SSRG International Journal of Electronics and Communication Engineering Volume 10 Issue 8, 36-47, August 2023
ISSN: 2348-8549/ https://doi.org/10.14445/23488549/IJECE-V10I8P104

Original Article

An Intelligent Model for Improved Breast Cancer Prognosis

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Received: 05 June 2023 Revised: 10 July 2023 Accepted: 05 August 2023 Published: 31 August 2023

Abstract - *This research suggests developing a deep learning model using customized CNN to categorize and predict breast cancer in a timely period. The model utilizes a large dataset of breast cancer images obtained from Kaggle, an online research repository. Pre-processing techniques were applied to the images to eliminate noise, such as shadows on the images, and resize the images to lessen the high computation cost. The dataset was separated into training set 80% (48, 852) and test set 20% (16, 284). CNN was employed to mine meaningful features from the images and to classify them based on predefined criteria, assessing the presence and severity of breast cancer. Additionally, the model could provide treatment recommendations depending on the patient's health account and other pertinent aspects. The model's performance was evaluated using a confusion matrix, revealing a 95% accuracy rate, 100% recall value, 90% precision value, and 95% F1 score. The classifier's AUC value was 88%, indicating high reliability for breast cancer prognosis. The proposed methodology may significantly increase diagnostic speed and accuracy, resulting in earlier detection and better patient outcomes.*

Keywords - *Breast cancer, Classification, CNN, Deep learning, Prognosis.*

1. Introduction

Breast malignancy is the principal reason for demise amongst womenfolk worldwide and is the most significant widespread malignant cells in womenfolk. In the United States, many women are diagnosed with invasive and non-invasive breast cancer. Nigeria has traditionally had a low incidence of breast cancer but has increased due to lifestyle changes and urbanization. Breast malignancy or growth is presently the prominent root of cancer-associated demises in Nigeria [1]. Survival rates for breast cancer have improved but vary significantly between individuals [2]. Accurately predicting breast cancer can help healthcare professionals make better treatment decisions, avoid unnecessary therapies, and reduce costs [3]. The Centers for Disease Control and Prevention (CDC) describes breast malignancy as an ailment that originates in the breast but can blow out to other portions of the human system through metastasis [4].

Fatima et al. [5] classified various types of breast cancer, including Mucinous Breast Cancer (MBC), Inflammatory Breast Cancer (IBC), Ductal Carcinoma in Situ (DCIS), Invasive Ductal Carcinoma (IDC), and Mixed Tumour Breast Cancer (MTBC). Diagnosing breast cancer accurately is crucial in bioinformatics and medical research, but it is a challenging process with potential errors and biases [6, 7]. Several techniques are used to diagnose breast cancer, such as breast examination, mammography[8], breast ultrasound, breast biopsy, breast MRI, and PET scan [9]. Nevertheless, the particular root reasons for breast malignancy are yet to be fully understood. However, factors like age, family history, breast abnormalities, hormonal factors, obesity, alcohol consumption, and radiation exposure have been identified as risk factors [10, 11].

The prognosis of breast malignancy depends on issues like malignancy phase, growth extent, lymph node involvement, treatment type, and method of diagnosis [12, 13]. Effective prevention, detection, and treatment approaches, including hormone therapy and chemotherapy, have decreased mortality rates and increased survival [14].

Machine learning techniques, including tumour classification, gene sequence prediction, and identification of prognostic factors, have revealed promise in breast cancer research [15, 16]. Breast malignancy or cancer presents challenges, particularly in Africa, where aggressive tumours and younger patient profiles contribute to high mortality rates [17]. Early detection and efficient diagnostic models are essential in reducing breast cancer-related deaths [18]. Breast self-examinations have limitations, causing anxiety and requiring further tests for confirmation [6].

Mammography, the primary screening tool, has limitations in detecting all types of breast cancer and can result in false positives [19]. Integrating artificial intelligence into mammogram interpretation can improve accuracy and early detection [6]. Developing a deep learning model for the prognosis of breast cancer using CNN is the primary focal point of this study.

2. Related Works

Dhahri et al. [20] utilized genetic program writing to spontaneously find a solution to the best-fit technique for breast cancer diagnosis by using hybridization of features pre-processing and classification techniques[21]. They demonstrated the effectiveness of genetic programming in accurately diagnosing breast cancer.

Abbas et al. [22] proposed a novel approach called BCD-WERT for breast malignancy or cancer detection. The authors employed a mighty randomized tree and whale optimization technique for feature grouping and selection. Results revealed that the BCD-WERT outperformed other machine learning algorithms, achieving high accuracy rates and demonstrating the usefulness of feature map collection methods.

Amrane et al. [16] presented a comparative study between K-Nearest Neighbor (KNN) and Naive Bayes (NB) techniques for breast malignancy classification based on the Wisconsin dataset for Breast Cancer. Results revealed that the KNN achieved a higher accuracy rate when compared to NB.

Asri et al. [23] also evaluated the strength of different techniques such as Support Vector Machine (SVM), Decision Tree (DT), K-NN and NB for breast malignancy risk prediction and prognosis. Findings revealed that SVM attained the uppermost accuracy rate of 97.13%.

Alanazi et al. [24] suggested an approach for breast malignancy prediction using CNN. The approach achieved a higher accuracy rate than traditional machine learning techniques, reducing human errors and improving the diagnostic process.

Taher and Shaimaa [25] utilized Probabilistic Neural Network (PNN), Multi-Layer Perceptron (MLP), and Radial Basis Function (RBF) for breast cancer classification. The MLP achieved high accuracy rates for both training and testing datasets.

Alickovic & Subasi [26] applied Genetic Algorithm (GA) and Random Forest (RF) techniques for breast malignancy classification. The RF with GA attribute selection achieved a higher accuracy rate of 99.48%.

Tice et al. [27] designed a prognostic model for estimating breast malignancy risk using clinical factors and mammographic breast density. The model showed minor insight comparing breast cancer survivors and those who do not, providing a 5-year risk assessment for invasive breast cancer. Rashed & Seoud [28] offer a CNN-based deep learning method for breast cancer prognosis. Their results outperformed well-known structures such as AlexNet, VGGNet, and GoogleNet, achieving high accuracy of 94% for micro-classification and masses.

Keikha & Tamandani [29], authors utilized a Recursive Convolutional Neural Network (R-CNN) for the organization and forecast for breast cancer. Results revealed that the R-CNN achieved good sensitivity, specificity, and AUC, indicating its potential accuracy rate of 90% for breast cancer detection.

Shwetha et al. [30] used deep learning techniques and the Inception V3 architecture for breast cancer detection. They found that the model attained an accuracy rate of 83% in breast cancer prediction.

Chtihrakkannan et al. [31] employed an MLP in a deep-learning neural network classifier for breast cancer detection, achieving an accuracy rate of 92%.

To sum up, these research studies illustrate the effectiveness of techniques in Machine Learning (ML), including neural networks, genetic programming, SVM, and deep learning, in precisely diagnosing and predicting breast cancer.

These approaches hold promise in enhancing breast cancer detection and classification, thereby contributing to early identification and treatment. However, one main area that the proposed study aims to address is the limited research on post-classification models for predicting the severity of breast cancer. While CNN-based models have been extensively studied for diagnosing breast cancer, there is a need for further research on models that can predict the severity of the disease.

This research gap is essential to bridge because accurate prediction of breast cancer severity is crucial for determining appropriate treatment strategies and improving patient outcomes.The proposed study aims to develop a post-classification model to fill this research gap and contribute to the advancement of more effective methods for breast cancer diagnosis and treatment.

3. Materials and Methods

3.1. Data Source

Sixty-five thousand one hundred thirty-six breast cancer images were acquired from the breast histopathology section on the Kaggle online research community.

3.2. Data Description

The dataset is 980 MB and is organized into two folders: one for testing and the other for training. The training dataset covers 75% of the total, with 48,852 images, while the test dataset represents the remaining 25%, with 16,284 images. Figure 1 depicts the dataset splitting ratio.

The sample test dataset, shown in Figure 2, refers to a portion of the entire dataset used to assess the effectiveness and precision of the suggested model. It is used to judge how commendably the model generalizes to new, unconfirmed data. The Sample test dataset, frequently different from the training dataset used to build the model, is used to evaluate the model's propensity to make predictions or assign categories to fresh data. It aids in assessing the model's efficacy and dependability in real-world circumstances.

3.3. System Architecture

The system architecture comprises a system's components, modules, and interactions, as well as its overall design and structure. It determines the best configuration for multiple components to achieve the system's goals and expected functioning. The proposed system's architecture covers data processing, image analysis, and classification related to the overall breast cancer diagnosis system design depicted in Figure 3.

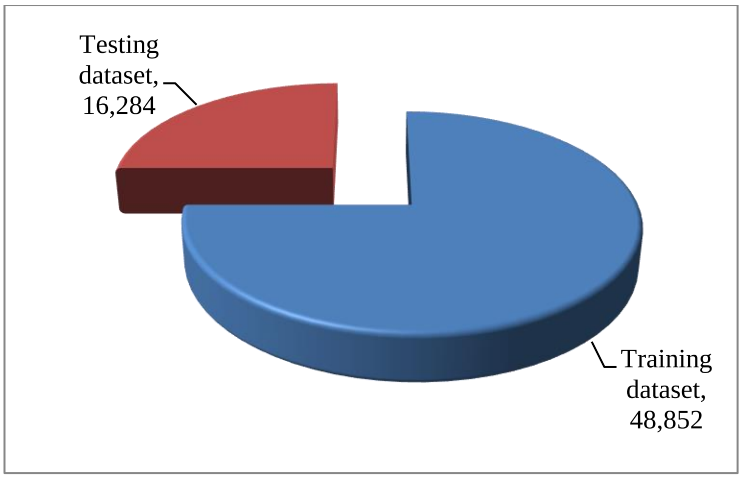

Fig. 1 Dataset split ratio

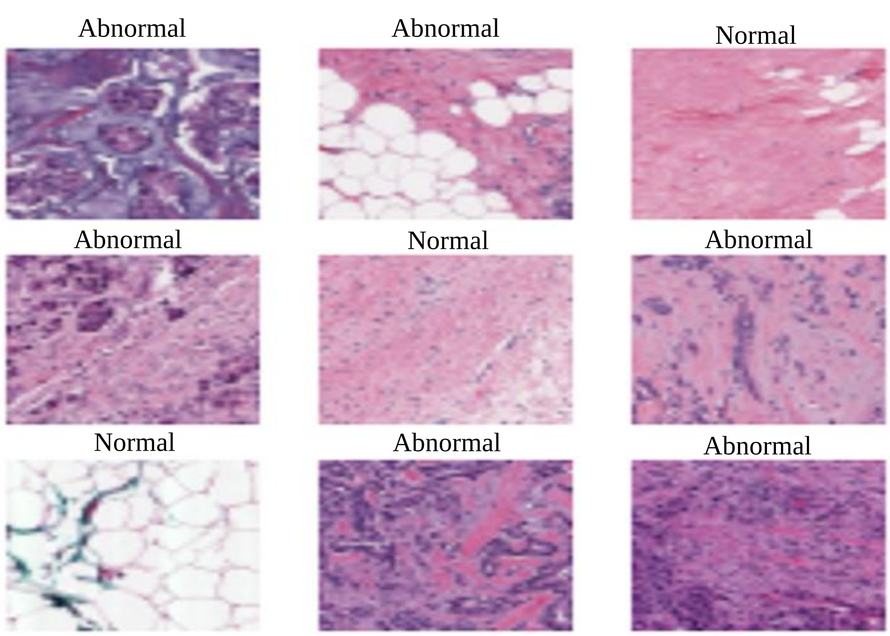

Fig. 2 Sample test dataset

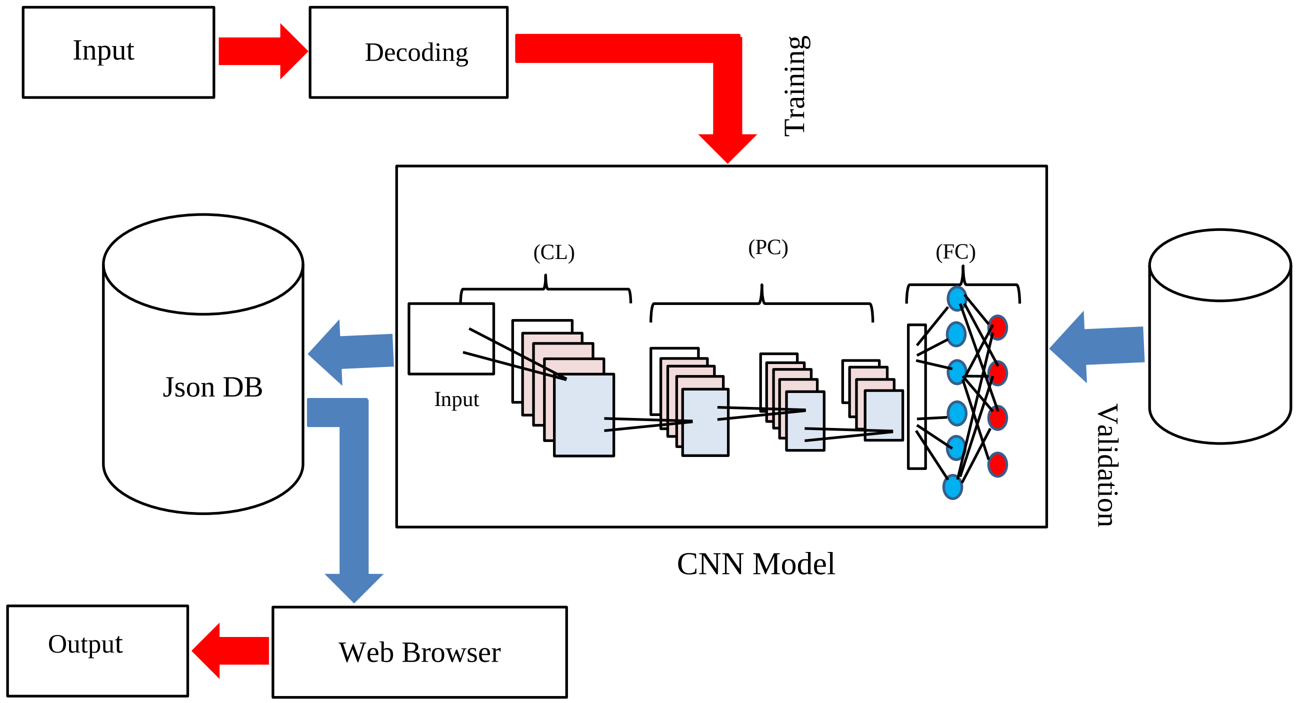

Fig. 3 The proposed system architecture

The proposed system blueprint or architecture, as depicted in Figure 3, illustrates the process flow of the entire system for breast cancer detection. The breast cancer images undergo various steps, including processing and encoding into RGB images, then training the model using CNN.

The CNN-based model consists of multiple convolutional and maximum pooling layers and a Rectified Linear Unit (ReLU) for feature extraction from the input images.

A Fully Connected layer (FC) is then utilized to flatten the extracted features, passed to the output layer for classification. The combination of the FC layer and output layer forms the CNN grouping procedure. In this process, an image is classified as 0 when no breast cancer is identified and one whenever the model identifies the presence of breast malignancy or cancer.

3.4. The CNN Algorithm Executed

An algorithm is a set of precise guidelines to solve a specific task or problem. This section focuses on implementing efficient algorithms to guarantee the usefulness of the developed classifier model in terms of time and space complexity. Table 1 provides a detailed explanation of the CNN algorithm employed in developing the proposed model. CNN is known for their superior performance in image classification. It contains three essential kinds of layers: (a) Convolution Layer (CL), (b) Pooling Layer (PL), and (c) Fully-Connected Layer (FC).

These layers play crucial roles in the CNN architecture, allowing for the mining meaningful features from input digital images. The CNN algorithm comprises these layers, contributing to the model's ability to classify images accurately.

Table 1. CNN algorithm implemented

CNN Algorithm	
Step 1:	Convolutional Layer: The convolution operation is represented as C = f(W * I + b), where f() is the activation function.
Step 2:	Activation Function: ReLU presents non-linearity by applying the element-wise operation R(x) = max(0, x) to each element of the feature map C.
Step 3:	Pooling Layer: The pooled feature map, P, is obtained by downsampling the feature map C using pooling operations such as max pooling or average pooling.
Step 4:	Repeated Convolution and Pooling: Multiple convolutional and pooling layers, denoted as C1, C2, ..., Cn, P1, P2, ..., Pn, can be stacked to capture hierarchical features.
Step 5:	Fully-Connected Layer: The flattened vector representation of the last pooled feature map, denoted as F, is multiplied with learnable weights, W_fc, and added with biases, b_fc, to obtain the output of the FC layer, denoted as O_fc. This can be represented as O_fc = W_fc * F + b_fc.

Step 6: Output Layer: The FC layer output is fed into the output layer, which applies an appropriate activation function, such as softmax, to produce a probability distribution over the classes.

Step 7: Loss Function: The categorical cross-entropy loss function, denoted as L, measures the discrepancy between the predicted probabilities, P_pred, and the true labels, P_true. It is calculated as L = -sum(P_true * log(P_pred)).

Step 8: Optimization: The network parameters, including the filter weights, biases, and fully-connected layer weights, are updated iteratively using optimization algorithms. The update rule for a parameter, θ, is given by θ_new = θ_old - learning_rate * gradient, where the gradient is computed through backpropagation.

Step 9: Training and Evaluation: The CNN is trained on a labelled dataset by minimizing the loss function through iterative updates.

The CNN layers play a crucial role in extracting convolutional features, which are essential for the decision support system. Equations (1) and (2) represent the mathematical operations involved in performing 2D convolutions.

$$\mathrm{y}[\mathrm{m},\mathrm{n}] = x[m,n]x\ h[m,n] \tag{1}$$

$$y[m,n] = \sum_{i=-\propto}^{\propto} \sum_{j=-\propto}^{\propto} x[i,j]\ .\ h[m-i,n-j] \tag{2}$$

Where x[m, n] = Input, m, n = number of rows and number of columns correspondingly, i, j = row index and column index.

Similarly, Equation (3) provides the size of the image following convolution:

$$size = \left[\left(\frac{m+2p-n}{s} + 1,\quad \frac{m+2p-n}{s} + 1\right)\right] \tag{3}$$

Where m = quantity of input characteristics; n = size of the convolution kernel; p = padding; s = stride.

The mini-batch mean is calculated mathematically using Equation (4):

$$\mu\beta = \frac{1}{m}\sum_{i-1}^{m} x_i \tag{4}$$

Equation (5) displays the variance in the mini-batch:

$$ {}^{2}_{\beta} = \frac{1}{m}\sum_{i-1}^{m}(x_i - \mu\beta)^{2} \tag{5}$$

While Equation (6) provides normalization:

$$\overline{x_i} = \frac{x_i - \mu\beta}{\sqrt{\sigma_\beta^2 + \varepsilon}} \tag{6}$$

In Equation (7), categorical cross-entropy is displayed:

$$L[y,y] = -\sum_{j=0}^{M} \sum_{i=0}^{M} [y_{ij}\ x\ Log(y_{ij})] \tag{7}$$

3.5. System Deployment

Making the developed breast cancer diagnosis system accessible to users in a production environment is known as system deployment. It involves setting up the infrastructure, configuring the parts, and ensuring appropriate connectivity. Once the system is in place, users can interact with it, upload images for analysis, and get diagnosis results.

As illustrated in Figure 4, after the model has completed its training and validation, it is deployed to run in a web browser using the Flask framework.

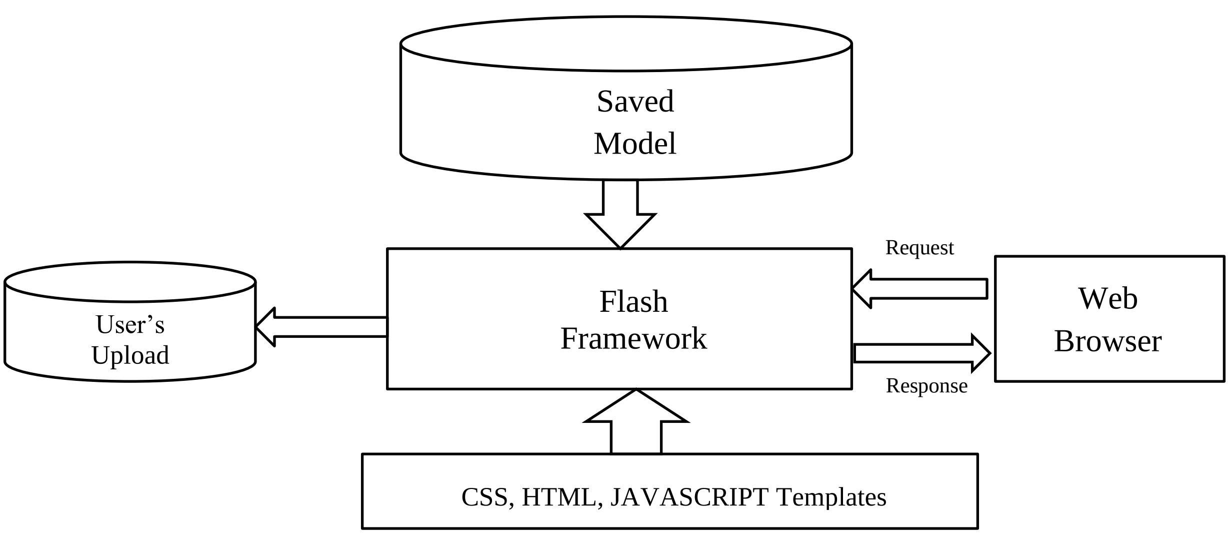

Fig. 4 Diagram showing the proposed model's deployment

The Flask framework handles the response and request interactions between the web browsers and the saved model, which is stored as a JSON file. The uploaded image is preserved in the Upload database when a user for testing uploads it. Flask then uses the previously saved model to execute the architecture's various steps. These steps involve processing and analysing the uploaded image before generating the final output, which is then sent back to the web browser. Finally, in conjunction with Flask, the deployed model enables users to upload images, process and analyse them, and receive the corresponding output through the web browser.

3.6. Experimental Setup

Table 2 presents the experimental setup environment used in the research, including the brand of the computer, processor details, RAM capacity, disk space, operating system, and the programming language and libraries utilized. The computer system was an HP Elitebook with an Intel Core i7-7300U CPU running from 2.60GHz to 2.71GHz. It had 32GB of RAM and a 1 Terabyte HDD for storage. Python 3.8.0, TensorFlow 2.6.1, Keras 2.2.4, Anaconda 3, and Google Colab with GPU were used as programming languages and libraries. The operating system utilized was Ubuntu 18.0.4 server core.

Table 2. Experimental setup environment

S/N	Computer Specification/Setup Environment
1	Computer brand: HP Elitebook
2	Processor: Intel Core i7-7300U CPU 2.60GHZ, 2.71GHZ
3	RAM: 32GB RAM
4	Disk space: 1 Terabyte HDD
5	Operating System: Ubuntu 18.0.4
6	Programming language & libraries used: Python 3.8.0, Keras 2.2.4, TensorFlow 2.6.1, Anaconda 3, Google Colab with GPU

4. Results and Discussion

4.1. Training Results

A customized CNN (Convolutional Neural Network) is the model type employed in the experiment. The input images were scaled between 0 and 1. The CNN's default input shape was 50x50 pixels with three channels (RGB). The model had 70,017 trainable parameters. The model had 240 minutes of training. Figures 5 and 6 show that the proposed model has an 85.6% training accuracy and an 86.4% validation accuracy. The proposed model's training progressed throughout ten epochs. A complete iteration of the training dataset is represented by one epoch. Based on the computed loss from the training phase, the model's weights are updated, and the learning rate is also modified. Loss, accuracy, validation loss, and validation accuracy are among the parameters that were recorded.

While accuracy counts the percentage of adequately identified samples, loss shows the inconsistency between the predictable and actual values. Analysis of the findings reveals that the loss and validation loss rapidly reduce across epochs, demonstrating that the model is improving its predictions, as shown in Figure 5. The accuracy and validation accuracy also improve, as shown in Figure 6, suggesting that the model's performance improves.

The reported Learning Rate (LR) remains constant at 1.0000e-05 throughout the training process. In all, these results demonstrate the progress and performance of the model during the training phase. Further analysis and evaluation of test datasets would be necessary to assess the model's generalization and effectiveness in real-world scenarios. These findings show that the customized CNN model worked reasonably accurately.

4.2. ROC/AUC Graph

The ROC curve illustrates the trade-off between a classifier's TPR (recall) and FPR. The sensitivity signifies the genuine positive rate, while specificity signifies the TNR. These values are plotted to create the ROC curve. As depicted in Figure 7, the ROC curve was created using the roc_curve function, which takes the FPR and TPR values as inputs and produces the curve. The curve was then visualized using Matplotlib. A good classifier strives to be as far from the dotted line in the plot, just before the top-left angle of the figure, which reflects the ROC curve of a random classifier. The ROC AUC is used to compare the breast cancer classifier. This value provides a quantitative measure of the classifier's performance. A random classifier would have a value of 0.5, and a perfect classifier would have a ROC AUC value near or equal to 1.

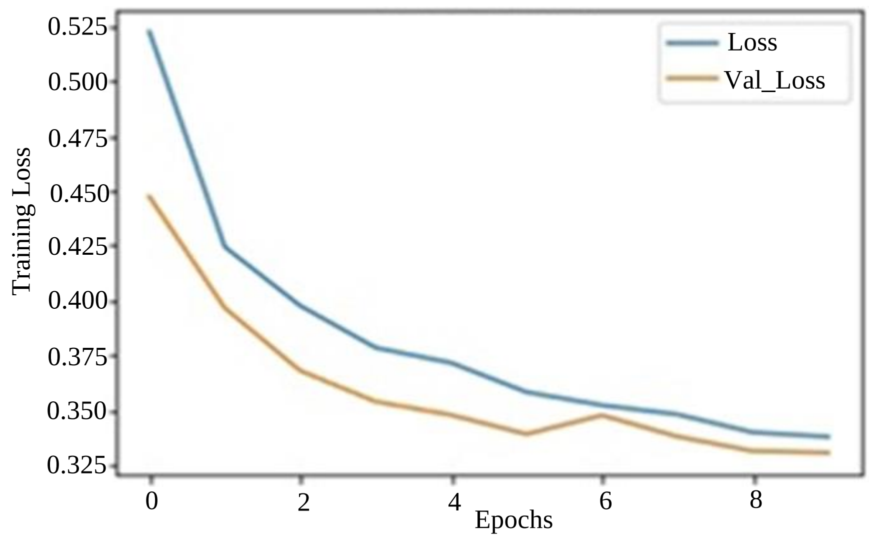

Fig. 5 Proposed CNN model's loss evaluation diagram

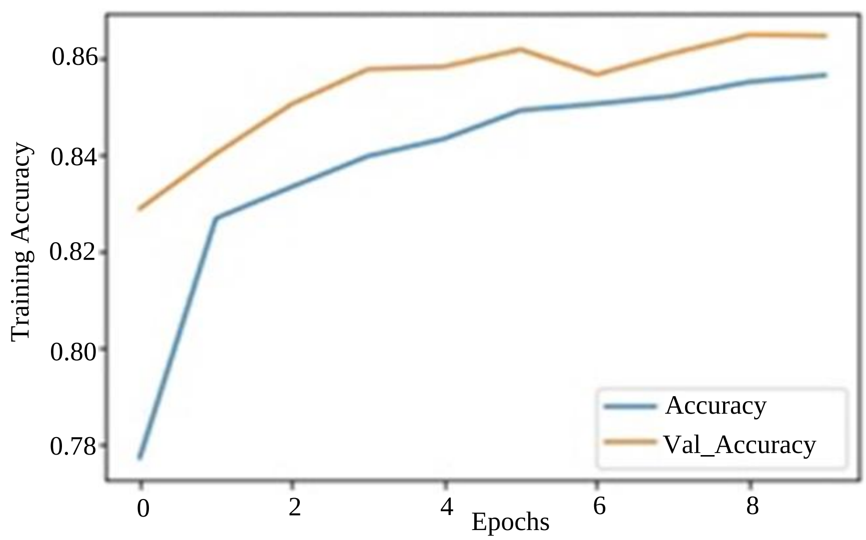

Fig. 6 Proposed CNN model's accuracy evaluation diagram

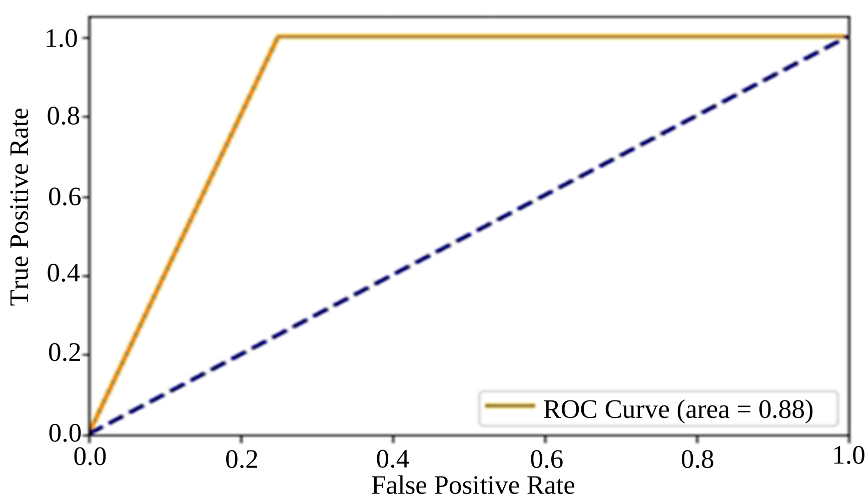

Fig. 7 ROC curve

The ROC AUC value for the discussed classifier is 0.88, indicating that it performs well and is recommended for breast cancer screening.

In conclusion, the ROC curve and ROC AUC value show how well the classifier identifies positive and negative cases in breast cancer screening. The classifier performs well, and a higher ROC AUC indicates it is good at spotting breast cancer instances.

4.3. Evaluation Procedure

The confusion matrix is a good technique for evaluating a classification model's effectiveness. We can use it to calculate other metrics such as accuracy, precision, recall, and F1 score because it gives us a complete breakdown of the anticipated and actual class labels. The genuine class labels from a test dataset are contrasted with the predicted class labels to create a confusion matrix. False Negatives (FN), True Negatives (TN), True Positives (TP), and False Positives (FP) make up the matrix's four values.

$$\text{Accuracy} = \frac{\text{TP} + \text{TN}}{(\text{TP} + \text{TN} + \text{FP} + \text{FN})} \quad (8)$$

$$\text{Precision} = \frac{\text{TP}}{\text{TP}+\text{FP}} \quad (9)$$

$$\text{Recall} = \frac{\text{TP}}{\text{TP}+\text{FN}} \quad (10)$$

$$\text{F1} - \text{Score} = 2 * \frac{(\text{Recall}*\text{Precision})}{(\text{Recall}+\text{Precision})} \quad (11)$$

Eighty test samples were used to assess the proposed breast cancer classifier created. We analyzed the test generator's prediction function to generate a binary class that was rounded up to provide a clear distinction between abnormal and normal breast cancer. The accurate or actual classes are set as y_true in the test generator classes for the test examples. y_val is assigned to the prediction's output. By developing a definition to plot and paint our confusion matrix accurately, we compared the two values and plotted a confusion matrix, as shown in Figure 8.

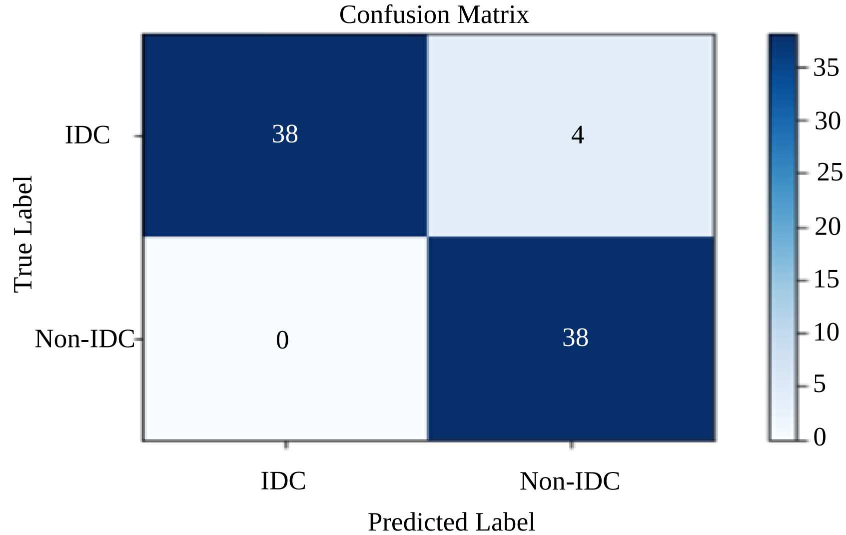

Fig. 8 Confusion matrix based on 80 test samples

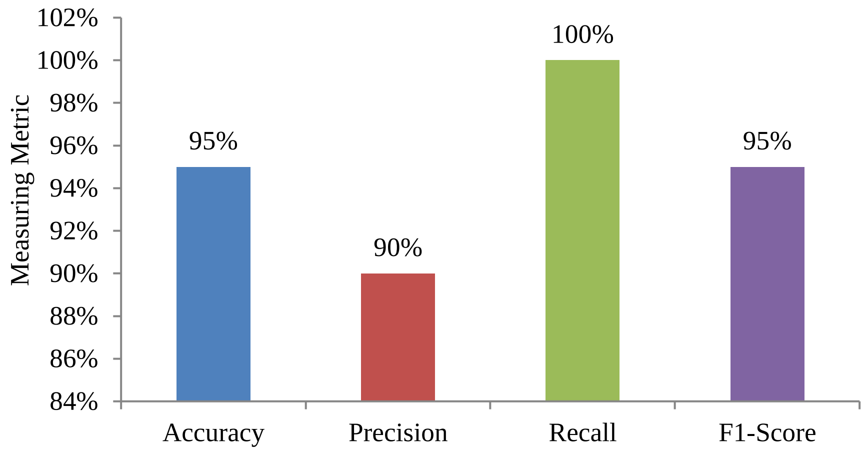

Fig. 9 Model's performance

Figure 9 demonstrates the proposed breast cancer classification model's performance with a high accuracy of 95%, which indicates that it correctly identified the majority of occurrences in the test dataset. It also displayed a 90% precision, meaning that 90% of predicted positive instances were genuinely positive. By accurately detecting every instance of positivity, the model attained a recall of 100%. In order to balance the precision and recall values, a statistic known as the F1-score was calculated; these measures show the model's excellent performance in correctly categorizing breast cancer cases as a whole. It is essential to consider these measures when addressing breast cancer diagnosis and therapy to guide medical judgment and improve patient outcomes.

4.4. System Comparative Analysis

Comparing several systems' accuracy levels can provide us with an understanding of how well they operate and point us in the direction of the system that will diagnose breast cancer the most accurately. Accuracy is a regularly used indicator to assess how well a system predicts outcomes. Higher accuracy translates to a more substantial capacity to correctly identify cases as either malignant or non-cancerous in the context of a breast cancer diagnosis.

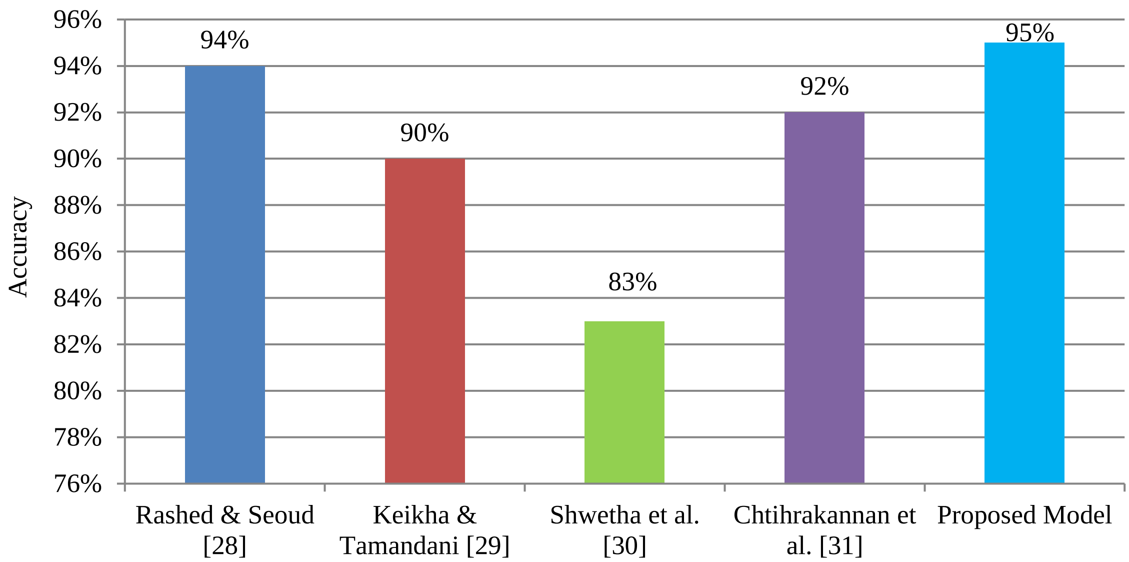

Fig. 10 Model performance evaluation

The accuracy of a model is an important metric to evaluate its performance in classification tasks. In Figure 10, various authors have reported the accuracy achieved by their respective models for breast cancer diagnosis.

Rashed & Seoud [28] achieved an accuracy of 94%, indicating a high level of accuracy in their model.

Keikha & Tamandani [29] reported an accuracy of 90%, slightly lower than Rashed & Seoud [28], but still demonstrates a reliable performance.

Shwetha et al. [30] achieved an accuracy of 83%, which is comparatively lower than the previous two models.

Chtihrakkannan et al. [31] reported an accuracy of 92%, indicating good performance in their model. This study's proposed model had a 95% accuracy rate, the highest among all the models discussed. This suggests that the proposed model performs well in accurately classifying breast cancer cases. Comparing the accuracies of the different models, it is evident that the suggested model outperforms other models evaluated, such as Rashed & Seoud [28], Keikha & Tamandani [29], Shwetha et al. [30], and Chtihrakkannan et al. [31]. This demonstrates the proposed model's potential efficacy for diagnosing breast cancer.

Remembering that accuracy might not give a complete picture of a model's performance is crucial. Additional evaluation metrics like precision, recall, and F1-score should also be considered to evaluate the models' overall effectiveness and dependability. In all, the high accuracy achieved by the proposed model suggests its potential usefulness in accurately diagnosing breast cancer, but further analysis and evaluation are necessary to validate its performance and compare it with other relevant models.

4.5. Model's Interface for Prognosis

The user-friendly interface of the breast cancer prognosis model offers a convenient means of entering pertinent data and generating predictions about the prognosis of breast cancer. These forecasts can aid medical professionals in making well-informed choices regarding treatment strategies and patient care. The interface is also helpful in oncology, helping with breast cancer assessment and prognosis.

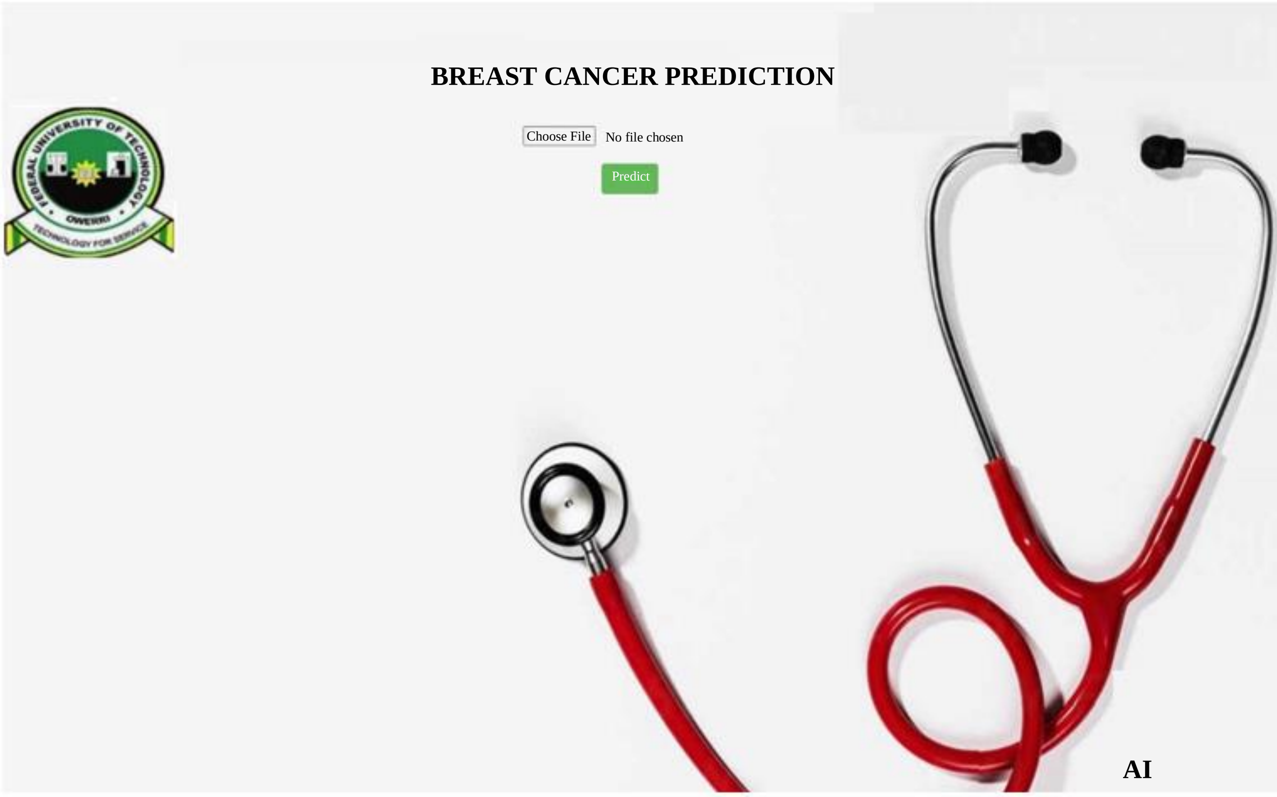

Fig. 11 Model's interface

The deployment landing page of the model, as shown in Figure 11, includes a file button for uploading a Breast cancer image and a foretell button to start the Flask program (app.py). The saved weights from training are loaded and initialized in the application code.

The model resizes the input image to match its learned dimensions of 50x50 pixels because the prediction process is size-invariant. A normalization step is then applied to ensure all image pixels fall between 0 and 1. An image from the test set is randomly chosen by the interface and sent to the model for forecasting. The sigmoid function causes the model's forecast to range between 0 and 1.

A prediction of 0 indicates that cancer is "Lacking," while a prediction of 1 indicates that cancer is "Present." Extra evidence is provided by the probability based on the projected class, with severe instances having a probability further away from 0.3 in the negative direction and moderate cases having a probability between 0.3 and 0.5.

The recommender system responds promptly based on the projected class and its corresponding likelihood. In addition, the deployed model's interface allows users to upload digital breast cancer images for prediction. The model predicts the existence or lack of cancer, along with the associated probability.

5. Conclusion

In conclusion, the research paper focused on creating and assessing a unique CNN method for breast cancer classification. The suggested method displayed a reasonable accuracy rate, recall value, precision and F1-score, demonstrating its efficacy in correctly diagnosing breast cancer cases. The system architecture included data processing, picture analysis, and classification, offering a thorough strategy for diagnosing breast cancer. The model was trained and assessed using a dataset of 65,136 images of breast cancer.The training procedure improved throughout epochs, with reduced loss and rising accuracy. The ROC curve analysis proved the model's capability to differentiate between positive and negative situations.

The deployment of the model on a web browser using the Flask framework provided a user-friendly interface for breast cancer prognosis. Users could upload breast cancer specimen images and receive predictions about the presence or absence of cancer, along with associated probabilities. The interface facilitated quick and easy to get to breast cancer diagnosis. Comparing the accuracy levels of diverse breast cancer classification models, the proposed method beat previous models examined based on their accuracy rates. However, further analysis and evaluation are needed to comprehensively assess the model's performance and compare it with relevant models using additional evaluation metrics. The study emphasized the significance of a precise breast cancer diagnosis to inform treatment choices and enhance patient outcomes. It stressed the need for effective diagnostic models and early diagnosis, particularly in areas with high incidences of breast cancer mortality. The use of artificial intelligence to improve accuracy and enable early detection in diagnostic instruments like mammography is one of the paths for future research. Additionally, the dataset must be expanded to confirm the model's efficacy in clinical settings, and test datasets must undergo in-depth analysis. Furthermore, it is advised to include explainable AI capabilities in the model. Future research should examine the utility of vision transformer and MLP auto-encoder models in predicting breast cancer prognosis.

The customized CNN model built shows promising potential for accurate breast cancer diagnosis and can change breast cancer screening and treatment recommendations.

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