensemble approach is

used by averaging predicted probabilities. The optimized VGG16 and VGG19 model ensemble exhibit competitive classification performance, with a sensitivity of 97.73% and an overall accuracy of 95.29%, especially for carcinoma. The architecture of VGG 16 is shown in Fig 3. Robust experimental results demonstrate the effectiveness of the proposed deep learning approach in automating the classification of difficult histopathology photos, particularly for carcinoma images.

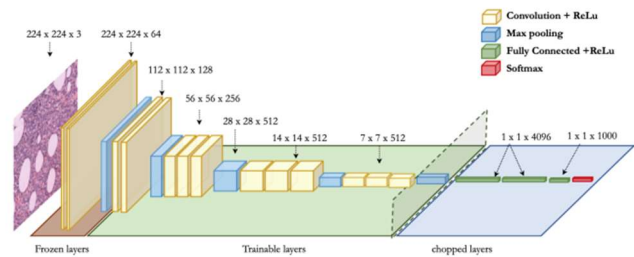


Fig 3. VGG 16 Architecture Source: [4]

Breast cancer is the second most common cancer in women worldwide, accounting for a large percentage of newly diagnosed cases in this context [5] seeks to create an exact algorithm that uses biopsy images to identify breast cancer. The study uses a deep learning strategy, creating a Convolutional Neural Network with transfer learning using a library of photos related to breast cancer. The accuracy obtained is higher than 96%, which is better than that of other state-of-the-art algorithms. This highlights the algorithm's accuracy in boosting early detection for better patient outcomes and its potential to considerably aid in diagnosing breast cancer. Due to their high prevalence and fatality rates, canine mammary tumours (CMTs) are valuable models for studying human breast cancer. So [6] discusses how difficult and time-consuming it is to diagnose human breast cancer and CMTs via histological investigation. Introducing the first dataset of CMT histopathology pictures (CMTHis), the paper presents a framework based on VGGNet-16 for automatic classification, as shown in Fig 4. The system uses support vector machines and is evaluated on the CMT and human breast cancer datasets. It obtains mean accuracies of 97% and 93% for binary classification of human breast cancer and CMT, respectively. The study highlights the potential of the suggested approach for automated diagnosis in veterinary and human medical contexts while validating its efficacy.

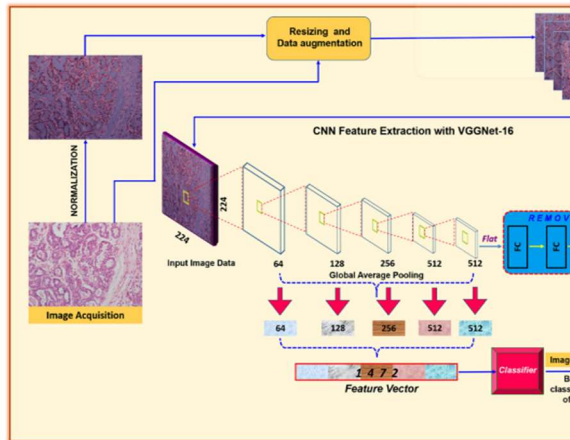


Fig 4. Histopathology Image Classification Frame Work Source: [6]

Another study [7] explores the diagnosis of breast cancer using histopathology pictures by contrasting deep learning (DL) and conventional machine learning (CML) techniques, as shown in Fig 5. The study fine-tunes VGG-19 for DL using histopathology images through a transfer learning approach. Evaluation of the BreakHis dataset and validation on KIMIA Path960 indicate DL outperforming CML, obtaining accuracies between 94.05% and 98.13% for binary classification and 76.77% to 88.95% for eight-class classification. Enhancing clinical interpretability through visual interpretation of learnt features, such as attention maps, increases confidence in DL techniques as trustworthy instruments for breast cancer diagnosis. [8] done a review on the breast cancer image classification. This review highlights the application of artificial deep neural networks in multiple medical imaging modalities, focusing on the categorization of cancer. AnalyzingAnalyzingcations from eight repositories, the review evaluates factors such as imaging modalities, datasets, preprocessing approaches, neural network types, and performance measures. Histopathologic pictures and mammograms are frequently employed, and available databases are used in 55% of investigations. Preprocessing methods are widely used, including scaling and normalization. A lot of research uses convolutional neural networks (CNNs), often using pre-trained networks. Accuracy, area-under-the-curve, sensitivity, precision, and F-measure are examples of evaluation metrics. The review lists ten open research issues, offering a comprehensive resource for both novices and advanced researchers in deep learning-based breast cancer category categorization.

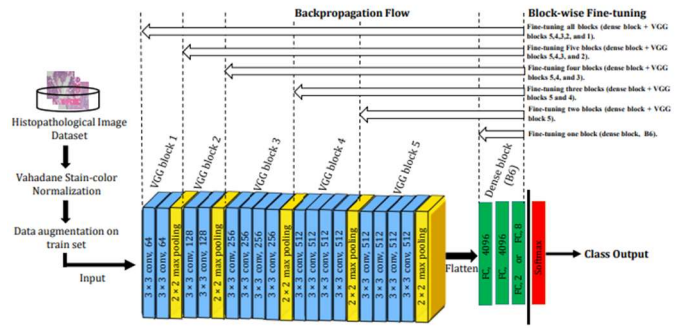


Fig 5. Proposed DL-Based Architecture Source: [7]

[9] The proposed method serves two purposes. First, it looks into different deep learning models for categorizing histology images of breast cancer and finds the best models for binary, fourth, and eighth classifications. Model accuracy is impacted by data augmentation, preprocessing, and transfer learning

techniques. Second, it evaluates state-of-the-art models (ResNeXt, Dual Path Net, SENet, NASNet) on the BreakHis and BACH datasets, which have not received much attention in previous research. Better results were obtained with Inception-ResNet-V2 for eight and binary classifications. The work provides a thorough analysis and discussion of experimental conditions used in investigations on histopathological images of breast cancer. Similarly, [10] offers Pa-DBN-BC, a novel patch-based deep learning algorithm utilizing Belief Network (DBN), for identifying and classifying breast cancer in histopathological images, as shown in Fig 6. The method consists of supervised fine-tuning stages and unsupervised pre-training for feature extraction from image patches. Patch classification uses logistic regression, which gives findings as a probability matrix showing positive (cancer) or negative (background) samples. By automatically identifying the best characteristics, the Model surpasses conventional techniques with an accuracy of 86% when evaluated and trained on a variety of whole slide histopathology image datasets.

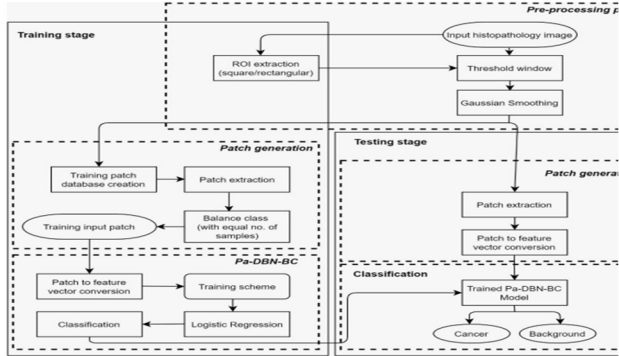


Fig 6. PA-DBN-BC Model Structure  
Source: [10]

[11] Focuses on creating a convolutional neural network (AlexNet)-based computer-aided diagnostic system for histopathology pictures of breast cancer. Conventional feature extraction techniques need to be more accurate and time-consuming. The system under consideration utilizes AlexNet generated from the BreakHis dataset, as shown in Fig 7. Experiments are conducted at various magnification factors. High accuracy (95%), sensitivity (97%), specificity (90%), and AUC (99.36%) of the results demonstrate the efficacy of the suggested method in differentiating between benign and malignant breast cancer.

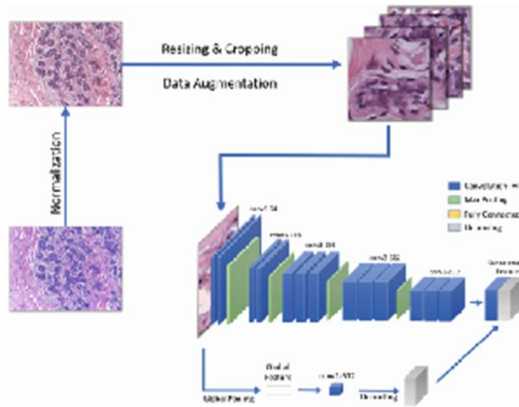


Fig 7. CNN & AlexNet Architecture  
Source: [11]

**B. Summary and Problem statement**

After conducting a brief literature review on the recent studies made by various researchers in the domain of breast cancer prediction, the following few of the observations are made. Manual diagnosis of breast cancer histopathology images is challenging due to its subjective and time-consuming nature. There is a need for automated and objective methods to improve diagnostic accuracy and efficiency. Early diagnosis of breast cancer is crucial for improving patient outcomes. Automated deep

learning-based approaches offer the potential to enhance early detection and facilitate timely interventions. Deep learning, particularly convolutional neural networks (CNNs), has shown promise in automating the classification of breast cancer histopathology images. These approaches have demonstrated high accuracy and sensitivity, outperforming traditional machine learning techniques.

With the literature review showing that pre-trained models are frequently used in breast cancer detection research and my project's strength being the use of a customized convolutional neural network (CNN) the problem statement can be summarized as follows. Pre-trained models, such as VGG16 and VGG19, are primarily used in the literature currently available on breast cancer detection for image classification tasks. Despite their excellent accuracy, these models might not be tailored to the particulars of breast cancer histopathology pictures. Consequently, a customized strategy based on CNN architectures created especially to handle the difficulties involved in breast cancer diagnosis is required. By creating a customized CNN for breast cancer diagnosis and prediction, my research seeks to close this gap. This research aims to increase the precision and generalizability of breast cancer detection models, ultimately leading to more efficient and dependable diagnostic instruments in clinical practice. It does this by utilizing the advantages of customized CNNs, such as their adaptability in model architecture and capacity to optimize for the particular task at hand.

**3. METHODOLOGY**

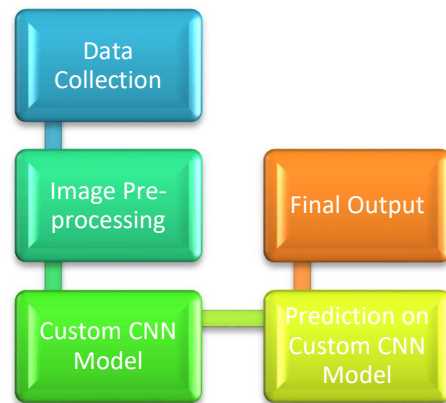


Fig 8. Proposed Methodology

A systematic approach that includes data collecting, image preprocessing, creation of a custom CNN model, prediction, and output analysis is used to

predict breast cancer, as shown in Fig 8. The meticulous completion of each phase is crucial to the predictive Model's effectiveness.

In this research, we are focusing on using a custom convolutional neural network (CNN) for the detection and prediction of breast cancer. The literature review revealed that many existing studies in this area have utilized pre-trained models, such as VGG16 and VGG19, for breast cancer image classification. However, the strength of our research lies in the development and implementation of a custom CNN architecture specifically tailored to address the challenges and nuances of breast cancer detection. By designing a custom CNN, we aim to improve the accuracy and generalizability of the classification model, particularly in scenarios where pre-trained models may not perform optimally. This approach allows for the customization of the network architecture to better capture the unique features of breast cancer histopathology images, potentially leading to more accurate and reliable predictions.

When compared to pre-trained models, employing a custom CNN for breast cancer detection and prediction has a number of advantages. First, a customized CNN that is tailored to the task at hand and takes into consideration the distinct features of images from breast cancer histopathology can be created. This gives the model architecture more flexibility, which could result in better accuracy and performance than if you used a pre-trained model that wasn't really suited for this kind of work. Second, creating a custom CNN from scratch gives you more control over the training procedure and enables you to adjust the model according to the available dataset. This can be especially helpful when there is a little dataset available or when the data distribution is very different from the dataset used to train the pre-trained model. Researchers can adjust a custom CNN to more closely match the features of the dataset, which could improve performance and generalization. Furthermore, avoiding any biases or restrictions seen in pre-trained models can be facilitated by employing a bespoke CNN. Large, diverse datasets are frequently used to train pre-trained models, which may not adequately represent the subtleties of a given problem area. Researchers may make sure the model is especially tuned for the goal of breast cancer detection by training a bespoke CNN, which could result in more accurate and trustworthy outcomes.

#### A. Data Collection

Carefully gathering data is the first step in the prediction of breast cancer. In this context, data from medical imaging, especially mammography, is collected from several sources. Images of breast tissues labelled with corresponding diagnostic results,

such as benign or cancerous, are included in this data set. A comprehensive dataset is essential for training a robust model to ensure that the CNN learns patterns and features indicative of breast cancer across different circumstances and patient profiles.

#### B. Image Preprocessing

The next crucial stage after gathering the data is picture preparation. Several actions are involved to improve the quality and relevance of the images for model training. To help in training convergence, rescaling is done to normalize lues to a standard range, usually  $[0, 1]$ . Furthermore, data augmentation methods, including rotations, flips, and random brightness modifications, are used. By subjecting the Model to various viewpoints on breast tissue, these augmentations add heterogeneity to the dataset and aid in the generalization of the Model.

#### C. Custom CNN Model

Creating a convolutional neural network (CNN) model is the foundation of the breast cancer prediction methodology. The architecture is painstakingly constructed to extract hierarchical information from the input photos. Convolutional layers for feature extraction, max-pooling layers for spatial reduction, and dropout layers for regularisation are found in each convolutional block that makes up the CNN. The retrieved features are combined by fully linked layers after the Model to get a final classification. Before the dense layers, batch normalization is used to stabilize the stabilizing process, and global average pooling is used to reduce spatial dimensions further. After that, the model architecture is constructed, defining suitable optimizer functions for jobs involving binary classification.

#### D. Prediction using CNN Model

The prediction phase involves feeding fresh, untrained mammography pictures into the trained CNN model. Using the features it has learnt, the Model uses its layers to interpret these images and forecast whether or not breast cancer will develop. The output layer's sigmoid activation function converts the Model's unprocessed predictions into probabilities, showing the malignancy likelihood. This stage is essential for evaluating the Model's capacity to provide precise predictions and generalize unseen data.

#### E. Final Output

AnalyzingAnalyzingl's outputs is the last stage in the approach for predicting breast cancer. Predictions are compared against ground truth labels to assess the Model's accuracy, precision, recall, and F1 score.

The discriminating power of the Model can also be evaluated using Area Under the Curve (AUC) metrics and Receiver Operating Characteristic (ROC) curves. Additionally, a confusion matrix provides insights into false positives and false negatives. This in-depth research informs future adjustments to increase the forecast accuracy of the Model and helps assess its dependability.

Developing the Model, predicting, preprocessing, and analyzing analyses are part of the multifaceted breast cancer prediction approach process. The quality and diversity of the dataset, the potency of picture preprocessing methods, and the structural integrity of the customized Model are all critical to the predictive Model's performance. The Model's dependability in practical applications is ensured by thoroughly verifying predictions against ground truth labels, which supports ongoing attempts to improve breast cancer diagnosis and therapy.

#### F. Data Collection

Data collecting is a crucial stage for breast cancer prediction research, which uses the abundant resources offered by Kaggle, an open-source platform well-known for housing various datasets. Kaggle provides a repository for several medical imaging datasets, particularly those linked to breast cancer. The procedure of acquiring the dataset entails gaining access to mammography images and well-labelled diagnostic results that indicate whether or not there are any malignant or benign diseases. Building a comprehensive dataset is made possible by the wide range of patient profiles, imaging modalities, and clinical variants included in the Kaggle collection. This diversity is essential for developing a robust predictive model to identify complex patterns linked to breast cancer in various contexts. Through the collaborative study of various datasets made available by the platform, researchers and data scientists can progress the field of breast cancer prediction by contributing to and benefiting from a shared pool of knowledge. This can be achieved by utilizing a collaborative environment. By improving data quality and encouraging openness and cooperation among scientists, this strategy eventually aids in creating more precise and broadly applicable breast cancer prediction models.

#### G. DataSet

The dimensions of the training and test datasets are essential factors that influence the predictive Model's effectiveness and generalizability in breast cancer prediction. With a size of (2582, 5), the training dataset denotes the existence of 2582 samples or instances, each of which is distinguished by five attributes. These elements likely include a range of

clinical and imaging-related factors, which serve as the required input for the custom convolutional neural network (CNN) to identify patterns that may suggest breast cancer. The Model is exposed to a broader range of cases thanks to the more extensive training dataset, which helps it generalize new examples. On the other hand, 1251 instances of the test dataset measuring (1251, 5) have the same five attributes. This set acts as an impartial baseline to assess the Model's performance on fresh, untested data. To evaluate the Model's resilience and make sure it can produce correct predictions outside of the training data, the size of the training and test datasets must be balanced. The Model's capacity to generalize is affected by the differences in size between the training and test datasets; therefore, preserving a harmonious proportionality to maximize maximum performance in breast cancer prediction is crucial.

#### H. Image Preprocessing

The preprocessing of the breast cancer prediction dataset entails transforming each mammography image to fit into this standardized image size. This stage guarantees consistency and interoperability for the training, validation, and testing stages. Furthermore, the dataset is suitably divided into test, validation, and training sets, enabling efficient model testing, tuning, and assessment. The uniform size of images reduces processing overhead. It facilitates the smooth incorporation of images into the customized neural network, which improves the Model's ability to extract pertinent features and patterns suggestive of breast cancer in all standard dimensions.

#### I. Custom Convolutional Neural Network

For the prediction of breast cancer, the custom Convolutional Neural Network (CNN) architecture is a potent tool. Its hierarchical structure is designed to pick up on minute details in breast cancer screening images, from convolutional blocks that extract local characteristics to fully connected layers that capture global patterns. When identifying minute anomalies that may be signs of breast cancer, CNN's capacity to automatically learn pertinent properties like textures, edges, and spatial hierarchies is essential. Including batch normalization layers and data augmentation approaches improves the Model's robustness and generalization, and overfitting is avoided during training. Spatial reduction is facilitated by using max-pooling layers, which highlight important features. The output layer's last sigmoid activation offers a probabilistic interpretation, which enables the Model to forecast the chance of malignancy. In reality, 224 x 224 breast cancer pictures are fed into the CNN, ensuring uniform dimensions for easy



processing. The Model can identify various anomalies in breast tissue because of its extensive training on various images. By streamlining the breast cancer prediction process and offering an automated and precise tool for early diagnosis, this

CNN-based method architecture is a helpful tool in the ongoing attempts to enhance patient outcomes and diagnosis of breast cancer because of its capacity to discern complicated patterns and adapt to different imaging parameters.

**J. CNN Architecture Model Summary**

*Table 1. CNN Architecture Model Summary*

Model: "CustomCNN"		
Layer (type)	Output Shape	Param #
random_brightness_1 (Random Brightness)	(None, 224, 224, 3)	0
random_flip_1 (RandomFlip)	(None, 224, 224, 3)	0
random_rotation_1 (random rotation)	(None, 224, 224, 3)	0
rescaling (Rescaling)	(None, 224, 224, 3)	0
batch_normalization (BatchNormalization)	(None, 224, 224, 3)	12
conv2d (Conv2D)	(None, 222, 222, 32)	896
max_pooling2d (MaxPooling2D)	(None, 111, 111, 32)	0
dropout (Dropout)	(None, 111, 111, 32)	0
conv2d_1 (Conv2D)	(None, 109, 109, 64)	18496
max_pooling2d_1 (MaxPooling2D)	(None, 54, 54, 64)	0
dropout_1 (Dropout)	(None, 54, 54, 64)	0
conv2d_2 (Conv2D)	(None, 52, 52, 128)	73856
max_pooling2d_2 (MaxPooling2D)	(None, 26, 26, 128)	0
dropout_2 (Dropout)	(None, 26, 26, 128)	0
global_average_pooling2d (GlobalAveragePooling2D)	(None, 128)	0
dropout_3 (Dropout)	(None, 128)	0
dense (Dense)	(None, 256)	33024
dropout_4 (Dropout)	(None, 256)	0
dense_1 (Dense)	(None, 32)	8224
dense_2 (Dense)	(None, 1)	33

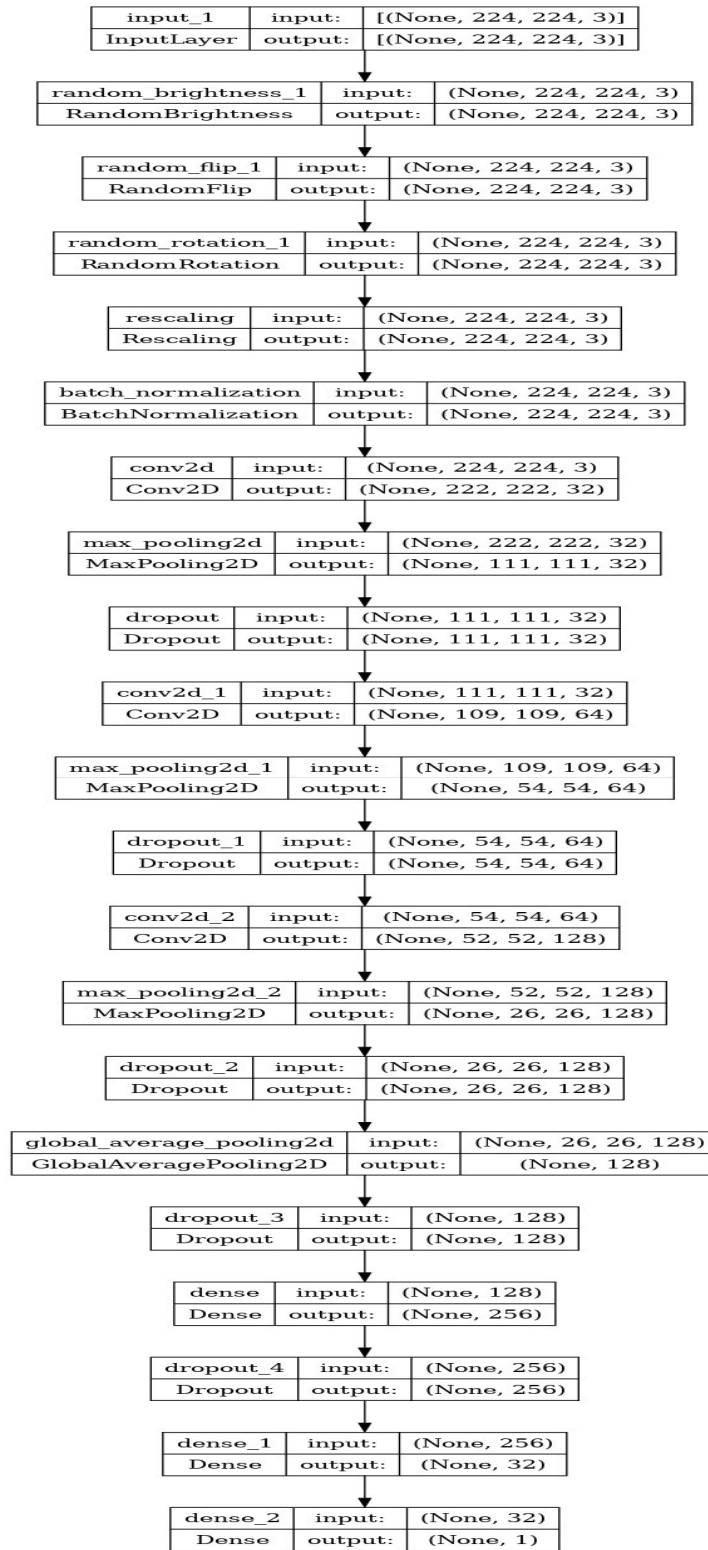


Fig 9. The architecture of Custom CNN

Table 1 shows the Convolutional Neural Network on each layer's output shape and number of (CNN) model's architecture, including information parameters. The same information is given in the

pictorial format in the Fig 9. The first layers comprise data augmentation methods, including rotation, flipping, and random brightness adjustment. These methods all help to diversify the training dataset without adding extra parameters. The Model then integrates necessary preprocessing layers, including batch normalization, adding 12 parameters for normalization calling. To capture complicated patterns, the convolutional layers (Conv2D) gradually increase the number of filters (32, 64, and 128) while extracting features from the input. Dropout layers are used for regularisation after max-pooling layers to reduce spatial dimensions. The Global Average Pooling layer reduces the spatial dimensions to a flat representation. The global feature representation is aided by fully connected layers (Dense) of different sizes (256, 32), and the final output layer, which has a sigmoid activation, predicts the probability of breast cancer. This architectural overview presents a balanced and organized approach to predicting breast cancer.

#### K. Activation Function

Convolutional neural networks (CNNs) are used to predict breast cancer. The selection of activation functions—Rectified Linear Unit (ReLU) and Sigmoid, in particular—is critical to the behaviour and predictive power of the Model.

ReLU is a popular activation function that allows the Model to activate when the input is positive and to activate zero otherwise, introducing non-linearity. It is exceptionally well suited for CNNs due to its ease of use and effectiveness in training. ReLU activation in convolutional layers aids the network in learning intricate patterns and features found in mammography pictures in the breast cancer prediction model. This non-linearity improves the Model's ability to identify minute details that may be signs of cancer.

Conversely, the last layer of binary classification models usually uses the Sigmoid activation function. Sigmoid activation in breast cancer prediction converts the Model's raw output into a probability score ranging from 0 to 1, signifying the probability that the mammogram is malignant. This probability helps physicians make decisions by making it easier to understand the Model's predictions. When diagnosing breast cancer, sigmoid activation plays a crucial role in transforming the continuous output of the Model into a functional binary classification that can differentiate between benign and malignant cases. To sum up, integrating Sigmoid and ReLU activation functions enhances the efficacy and comprehensibility of CNNs in predicting breast cancer, permitting more precise and practically applicable results.

#### L. Augmentation

In breast cancer prediction, augmentation is vital in strengthening the robustness and generalization model. An example image from the training dataset is applied with different augmentations in the provided code snippet. The dataset is more diverse by applying various circumstances to the image, such as rotations, flips, and random brightness modifications. By introducing variability, this augmentation method helps the Model better adapt to a wide range of scenarios and, in the end, enhances its capacity to identify patterns suggestive of breast cancer across various patient cases and imaging settings. Enhancing the Model's performance on unknown data and preventing overfitting are two essential augmentation goals.

### 4. RESULT AND ANALYSIS

#### A. Confusion Matrix

A crucial evaluation tool for classification models, such as those used in the prediction of breast cancer, is the confusion matrix. In the binary classification scenario inherent to breast cancer diagnosis, this matrix comprehensively captures the performance of the Model by categorizing it into four components: True Positive (correctly identified malignant cases), True Negative (correctly identified benign cases), False Positive (false alarms, benign cases misclassified as malignant), and False Negative (missed diagnoses, malignant cases misclassified as benign). Critical performance indicators, including accuracy, precision, recall, and the F1 score, are derived from these constituents. In the context of breast cancer prediction, this matrix provides a nuanced viewpoint on the Model's advantages and disadvantages, facilitating the evaluation of the Model's clinical significance and possible influence on patient outcomes.

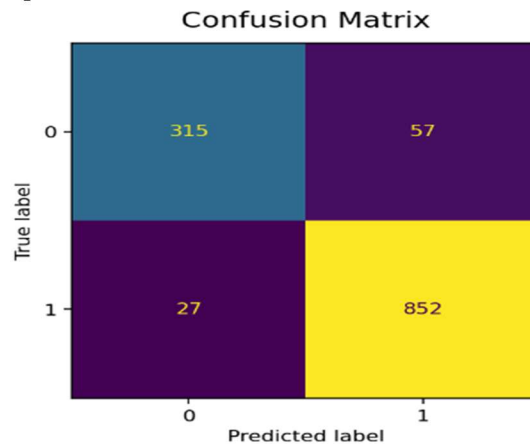


Fig 10. Confusion Matrix

When considering two classes, Class 0 and Class 1, the confusion matrix that is produced provides

insightful information about how well a classification model performs, as shown in Fig 10. The diagonal members represent the accurate optimistic and true pessimistic predictions in these matrixes, and the off-diagonal elements represent the false positives and false negatives. Remarkably, the high number of true positives (852) indicates that the Model is adept at correctly detecting occurrences of Class 1. Nevertheless, the 57 false positives—cases mistakenly classified as Class 1—show that there is still room for improvement in the Class 0 prediction. This implies that it might be challenging to discern between the two classes, which could cause Class 1 to get needless alerts.

Furthermore, the 27 false negatives show that there have been cases where Class 1 was mistakenly forecasted as Class 0. This misclassification is significant because it shows occasions in which the Model cannot detect actual positive cases, particularly in the context of breast cancer prediction. The Model's accuracy depends on how well it balances, reducing false positives and negatives. In breast cancer prediction, an additional study that includes precision, recall, and F1 score estimates would offer a more thorough knowledge of the Model's advantages and shortcomings.

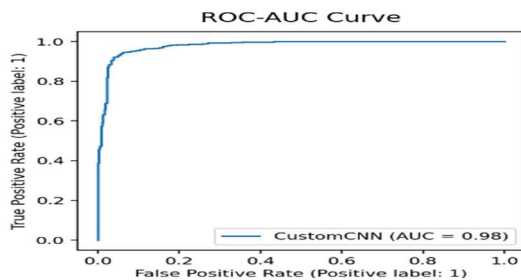


Fig 11. Roc-Auc Curve

In the context of breast cancer prediction models, the Area Under the Receiver Operating Characteristic (ROC) Curve, or AUC-ROC, is a crucial performance indicator. An elevated AUC value, like the noteworthy 0.98 previously mentioned, signifies an extraordinary discriminatory capacity of the Model. The ROC curve provides a detailed evaluation of the Model's classification ability by visually representing the trade-off between the actual positive rate (sensitivity) and false positive rate across different threshold settings, as shown in Fig 11. A 0.98 AUC in the prediction of breast cancer suggests that the Model has a solid capacity to discriminate between benign and malignant cases. The discriminating power of the Model is better the closer its AUC value is to 1. With a high AUC value, the Model can minimize false positives and false negatives by properly balancing sensitivity and

specificity. This kind of performance is critical for the prediction of breast cancer, as early detection and treatment of the disease depend on the correct diagnosis of malignancies. A high AUC-ROC value indicates a well-performing model, which adds credence to its clinical application and supports its potential as a valuable tool for helping medical professionals diagnose breast cancer accurately.

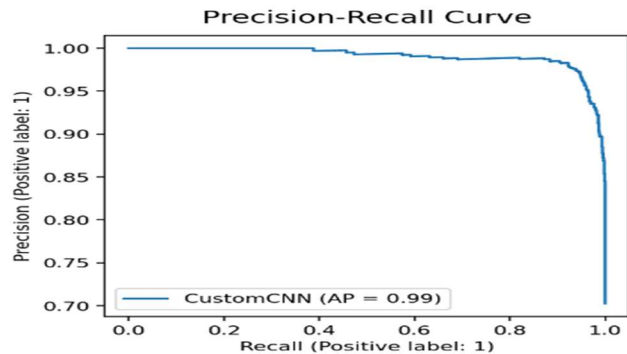


Fig 12. Precision-Recall Curve

Fig 12 shows the precision-recall curve for the breast cancer custom CNN model. The curve for the CustomCNN model is very close to the top-left corner of the graph, which is the ideal location for a precision-recall curve. This means that the Model is very good at both precision and recall. The curve is smooth and has no sharp drops, suggesting that the Model is well-calibrated. The AP (average precision) for the Model is 0.99, which is very high. This means the Model is, on average, precise and has a high recall.

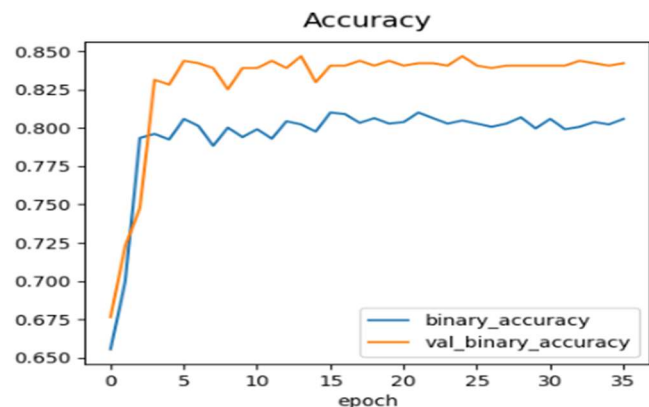


Fig 13. Accuracy For Training And Validation Set

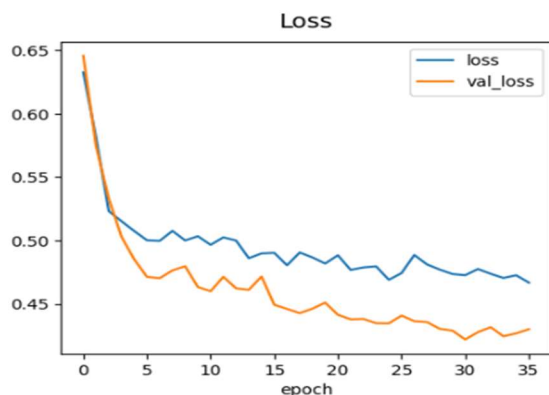


Fig 14. Loss For Training And Validation Set

Figs. 13 and 14 show the training accuracy, validation accuracy, training loss, and validation loss. The effectiveness of the custom CNN model in predicting breast cancer was revealed by the performance metrics acquired from it. The Model's capacity to reduce mistakes throughout the training phase is reflected in the training loss of 0.4667. The Model's ability to discriminate between positive and negative instances is demonstrated by the ROC AUC (Receiver Operating Characteristic Area Under the Curve) score of 0.8138; higher values indicate more substantial discriminatory power. Furthermore, a binary accuracy of 0.8058 highlights how well the Model classifies cases into binary categories.

The validation results further support the robustness of the Model. The validation loss of 0.4300 demonstrates effective data generalization, while the ROC AUC value of 0.8703 represents the Model's enhanced discriminatory ability on the validation set. The Model's ability to accurately predict binary outcomes in new situations is demonstrated by its validation binary accuracy of 0.8421.

One key hyperparameter that affects the Model's convergence during training is the learning rate (LR) of  $2.5000e-05$ . This extensive collection of metrics provides a thorough knowledge of the custom CNN's performance, including binary accuracy, learning rate, ROC AUC, and loss. This gives confidence in the custom CNN's potential value for accurate breast cancer prediction in real-world scenarios.

## B. Comparison of Results

The literature review highlights various deep learning approaches for breast cancer detection and prediction, showcasing notable achievements in accuracy, AUC, and precision-recall metrics. The hybrid convolutional and recurrent deep neural network used by [3] achieved an accuracy of 91.30%, demonstrating the potential of combining different network architectures. The ensemble of pre-trained

VGG16 and VGG19 models used by [4] achieved a higher accuracy of 95.29%, showcasing the effectiveness of leveraging pre-trained models. Transfer learning with CNNs used by [5] achieved an accuracy exceeding 96%, indicating the benefits of using pre-trained models for feature extraction. Additionally, using VGG16 for feature extraction and SVM used by [6] for classification resulted in high accuracies of 97% and 93% for binary classification of human breast cancer and canine mammary tumors, respectively. Transfer learning with VGG19 used by [7] achieved accuracies between 94.05% and 98.13%, highlighting the effectiveness of transfer learning. Lastly, the use of Alex-Net used by [11] achieved an accuracy of 95% and an impressive AUC of 99.36%, showcasing the power of deep learning in histopathology image analysis.

Comparing these results to our custom CNN model, we note that our model achieved an accuracy of 93.20% and an AUC of 98%, which is slightly lower than some of the top-performing techniques in the literature. However, it is crucial to highlight that our model is a custom CNN, unlike the others that used pre-trained models. This distinction is significant as it indicates that our model was specifically designed and trained for breast cancer detection and prediction, rather than being adapted from models trained on unrelated tasks. While our model's accuracy is slightly lower than some pre-trained models, it demonstrates competitive performance, especially considering its customized architecture. Additionally, our model achieved a precision-recall of 99%, indicating its ability to correctly identify positive cases with high precision. Overall, our custom CNN model offers a unique approach to breast cancer detection and prediction, focusing on customization and task-specific optimization, which sets it apart from the pre-trained models used in the literature.

## 5. CONCLUSION

To sum up, the methodology for predicting breast cancer that has been provided is methodical and all-inclusive; it includes data gathering, image preprocessing, building bespoke CNN models, making predictions, and analyzing. Training a robust custom CNN model starts with carefully selecting various datasets from sites like Kaggle and applying rigorous picture preprocessing methods like rescaling and data augmentation. Convolutional blocks, dropout layers, and global average pooling show how well-thought-out CNN's architecture is for hierarchical feature extraction. The Model's ability to distinguish between benign and malignant instances

is demonstrated by the evaluation metrics, which include the confusion matrix, AUC-ROC, and precision-recall curve. Additionally, the Model's performance is noteworthy for its potential clinical relevance, as evidenced by its outstanding accuracy of 0.93285, ROC AUC (0.98051), and binary accuracy scores. This methodology advances the field of breast cancer prediction by providing a valuable instrument for early diagnosis and intervention in practical situations.

#### Future Research Directions

- **Enhancing Model Generalization:** In spite of the custom CNN architecture's encouraging results in classifying images of breast cancer, more investigation is required to improve the model's generalisation over a wider range of datasets and clinical contexts. It might be possible to adapt the model to different imaging protocols and tissue preparation techniques that are frequently encountered in real-world scenarios by looking into transfer learning techniques or domain adaptation methods.
- **Validation on Diverse Patient Populations:** The majority of the images in the BreakHis dataset used in this study come from a particular demographic or geographic area. Future studies should confirm how well the customised CNN architecture performs on a wider range of patient populations to guarantee that it can be applied to a variety of age groups, ethnicities, and healthcare environments.

#### REFERENCES

- [1] Amethiya Y, Pipariya P, Patel S, Shah M. Comparative analysis of breast cancer detection using machine learning and biosensors. *Intelligent Medicine*. 2022;2(2):69-81.
- [2] Balasubramaniam S, Velmurugan Y, Jaganathan D, Dhanasekaran S. A modified LeNet CNN for breast cancer diagnosis in ultrasound images. *Diagnostics*. 2023;13(17):2746.
- [3] Yan R, et al. Breast cancer histopathological image classification using a hybrid deep neural network. *Methods*. 2020; 173:52-60.
- [4] Hameed Z, Zahia S, Garcia-Zapirain B, Aguirre JJ, Vanegas AM. Breast cancer histopathology image classification using an ensemble of deep learning models. *Sensors*. 2020;20(16):4373.
- [5] Sharma T, Nair R, Gomathi S. Breast cancer image classification using transfer learning and convolutional neural network. *International Journal of Modern Research*. 2022;2(1):8-16.
- [6] Kumar A, et al. Deep feature learning for histopathological image classification of canine mammary tumours and human breast cancer. *Information Sciences*. 2020; 508:405-421.
- [7] Boumaraf S, et al. Conventional machine learning versus deep learning for magnification dependent histopathological breast cancer image classification: A comparative study with visual explanation. *Diagnostics*. 2021;11(3):528.
- [8] Murtaza G, et al. Deep learning-based breast cancer classification through medical imaging modalities: state of the art and research challenges. *Artificial Intelligence Review*. 2020; 53:1655-1720.
- [9] Shahidi F, Daud SM, Abas H, Ahmad NA, Maarop N. Breast cancer classification using deep learning approaches and histopathology image: a comparison study. *IEEE Access*. 2020; 8:187531-187552.
- [10] Hirra I, et al. Breast cancer classification from histopathological images using patch-based deep learning modelling. *IEEE Access*. 2021; 9:24273-24287.
- [11] Senan EM, Alsaade FW, Al-Mashhadani MIA, Theyazn HH, Al-Adhaileh MH, et al. Classification of histopathological images for early detection of breast cancer using deep learning. *Journal of Applied Science and Engineering*. 2021;24(3):323-329.