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ORIGINAL RESEARCH ARTICLE

An integrated system for breast cancer diagnosis using convolution neural network and attention mechanism

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ABSTRACT

In most malignancies, breast cancer is fatal, accounting for approximately 500,000 annual deaths. The subtype of breast cancer known as Invasive Ductal Carcinoma (IDC) is surprisingly common. Pathologists commonly focus on IDC-containing regions when trying to determine if a patient has breast cancer. Although extremely fatal, survival rates and expected lifespans improve dramatically with prompt diagnosis and treatment. The treatment strategy also varies based on the breast cancer patient's stage. In this research, we use a classification method for a publically available dataset of breast histopathology images obtained from the Kaggle. The IDC regions of the images in this dataset have been restricted for easy retrieval. The breast cancer IDC data set contains 277,524 records, of which 78,786 are positive. The 277,524 images were classified using an IDC breast cancer dataset, with 78,786 positive IDC and 198,738 negative IDC, respectively. The authors introduce a new architecture of deep convolutional neural networks and attention mechanism for classification. The model achieves state-of-the-art levels of accuracy for IDC identification, setting a new benchmark for future studies.

Keywords: breast cancer; histopathology; convolutional neural networks; deep learning

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1. Introduction

The International Agency for Research on Cancer (IARC) reports that breast cancer is one of the most prevalent malignancies diagnosed as well as one of the significant causes of cancer death in women[1]. Invasive ductal carcinoma (IDC), often referred to as infiltrating ductal carcinoma, is the most common subtype of breast cancer, accounting for about 80% of cases[2,3]. IDC forms inside a milk duct and spreads to the nearby fatty or fibrous breast tissue. Lymph nodes and other organs may also be affected. Breast cancer patients have a relative 5-year survival rate of 89%. Survival rates from breast cancer can be predicted, in part, by the stage of the disease at diagnosis[4].

However, only 61% of breast cancers are detected at this early stage, where the 5-year relative survival rate is nearly 100%. When patients reach stage 4, the relative 5-year survival rate plummets to 22%. Finding cancer in its earliest stages is crucial. IDC's "special subtypes" cannot be reliably identified by their morphological characteristics[5]. Pathologists must visually examine histology samples for IDC, which is laborious and time-consuming. A faster and more accurate diagnosis of this type of cancer could be achieved by automated detection by pathologists. Over the past decade, automated detection in medical imaging has been a hot topic of study. Histopathological pictures are classified as benign or malignant using convolutional neural networks (CNNs). Breast cancer photo classification is difficult because of high inter-class variation and complex geometrical shapes. Histopathological pictures of breast tumours at four different magnifications and two different malignancy stages are used from the dataset available at the Kaggle repository[6]. Classifying images as cancerous or noncancerous has received less attention than benign or malignant classification[7].

Combining deep learning and healthcare provides intelligent data analysis with security, which can be helpful in healthcare applications. Due to its potential to enhance early detection and treatment results, breast cancer prediction is receiving more and more attention. In this paper, we describe a revolutionary method that combines the strength of convolutional neural networks with attention mechanisms. This study presents a unique CNN architecture with an attention mechanism for identifying malignant and noncancerous tissue samples in publically available histopathology pictures. On a benchmark set of 27,553 images, our proposed architecture has an Area Under the Curve of 0.965 for detecting IDC. The suggested method uses a convolutional neural network (CNN) with an attention mechanism to aid in forecasting breast cancer.

2. Related work

Other authors conducted the research using deep learning technologies, convolutional neural networks, and breast histopathology images, which are explained below. Improved performance and accuracy in detecting breast cancer can be achieved through the use of deep learning-based CNN models.

On the CBIS-DDSM dataset, Salama and Aly[8] proposed a CNN-based deep learning model for image segmentation and classification in 2021. The authors trained U-Net and Inception-v3 models to extract breast tissue from mammograms. The model aids the radiologist's aides in making timely diagnoses. The model achieves an accuracy of 98.87%. The study of Gravina et al.[9] focuses on the enhancement of photographs through the extraction of shape-related features and the identification of the precise location of the image. When high-dimensional images were tested, they found that the CNN had no effect. Ukwuoma et al.[10] suggested a multi-classification approach for breast cancer that uses histopathology pictures and deep learning to categorise photos at varying magnifications.

According to Yala et al.[11], have also developed into superior problem-solving approaches with numerous academic and industrial uses. Trends in modern medicine, security, schooling, and technology have all been explored in deep learning's application to computer vision research. A blockchain-oriented multi-agent system for breast cancer diagnosis was introduced in the study paper by Ramanath et al.[12]. Integrating blockchain-based security measures into healthcare monitoring is a valuable approach. The system has a reliability of 96.49 per cent in patient classification.

However, a hybridised model based on IMPA and ResNet50 was developed by Houssein et al.[13] employing CNN and IMPA. With the CBIS-DDSM dataset, the model achieves an accuracy of 98.32%, while the MIAS dataset achieves an accuracy of 98.88%. In addition, Narayanan et al.[14] used a CNN trained on a histological dataset to classify breast cancer. Histogram equalisation, colour consistency, and comparison to established CNN benchmarks were employed.

Some researchers have developed a transfer learning approach for labelling breast cancer images obtained by histopathology. The authors employed a block-wise fine-tuning strategy with the ResNet-18 model. Data augmentation methods and global contrast normalisation helped the model perform better. In addition, Zhou et al.[15] proposed a classification method for thermal pictures that uses a CNN model to merge thermal images from multiple perspectives. The approach attained a 97% sensitivity and a 100% specificity with a 0.99 AUC. Ambika et al.[16] introduced a DL framework (DenseNet) for distinguishing between malignant and benign cells by ingesting image information into a fully connected (FC) layer. Hyperparameter tuning was used to assess the method's efficacy. Zhou et al.[17] a deep classification system called CNNI-BCC (CNN improvement for breast cancer) was developed with mammography images. Breast images can be classified as cancerous, average, or healthy using the CNNI-BCC model. Their precision was 90.50%, and their sensitivity was 90.71%. Abdelrahman et al.[18] show that TL enhances performance using Inception-v4, which had already been pretrained on the ImageNet and DDSM datasets.

The research concluded that CNN and attention mechanisms had gained success in detecting breast cancer, but the high number of hyperparameters prevented further improvements. Therefore, optimising CNN hyperparameters is crucial for improving CNN performance. Healthcare providers may benefit from this paper's proposed C-ATT model for breast cancer classification based on an attention mechanism.

3. Preliminary study

This section of the research paper described the idea of a convolutional neural network (CNN), encompassing various layers and additional intricacies of CNN, including the focus system.

CNN architecture

The convolutional layer, the activation layer using the rectified linear unit (ReLU), the batch normalisation layer, the pooling layer, the dropout layer, the fully connected layer, and the softmax layer are all essential parts of the CNN architecture[19]. The convolutional neural network (CNN) model's architectural layout is shown in **Figure 1**, which also shows how many layers are connected. For classification, a fully connected layer and a softmax layer are added after the convolutional layers in the design[20]. Several reduced-dimension filters convolve to extract separate features from the input data. A rectified linear unit (ReLU), a batch normalisation layer, a maximum pooling layer, and convolution filters comprise each convolutional layer.

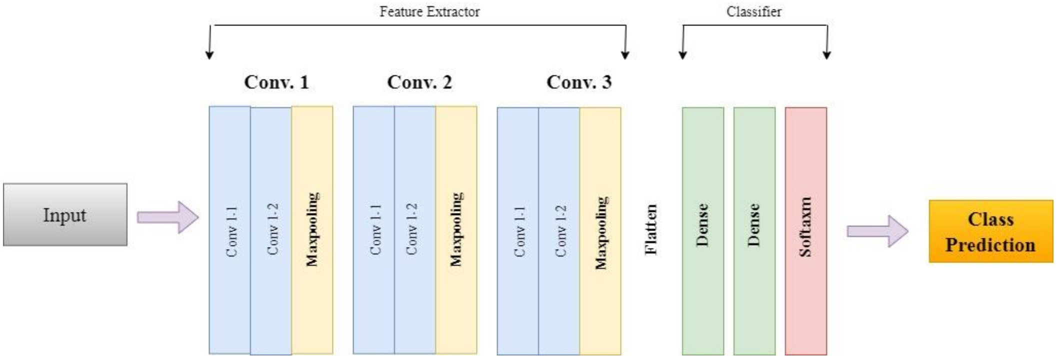

Figure 1. The architecture of the CNN model.

The batch normalisation layer is responsible for normalising the activated values. Batch normalisation is a method utilised to standardise the activations within the intermediate layers of deep neural networks. The system's effectiveness is demonstrated by its ability to enhance accuracy and expedite the training process[21]. The pooling layer is responsible for downsampling on the input's spatial dimension, reducing parameters within the activation[22].

Convolutional neural networks (CNNs) have demonstrated significant efficacy in image analysis due to their ability to leverage pattern-specific filters, effectively retaining the spatial characteristics of the images. Convolutional neural networks (CNNs) frequently perform better than dense neural network approaches because fully connected architectures tend to flatten input images, disregarding crucial spatial patterns.

Applying deep learning-based convolutional neural networks (CNNs) represents a highly stimulating area of investigation within healthcare and pharmaceutical sciences. Based on empirical research, it has been determined that approximately 5% of medical diagnoses are found to be inaccurate. Annually, an estimated global population of approximately 12 million individuals experiences mortality rates ranging from 40,000 to

80,000 due solely to erroneous diagnoses. Deep learning systems have the potential to aid in accurate disease diagnosis, thereby potentially contributing to patient survival[23].

Layer 1: Convolutional layer:

The task of getting beneficial characteristics via an image typically begins with convolution. Convolutional operations are executed through the utilisation of diverse filters that are incorporated within the convolutional layers.

The initial convolutional layer of a convolutional neural network (CNN) can be regarded as a conventional image filter. This process aims to acquire an unprocessed image and extract its fundamental characteristics. These entities are commonly known as low-level features. The second convolutional layer receives the extracted features from the first layer as input rather than the raw image. It enables the entity to integrate these fundamental geometric forms into more intricate structures. The complexity of the extracted features increases as we traverse more profoundly into the network[24].

Let *i* denote the input signal, *W* represent the weight matrix of the filter, *v* symbolises the bias vector, and *f* means the activation function, specifically the rectified linear unit (ReLU) in this context. The symbol * represents the mathematical operation of convolution, and the resulting output O of the convolutional layer can be expressed as:

$$O = f(i \times W + v)$$

To enhance the model's efficacy and standardise the output, batch normalisation is implemented after each convolutional layer. Let "i" represent the input and "μ" denote the learning rate of the shift parameter. The variable n represents the batch size in this context. The calculation of the output of batch normalisation is determined by:

$$\mu_B = \frac{1}{n}\sum_{i}^{n} y_i$$

ReLU layer:

The acronym ReLU represents the rectified linear unit. After extracting feature maps, the subsequent procedure involves transferring them to a Rectified Linear Unit (ReLU) layer. The fixed linear unit (ReLU) function conducts an element-wise operation by assigning a value of 0 to all pixels with negative values, including non-linearity in the network, generating a rectified feature map as the output. The initial image is subjected to convolutions and rectified linear unit (ReLU) layers to identify and localise the distinctive features.

Attention layer:

An attention layer is incorporated into the model after the third convolutional layer to enhance the framework's efficiency. This addition enables the identification of the image region containing the most crucial information about the input signal. The equation that characterises the layer is defined as:

$$q = \tan h(iW + v)$$

In the above equation, q is the score of the attention, W is the weight matrix, and *v* is the bias vector.

$$a = \mathrm{softmax}(q)$$

$$\mathrm{attended}_{\mathrm{signal}} = a \times i$$

To calculate the weights of attention, the softmax function is applied to q, and to obtain the attended attention signals, it is further multiplied with the input signals[25].

Layer 2: Pooling layer:

The pooling layer is an additional convolutional neural network (CNN) component. Dimension reduction techniques are employed to decrease the dimensions of feature maps. As a result, it reduces the number of parameters that need to be learned and the computational workload carried out within the network. The subsequent operations are conducted on condensed rather than precisely localised features produced by the convolution layer[26]. This enhances the model's resilience to fluctuations in the spatial arrangement of the features within the input image.

Layer 3: Dropout layer:

A small subset of nodes' weights are made zero in a dropout layer. It removes a small number of nodes and then uses the newly distributed set to train a CNN model. Over-fitting is a problem that this aids the model in overcoming.

Dropout is a method for pruning the model's nodes at random throughout each training iteration. When the weights of the nodes are set to zero, the model itself learns for the loss of neurons. As a result of this random ablation, models can better generalise findings from the training data to the testing data. Researchers have demonstrated that the approach leads to more robust CAD models with improved performance.

Layer 4: Flatten layer:

Using the flattening operation, all the generated 2-vectors are flattened into a single long continuous linear vector. After the convolutional or maxpool layers, flattening is a crucial step for utilising the fully linked network[27].

Layer 5: Dense layer:

The standard, strongly connected neural network layer is called the "dense layer." The output layer of a convolutional neural network (CNN) is conceptually identical to a fully connected layer.

The image is segmented using many pooling layers and a variety of filters. The output is obtained by feeding a flattened version of the pooled feature map into a fully linked layer.

Layer 6: Fully connected layers:

Two fully connected layers receive the flattened signal from the attention layer.

Here, we'll refer to ReLU's activation function as f, the weight matrix as W, the bias vector as b, and the input x as the bias. Then, the completely connected layer's output y is given by:

$$y = f\,(xW + b)$$

Then, each layer's inputs are normalised using the batch normalisation technique to speed up training and lessen the model's sensitivity to weight initialisation.

Layer 7: Output layer:

The probabilistic distribution of the network's output is normalised using the softmax activation function in the final output layer. In this case, we will use the preceding layer (z) output and the softmax function (s). Then, the softmax layer's output y is defined as follows:

$$\sigma(\vec{z})_i = \frac{e^{zi}}{\sum_{j=1}^{K} e^{zj}}$$

In the above equation, e specifies the standard exponential function for input, z is the input vector, k represents the number of classes, and e^{zj} displays the standard exponential for output[28].

Loss function

Binary cross entropy loss (or log loss) was chosen because it is a popular loss function in machine learning for binary classification problems. Binary cross entropy provides valuable insights by comparing each output probability with its actual output. The estimated probability is given a score considering how far they deviate from the expected result. The usefulness of this loss increases exponentially as the deviation of the anticipated chance from the predicted outcome increases.

Optimizer

Given the profound nature of the CNN model and the associated complexity, it is essential that as few hyper-parameters as possible need to be tuned. The tuning of a CNN's hyperparameters is shown in **Figure 2**. Compared to more conventional optimisation algorithms like stochastic gradient descent (SGD), adaptive learning rate optimisation techniques offer superior out-of-the-box performance thanks to their fast convergence and less need for fine-tuning algorithm parameters. Adam (adaptive moment estimation), a hybrid of momentum (which allows for longer steps in the direction of the steepest gradient) and root mean square propagation (which allows for stronger acceleration on steep slopes), is the most popular adaptive optimiser. Although there are many distinct optimisers and various varieties of Adam, he was chosen because he possesses these attributes. Ideally, research on the optimum optimiser for the breast cancer data set would be conducted empirically[29–31].

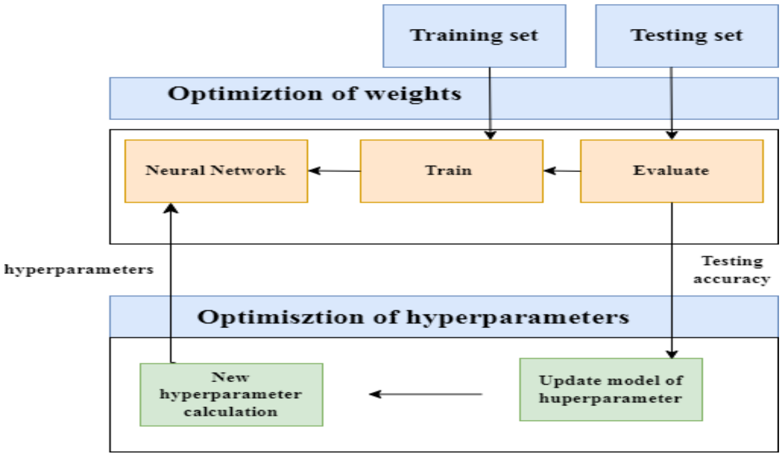

Figure 2. Standard process of hyperparameter optimisation.

4. Proposed CNN-attention mechanism based model

The complete process of breast cancer classification of invasive breast cancer images is implemented using the proposed C-ATT (CNN-attention) model described in the subsequent sections:

4.1. Dataset description

We use a publicly available database obtained from Kaggle to evaluate the efficacy of our suggested methods. There are 162 scanned whole-mount slides of breast cancer tissue samples. Each image has a unique patient ID and a positive (IDC present) or negative (IDC absent) label applied by a medical professional[32].

The IDC breast histopathology image dataset was used for this study. Initially, there were 162 WSI-scanned breast cancer tissues in the original collection. From those WSI, 277,524 patches were taken, each measuring 50 by 50 pixels. There were 78,786 IDC(+) photos and 198,738 IDC(-) images. **Figure 3** displays examples of histopathology photos from the current dataset.

In this study, we use a dataset of 277,524 photos from the IDC breast cancer database and classify them as IDC(+) or IDC(-). The dataset contains 78,786 IDC constructive images and 198,738 IDC undesirable images.

4.2. The proposed C-ATT model

The proposed model is provided in this section, and it is based on a CNN architecture, which is already pretrained and the CNN-Attention-based model, as shown in **Figure 3**. The pretrained CNN model is hyperparameter optimised using an algorithm to improve the proposed model's performance. Once the optimal parameter settings had been determined, the adaptive moment estimation model was trained using various techniques. After finishing training, the model is checked against the test data. The proposed model was implemented using Python with the help of the Keras and TensorFlow libraries. In the following part, the structure of the model is described in depth. Attention, flatten, thick, and dropout layers round out the proposed model's eight total layers.

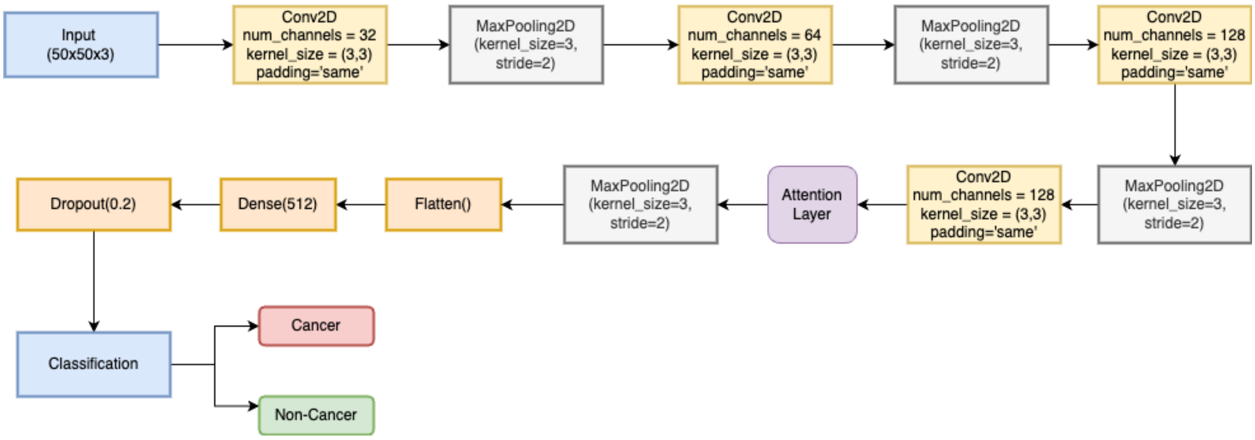

Figure 3. Architecture of the proposed C-ATT model.

The initial step was improving the datasets and splitting them into a training set and a test set with a 75:25 split, respectively. Training sets have also been augmented via various data preparation processes. The dataset breast cancer historiography was used to test the suggested model. Second, the pretrained CNN architecture's hyperparameters are optimised with the help of the adaptive moment estimation (Adam). Third, the model was fully trained with the hyperparameter values found in the previous phase, which allowed the architecture to correctly diagnose the test set. The stages of the suggested model will be described in depth in the following paragraphs.

Step 1: Data preprocessing step:

Histopathological breast cancer datasets underwent preprocessing at this stage. Initially, noise was digitally removed from each image, and the size of every image was 50 × 50 × 3, saving space and processing power. Linear interpolation is utilised to obtain these missing data points during preprocessing. Second, various data augmentation techniques have been used to expand the size of training sets, reduce the likelihood of overfitting, accelerate convergence, and enhance generalisation.

Phase 2: Optimisation of parameters step:

The effectiveness of a CNN's categorisation is heavily influenced by its tuning parameters. As an optimiser, the suggested model uses the adaptive moment estimation (Adam) algorithm. Eight hyperparameters, including learning rate, batch size, dropout rates for three layers, and dense layer unit count, are optimised in the proposed CATT model.

Step 3: Model learning step:

Feature extraction is carried out to make the model more amenable to learning from the datasets in use. The convolutional base is left untouched during feature extraction, while the underlying classifier is updated to the most recent version to better suit the datasets. Four 2D convolutional layers, four 2D MaxPooling layers, an attention layer, a flattened layer, a dense layer, and a dropout layer make up the new classifier's twelve layers. To determine the convolutional layer's learning rate, the number of neurons in the first four dense layers that employ the activation function (ReLU) to prevent gradient vanishing and the rates of all dropout layers are all computed using the adaptive moment estimation. Only one of the neurons in the final dense layer uses a softmax function. Fine-tuning is accomplished by retraining the last two blocks of the convolutional section after the new classifier has been trained for some epochs. The model employs a loss function of binary cross entropy.

Step 4: The performance evaluation step:

Accuracy, precision, recall and the AUC are the performance metrics used to evaluate the performance of the proposed model. All the metrics are explained here accordingly:

- Accuracy: It defines the total correctly classified instance in perspective of total instances.

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

- Precision: The precision of a model depends on how many positive instances it correctly predicts against how many are really present.

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

- Recall: In statistics, recall is defined as the percentage of positive samples that actually are positive.

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

5. Experimental results and performance analysis

5.1. Experimental setup

Python 3 and Keras simulate the suggested model[33]. Keras is a high-level NN API compatible with popular frameworks like TensorFlow and OpenCV and popular Python libraries like Pandas and Numpy. It is widely considered to be the best deep learning framework. Its user-friendly design and ability to run several tests and retrieve results quickly and with minimal delay have provided sufficient paper. We used TensorFlow in a simulated setting for the experiment design and validation. At first, there were a total of 277,524 photos in the collection, 198,738 of which were deemed to be free of cancer and 78,786 of which showed evidence of an active tumour. There is a 75:25 split between the train and test datasets. During preprocessing, the input pictures are downscaled to 50 × 50 × 3 using the inter-linear polation technique INTER_LINEAR (INTER_CUBIC/INTER_AREA/INTER_NEAREST). Train and test data have the following shapes: X_train = (208143, 50, 50, 3); X_test = (69381, 50, 50, 3); Y_train = (208142, 2); Y_test = (69381, 2); Y can be in one of two classes: cancer or non-cancer. To achieve optimal performance, the adaptive moment estimation (Adam) determines the best settings for our model's hyperparameters, such as the number of filters, kernel size, dropout rate, and learning rate. The model's learning rate is 0.00002, and its beta_1 and beta_2 values are respectively 0.9 and 0.999.

The attention layer set up the squeeze layer, which averaged data from axis = 2, 3. After that, use the first convolutional layer and transpose on the compressed output. To draw focus, the sigmoid function is applied to the transposed layer. After that, the input is amplified by the determined focus. Since the first layer only extracts the dataset's global features, the convolution layer's number of filters must increase over time to remove the finer-grained features (local features). Filter sizes of 32, 64, 128, and 256 were ultimately chosen to best represent the model. A total of 512 neurons were used to create the dense layer. The filter sizes and the number of neurons were established through a grid search. In addition, we examined three distinct dropout levels (0.1, 0.2, and 0.5) and discovered that the latter performed best.

Similarly, we experimented with several choices for the learning rate (including 0.1, 0.01, 0.2, 0.002, 0.0001, 0.002, 0.00001, and 0.00002) before settling on 0.00002 as the best option. The last experiment employs a batch size of 75, trained for 20 iterations. Binary cross entropy is used to determine the model's loss function, which is graphically shown in **Figure 4**.

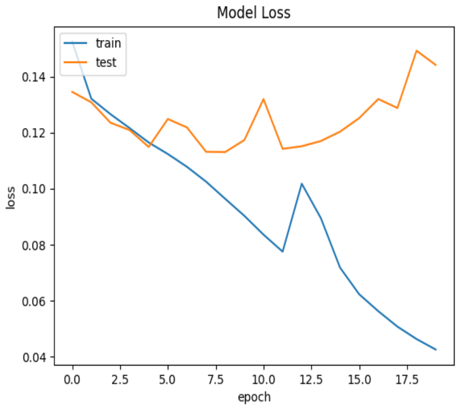

Figure 4. Epochs loss chart of the proposed model.

5.2. Analysis of the proposed model for IDC histopathological images

The integration of CNN and attention is hugely significant for managing healthcare and predicting breast cancer. Our model can forecast events with more accuracy and promptness, which could result in earlier diagnosis and treatment. The proposed model empowers patients by enabling restricted data sharing, allowing them more control over their health information while retaining privacy.

To analyse the outcomes of the suggested hyperparameter-based approach. Accuracy, precision, recall, and area under the curve (AUC) are used to assess the proposed model on the breast cancer histopathology dataset. For the validation set, the suggested technique has an accuracy of 96.61%, precision of 97.45%, recall of 99.03%, and area under the curve (AUC) of 98.02%.

The table below displays how the suggested model performs compared to the training dataset's results. 97.57%, 99.23%, 99.77%, and 99.58% are the precision, recall, and area under the curve, respectively, for the training dataset. Using a breast cancer histopathology dataset, we compared the suggested model's accuracy to previously published research. Studies based on CNN architectures were chosen for comparison[33]. Xioli et al.[34] in 2021, CNN enhanced with human attention in their research. Another author[35] examined the performance of several CNN and attention-based classifiers on the same real-world dataset in 2022. The IDC breast cancer dataset was utilised by Wang et al. [36] to test their CNN and GRU for breast cancer detection. Accuracy, recall, precision, and AUC were all measured and compared among the various approaches. **Figure 5** depicts the graphical representation of the comparison between the accuracies achieved by different researchers. A minus sign in **Table 1** signifies that a comparable measure is unavailable for that comparison technique.

Table 1. Comparison of the proposed model with the recent studies.

Year of the research	Authors	Accuracy	Precision	Recall	AUC
2021	S. Roy et al.[33]	92.5	93.4	88.8	-
2021	Xioli et al.[34]	83.15	83.5	83.1	94.87
2022	Pinky A. et al.[35]	94.67	92.60	80.52	-
2023	Md Ishtyaq et al.[37]	90.02	-	94.7	90
2023	Xiaomei et al.[36]	86.21	85.50	-	89
2023	Sushovan et al.[38]	90.3	-	-	-
2023	**Proposed model**	**96.61**	**97.45**	**99.03**	**98.02**

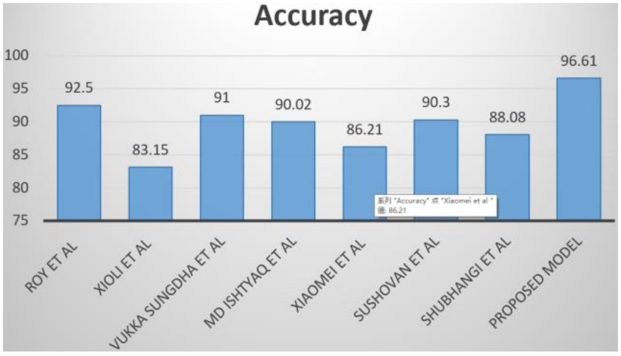

Figure 5. Comparison of accuracies between other authors and proposed study.

6. Conclusion and future work

The CNN and attention mechanism system is proposed in this study for early breast cancer detection. The goal was to run the input picture data through a CNN with an attention layer that had already been pre-trained. Breast tumours are successfully separated into benign and malignant categories using the suggested approach. Cancer is a terrible disease, but if caught early and at the proper stage, an oncologist can take the necessary steps to preserve their patients' lives. When doctors in underdeveloped nations like India can classify their patients as having invasive (malignant) or noninvasive (benign) breast cancer, they may allocate their limited medical resources more effectively.

IoT-based, real-world health monitoring devices and deep learning technology have demonstrated their vital role in tracking health and predicting illness. Creating deep learning models for health problem categorisation has the potential to improve accuracy and lessen the need for human intervention in the process of gathering features. Proactive disease prevention, remote monitoring, and early identification of health concerns will be made possible by the convergence of IoT-based real-time health monitoring devices, deep learning technologies, and blockchain-integrated protected frameworks.

In the future, combining IoT and blockchain in health care will help decentralise data to enhance resilience and security. CNN models work effectively to analyse image and sensor data from IoT devices. IoT data may be analysed in real-time or almost real-time with the processing capacity of CNNs to glean insightful information and make prompt decisions. The combination of blockchain, IoT, and CNN models has enormous potential to revolutionise businesses by delivering secure, open, and effective data administration and analysis solutions. However, a successful deployment necessitates carefully evaluating the particular use case, the selected blockchain platform, scalability issues, and adherence to pertinent laws. When used carefully, this combination can spur creativity and enhance different facets of automation and data-driven decision-making.

In keeping with the above, the proposed model is to test an actual breast cancer dataset collected from self-built IoT devices and to integrate blockchain security into the model. To evaluate the efficacy of the proposed model, it may be applied to various other disease image datasets, such as those about lung and cervical cancer.

Author contributions

Conceptualization, DS; methodology, DS; software, DS; validation, DS, RK and AJ; formal analysis, DS; investigation, DS; data curation, RK; writing—original draft preparation, DS; writing—review and editing, AJ; visualization, RK; supervision, RK; project administration, RK and AJ. All authors have read and agreed to the published version of the manuscript.

Conflict of interest

The authors declare no conflict of interest.

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