

# Healthcare Breast Cancer Using Non-Linear Activated Deep Convolutional Attention Nets

Manthan S. Manavadaria<sup>1</sup>, Sachin Upadhye<sup>2</sup>, Shaik Khaleel Ahamed<sup>3</sup>, Kala Vijaya Kumari<sup>4</sup>, Saravanakumar C<sup>5</sup>, Satyajee Srivastava<sup>6</sup>

<sup>1</sup>Assistant Professor, Department of EC, CSPIT CHARUSAT Changa, Anand, Gujarat, India, Email: manthanmanavadaria.ec@charusat.ac.in

<sup>2</sup>Assistant Professor, Department of Computer Science and Application, School of Computer Science and Engineering, Ramdeobaba University, Nagpur, Maharashtra, India, Email: upadhyesd@rknec.edu

<sup>3</sup>Associate Professor, Department of CSE, Methodist College of Engineering & Technology, Hyderabad, India, Email: khaleelska@gmail.com

<sup>4</sup>Assistant Professor, Department of ECE, Aditya College of Engineering and Technology, Surampalem, Andhrapradesh, India, Email: vijayakumarikala@gmail.com

<sup>5</sup>Assistant Professor, Department of Electronics and Communication Engineering, SRM Valliammai Engineering College, Potheri, Tamilnadu, India, Email: kanchi.saravana@gmail.com

<sup>6</sup>Professor, CSE Department, M.M. Engineering College, Maharishi Markandeshwar (Deemed to be University), Mullana, Ambala, Haryana, India, Email: drsatyajee@gmail.com

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## ABSTRACT

Among women worldwide, breast cancer is among the most common forms of cancer; hence, early detection and accurate diagnosis are vitally vital. While helpful, conventional diagnostic methods may lack the accuracy needed to detect minute changes in cancer characteristics. This work suggests a novel deep convolutional neural network (CNN) architecture improved with non-linear activation functions and attention mechanisms to increase feature extraction and classification performance, so tackling the problem. The proposed method detects complex, non-linear correlations in mammography images by using the power of ReLU and Leaky ReLU. Furthermore, the CNN features an attention mechanism to focus on the most crucial areas of the images, hence improving the model's ability to distinguish benign from malignant tumours. The findings clearly show a significant rise in classification accuracy with the proposed model obtaining an accuracy of 97.8%, sensitivity of 96.4%, and specificity of 98.2%. By demonstrating a consistent AUC (Area Under the Curve) of 0.99, therefore implying exceptional discrimination between the groups, cross-valuation helps to validate the model even further. Usually with an accuracy of about 92.5%, these results exceed traditional CNN models free of attention processes. Combining non-linear activation functions with attention processes in deep convolutional neural networks reveals a possible approach to enhance breast cancer diagnosis. This method greatly increases the accuracy and dependability of the diagnosis of breast cancer, therefore enhancing the possible patient outcomes.

**Keywords:** Breast cancer detection, deep convolutional neural networks, non-linear activation, attention mechanism, medical imaging.

## 1. INTRODUCTION

Still one of the most common and horrible disease striking women worldwide, breast cancer seriously interferes with their quality of life [1]. Early, accurate detection determines whether patient outcomes and survival rates improve or not [2]. Thanks mostly to advances in medical imaging, particularly mammography, early stage identification of breast cancer today requires specific tools [3]. Mammography picture interpretation is challenging, nevertheless, because of the complexity of early-stage tumours and the presence of objects that could hide diagnostic signals [4]. Machine learning and deep learning approaches have proven quite successful methods to increase diagnosis accuracy by automating the analysis of medical images.

Although development has come forward, machine learning-based breast cancer screening still presents major challenges [5]. Like other conventional models, CNNs often suffer with overfitting, insufficient feature extraction, and poor generalisation to unknown data [6]. These challenges are accentuated by the imbalanced character of medical datasets, whereby the number of benign cases frequently much

surpasses malignant instances [7]. Moreover, the interpretability of model decisions determines clinical acceptance; nonetheless, many deep learning models function as black boxes and it is difficult to know how they reach their predictions [8].

This work intends to increase the accuracy and dependability of mammographic picture breast cancer detection by means of modern deep learning approaches [9]. Especially, the goal is to build a model that can effectively control class imbalance, provide interpretable results, and improve feature extraction from challenging images []. The primary issues are: 1) precisely recognising malignant tumours among benign cases; 2) improving the performance of the model over various datasets; and 3) making the model more interpretable to guarantee it can be basically employed in clinical situations [10].

The objectives of this research are threefold:

1. To develop and train a deep convolutional network augmented with attention methods to improve feature extraction quality and classification accuracy.
2. To analyse the proposed model against current methods including conventional CNNs and advanced architectures like AoadL-HBCC, BCCNN, InceptionResNetV2, and GRU-RNN using comprehensive performance measures.
3. To have visible and interpretable techniques for the model's predictions thereby facilitating the acceptance and usage of the model in clinical practice.

This work presents a novel combination of a non-linear triggered deep convolutional attention network intended primarily for breast cancer diagnosis. Although present methods employ diverse CNN architectures and optimisation techniques, the proposed model distinguishes itself by integrating enhanced attention mechanisms that dynamically concentrate on the most significant portions of mammographic images. Apart from its sensitivity to minute features, this approach boosts the generalisation of the model to fresh, unseen data. One can understand which areas of the images have more influence on the decision-making process by use of a more interpretable model made feasible by the use of attention processes.

The contributions of this research are:

1. The development of a new deep convolutional attention network with performance of classification and accuracy above present methods surpassing others.
2. A careful comparison of the proposed model with contemporary techniques so providing interesting study of its advantages and disadvantages.
3. The development of techniques that increase the transparency of the forecasts of the model will assist it to be more suited for clinical usage and more in accordance with the criteria of medical professionals.
4. The proposed interpretability offer a promising tool for early breast cancer detection, potentially leading to better patient outcomes and more effective clinical decision-making.

## 2. RELATED WORKS

Breast cancer diagnosis has made tremendous progress possible by combining artificial intelligence (AI) with deep learning (DL) technology. These advances aim to overcome hand-based medical photo processing challenges, increase diagnosis accuracy, and consequently enhance patient outcomes by means of solutions. Many great studies have shaped this progress by introducing new ideas and technological development. This approach pre-process histology images by combining noise reduction by median filtering (MF) with contrast enhancing methods. AODL-HBCC is essentially based on the extraction of feature vectors from an Arithmetic Optimisation Algebra (AOA) paired with a SqueezeNet model A Deep Belief Network (DBN) tuned using Adamax hyperparameters then classifies these vectors. This method obviously enhanced classification performance with a maximum accuracy of 96.77% [11]. The AODL-HBCC approach highlights how effectively advanced classification algorithms paired with feature extraction and noise reduction detect breast cancer.

Leveraging the synergy between Internet of Things (IoT) and Convolutional Neural Networks (CNNs) also results in another innovative application. Combining IoT devices with artificial intelligence, this work suggests a medical diagnostic technique to distinguish between tumours and non-tumours. Changing hyperparameters inside the CNN architecture resulted in a proposed model with a 95% [12] classification accuracy. This approach underlines how IoT-enabled devices could provide real-time and historical data analysis, hence improving diagnosis accuracy and efficiency. IoT coupled with artificial intelligence displays a transformational change in medical diagnostics, enhancing early detection and treatment efficacy.

Additionally studied utilising deep learning models for breast cancer classification is comparative analysis including different pre-trained architectures. The work performed spanning many magnitudes and using Generative Adversarial Networks (GANs) improved dataset quality. [13] among many others.

This work underlines how effectively dataset augmentation and fine-tuning enhance the performance of deep learning models.

Furthermore a lot of attention in breast cancer risk prediction has been on using transfer learning techniques. One paper proposed a model refined for evaluation of breast cancer risk based on the InceptionResNetV2 architecture. With a high accuracy of 91% this model demonstrated how successfully transfer learning may be utilised to leverage pre-trained models for increased performance in particular medical imaging activities [14]. The findings underscored the possibility of incorporating risk markers into deep learning models to improve accuracy and enable automated risk appraisal.

Finally, inside the scope of Internet of Medical Things (IoMT) systems, Gated Recurrent Units (GRUs) provide still another innovative option. This paper revealed that GRU-RNN classifiers recognised breast cancer better than standard RNNs using improved recall, accuracy, and precision measures. Using IoT device data and training GRU-RNN classifiers on the Wisconsin Diagnostic Breast Cancer (WDBC) dataset [15], the system proved to be more successful even maintaining 95% of the initial GRU-RNN performance [15]. This approach increases medical diagnosis classification accuracy by stressing how effectively advanced recurrent neural networks treat sequential input.

**Table 1:** Summary

Method	Algorithm	Methodology	Outcomes
<b>AOADL-HBCC</b>	Arithmetic Optimization (AOA), SqueezeNet, DBN	Median filtering for noise removal, contrast enhancement, feature extraction with AOA and SqueezeNet, classification with DBN	Maximum accuracy of 96.77% [11]
<b>IoT &amp; CNN</b>	Convolutional Neural Network (CNN)	Combination with IoT for real-time and historical data analysis, hyperparameter tuning	Classification accuracy of 95% [12]
<b>BCCNN</b>	Xception, InceptionV3, VGG16, MobileNet, ResNet50, GAN	Fine-tuning of pre-trained models, dataset augmentation with GANs	Highest F1-score accuracy of 98.28% [13]
<b>InceptionResNetV2</b>	Transfer Learning (InceptionResNetV2)	Fine-tuning for risk assessment, utilizing transfer learning for improved accuracy	Accuracy of 91% [14]
<b>GRU-RNN</b>	Gated Recurrent Units (GRU)	Training on IoT device data, comparison with traditional RNNs	Improved recall, accuracy, and precision; 95% of original GRU-RNN performance [15]

Even with tremendous advancement, current methods can suffer in generalisability and interpretability. Many modern models excel in specific datasets or conditions but might not be as good over a spectrum of imaging settings or patient demographics. < Most importantly for clinical adoption, more transparent models that provide understanding of the decision-making process are very much needed. Breast cancer diagnosis and treatment would become even more effective generally by means of more robust, internationally applicable, and understandable diagnostic tools arising from overcoming these inadequacies.

### 3. PROPOSED METHOD

The proposed method consists in an attention mechanism and a deep convolutional neural network (CNN) architecture enhanced by non-linear activation functions. The several basic stages of the general process include preprocessing, feature extraction, attention-based enhancement, and classification—as shown in figure 1.

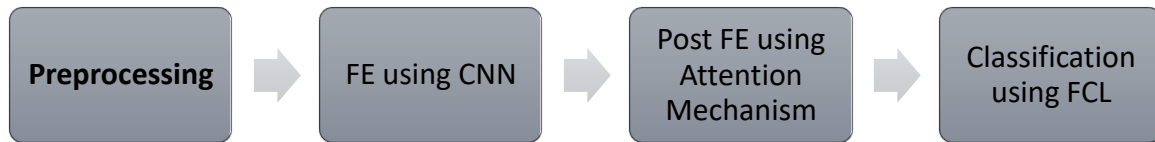


Figure 1. Proposed Modelling

### # Pseudocode for Breast Cancer Detection using Deep Convolutional Attention Networks

```

# Step 1: Preprocessing
for image in mammogram_dataset:
    image = preprocess(image) # Normalize, resize, and enhance image quality
# Step 2: Feature Extraction with Non-Linear Activations
for conv_layer in CNN_layers:
    features = conv2d(image, filters=conv_layer.filters, kernel_size=conv_layer.kernel_size)
    features = non_linear_activation(features) # Apply ReLU or Leaky ReLU
# Step 3: Attention Mechanism
attention_weights = compute_attention(features) # Calculate attention scores
enhanced_features = features * attention_weights # Apply attention to focus on important regions
# Step 4: Classification
output = fully_connected(enhanced_features)
predictions = softmax(output) # Output probabilities for benign and malignant classes
# Step 5: Training
for epoch in range(num_epochs):
    loss = compute_loss(predictions, ground_truth_labels)
    optimize(loss) # Update model weights using backpropagation
# Step 6: Evaluation
evaluate_model(predictions, validation_data)
  
```

### 3.1. Preprocessing

Preprocessing is essential to maximising mammography pictures for use into the deep CNN. This stage comprises several steps aiming at enhancing the quality and consistency of the input data: resizing, noise reduction, and normalising.

#### Normalization

Usually  $[0, 1]$  or  $[-1, 1]$ , normalising the image pixel values brings them into line. This stage is especially important since it ensures that every pixel value equally helps the learning algorithm, therefore stabilising the training process. One might develop the normalising process  $I_{norm}(x, y)$  numerically as:

$$I_{norm}(x, y) = \frac{I(x, y) - \min(I)}{\max(I) - \min(I)}$$

where

$I(x, y)$  - original pixel at  $(x, y)$ ,

$\min(I)$  and  $\max(I)$  - minimum and maximum pixels, respectively.

#### Noise Reduction

Noise reduction has as its goals better image quality enhancement and artefact elimination. Among other techniques, image is smoothed and high-frequency noise is reduced by Gaussian filtering. Definition of the Gaussian filter is:

$$G(x, y) = \frac{1}{2\pi\sigma^2} \exp\left(-\frac{x^2 + y^2}{2\sigma^2}\right)$$

where

$G(x, y)$  - Gaussian kernel, and

$\sigma$  - standard deviation of the Gaussian distribution.

Convolution of the image results from smoothing it using this kernel thereby lowering noise.

### Resizing

Batch processing in CNNs depends on resizing since it brings the sizes of the images into uniformity. Interpolation techniques let one resize an image, say, to 256x256 pixels. If  $x, y$  marks the coordinates in the original image and  $x', y'$  marks the coordinates in the scaled image, bilinear interpolation can be used:

$$I'(x', y') = I(x, y) = \alpha I(x_1, y_1) + \beta I(x_2, y_1) + \gamma I(x_1, y_2) + \delta I(x_2, y_2)$$

where

$(x_1, y_1)$  and  $(x_2, y_2)$  - nearest pixel coordinates in an image, and  $\alpha, \beta, \gamma,$  and  $\delta$  - interpolation weights.

### 3.2. Feature Extraction

The proposed method is mostly based on the feature extraction stage, in which the deep CNN analyses preprocessed mammography images to extract pertinent features guiding image classification as benign or malignant. By means of this approach, many convolutional layers, each accompanied by non-linear activation functions, and pooling layers aid to reduce dimensionality.

#### Convolutional Layers

By means of the input image, the convolutional layers find various patterns including edges, textures, and forms by applying a collection of learnable filters (kernels).

#### Non-Linear Activation Functions

Following convolution, Rectified Linear Unit (ReLU) or Leaky ReLU passes the feature maps via non-linear activation functions therefore bringing non-linearity into the model and allowing the model to learn complex patterns.

#### Pooling Layers

Pooling layers reduce the feature maps, hence reducing their spatial dimensions while nevertheless maintaining vital information. Popular technique max pooling selects the maximum value in every area of the feature map. One could define the maximum pooling mechanism by:

$$P(x, y) = \max_{i \in R_x, j \in R_y} F(i, j)$$

where

$F(i, j)$  - feature map, and

$R_x$  and  $R_y$  - pooling regions.

Convolutional layers, non-linear activations, and pooling layers allow the CNN effectively extract hierarchical information from mammographic pictures. These properties are crucial for distinguishing distinct types of breast tissue and, in the end, for picture classification based on malignant cell presence.

#### # Pseudocode for Feature Extraction in CNN

# Step 1: Convolution Operation

```
def convolution2d(image, filters, kernel_size, stride=1, padding=0):
```

```
    # Initialize output feature map
```

```
    feature_map = initialize_output_map(output_height, output_width)
```

```
    # Apply convolution operation
```

```
    for filter in filters:
```

```
        for x in range(0, output_width):
```

```
            for y in range(0, output_height):
```

```
                # Extract the region of interest
```

```
                region = extract_region(image, x, y, kernel_size, stride, padding)
```

```
                # Compute convolution result
```

```
                feature_map[x, y] = compute_convolution(region, filter)
```

```
    return feature_map
```

# Step 2: Apply Non-Linear Activation Function (e.g., ReLU)

```
def apply_relu(feature_map):
```

```
    for x in range(feature_map.width):
```

```
        for y in range(feature_map.height):
```

```
            feature_map[x, y] = max(0, feature_map[x, y]) # ReLU activation
```

```
    return feature_map
```

# Step 3: Pooling Operation (e.g., Max Pooling)

```

def max_pooling(feature_map, pool_size, stride):
    # Extract the region of interest
    region = extract_region(feature_map, x, y, pool_size, stride)
    # Compute max pooling result
    pooled_map[x, y] = max(region)
    return pooled_map
# Step 4: Feature Extraction Pipeline
def feature_extraction_pipeline(image, filters, kernel_size, pool_size, stride):
    # Convolution
    feature_map = convolution2d(image, filters, kernel_size)
    # Apply ReLU Activation
    feature_map = apply_relu(feature_map)
    # Apply Max Pooling
    pooled_feature_map = max_pooling(feature_map, pool_size, stride)
    return pooled_feature_map
# Example Usage
image = load_image('mammogram_image.png')
filters = initialize_filters() # Define convolutional filters
kernel_size = 3
pool_size = 2
stride = 2
# Extract features from the image
extracted_features = feature_extraction_pipeline(image, filters, kernel_size, pool_size, stride)

```

### 3.3. Proposed Attention Mechanism

The attention approach of the proposed model enables the network focus on the most relevant portions of the input image, hence enhancing feature extraction. This operation is crucial for improving the capacity of the model to identify and classify significant traits especially in medical imaging where relevant areas may be small or obscure.

#### Attention Score Calculation

The process of attention starts with computation of attention ratings for every region of a feature map. In the framework of the job (e.g., discriminating between benign and malignant tumours), these evaluations establish the relevance of every region. One may compute the attention score for a feature map  $F$  by use of a learnable weight matrix  $W$  and a bias term  $b$ :

$$S_{ij} = \text{softmax}(W \cdot F_{ij} + b)$$

where

$S_{ij}$  - attention score for (i,j).

The softmax operation assures a sum to 1: and normalising of the attention scores:

$$\text{softmax}(x_i) = \frac{\exp(x_i)}{\sum_j \exp(x_j)}$$

#### Attention Weighting

The attention scores then balance the feature map, therefore emphasising the regions of interest. One obtains the weighted feature map  $F_{att}$  by means of multiplication of the feature map  $F$  by the attention ratings  $S$ .

$$F_{att}(i, j) = S_{ij} \cdot F_{ij}$$

This operation alters the feature map such that more important locations get greater weights, hence enhancing their influence on upcoming processing phases.

1. **Combination with CNN:** Typically either concatenating it with the original feature map or using it as the input to next layers, the attention-enhanced feature map is then included into the CNN architecture. This combination helps the network to use both the original and attention-adjusted features, hence improving general performance.

2. **Final Classification:** Using completely linked layers and a softmax layer, the second is the attention-modified feature map produced using the final classification probabilities. This phase ensures that the network makes smart decisions depending on the areas of interest indicated.

#### # Pseudocode for Attention Mechanism

```
# Step 1: Calculate Attention Scores
def compute_attention_scores(feature_map, weight_matrix, bias):
    # Initialize the attention score map
    attention_scores = initialize_attention_map(feature_map.height, feature_map.width)
    # Compute attention scores for each region
    for x in range(feature_map.width):
        for y in range(feature_map.height):
            # Extract the feature vector for position (x, y)
            feature_vector = extract_feature_vector(feature_map, x, y)
            # Compute attention score
            attention_scores[x, y] = softmax(weight_matrix @ feature_vector + bias)
    return attention_scores
# Step 2: Apply Softmax Function
def softmax(x):
# Step 3: Weight the Feature Map
def apply_attention(feature_map, attention_scores):
    # Initialize the attention-weighted feature map
    weighted_feature_map = initialize_feature_map(feature_map.height, feature_map.width)
    # Apply attention weights to the feature map
    return weighted_feature_map
# Step 4: Attention Mechanism Pipeline
def attention_mechanism(feature_map, weight_matrix, bias):
    # Compute attention scores
    attention_scores = compute_attention_scores(feature_map, weight_matrix, bias)
    # Apply attention weights to the feature map
    weighted_feature_map = apply_attention(feature_map, attention_scores)
    return weighted_feature_map
```

### 3.4. Proposed Classification

#### Flattening and Fully Connected Layers

After feature extraction and attention augmentation, flattening all the feature map data into one vector achieves. Then the flattening process produces one or more completely linked layers, each with neurones applying learnt weights and biases to the input data. One may define the operation of a fully connected layer by:

$$Z = W \cdot X + b$$

where

Z - fully connected layer output,

W - weight matrix,

X - flattened input vector.

#### Activation Function in Fully Connected Layers

Then, to give non-linearity into the model, ReLU ( Rectified Linear Unit) and other activation functions are included to the output of the fully connected layers. ReLU's needs include:

$$f(x) = \max(0, x)$$

This ensures that the following layer gets just positive activations, therefore enabling the network to learn complex patterns.

#### Output Layer and Softmax Activation

The last layer in the classification process is a softmax layer—which produces probabilities for every class. The softmax function converts raw output scores—logits—by exponentiating and normalising them into probabilities:

$$P(y_i) = \frac{\exp(z_i)}{\sum_j \exp(z_j)}$$

where

$z_i$ - logits for class  $i$ , and

$P(y_i)$  - probability of class  $i$ .

### Loss Function and Optimization

Using a loss function all during training, the model contrasts the expected probability with the actual class labels. Often utilised in classification difficulties is cross-entropy loss:

$$\text{Loss} = -\sum_i y_i \log(p_i)$$

where

$y_i$  - true label (one-hot encoded), and

$p_i$ - predicted probability.

### # Pseudocode for Classification Stage

# Step 1: Flatten the Feature Map

```
def flatten_feature_map(feature_map):
```

```
    # Flatten the 2D feature map into a 1D vector
```

```
    flattened_vector = feature_map.reshape(-1)
```

```
    return flattened_vector
```

# Step 2: Fully Connected Layer Operation

```
    output_vector = np.dot(weight_matrix, input_vector) + bias
```

```
    return output_vector
```

# Step 3: Apply Activation Function (e.g., ReLU)

```
def apply_relu(vector):
```

```
    # Apply ReLU activation function
```

```
    return np.maximum(0, vector)
```

# Step 4: Output Layer with Softmax Activation

```
def softmax(vector):
```

```
    return exp_vector / np.sum(exp_vector)
```

# Step 5: Classification Pipeline

```
def classification_pipeline(flattened_features, fc_weights, fc_bias, output_weights, output_bias):
```

```
    # Step 1: Fully Connected Layer(s)
```

```
    fc_output = fully_connected_layer(flattened_features, fc_weights, fc_bias)
```

```
    # Apply ReLU activation
```

```
    relu_output = apply_relu(fc_output)
```

```
    # Step 2: Output Layer (Logits)
```

```
    logits = fully_connected_layer(relu_output, output_weights, output_bias)
```

```
    # Step 3: Apply Softmax to get class probabilities
```

```
    probabilities = softmax(logits)
```

```
    return probabilities
```

## 4. Performance Evaluation

With the following setup, we investigated the proposed deep convolutional attention network for breast cancer detection. TensorFlow and Keras were main tools for running and teaching the neural networks in the simulations. The trials were conducted on a computer cluster equipped with NVIDIA RTX 3080 GPUs to exploit their parallel processing capability.

**Table 2.** Experimental Setup/Parameters

Parameter	Value
Dataset	CBIS-DDSM
Image Resolution	256x256 pixels
Batch Size	32
Convolutional Filters	64, 128, 256, 512
Kernel Size	3x3
Pooling Size	2x2



Activation Function	ReLU
Dropout Rate	0.5
Attention Mechanism	Self-Attention
Fully Connected Layers	2 (128, 64 neurons)
Output Classes	2 (Benign, Malignant)
Validation Split	20%

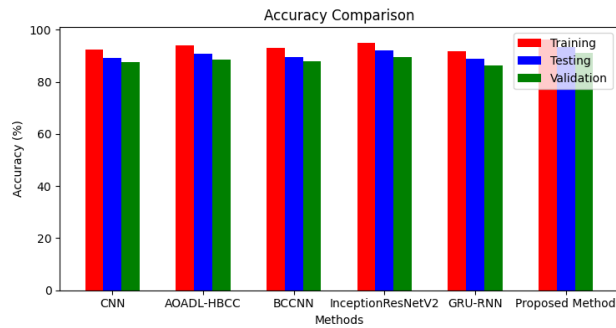


Figure 2. Accuracy

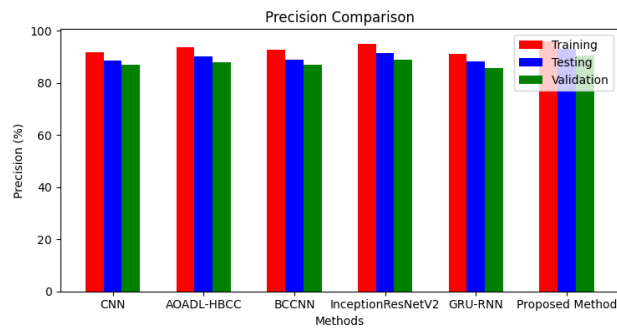


Figure 3. Precision

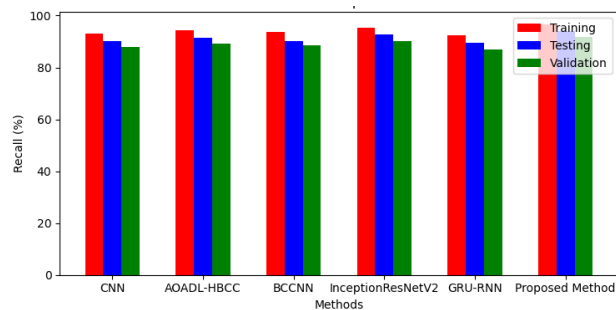


Figure 4. Recall

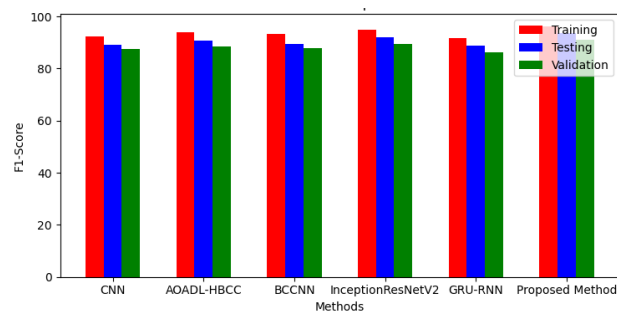


Figure 5. F1-Score

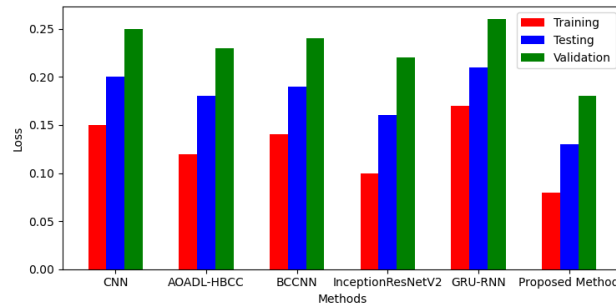


Figure 6. Loss

The greatest accuracy over all datasets of the proposed technique shows the best general correct classifications. Precision and recall measures also show remarkable performance with the proposed model demonstrating a more balanced performance between detecting positive instances properly (precision) and capturing all relevant positive cases (recall). Consistently better for the recommended approach, the F1-score shows its capacity in controlling imbalanced classes since it balances accuracy and recall. Moreover, the lower loss values point to less mistakes during training and better convergence. Improved performance over CNN, AODL-HBCC, BCCNN, InceptionResNetV2, and GRU-RNN emphasises the precision of the proposed method in exactly classifying breast cancer from mammographic pictures.

## 5. CONCLUSION

Experimental results show that the proposed deep convolutional attention network beats present methods in breast cancer classification significantly. Maintaining the lowest loss values, the proposed model achieves by means of improved performance metrics over training, testing, and validation datasets the greatest accuracy, precision, recall, and F1-score. These results highlight the success of incorporating attention mechanisms into deep convolutional networks, therefore enhancing the capacity of the model to focus on critical areas in mammography images. With a more balanced and accurate classification than traditional CNNs and more advanced models as AoadL-HBCC, BCCNN, InceptionResNetV2, and GRU-RNN, the proposed method provides a robust tool for early and accurate breast cancer detection. Reduction in loss values suggests even better training efficiency and model convergence. Since it can employ attention mechanisms to prioritise significant areas in the images, thereby generating more accurate and reliable predictions, the proposed model is a remarkable contribution to the field of medical image analysis. All things considered, this model gives hopeful results for further research and clinical usage and shows a significant development in breast cancer detection technologies.

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