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BCDNN: Enhancing CNN Model for Automatic Detection of Breast Cancer Using Histopathology Images

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ABSTRACT

The United Nations has identified health and well-being for all as one of its sustainable development goals. Research efforts in the healthcare domain worldwide are aligned with this goal. According to the World Health Organization (WHO), there has been an increasing incidence of breast cancer globally. The emergence of Artificial Intelligence (AI) has enabled learning-based approaches for diagnosing various ailments in the healthcare domain. Numerous efforts have been designed to efficiently diagnose breast cancer using deep learning algorithms, with the Convolutional Neural Network (CNN) being the widely used model due to its efficiency in processing medical images. However, CNN-based models may experience deteriorated performance without empirical studies to improve the underlying architecture. Motivated by this fact, our paper proposes a deep learning-based system for breast cancer diagnostic automation by enhancing a CNN model called the Breast Cancer Detection Neural Network (BCDNN). We also introduce an algorithm called Enhanced Deep Learning for Breast Cancer Detection (EDL-BCD), which leverages the enhanced deep learning model for better disease diagnosis performance. Our evaluation with a benchmark dataset comprising breast histopathology images shows that our suggested framework significantly outperforms state-of-the-art models, achieving an impressive accuracy of 97.99%. Therefore, the proposed system can be integrated with healthcare applications to assist in automatic screening by utilizing histopathology pictures to visualize breast cancer.

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1. INTRODUCTION

Breast cancer is a complex and prevalent sickness that raises health issues globally and may even be fatal. It is caused by the aberrant growth of malignant cells that originate in the ducts or lobules of the breast tissues. Many different variables might contribute to breast cancer, such as genetics, lifestyle, gender, and family history. MRIs, mammograms, ultrasounds, and histopathological images are various imaging modalities used to identify the condition [1]. Technology-driven solutions for breast cancer screening have been made feasible by artificial intelligence. These techniques employ machine learning and deep learning models for detection. Because these learning-based methods use previous data to learn, they may be able to provide well-informed diagnoses [2]. The automated identification of breast cancer from histological images has shown promise when employing deep learning models, ensemble techniques, and compelling feature extraction strategies [3]. Histopathology photos have been proven to help improve breast cancer detection despite the

difficulties presented by the nature of crystal pathology imaging. CNN variations are also appropriate for medical image analysis; nevertheless, these models must be improved to handle histopathological images for automated breast cancer identification [4], [5].

This study aims to discuss the shortcomings of the available breast cancer detection techniques. Our suggested method entails creating a deep learning framework for breast cancer diagnosis on auto-pilot. We have enhanced a CNN model, the Breast Cancer Detection Neural Network (BCDNN), and introduced an algorithm called Enhanced Deep Learning for Breast Cancer Detection (EDL-BCD). These improvements have led to better disease diagnosis performance. Our evaluation using a benchmark dataset of breast histopathology images demonstrates that the remarkable precision that our suggested model obtains of 97.99% outperforms existing models. Compared with the current CNN-based approaches which are mainly based on standard normalization layers and heavy architectures, the proposed BCDNN embeds Instance Normalization for small medical datasets and lightweight fully connected architectures to enhance classification accuracy and generalization capability on the breast histopathology images. This emphasis on stability, efficiency, and improved performance is the main novelty of our work. Our system can be integrated into healthcare applications to automatically screen histopathological scans for breast cancer. The rest of the document is organized as follows: - Section 2 examines current deep learning techniques for various imaging modalities-based automated breast cancer diagnosis. - Section 3 - Section 4 presents our empirical study and results, along with various insights and observations, and the process for improving the CNN model's breast cancer detection performance. - Section 5 discusses the research, providing the study's limitations. - Section 6 provides conclusions and guidelines for future studies to further the state of the art in breast cancer detection.

2. RELATED WORK

Multiple Models of deep learning have been applied in the research of breast cancer detection with various imaging modalities. Mahmud et al. [1] achieved a 90.2% accuracy using the ResNet50 model. Both men and women can be affected by breast cancer, and histopathological scans can assist in diagnosis. Abbasniya et al. [2] focused on preventing breast cancer, which is common in women. They proposed a CAD system using histology and achieved an accuracy of 96.82%-97.01% with the IRv2-CXL model on the BreakHis dataset. Gecer et al. [3] produced a deep learning system that achieved accuracy comparable to pathologists' diagnoses for five classes of breast histopathology. Budak et al. [4] created a full model including layers of FCN and Bi-LSTM to detect breast cancer, demonstrating exceptional accuracy on the BreaKHis database. Aresta et al. [5] enhanced the categorization by capturing pictures from breast cancer histopathology using convolutional neural networks, achieving 87% accuracy.

Yang et al. [6] presented a directed attention strategy for classifying breast cancer histology pictures that outperformed state-of-the-art techniques on the BACH dataset. Vo et al. [7] proposed a convolution network with incremental boosting for the detection of breast cancer, which outperformed conventional techniques. Sharma and Mehra [8] investigated the categorization of pictures from breast cancer histology and discovered that transfer learning with VGG16 + SVM (L, 1) achieved high accuracies across all magnifications. Dabeer et al. [9] highlighted the importance of using machine learning to detect breast cancer early and applied it to histopathological images, with CNN accuracy rates reaching the highest level. Shallu and Mehra [10] found that VGG16 outperformed VGG19 and ResNet50 in accuracy at 92.60% when trained with transfer learning. They highlighted the importance of network bias in performance and emphasized the need for larger datasets, sophisticated augmentation methods, and fine-tuning layers for future improvements. Li et al. [11] improved network training with the "concentric loss" function, achieving F-scores of 0.562 to 0.673 on datasets and showing promise for mitotic detection model improvement. Kumar et al. [12] introduced a VGGNet-16 framework for automated CMT binary classification and human breast cancer detection, achieving high accuracies. Talo et al. [13] demonstrated the effectiveness of automated histopathology image analysis using transfer learning with DenseNet-161 and ResNet-50. Roy et al. [14] suggested a classifier based on patches (PBC) for histological breast image classification, achieving 87% accuracy on the ICIAR-2018 dataset. Naylor et al. [15] suggested using open code and annotated datasets to differentiate cell nuclei on tissue slides stained with hematoxylin and eosin using fully convolutional networks.

Sudharshan et al. [16] emphasized the importance of using MIL to help computer-aided diagnosis and identify breast cancer histopathology photos. Komura et al. [17] discussed how the growing usage of digital histopathology photos necessitates computer-assisted diagnosis and offered enhancements for improved analysis. Roy et al. [18] emphasized the use of histopathology images to diagnose the significance of color normalization successfully and suggested the use of stain separation and histogram definition. Hou et al. [19] highlighted the effectiveness of cross-sectional sparse CAE by providing a simple convolutional autoencoder for detecting nuclei in histopathology images. Plans for upcoming instance-level segmentation testing were also suggested. Gandomkar et al. [20] designed a system to categorize digital breast slides into four types, each

for benign and cancerous conditions. They used Deep ResNets in the MuDeRN for classification and combined the results to make a patient diagnosis. However, they noted that the manual region selection process and non-invasive BCa exclusion have limitations, indicating the need for further development.

Karuppasamy et al. [21] highlighted how crucial feature learning is for efficiency in picture categorization, particularly in datasets related to breast cancer. They found that feed-forward techniques such as CLR and CSVM-H outperformed back-propagation, achieving superior AUCs, quicker training, and lower memory requirements. They also highlighted that in the future, model design's primary focus will be explainability and hyperparameter optimization. Parshionikar et al. [22] utilized automated technologies to identify breast cancer, particularly in the BreakHis and IR Thermal Images datasets, where the suggested Capsule Neural Network outperformed previous techniques in terms of accuracy. They also emphasized the need to improve real-time monitoring as a future priority. Ortiz et al. [23] focused on identifying cancer zones in WSI pictures using deep-learning algorithms for early cancer diagnosis. They improved detection accuracy with a novel patch overlap approach, reaching 94.6%. Mohan et al. [24] emphasized the essential role of AI and data mining in breast cancer diagnosis in IoT environments. They used ABER-CSDNN, which employed U-Net for classification improvement and semantic segmentation, achieving 99.12% accuracy. Si et al. [25] proposed an approach that enhances feature extraction and fusion by combining the condensation of prior information via multi-view contrastive learning. Their tests on the BreakHis dataset validated the efficacy of categorization.

Perez et al. [26] provided deep learning solutions for automated Computational Pathology (CPATH) segmentation. Their suggested techniques achieved scalability and exceeded STAPLE by combining segmentation with annotator expertise learning. Xiao et al. [27] suggested TCGN, which combines graph neural networks, transformer encoders, and convolution to estimate gene expression. They highlighted its greater accuracy, easy interpretability, and ability to handle large amounts of RNA-seq data with few parameters and low memory consumption. Krishna et al. [28] introduced an attention branch to achieve 98.7% accuracy in cancer diagnosis while improving interpretability and performance with their ABNDCN model. Shovon et al. [29] used DenseNet201-Xception-SIE in an ensemble method, outperforming previous models and achieving 97.12% accuracy on H&E data and 97.56% on IHC data. They emphasized the efficient interpretation provided by Grad-CAM. Kausar et al. [30] achieved 96.25% accuracy on datasets using a lightweight CNN with WT to lessen the computational load. They also emphasized the importance of early detection due to increasing global breast cancer death rates.

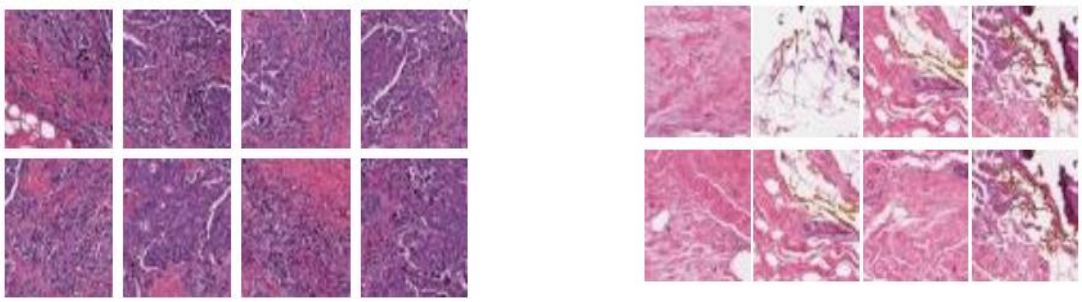
Aziz et al. [31] emphasized the global significance of prompt detection of breast cancer. IVNet achieves 97% accuracy by utilizing ImageNet and VGG16, and its real-time tracking capabilities are beneficial for treatment planning in resource-limited environments. Yu et al. [32] demonstrated that CA-BreastNet achieved 99.75% binary and 95.69% eight-class accuracy with the BreakHis dataset by combining DenseNet with coordinated attention. The expertise in histopathology is crucial to diagnose breast cancer properly. Joseph et al. [33] highlighted the importance of categorization due to the high death rate of breast cancer. Their work uses DNN and hand-crafted features to multi-classify histopathology pictures with improved accuracy. Yang et al. [34] focused on predicting metastasis and, by merging H&E images and clinical information, recurrence in HER2-positive breast cancer. Gupta et al. [35] emphasized the necessity of effective diagnosis to reduce death rates from breast cancer. Their modified version of the ResNet-based algorithm outperforms previous methods with the highest accuracy on the BreakHis dataset.

Burcak et al. [36] suggested a DCNN model to attain higher accuracy on histopathology pictures for breast cancer detection. Hirra et al. [37] introduced a novel Pa-DBN-BC model utilizing DBN with 86% accuracy to categorize breast cancer using histopathology images. Demir et al. [38] combined the CLSTM model with MWSA preprocessing and an improved SVM classifier to produce outstanding performance in breast cancer identification on HPIs using the BreakHis dataset. Wang et al. [39] suggested FE-BkCapsNet for histopathology picture classification of breast cancer, integrating CNN and CapsNet with high accuracy potential in clinical diagnosis. Rachapudi et al. [40] presented an effective CNN architecture, achieving a 22.7% error rate for histopathology image categorization of colorectal cancer pictures.

Despite widespread use of deep learning models like ResNet, DenseNet, and VGG-based networks for breast cancer detection with histopathology images, problems such as small dataset, overfitting, and good feature extraction are yet to be addressed. Specific architectural adaptation for these problems has not been made in many of the previous works. This inspired us to design the BCDNN model, which is tailored to improve CNN stability and performance within the challenging scenario of small-scale medical imaging datasets.

3. MATERIALS AND METHODS

Using pictures from histopathology, this section explains the tools and supplies used in breast cancer detection research. Referendum [41] provided the dataset used in this investigation. Imaging from pathology is crucial for the diagnosis of breast cancer as it shows tissue samples that have been analyzed under a microscope to find aberrant cells or structures that point to the disease. These samples are collected through biopsy, providing valuable information for detecting the disease. The tissue samples undergo processing and staining using various colors to distinguish cell structures. Pathologists examine these stained slides to determine the likelihood of cancer, the type of tumor, its grade, and its hormone receptor status. Various histological features indicate the nature and spread of cancer, providing essential details for treatment planning, which may include targeted therapy, hormonal therapy, chemotherapy, radiation therapy, or surgery. Figure 1 (a) shows an excerpt from the dataset with cancerous breast histopathology images. Histopathology images are made with the help of biopsy under their procedures, to help pathologists use microscopes to understand the probability of breast cancer. This study aims to develop an automated breast cancer detection system using a histopathology data set and artificial intelligence. Figure 1 (b) shows an excerpt from the dataset with non-cancerous breast histopathology images.



(a) Cancerous samples (b) Non-cancerous samples

Figure 1. An excerpt from the dataset with cancerous and non-cancerous breast histopathology images

The empirical study uses two pathology data sets to detect breast cancer automatically. The methodology followed in this paper towards achieving breast cancer detection is founded on a deep learning paradigm, namely one that Al enables. The literature in section 2 shows that a convolutional neural network efficiently processes medical images. Our empirical study revealed that no one-size-fits-all solution produces optimal results with different diagnosis methods and imaging modalities on CNN. We recognize the need to enhance the CNN model with empirical investigations to leverage its number of layers or architecture to deal with breast histopathology images. This fact has motivated us to develop an innovative deep-learning architecture that utilizes the CNN Model. The Breast Cancer Detection Neural Network (BCDNN) is the proposed enhanced CNN model. Figure 2 illustrates the architectural overview of the BCDNN model.

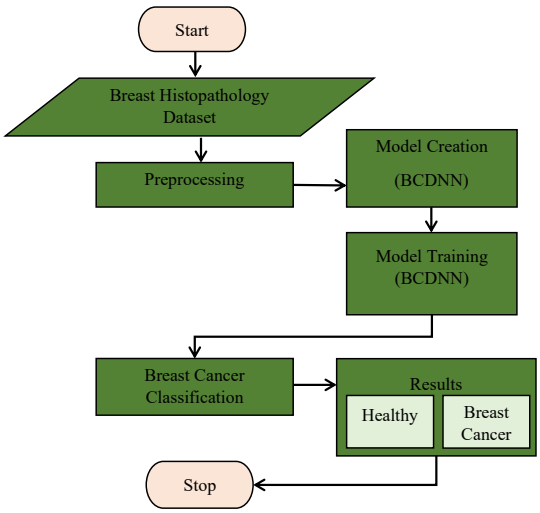


Figure 2. Overview of the proposed deep learning-based framework for breast cancer detection using histopathology images

Figure 2 shows the suggested deep learning-based architecture for identifying breast cancer using histopathology pictures. The first step in the identification of breast cancer is gathering a dataset on breast histology. The dataset then undergoes preprocessing, which includes data normalization, image resizing, and data augmentation to enhance sample diversity. The preprocessing steps consisted of resizing all histopathology images to 128×128 pixels for standardizing the image size of the inputs, and then normalizing pixel values between 0 and 1 to make neural training more stable. In addition, data augmentation (e.g., random rotations (±15°), horizontal flipping, slight zooming (up to 10%)) was exploited to improve the diversity of the training dataset and reduce overfitting. These preprocessing procedures were necessary to deal with the slight variations in histopathology images.

Subsequently, the model creation process involves constructing a deep learning model, BCDNN, as presented in Figure 3. This model operates on preprocessed images and is trained using 80% of the dataset. The trained model acquires knowledge, which is then persisted. When required, the persisted model is loaded to automatically detect breast cancer using the remaining 20% of the dataset as test samples. The classification results indicate whether each histopathology test sample is healthy (labeled as 0) or potentially indicative of breast cancer (labeled as 1). Overall, the framework is designed to automate breast cancer detection using histopathology imagery through supervised learning, encompassing training and testing phases.

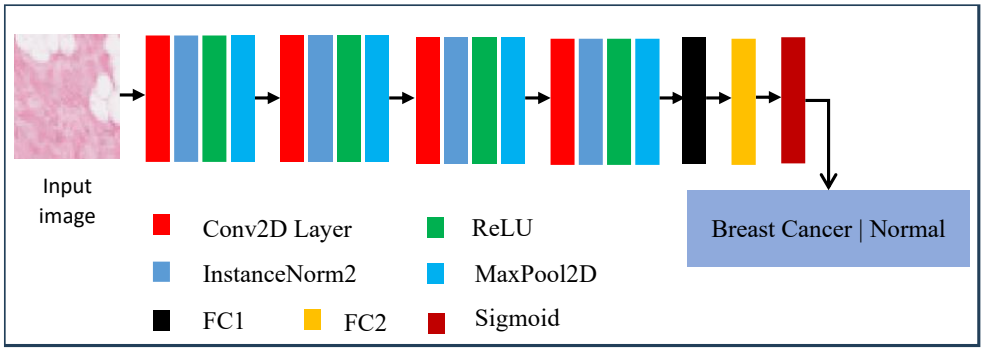


Figure 3. Proposed enhanced CNN model known as BCDNN

The suggested improved deep learning model, or BCDNN, is modeled after the architecture shown in Figure 3 and is intended to classify breast cancer cases automatically. The model can predict class label for each test sample using the supplied histopathological test samples. After training on training data samples, the model gains the information required to process test photos for automated breast cancer diagnosis. The model starts by taking a given input image as a histopathology slide of the breast. As the model is trained for this imaging modality, it can efficiently process the image to detect breast cancer probability. The proposed tape learning model is found to be efficient in processing medical images in the form of histopathology slides. The suggested deep learning model uses convolutional layers to progressively extract features from the given histopathological image. The 2D (2-dimensional) convolutional layer examines histopathological characteristics to identify patterns suggesting the likelihood of malignant tissues in the sample. These layers add filters to comprehend the aspects of the provided medical picture. A feature map with information on the features of the medical picture is produced due to the convolutional procedures applied to it. When detecting breast cancer using histopathology slides, convolutional layers gather features from the image and gradually construct complex patterns that help identify harmful cells in the presented medical image.

The proposed BCDNN differs from existing CNN models (VGG16, ResNet50) by using Instance Normalization, instead of Batch Normalization, to train effectively with limited histopathology data. In addition, the numbers of kernels (3×3) are also reduced for fine-level feature extraction. A simplified two-stage downsampled fully connected (FC) layer replaces the heavier FC layer to avoid the risk of overfitting. Such a maneuver enables BCDNN to achieve the higher accuracy with less parameters on the breast histopathology datasets. Table 1 outlines the BCDNN model's complete layer configuration, parameters, and output dimensions.

The Breast Histopathology used in this work contains 277,524 image patches, where each patch is annotated as cancerous (label 1) or non-cancerous (label 0). It is a 2-class system, with no further severity grading - for example, stages of benign or malignant. The data is moderately unbalanced, consisting of 198,738 non-cancerous and 78,786 cancerous samples. To mitigate this imbalance, we performed data augmentation (e.g. random rotations, flips, zooming) on the minority class at the time of training to prevent the model from being tilted towards the majority class.

Table 1. Layer-Wise Architecture Details of the Proposed BCDNN Model

Layer Type	Parameters	Output Size
Conv2D	32 filters, 3×3 kernel, stride=1, padding=same	128×128×32
InstanceNorm2D	-	128×128×32
ReLU	-	128×128×32
MaxPool2D	2×2 pool size	64×64×32
Conv2D	64 filters, 3×3 kernel, stride=1, padding=same	64×64×64
InstanceNorm2D	-	64×64×64
ReLU	-	64×64×64
MaxPool2D	2×2 pool size	32×32×64
FC1	128 neurons	128
FC2	1 neuron (Sigmoid)	1 (binary output)

The proposed deep learning system introduces non-linearity using the Rectified Linear Unit (ReLU). It is an activation function that adds non-linearity to the provided data to help learn complicated patterns. It detects all the negative pixel values that neurons supply as output and sets them to 0 without altering the positive values corresponding to the neurons. This neural network feature can help reduce the vanishing gradient problem and speed up the convergence of the training process. The recommended deep learning model uses instance normalization to improve network performance. It guarantees uniform data delivery throughout the network's tiers. By applying instance normalization, one may better know the features of a specific histology sample and use it to identify breast cancer in histopathology pictures. Table 1 lists the size of feature maps for each stage of BCDNN, starting from 128×128 and shrinking down through MaxPooling.

Through downsampling feature map data produced by the convolutional layers, the Max Pooling layers of the proposed deep learning model aim to reduce the spatial dimensions of the input. However, the Max Pooling layers in the model help to minimize computational complexity and control overfitting issues by gradually decreasing the spatial size in the data representation. By obtaining the most crucial characteristics in different areas of the provided picture, these layers further strengthen the network's resistance to fluctuations related to the input data. Max Pooling layers aid in getting the most significant characteristics necessary to differentiate between healthy and diseased samples when it comes to histopathology pictures used for breast cancer screening. Consequently, to help identify breast cancer, Max Pooling layers are positioned throughout the suggested model. The fully connected layers of the proposed model are intended for data analysis and breast cancer prediction. These layers are necessary to distinguish between malignant and benign samples. Their creation of connections between every neuron in the layer above and every single neuron in the layer below enables the network to find complex patterns and underlying linkages concealed in the input. The fully linked layers in processing histopathology slides for breast cancer diagnosis use the characteristics retrieved by the preceding layers to make well-informed choices about the presence of malignant cells in the provided medical picture.

The proposed deep learning model uses the sigmoid activation function to classify breast histopathology pictures in a binary classification. This function returns a number between zero and one, determining the risk of breast cancer in a given histopathological sample. A result closer to zero indicates the absence of cancerous cells, while a result closer to one indicates their presence. The sigmoid function in the model ultimately determines whether a given sample contains cancerous or non-cancerous cells.

Table 2. Configuration details of convolutional and Max Pooling layers in the proposed framework

Attribute of Layer	L1	L2	L3	L4	L5	L6	L7	L8
Pooling Size	-	3*3	-	3*3	-	3*3	-	3*3
Pooling stride	-	1*1	-	1*1	-	1*1	-	1*1
Conv. Stride	1*1	-	1*1	-	1*1	-	1*1	-
Channel	32	-	64	-	128	-	128	-
Filter size	5*5	-	5*5	-	5*5	-	5*5	-
Type	Conv	pool	Conv	pool	Conv	pool	Conv	pool
Activation	ReLu	-	ReLu	-	ReLu	-	ReLu	-
Padding Size	Same	None	-	None	-	None	-	None

Table 2 presents various attributes associated with the proposed deep learning model and configuration details for various layers constituting the convolutional layers and Max pooling layers.

The BCDNN algorithm treats a histopathological input image, with a convolutional first-layer processing to extract local patterns to include edges and textures. Instance normalization is used after all the

convolutions for stable learning. · Non-linear activation (ReLU) introduces non-linearity and increases feature representation levels, followed by Max Pooling, which reduces spatial dimensions, while preserving dominant features. This stack of feature extractivities is repeated in series, refining the information. The feature maps are then flattened and input into two fully connected layers for the fusion of high-level features. The last activation function is used as a Sigmoid function that gives a probability score of the cancerous tissue. The BCDNN has an end-to-end pipeline that allows efficient and accurate breast cancer classification in breast cancer histopathology images.

Algorithm 1. Enhanced Deep Learning for Breast Cancer Detection (EDL-BCD)

Algorithm: Enhanced Deep Learning for Breast Cancer Detection (EDL-BCD)
Input: Breast histopathology dataset D
Output: Breast cancer classification results R, performance statistics P

1. Begin
2. D'←Preprocess(D)
3. (T1, T2)←DataSplit(D') //80% training (T1) and 20% testing (T2)
4. Configure BCDNN model m //as in Figure 3
5. Compile m
6. m'←TrainBCDNN(m, T1)
7. Save m'
8. Load m
9. R←BreastCancerClassification(m', T2)
10. P←FindPerformance(R, ground truth)
11. Display R
12. Display P
13. End

Algorithm 1 is designed to categorize breast cancer utilizing histopathology datasets. The algorithm begins by preprocessing the input dataset (D) to prepare it for analysis. The preprocessed dataset (D') is then divided into two sections: 80% for training (T1) and 20% for testing (T2). The algorithm configures a Breast Cancer Detection Neural Network (BCDNN) model (m), as illustrated in Figure 3, which is not included in the provided text. The model is compiled and after which the TrainBCDNN function was trained on the training dataset (T1). After training, the model is saved and loaded for the classification phase. The classification results (R) are obtained by applying the trained model (m') to the testing dataset (T2) using the Breast Cancer Classification function. The performance statistics (P) are calculated by employing the Find Performance function, compare the categorization outcomes with the ground truth data. The user is then shown the performance statistics (P) and the classification results (R) by the algorithm.

The BCDNN model was trained using the Adam optimizer due to its adaptive learning rate capabilities and computational efficiency. A learning rate of 10^{-3} was selected based on experimental tuning (refer to Figure 6), and a batch size of 32 was used. The model was trained for 100 epochs, with early stopping based on validation loss monitoring. Hyperparameter tuning experiments revealed that lower learning rates and moderate batch sizes yielded optimal convergence for the histopathology dataset. The supervised learning approach in the domains of deep learning and machine learning research usually includes using many performance indicators to assess model performance. The confusion matrix, which enables researchers to compute several performance indicators and compare algorithm predictions with the ground truth, is one of the tools often used for this purpose. Using equations 1 through 4, which represent various metrics utilized in the performance evaluation, we may construct performance statistics by comparing the predicted labels of our technique with the ground truth.

$$\text{Precision (p)} = \frac{TP}{TP+FP} \quad (1)$$

$$\text{Recall (r)} = \frac{TP}{TP+FN} \quad (2)$$

$$\text{F1-score} = 2 * \frac{(p * r)}{(p+r)} \quad (3)$$

$$\text{Accuracy} = \frac{TP+TN}{TP+TN+FP+FN} \quad (4)$$

A number between 0 and 1 is produced by the performance evaluation metrics. In machine learning research, these measures are often employed.

4. EXPERIMENTAL RESULTS

This publication uses breast histopathology pictures for studies on breast cancer detection [41]. Stated otherwise, the dataset consists of photos related to histology that are utilized to train the suggested deep learning model. The findings of our empirical investigation are shown in this part together with an analysis of the exploratory data and an assessment of the efficacy of histopathology pictures for the identification of breast cancer. Several cutting-edge models are used to compare the suggested deep learning model's performance: VGG16, VGG19, ResNet50, and ResNet101, as detailed in [1]. A baseline CNN model is also used to compare results.

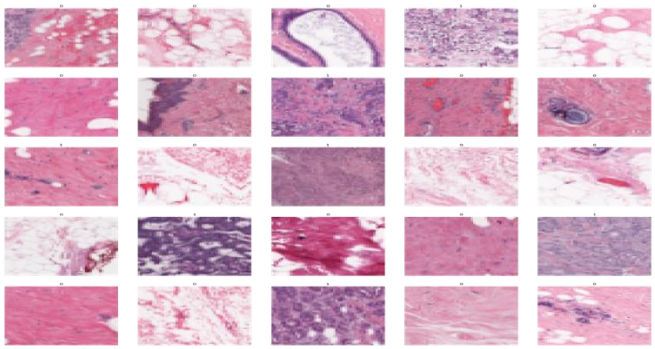


Figure 4. An excerpt from the dataset with cancerous (1) and non-cancerous (0) samples

Figure 4 shows a grid of microscopic images of tissue samples, with each image labeled as either cancerous (1) or non-cancerous (0). The samples exhibit varying degrees of cellular and structural detail, characteristic of histopathological examination. The visual differences between cancerous and non-cancerous samples include variations in cell density, tissue organization, and staining patterns, which are crucial for distinguishing between the two categories. The figure serves as an excerpt from a dataset used for training or evaluating a model to classify these tissue samples based on their histopathological characteristics. The bright purple color seen in the cancerous samples resulted from counterstaining of Hematoxylin in the histopathological preparation, which binds with nucleic acids and stains the nuclei of cells. This is a common Staining "routine" that is followed across the dataset samples. The images in Figure 5 are directly from the original dataset and have not been resized or normalized.

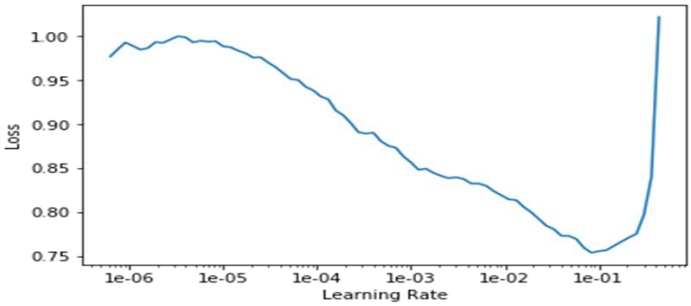


Figure 5. Experimental results to ascertain the relation between loss function and learning rate

Figure 5 depicts a graph demonstrating the connection between the learning rate and the loss function. A logarithmic scale, from \(10^{-6}\) to \(10^{-1}\), shows the learning rate on the x-axis, while the loss is shown on the y-axis, with values between 0.75 and 1.0. The curve shows that as the learning rate increases, the loss initially decreases, reaching a minimum, and then sharply increases. This suggests an optimal learning rate around \(10^{-2}\), where the loss is minimized. Beyond this point, further increasing the learning rate causes the loss to proliferate, indicating that the model's performance deteriorates at higher learning rates. This experiment likely aims to identify the best learning rate for training a model to achieve the lowest possible loss.

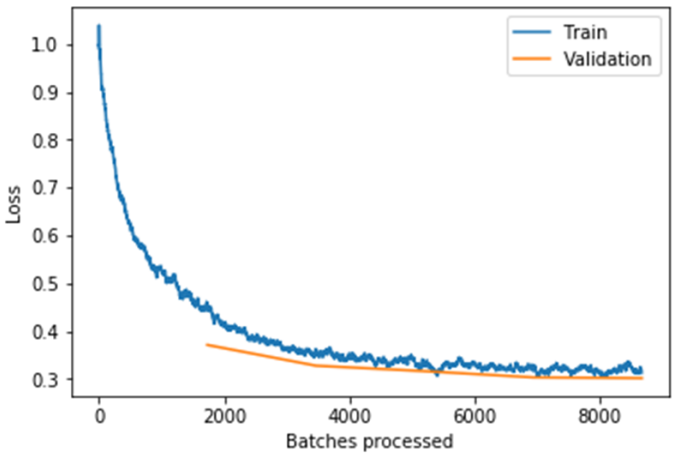


Figure 6. Illustrates the relationship between loss function and batches processed with the training and validation data

A graph depicting the loss values during training and validation over time is shown in Figure . The y-axis may show the loss and the x-axis the number of epochs or repetitions. The training loss is represented by the blue line, which first declines quickly before progressively declining more slowly over time with minor oscillations. Compared to the training loss, the validation loss reduces at a slower and more consistent rate, as seen by the orange line. The model appears to be learning well and generalizing well to new data without experiencing severe over-fitting as the difference between the training and validation losses gets smaller over time. During training, a machine learning model's performance and convergence are frequently assessed using this graph.

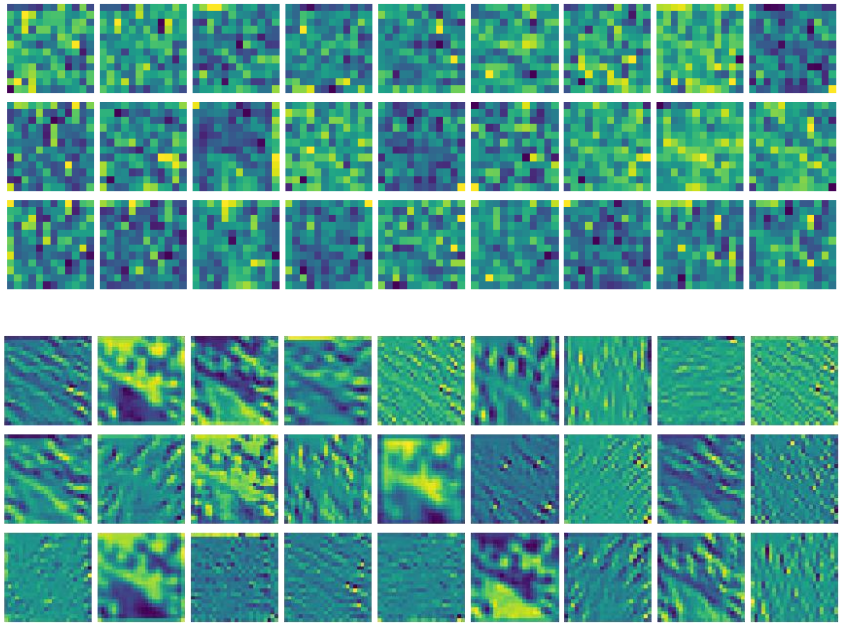


Figure 7. Illustrates the visualization of feature maps generated by convolutional layers

Figure 7 depicts the display of feature maps produced by a BCDNN model's convolutional layers. The outputs of convolutional operations performed on the input data are feature maps, which display various patterns and characteristics that the network has been trained to identify. The feature maps show clearer, more organized patterns in the upper part, suggesting that the convolutional layer is probably collecting lower-level elements like edges and textures. The feature maps become less organized and more abstract as we proceed to the bottom part, indicating that these layers are extracting more intricate and higher-level information from the input data. Deep learning models are characterized by this trend from simple to sophisticated feature

representation, where deeper layers capture more abstract notions and earlier levels collect fundamental information. Understanding a model's interpretation and processing of input data requires the use of visualization, which offers insights into the learnt characteristics at different network phases.

Figure 7 shows the feature maps of the first convolution layer of the trained BCDNN model at the inference stage for a representative cancerous histopathology sample. Feature maps were obtained using visualization hook during forward pass, demonstrating low-level features including edges and textures learned by the initial layers.

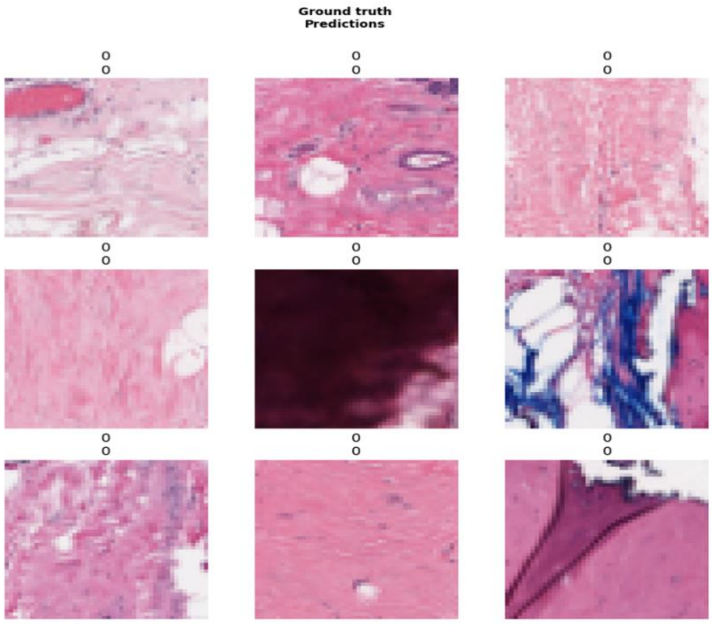


Figure 8. Illustrates model predictions and ground truth for some test samples

Figure 8 shows a number of histopathological image samples that are probably utilized for medical diagnosis together with the accompanying ground truth values and forecasts. Each sub-image represents a patch from a histology slide, with the top label indicating the prediction, and the bottom label showing the ground truth, both represented numerically. In this case, all predictions and ground truth values appear to be '0', suggesting a binary classification task where '0' may denote a non-cancerous or normal condition. The consistency in predictions and ground truth values implies that the model is performing accurately on these test samples. Such visual aids are essential to medical image analysis because they provide a clear and understandable understanding of how the model's predictions match real diagnoses, which helps determine the model's accuracy and dependability.

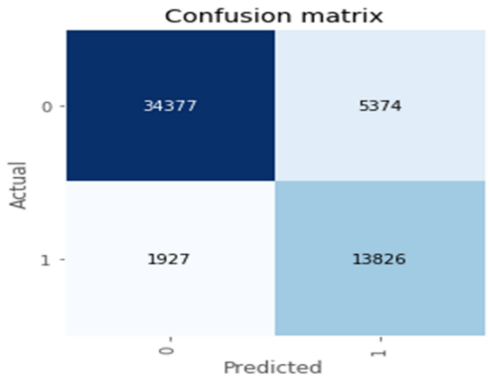


Figure 9. Illustrates confusion matrix reflecting the performance dynamics of the proposed deep learning model

An overview of a deep learning model's performance on a classification challenge is provided by the confusion matrix shown in Figure 9. Four cells comprise the matrix, representing the true positive, false

positive, true negative, and false negative rates. The matrix is specific in that it reveals 13,826 cases were successfully predicted as class '1' (true positives) and 34,377 instances were correctly projected as class '0' (true negatives). False positives, or 5,374 cases, occurred when the model predicted class '1' for instances of real class '0'; false negatives, or 1,927 instances, occurred when class '0' was projected wrongly for occurrences of actual class '1'. The aforementioned matrix offers significant insights into the model's precision, recall, accuracy, and overall efficacy in differentiating between the two classes. It highlights the model's strengths in correctly identifying both classes while also indicating areas where misclassification occurs, which can be targeted for further optimization.

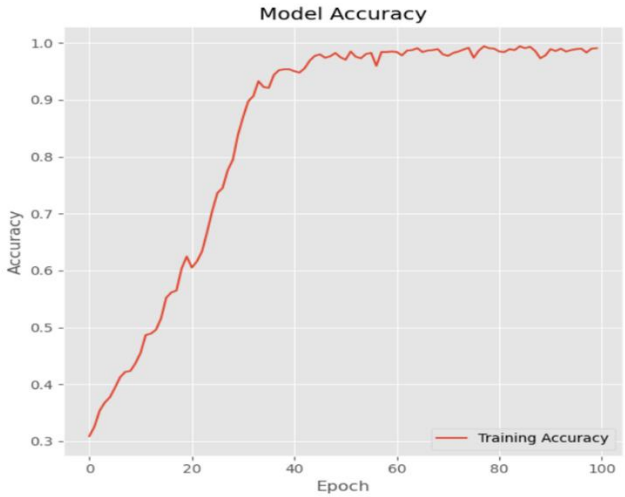


Figure 10. Model accuracy dynamics against number of epochs

Figure 10 illustrates the training accuracy of a model over 100 epochs. The precision begins at about 0.3 and steadily increases, with a rapid rise in the first 30 epochs. After reaching around 0.95, the accuracy growth slows and fluctuates slightly, eventually stabilizing close to 1.0. The plot shows that during the course of training, the model's accuracy increases continuously, and ultimately achieving near-perfect accuracy by the end of the training period.

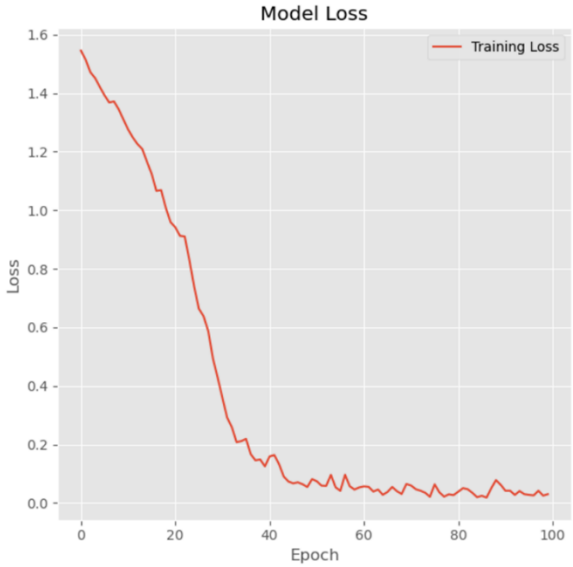


Figure 11. Model loss dynamics against number of epochs

Figure 11 illustrates the training model loss during a period of 100 epochs. at first, the lack of training is high, around 1.6, but it decreases sharply in the first 20 epochs, indicating rapid learning by the model. As the epochs progress beyond 20, the rate of decrease in loss slows down. By around 60 epochs, the loss stabilizes and fluctuates slightly around a minimal value close to zero, suggesting indicates the model is well-versed on the training set and is no longer improving significantly with additional epochs. This pattern is typical in

training machine learning models, where an initial period of significant learning is followed by diminishing returns as the model approaches its optimal performance.

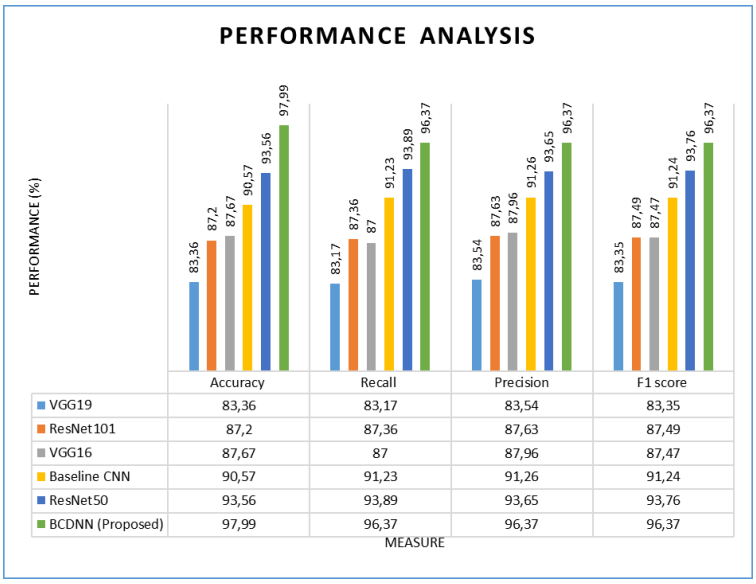


Figure 12. Performance comparison among deep learning models used for breast cancer detection using histopathology images

Figure 12 compares different models according to F1 score, accuracy, recall, and precision. Among the models, the proposed BCDNN demonstrates the highest performance across all measures, achieving 97.99% accuracy, 96.37% recall, 96.37% precision, and 96.37% F1 score. Other models like ResNet50 and Baseline CNN also perform well, with ResNet50 showing a notable accuracy of 93.56% and Baseline CNN achieving a recall of 91.23%. VGG19, VGG16, and ResNet101 show lower performance across these metrics, with VGG19 having the lowest accuracy at 83.36%. Overall, the BCDNN model significantly outperforms the others, indicating its effectiveness in the analyzed context.

5. DISCUSSION

Globally, breast cancer is a major health problem, leading to severe health issues and fatalities. Timely detection is crucial for informed decision-making and better patient outcomes. Artificial intelligence has made it possible to automatically detect breast cancer, utilizing various advanced modalities for training deep learning models. Histopathology, an imaging modality developed using biopsy, has proven effective in accurately detecting breast cancer. Research shows that CNN are often utilized in processing medical images due to their efficiency in progressively extracting features and optimizing feature maps through variants like Max pooling layers. However, CNN may not perform optimally with all modalities. To address this, we've put out an improved deep learning framework called BCDNN, designed to leverage the latest advancements. Our model, evaluated using breast histopathology images, has demonstrated superior performance compared to existing deep learning models. We believe that integrating this proposed deep learning model into existing healthcare systems could facilitate the development of a clinical automated decision support system for histopathology image-based breast cancer screening.

Compared to traditional CNN models such as VGG16, VGG19, and ResNet50, the proposed BCDNN demonstrates superior performance owing to the introduction of Instance Normalization layers, optimized convolutional kernels, and simplified fully connected structures. These enhancements enable BCDNN to achieve higher classification accuracy (97.99%), outperforming ResNet50 by over 4.4% and VGG19 by 14.63%. The empirical results affirm the effectiveness of the proposed modifications for breast cancer detection from histopathological images. However, as mentioned in section 5.1, there are several restrictions with the suggested system.

5.1 Limitations

When compared to the most sophisticated algorithms, the approach described in this article accurately identifies breast cancer using images from the histology. It does, however, have certain restrictions. The suggested deep learning method does not support additional modalities, such as mammography, and is only appropriate for histopathological breast pictures. Furthermore, just a small number of training samples are used in the system's assessment, underscoring the necessity of expanding sample variety in order to improve

performance even further. The system's exclusive reliance on an improved deep learning model, without taking into account the possible advantages of other hybridized deep learning models that improve breast cancer diagnosis, is another important drawback. Given the restricted quantity of training samples, generative adversarial network designs must be used to diversify data in order to enhance training quality and eventually improve the efficacy of breast cancer detection.

6. CONCLUSION AND FUTURE WORK

This paper presents a deep learning-based automated breast cancer detection system that is created by optimizing the CNN model known as BCDNN. After conducting an empirical investigation into various layers and configurations, the deep learning model's recommended design is finally used to develop the proposed deep learning architecture. The experimental study has shown that the CNN model is efficient in medical image processing. It is observed that one size does not fit all, and there is a need to tailor its architecture must fulfill the conditions of specific imaging modalities. In this paper, we focused on histopathology imagery for breast cancer detection, as this kind of imagery is suitable and provides more accurate results in detecting breast cancer. We also introduce an algorithm called Enhanced Deep Learning for Breast Cancer Detection (EDL-BCD), which leverages the enhanced deep learning model for better disease diagnosis performance. Our evaluation with a benchmark dataset comprising breast histopathology images shows that our suggested model performs noticeably better than cutting-edge ones, achieving an impressive accuracy of 97.99%. Going forward, we intend to introduce hybrid deep-learning models that exploit the benefits of underlying models to improve breast cancer detection performance, particularly with histopathology images. Another direction for future work is to explore generative adversarial network model architectures to address the problems associated with inadequate training samples.

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