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Research Article

Computer Aided Diagnosis System for Breast Cancer Detection

Mehreen Tariq[1, *], Hareem Ayesha[2]

[1]Department of Computer Science, Bahauddin Zakariya University, Multan, 60000, Pakistan.
[2]Institute of Computer Science and Information Technology, The Women University, Multan, 60000, Pakistan.
[*]Corresponding Author: Author's Name. Email: mehreentariq97@gmail.com

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Abstract: Recent developments in medical imaging have substantially enhanced the capacity to identify early-stage breast cancer. Medical practitioners frequently employ radiographic and microscopic imaging methods to detect a wide range of breast disorders. Accurately classifying these anomalies is challenging because of the similarities in appearance between benign and malignant breast cancers as well as the imprecision of imaging data. The integration of AI into healthcare applications has stoked the fires of research into intelligent computer-aided detection and diagnostic systems. The combination of computer vision (CV) and image processing allows these systems to identify breast cancer effectively. Despite the abundance of literature on the subject, most of it has focused on treating breast mammography as a binary test for benign or malignant abnormalities. Machine learning-based techniques have restricted accuracy due to their insufficient feature extraction capabilities, despite extensive exploration. However, because of their capacity to extract hundreds of characteristics, deep learning-based methods have demonstrated better performance in several experiments. A prevalent method in these examinations has been transfer learning utilizing pre-trained deep models. In order to semantically detect breast abnormalities in ultrasound pictures, our research presents a new deep architecture. Our suggested model demonstrated outstanding efficiency when compared to three top-tier deep semantic segmentation architectures: UNet, UNet++, and SegNet. We tested our model's generalizability using UDIAT, another publicly accessible BUS imaging dataset, in addition to training it on 546 pictures from a publicly available breast ultrasound imaging dataset. Our model's remarkable performance in semantic breast lesion identification was highlighted by its Jaccard scores of 0.77 on Dataset 1 and 0.748 on Dataset 2.

Keywords: Medical Imaging; Breast Cancer Detection; AI in Healthcare; Deep Learning in Medical Imaging; Computer-Aided Diagnosis;

1. Introduction

Many of areas of medical practice have been impacted by the revolutionary rise of artificial intelligence (AI). Applications in the medical industry have experienced a major spike due to the fast development of new medical data sources and the growth of AI-based technology. Automated computer-aided systems are being developed to automate many processes in healthcare using a variety of artificial intelligence (AI) technologies, such as rule-based expert systems, deep learning (DL), and natural language processing (NLP). Predicting illness risks, detecting and diagnosing diseases, generating reports, monitoring patients,

operating on patients, providing virtual support, and doing administrative duties are all part of this scope of work.

A big and very successful area among the many AI applications in healthcare is automated illness detection [1]. Not only can the use of AI-based systems in healthcare assist reduce the occurrence of pharmaceutical mistakes such medical picture misinterpretation [2], but it also allows for more accurate and prompt patient treatment, which in turn improves survival rates for potentially deadly diseases. Artificial intelligence also helps doctors by cutting down on unnecessary expenses and saving them time. People living in impoverished regions are even more able to get healthcare as a result.

A plethora of CAD systems have been created to help in the detection of several devastating diseases, including as those affecting the cardiovascular system, the nervous system, and the lungs. These systems also seek to diagnose fungal and viral diseases, such as Ebola and Coronavirus, and to identify malignancies in their early stages, including those of the brain, lungs, breast, prostate, and colorectal areas. The necessity to develop a deep learning-based system that can efficiently use a collection of film-mammography breast pictures for early-stage automated diagnosis of breast cancer is what drives this project.

The World Health Organization (WHO) reports that, worldwide, breast cancer ranks second among all cancers followed by lung cancer, making it a serious public health problem. Stages III or IV are the most common outcomes for breast cancer diagnoses in Pakistan, accounting for more than half of all cases [23]. About 90,000 new cases are recorded in Pakistan each year, with 40,000 people losing their lives as a direct result [21]. Delays in medical consultations, caused by variables including low levels of education, widespread poverty, and general lack of knowledge, are a major contributor to the high death rate [22]. The survival rate and the range of treatment for breast cancer can be greatly improved with early identification [31]. When it comes to early-stage diagnostics, CAD systems powered by AI show a lot of promise.

Automated breast cancer detection utilizing a variety of medical imaging modalities (e.g., thermography, histology, MRI, BUS, CT-scans, etc.) has been the subject of much literature, but there are still many obstacles to overcome. Among the several breast imaging modalities available, "Modality Selection" refers to the process of selecting the one most suited for early-stage diagnosis. To effectively differentiate benign from malignant tumors and enable informed decision-making, tumor discrimination is of utmost importance. Many research relies on manual parameter tuning, which is a time-consuming procedure, to determine the ideal values through experimentation and failed approaches.

Building effective and accurate automated CAD systems relies on having access to large-scale, high-quality datasets, yet publicly available datasets of this kind are in short supply. The reliance on pre-trained models and the paucity of newly-developed models both lead to overfitting and other problems. In addition, previous study has frequently ignored the automated tumor detection phase in favor of statistical approaches and handmade criteria for breast cancer diagnosis; these features typically include color, texture, and morphology.

Rest of the paper is organized as follow: In the next section contribution and objectives of this research are given. In section 2, a detailed literature review is provided. Proposed deep-learning based architecture for breast cancer detection is presented in section 3. In section 4, Experimental results are shown. Finally, a conclusion is given in section 5.

1.1. Contribution

Because most models only know how to label pictures as benign or malignant, they fail to account for the wide variety of breast cancers, including lobular, invasive, and ductal carcinoma in situ. This is a significant shortcoming of current systems that deal with multi-classification. The main goal of this study is to review all the cases where computer-assisted breast cancer screening has benefited from artificial intelligence (AI). We conducted a thorough literature review to identify the challenging factors that affect the accuracy of computer-aided diagnosis in various imaging modalities. A state-of-the-art deep learning method has been created to overcome these challenges in automated breast cancer diagnosis. By delving into topics including modality selection, tumor discrimination, dataset availability, overfitting, scarcity of

new models, handmade features, multi-classification, and manual parameter tweaking, this research hopes to make a significant contribution to the area.

Finally, there is great potential for AI to improve patient outcomes, decrease mistakes, and increase accessibility to healthcare services in healthcare, especially in breast cancer detection. Given these challenges, new approaches are required; this study aims to contribute to this dynamic area by developing a cutting-edge deep learning-based system to aid in the automated early detection of breast cancer.

1.2. Objectives

The goal of this research is to design a deep learning-based computer aided diagnosis system for breast cancer diagnosis. In particular our objective is to work in the following directions.

- Assessing the role of AI in computer aided breast cancer diagnosis: In our study, firstly we have done a comprehensive analysis of applications of AI in automated diagnosis of breast cancer.
- Reviewing Literature: Secondly, we have performed an extensive literature review to identify the challenging parameters (i.e., factors that greatly impact computer aided diagnosis performance). We have considered all imaging modalities during our literature survey.
- Designing a deep model for automated breast cancer diagnosis: A state of the art deep learning-based methodology has been designed for the automated diagnosis of breast cancer.

2. Literature Review

This chapter examined current automated breast cancer diagnosis technologies and their drawbacks. The preceding chapter's assessment parameters are used for a review. We assessed recent computer-aided breast cancer diagnostic classification approaches.

In order to identify breast cancer, mammograms were segmented using dual thresholding in [32]. This method outperforms manual segmentation in terms of speed and memory use. Four sample images with a resolution of 1024 × 1024 pixels are included in the Mini MIAS dataset [43]. Using the input image, the two-stage thresholding algorithm chooses L and U intensity values. A white pixel is located between L and U, whereas all the rest are black. Improve the thresholder image using a 1024 × 1024 mask and morphological border smoothing methods. Restoring the result to the original image reveals any irregularities. To cut down on processing time and expenses for machine learning-based breast tumor identification, another approach [38] proposes an automated image processing technique for segmenting breast lesions in breast MRI images. The method is composed of three steps: first, improving contrast and reducing noise using a median filter; second, using Otsu's thresholding to segment images; and last, using morphological methods to eliminate unwanted regions. The RIDER breast MRI dataset was used for validation, and the results show an accuracy of 97.33% over 150 test photos.

Using breast CT scans, a semi-automated technique for identifying breast lesions is shown in [46]. The three-stage process begins with manually drawing bounding boxes, then uses a four-seed random walk method to partition tumor regions, and last, improves histogram equalization contrast enhancement. A DICE coefficient and a locally acquired dataset consisting of fifty patients are used to validate the proposed method. Using a pseudonymous breast image, [41] demonstrates a basic semi-automated tumor segmentation method. Among the methods employed are sharpening, manual cropping for ROI extraction, global thresholding segmentation, noise reduction, and Sobel edge detection for boundary identification. Shifting gears to more traditional ML models, [17] evaluates SVM performance in binary breast mammography classification using ML and DL characteristics. The work feeds the SVM with size, shape, margin, and intensity for classification after using a region-growing approach to find regions of interest. Based on 607 images, the SVM achieved an area under the curve (AUC) of 0.81. Local Binary Patterns (LBP) for texture feature extraction is suggested in [26] for mammographic image classification into normal and malignant categories. Otsu's thresholding eliminates mammography backgrounds, and the LBP picture

serves as a grid for extracting feature vectors. Using 0.5 as the threshold, SVM classification achieves 84% accuracy on 17,639 DDSM and MIAS images.

Another technique that uses support vector machines to categories mammograms as normal or abnormal is [44]. Using 600 mammography images for training, SVMs with Harris corner detection features achieve 96.8 percent accuracy and 92.5 percent recall on 400 test images. In order to classify breast tumors as either benign or cancerous, a support vector machine (SVM) CAD system is proposed in [20]. Fifty images from the MIAS dataset were cleaned up using median filtering and areas of interest were extracted using split-and-merge segmentation. With a 94% estimation rate, support vector machines (SVMs) employ 13 texture-based characteristics with a grey level co-occurrence matrix (GLCM). A non-linear support vector machine classifier determines if a breast mammography is normal, benign, or malignant in [6]. One hundred and ten Mini-MIAS images make up the training set. Use of a proposed automated pectoral muscle removal method during preprocessing yields 90% correct segmentation features using a Gaussian Mixture Model (GMM). Classification of normal and abnormal breast mammography images using support vector machines is suggested [45]. In preprocessing, masking gets rid of artefacts and maximization gets rid of pectoral muscle. The accuracy rate is 94% when intensity-based features are extracted.

Using K-Nearest Neighbors (KNN) to categories mammographic pictures as normal or abnormal, a computer-aided detection system (CAD) can identify breast cancer at an early stage [15]. Running the algorithm via 120 MIAS pictures yields an accuracy of 92%. [12] employs KNN for binary classification of 110 Mini-MIAS breast mammography as either benign or malignant. A retrieval and normalization of six first-order texture characteristics yields an accuracy of 91.8%. In order to determine if breast micro-calcification is benign or malignant, the CAD system described in [24] employs KNN, SVM, and Decision Tree voting classifiers. For optimal performance, train your top-hat transformation segmentation model on mammograms from the MIAS dataset. One way to detect breast cancer using magnetic resonance imaging (MRI) is outlined in [18]. Using a publicly accessible breast MRI dataset, we can accurately classify normal and abnormal images using a median filter, discrete wavelet feature extraction, and support vector machine classification. Breast tumors may be automatically classified as benign or malignant using a collection of breast MRI images collected locally [34]. The "Relief" feature selection is used to extract and minimize handmade characteristics such as morphological, GLRLM, GLDM, Gabor, and GGLCM. Adaboost fixes data imbalance, which leads to an AUC of 0.9617.

Detailing an automated approach to differentiate between in-situ and infiltrating breast tumors [10]. Radiomics feature extraction, false-positive reduction, and breast area recognition are all accomplished using pre-trained Google Net architecture. An area under the curve (AUC) of 0.70 was achieved on 55 DCE-MRI images using XGBoost classification. In [42], a publicly available thermal imaging dataset is used to validate an automated breast cancer detection algorithm. Some of the preprocessing steps include converting colors to grayscale, reducing noise, improving smoothness, and identifying edges. Using a backpropagation neural network, the extracted features achieve an accuracy of 96.51%. [3] provides a novel strategy to detecting breast cancer by utilizing six methods of texture analysis for feature extraction. The DMR-IR dataset achieves an AUC of 0.989 when a learning-to-rank (LTR) method and multi-layered perceptron are applied.

Automated radiomics features are utilized to categories benign and malignant breast cancers from CT images of the breast [40]. Applying SVM on datasets that are both publicly available and collected locally yields an accuracy rate of 72.54 percent. This is compatible with the recommendations of a recently developed deep Convolutional Neural Network (CNN) model for binary classification that uses extracted features from breast mammography mass images [19]. We use 600 mammographic mass photos from the Digital Database for Screening Mammography (DDSM) to fine-tune and assess the model after training it on ImageNet [11]. We do PCA image whitening after we normalize the recovered images. Upgraded images are subsequently enhanced via data augmentation. High-level and middle-level features are generated using CNN feature extraction. These features are used to train two linear SVM classifiers independently. The testing process involves running both classifiers on an example and prioritizing the results that are consistent. Otherwise, the distance between the test case and the training data designated benign and

malignant examples is calculated and categorized. The proposed model achieved a classification accuracy of 96.7%.

Classifying mammograms as benign or malignant is accomplished using a 7-layered CNN model in an alternative approach [13]. The dataset created by the Medical Image Analysis Society (MIAS) is used for both training and evaluating the models. The dataset contains 95 randomly chosen Regions of Interest (ROIs) for each mammogram, with a 15:4 split between the training and testing datasets. After 500 epochs of CNN model training with the returned ROIs, the highest accuracy was achieved at 0.751. You Only Look Once (YOLO) architecture-based deep convolutional neural network (CNN) for breast tumor identification and malignant/benign classification is also available in [37]. In order to train the model, DDSM mammograms are used. Images are normalized and noise and background are removed during preprocessing. Random rotation is one example of the data augmentation applied to images. Bounding boxes are used to extract and resize mass patches. Prior to training all mammography patches, mass patches are taught. Main training uses initial training weights to initialize modified CNN weights. The proposed system achieves a detection accuracy of 90% and a classification accuracy of 93.5%. For breast mammography classification, [9] presents a 9-layered CNN trained on MIAS. Images from the training dataset are used to conduct morphological closure and masking in order to segment ROIs. The suggested model, when fed resized images, obtains a multi-classification and binary accuracy of 65%.

An additional CNN is presented in [28] for the purpose of binary breast mammography classification. 116 MIAS anomalous photos are used to train. Image preprocessing includes global contrast normalization and cropping to eliminate noise and backgrounds. The next stage is to eliminate ROIs and replenish the data to minimize overfitting and achieve dataset balance. By feeding data into the CNN, we can see how the model's generalizability is affected by the CNN's depth and dropout adaptation. The results show that deep CNN classification is improved when a dropout approach and a smaller filter size are used. This study details a web-based CAD system that uses deep convolutional neural networks (CNNs) to binary classify breast histopathology images [7]. To teach the model, we drew from BreaKHis, an open-source database of high-resolution breast images. The input images to a seven-layer deep convolutional neural network (CNN) are 192 × 192 pixels in size. With 6327 examples trained and 1582 cases tested, the model achieved a 99% training accuracy and a 91.4% testing accuracy. [39] demonstrates a U-Net-inspired deep encoder-decoder CNN design for mammography-based early breast cancer detection. Microcalcification and bulk detection subsets of the CBIS-DDSM database are used to train the model. The training and assessment phases involved retrieving 692 masses and 603 microcalcified people from the database. We equalize the contrast of the histogram and randomly rotate it as part of the preprocessing.

The proposed CNN achieves an accuracy of 95.01% when classifying masses and 94.31% while classifying micro-calcifications. Uses both subjective and objective criteria to classify mammograms [47]. A proprietary dataset consisting of 400 mammography images is used to train the algorithm. Adaptive mean filter is used to reduce noise and increase the mass-environment contrast. Partitioning the ROIs into 48x48 subregions, bounding boxes are used to extract them. A feature vector of 24 lengths is generated from these subregions by use of a 7-layer convolutional neural network (CNN). Using the recovered attributes, an Unsupervised Extreme Learning Machine (US-ELM) technique may cluster areas that are suspicious and those that are not. The proposed method employs an ELM classifier for the classification of five morphological, five textural, and seven density-based attributes. When it comes to classification using all four characteristics, experimental results show that ELM is superior to SVM.

For the purpose of automatically distinguishing between benign and cancerous breast thermograms, [35] also details a deep learning architecture. The author uses the publicly available breast thermal imaging DMR-IR dataset for training and validation purposes. Normalization, scaling, and RGB-to-gray conversion are all part of the preprocessing. This proposed network uses 5 2D-convolution, 3 max-pooling, 2 fully connected, batch normalization, and dropout layers to get an accuracy of 95.8%. Three ResNet-34/50/101 ensemble classifiers are compared in this study: one that trains from scratch, one that fine-tunes the whole learned model, and one that tweaks only the last layer. Without the use of pre-trained weights, the suggested ensemble classifier is trained on the BACH-2018 dataset of microscopic breast images. We employ data

augmentation and image patching. Validation accuracy for the model is 97.3% and test accuracy is 86%. Not only that, but [14] evaluates several Transfer Learning (TL) approaches to binary categorization of breast histology WSI patches. Starting with 5,000 patches extracted from the locally collected WSIs dataset, the AlexNet and GoogLeNet architectures undergo a full training cycle. Augmenting data increases the size of datasets. Compared to GoogLeNet's 94.12% final accuracy, AlexNet's is 93.40%. In [27], the author employs an IRRCNN to identify binary and multi-class breast cancer images from histology slides. To put the model to the test, data is supplemented to the BreakHis and BioImaging-2015 datasets. By integrating residual networks with recurrent convolutional neural networks, the proposed architecture enhances performance.

Using a specially developed mammography dataset, [17] evaluates three support vector machine classifiers for the subjective and objective classification of benign and malignant breast lesions. Before normalization, mammograms are down sampled to 256 × 256 and divided into 512 × 512 patches. Each of the three classifiers undergoes a mixed-methods training process that includes deep learning, handcrafted features, and a pre-trained convolutional neural network (CNN) called AlexNet [27]. Because of its low dimensionality and good performance, Fc6 is used in feature selection by layer-wise support vector machine classifiers. [8] uses six features to categories BACH-2018 microscopic images. The feature extraction process makes use of five pretrained deep CNNs from ImageNet: ResNet-18, ResNet-152, ResNeXt, NASNet-A, and VGG16, as well as two new features, PFTAS and GLCM. In order to get an accuracy of 79% on Part A of the BACH challenge, the features are processed using Multi-View Random Forest Kernel SVM (RFSVM). A radiomics model separates benign from malignant breast tumors utilizing shape and GLGM, in addition to deep learning (AlexNet) [30]. With 212 unique digital mammography images, the model achieves a 96.4% success rate. In [14], 121 cases are used to construct a hybrid approach for classifying histopathological full slide photos. After removing noise and extracting patches, CNN obtains enhanced data. Different approaches to transfer learning are investigated for AlexNet and GoogLeNet, both with and without pretrained weights. For the purpose of picture texture characterization, GLCM and LBP features are recovered, and SVM trained over them attains a 98.90% accuracy rate. [49] evaluates a pretrained VGG16 CNN and a hybrid model (VGG-16 + SVM) for multi-classification accuracy on breast histopathology photos. With a validation accuracy of 81.25% and a Bioimaging 2015 accuracy of 80.6%, the hybrid approach fine-tunes a pretrained VGG-16 utilizing BACH-2018. There is a hybrid approach to classifying mammograms for the purpose of detecting breast cancer [4]. It employs a pretrained convolutional neural network (CNN) based on transfer learning (VGG-16) and a set of linear classifiers. The MIAS dataset is used to enhance classification accuracy with linear classifiers such as KNN, Decision Tree, and Gradient Boosting. One method for classifying mass patches found in many mammograms is the MV-DNN Deep Neural Network, which is shown in [48]. Thanks to its 0.89 AUC and 85% accuracy, MV-DNN shines on the BCDR-F03 dataset.

To locate and categories breast lumps, a Faster Recurrent CNN employs five feature extraction models [53]. With a typical accuracy of 0.85, Inception ResNet-V2 outperforms MobileNet, which has the lowest at 0.60. A recent study employed the DeepLab-V3 and Mask-RCNN frameworks to semantically segment and categories breast masses [5]. Applying Mask-RCNN and DeepLab-V3, we achieve 98% and 95% accuracy, respectively, using both MIAS and CBIS-DDSM datasets. Automating BUS ROI extraction is achieved by combining Faster RCNN with Inception-ResNet-v2 for object recognition [50]. Significant improvement in intersection over union (IOU) is demonstrated with the approach on two BUS image datasets. takes a look at five distinct methods to binary breast tumor classification using multi-parametric MRI [16]. With the help of a pretrained VGG-19 CNN, features are extracted, and SVM carries out the classification. We look into methods that combine features, images, and classifiers, and we find that they work. [33] proposes automatically classifying breast thermograms using pretrained Inception-V3 architecture. It takes 15 epochs for SVM to classify the feature vector accurately if the probability of a cancerous zone is 0.5 to 0.6. In order to classify breast images from tomosynthesis and 2D and 3D mammography, [52] examines eleven different deep learning architectures. ROCs of 0.7274 and 0.6632 for

2D and 3D photos, respectively, show that AlexNet's transfer learning outperforms other networks in categorization.

3. PROPOSED ARCHITECTURE

Our study's recommended architecture is shown below:

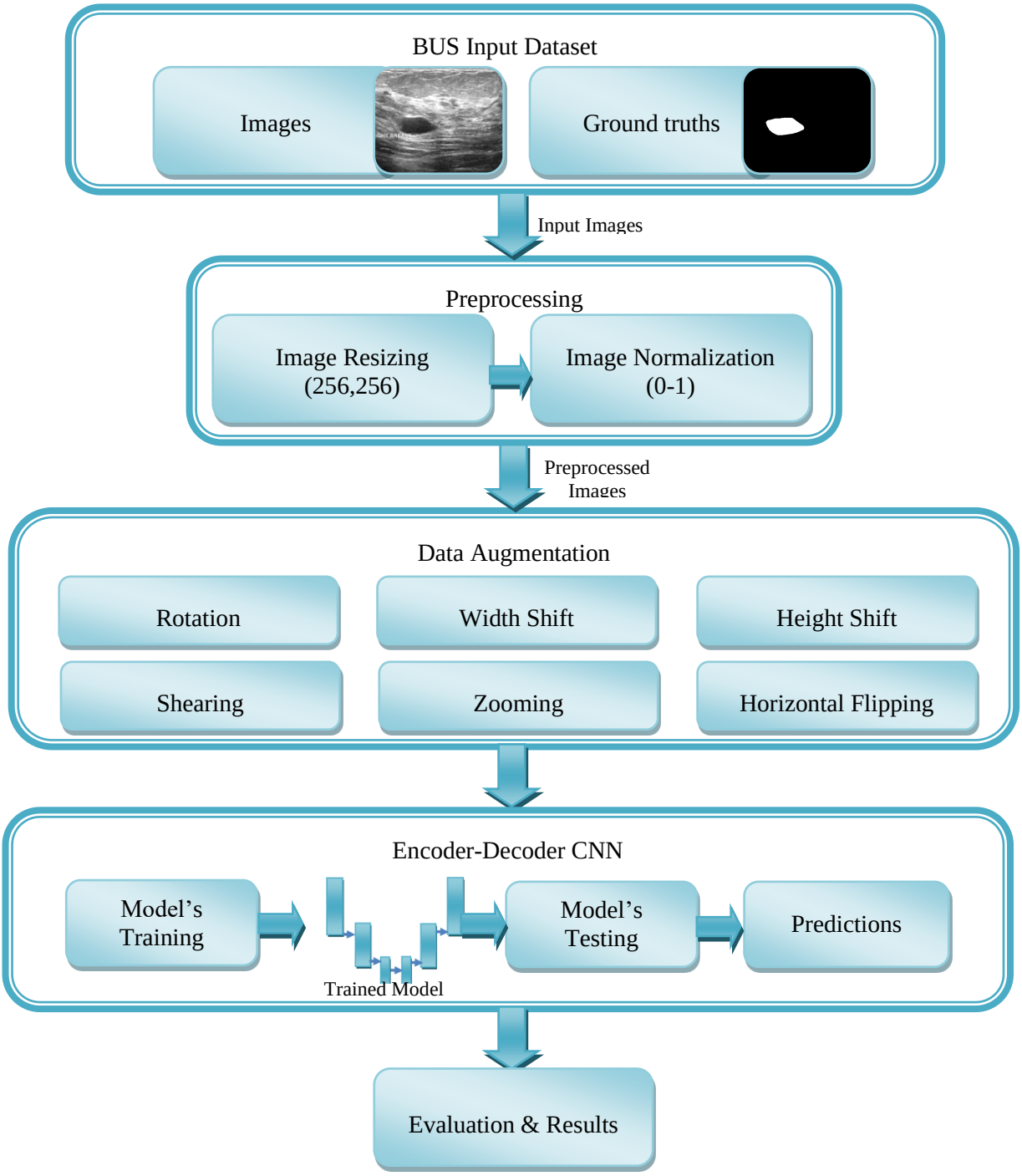

Figure 1: Proposed Architecture

3.1. Datasets Description

3.1.1. Dataset 1

In this investigation, we used a publicly accessible breast ultrasound imaging dataset [29] of 780 ultrasound pictures for training and evaluating the suggested deep learning architecture. This dataset was gathered in 2018 at Baheya Hospital in Egypt. The data was originally collected in 1280*1024 resolution DICOM format and subsequently transformed to 500*500 pixels average PNG size. The three main categories of images are benign, normal, and malignant.

Table 1: Training dataset description

Case	No of Images
Malignant	210
Benign	487
Normal	133
Total	780

3.1.2. Dataset 2

We also used a publicly accessible BUS imaging dataset, UDIAT [51], to evaluate trained models, which contains 163 BUS pictures (110 benign & 53 malignant) in PNG format with a size of 760*570 pixels.

3.2. Preprocessing

Dataset images are first preprocessed before being fed into the proposed deep architecture. During the preprocessing stage, two tasks are completed:

3.2.1 Image Resizing

All of the images in the collection are of different sizes, but on average they have a 500*500 pixel resolution. In contrast, deep convolutional neural network design strictly enforces the use of identically sized input images. To address this issue, two potential options are as follows: The first is padding, which can be either zero, the same, or constant. image resizing by the inclusion of extra columns and rows, which might result in higher processing expenses. 2) Resizing photos: Reducing the computational cost involves resizing photos to make their sizes equal. In this example, we resized the input photographs to 256*256 pixels so that they would all be the same size.

3.2.2. Image Normalization

Starting deep model weights with small, arbitrary values between 0 and 1 and adjusting them according to the loss calculated through an optimization process is a common practice. A wide intensity range (i.e., 0-255) is typically present in input images and ground facts. In the absence of intensity normalization or rescaling, problems such as an inflated gradient could arise from using such images, rendering the learning process useless. To avoid these kinds of issues, we rescale input photos and ground facts, also known as 0-1 normalization, before delivering them to the network.

3.3. Data Augmentation

Over-fitting is a key issue that arises during the training of deep learning architectures (i.e., the model memorizes input data and produces better results during training than testing outcomes). One of the primary reasons of this problem is model training on a little amount of data. Due to the scarcity of large-scale medical imaging datasets, this problem frequently occurs during automated illness diagnosis. To prevent such issues, a data augmentation approach is used (i.e., multiple transformations are done to input photos to increase the size of the dataset). We used six distinct forms of transformation of input data in our suggested technique, including:

- Rotation: photos are rotated at random in a range of 0.2 degrees.
- Width Shift: In this method, input photos are randomly horizontally moved to the left or right by a factor of 0.05% of their overall width.
- Height Shift: In this method, incoming photos are randomly vertically moved higher or lower by 0.05% of their entire height.
- Shearing: the input pictures are sheared counterclockwise in a 0.05-degree range.
- Zoom: input photos are randomly zoomed in the range [1-0.05, 1+0.05].
- Horizontal Flipping: This method randomly flips input photos horizontally.

3.4. Model's Architecture

Using our suggested semantic segmentation architecture as a benchmark, we evaluated its performance against that of three leading encoder-decoder semantic segmentation CNN designs: UNet [25], UNet++, and SegNet [36]. We will quickly go over these three state-of-the-art semantic segmentation architectures.

3.5. Existing Semantic Architectures

3.5.1. UNet

UNet design is divided into two sections: a contracting road (encoder) and a costly path (decoder). The encoder section comprises of two successive 3*3 convolution layers, followed by a ReLU and 2*2 Max pooling layers for picture downsampling, with the number of convolutional filters increased (from 64 to 128) for each downsampling layer.

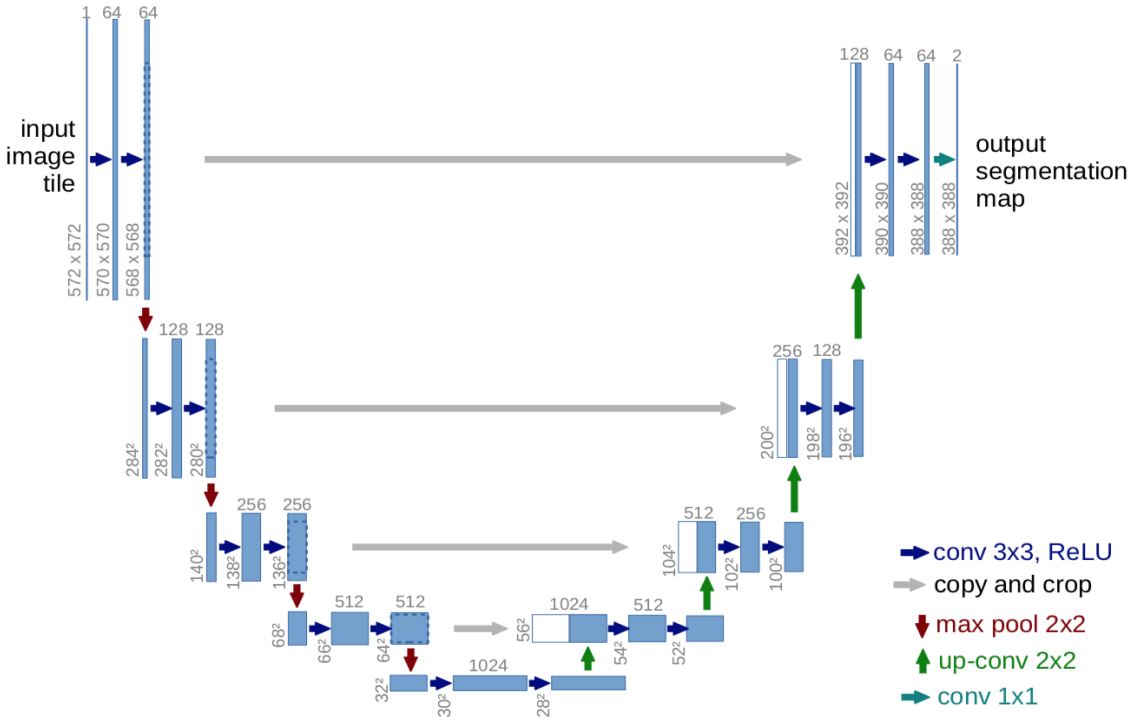

Figure 2: UNet Architecture

The decoder or expanding section includes feature modules for up-sampling, such as a 2*2 convolutional layer (up-convolution) that reduces the amount of feature maps by half (from 128 to 64) and a concatenation layer. Finally, 1*1 convolutional layer is integrated at the final layer to map 64*64 feature mappings to the necessary number of classes. The graphic above depicts the basic UNet architecture.

3.5.2. UNet++

The currently available UNet++ is built on top of the UNet architecture, and it uses dense convolutional blocks along each skip link to gather each previous feature map. UNet++ achieves this by adjusting the skip connections between the encoder and decoder. There are three main ways in which UNet++ differs from UNet: 1) A deep supervision mechanism is used; 2) dense skip connections are used to improve gradient flow; and 3) encoder and decoder feature maps are connected using convolutional blocks to bridge the semantic gap. The following diagram depicts the fundamental architecture of UNet++.

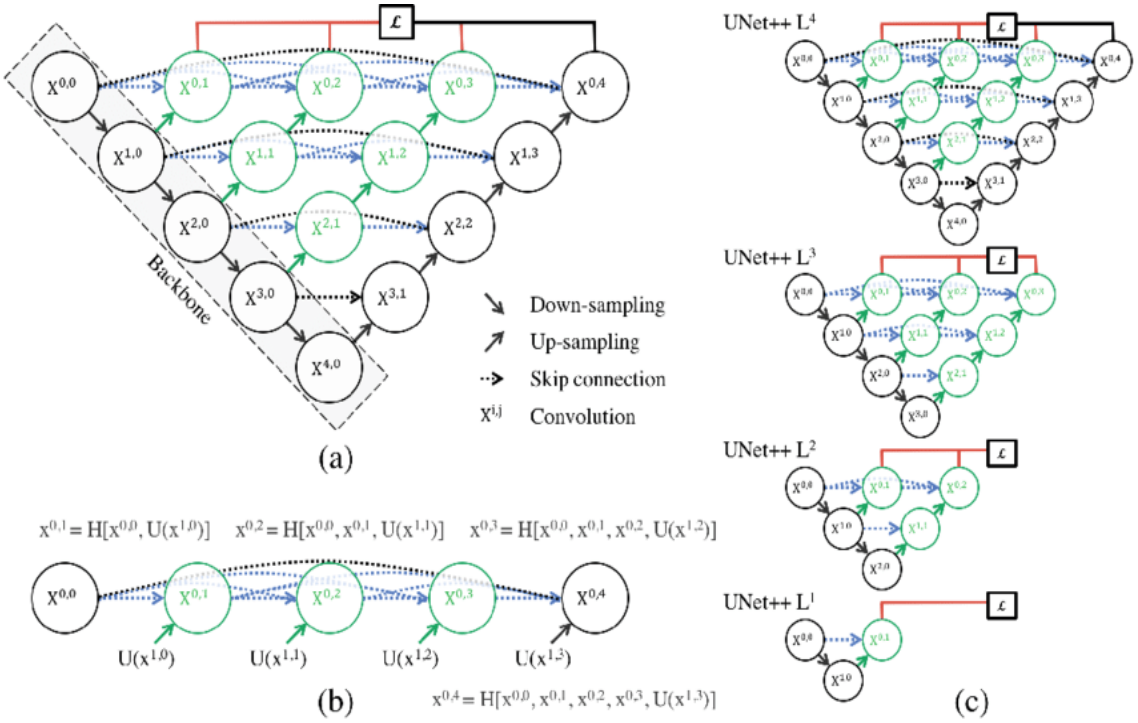

Figure 3: UNet++ Architecture

3.5.3. SegNet

The state-of-the-art SegNet architecture is another unique fully convolutional neural network whose performance was examined in our study. This design is also divided into two parts (encoder and decoder). The architecture of the encoder part is similar to a 13-layer convolutional neural network (CNN), more especially VGG-16, with 13 layers in the decoder part for every layer of the encoder. In each encoder block, you'll find convolutional layers, batch normalization, ReLU, and max pooling layers; in each decoder block, you'll find an up-sampling layer in place of the pooling layer. SegNet's encoder and decoder components do not share any skip links with UNet or UNet++. The picture below shows the SegNet architecture.

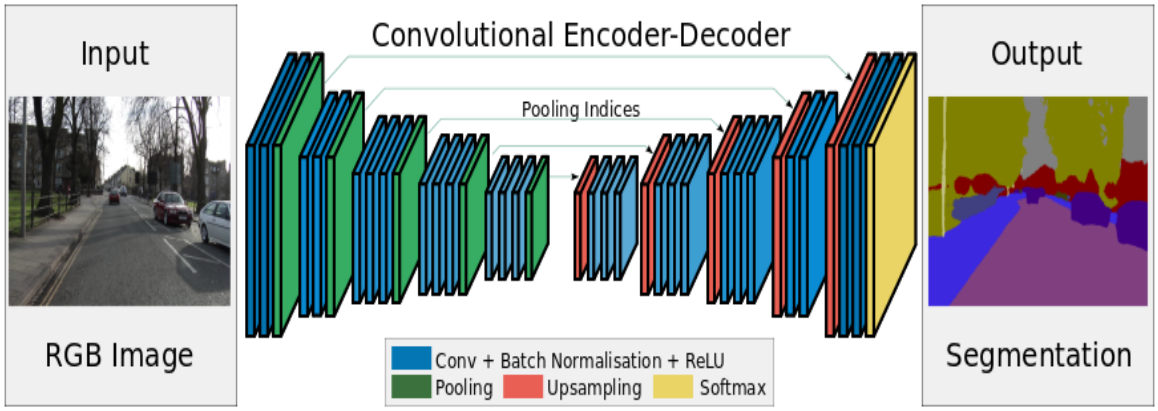

Figure 4: SegNet Architecture

3.5.4. Proposed Semantic Architecture

The proposed design is an upgraded variant of the state-of-the-art SegNet architecture. What sets SegNet apart from SegNet-xd is the inclusion of skip connections in the updated proposed architecture. The newly proposed model is simpler and uses less computing power than conventional SegNet since SegNet-xd has fewer convolutional layers. There are two kinds of skip connections in the updated model: 1) between the encoder's convolutional layers, and 2) between the decoder's and encoder's corresponding convolutional layers. Batch normalization also happens after every convolutional layer in SegNet, while in SegNet-xd it happens only after the second convolutional layer in each encoder and decoder block. Below is a diagram demonstrating the proposed SegNet-xd architecture.

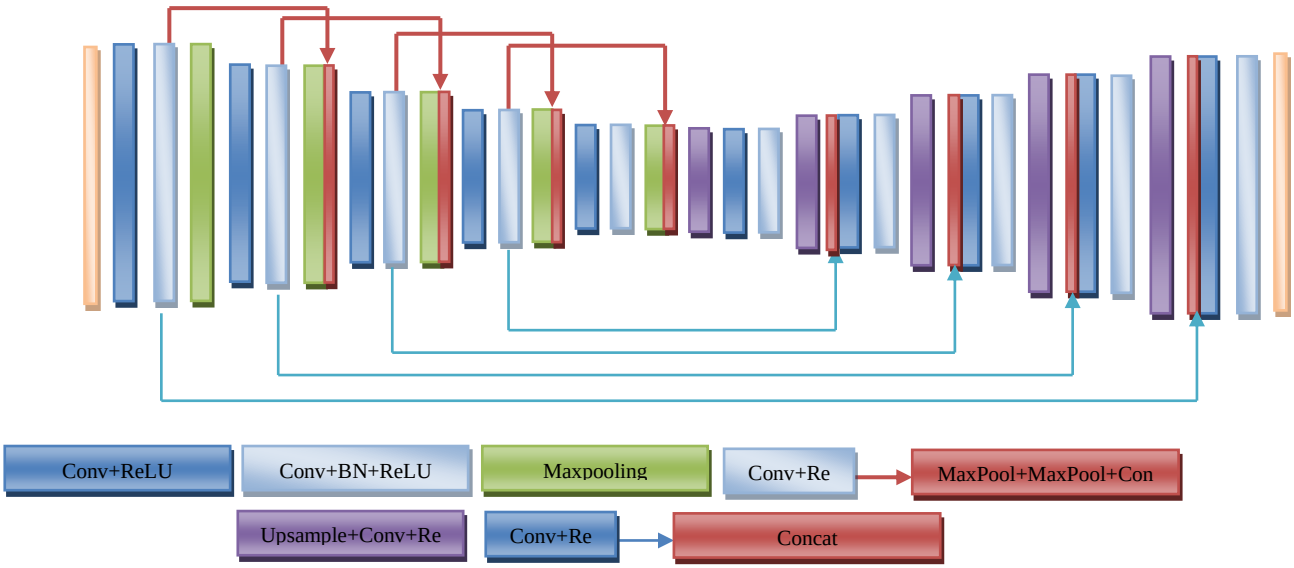

Figure 5: Proposed Semantic Segmentation Architecture

3.6. Training Parameters

The proposed deep CNN is trained over 500 epochs, utilizing 70% of the training data and a batch size of 10. Three sections of Dataset1 70% for training, 20% for validation, and 10% for testing, are utilized to

train the proposed model. We keep track of validation loss and the best model's weights throughout training. A binary cross-entropy loss and a learning rate of lr = 1e-4 were employed by the Adam optimizer.

4. Results and evaluation

In this chapter, we examined the outcomes of a suggested deep CNN architecture for automated breast lesion segmentation. The following are the outcomes of the experiments:

4.1. Experimental Results

Using 546 images for testing and 156 images for validation, with an equal percentage of benign, malignant, and normal cases, the newly proposed semantic segmentation architecture and the three leading ones are trained over 500 epochs. The training and validation loss of distinct architectures are shown in the following graphs.

4.1.1 Training and Validation Loss Plots

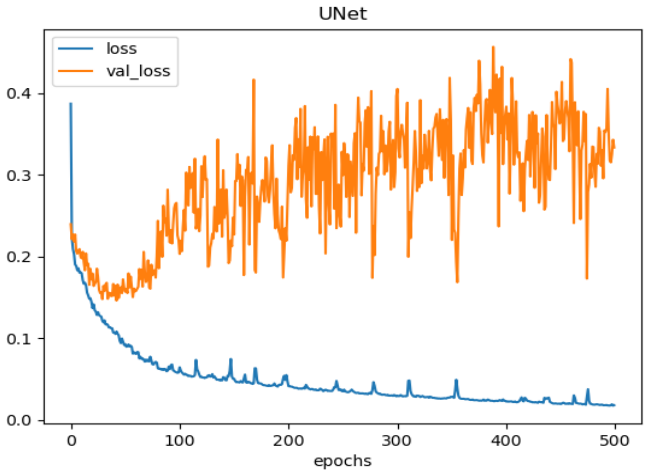

Figure 6: Training and Validation Loss of UNet Architecture

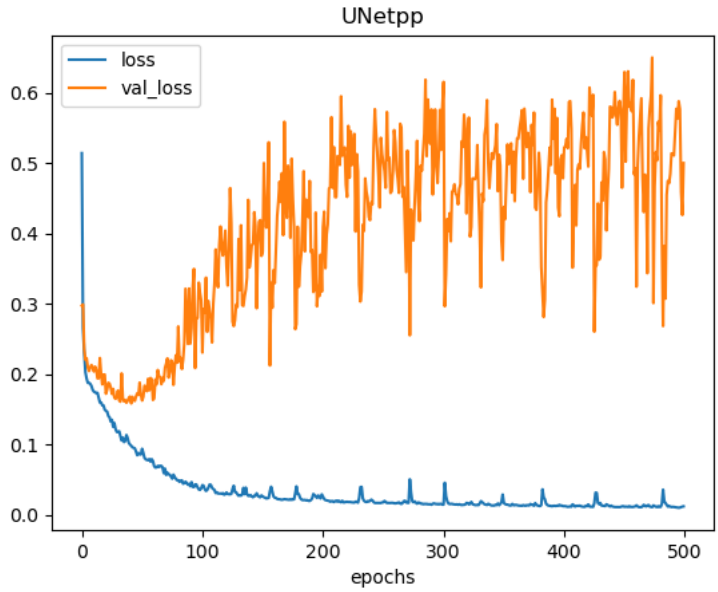

Figure 7: Training and Validation Loss of UNet++ Architecture

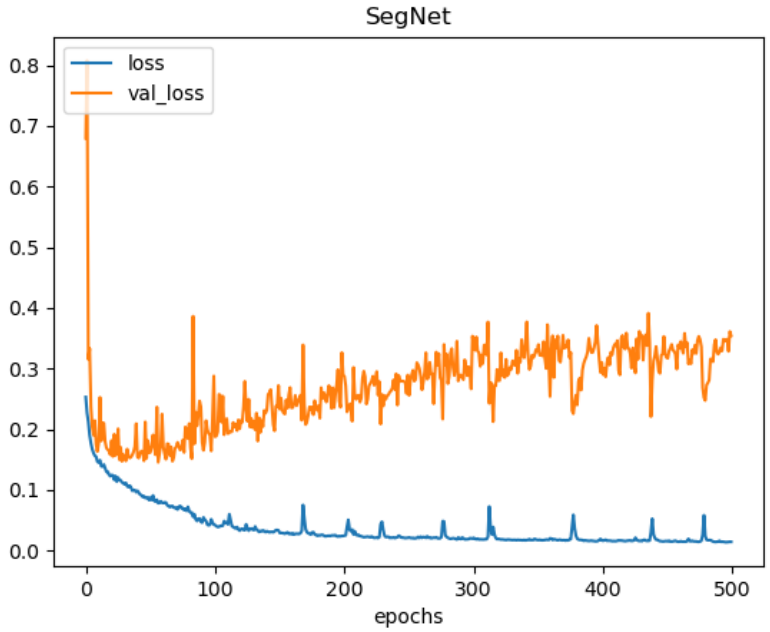

Figure 8: SegNet Architecture Training and Validation Loss

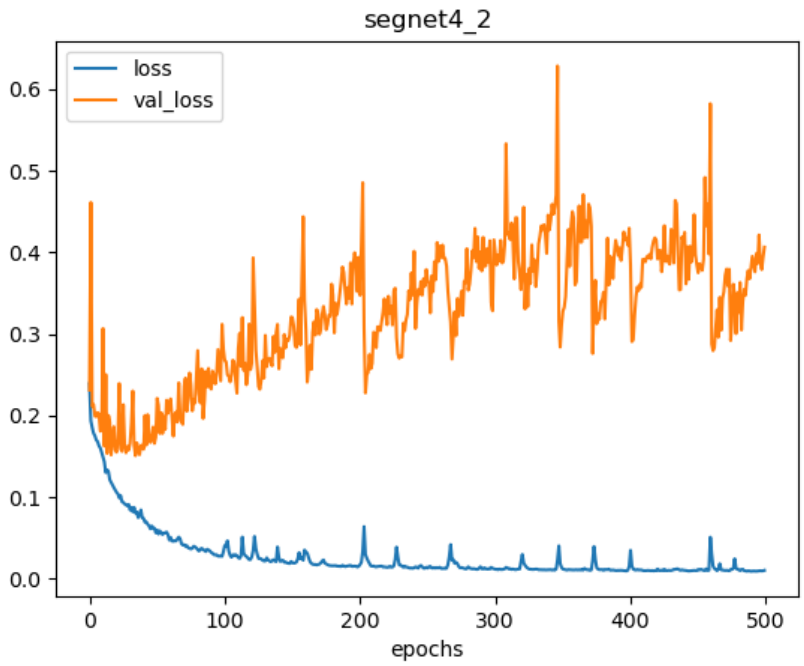

Figure 9: Proposed Architecture Training and Validation Loss

4.1.2. Model's Predictions

The following figures display the forecasts of the current architecture, two test photographs, and the original mask images, as well as the suggested design and three other architectures:

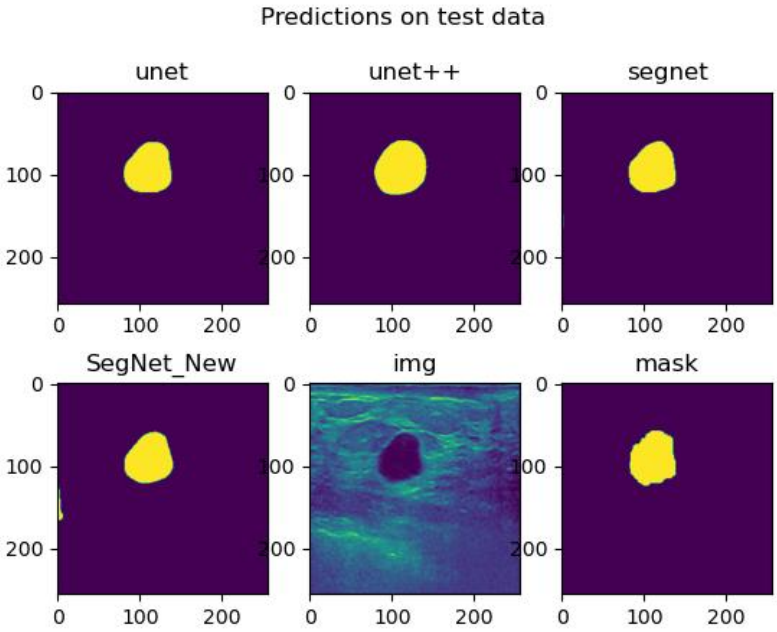

Figure 10: Predictions over 1st testing image

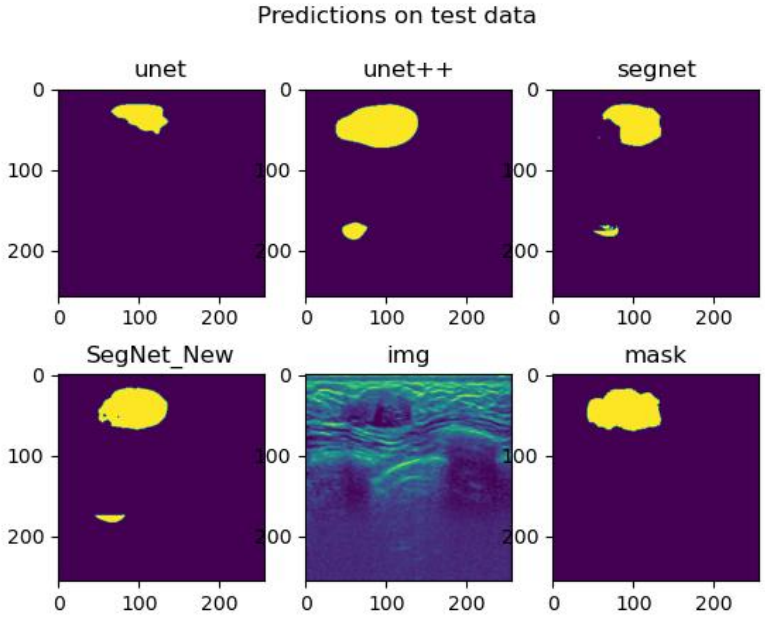

Figure 11: Predictions over 2nd testing image

4.1.3. Jaccard Scores over Dataset1

Table 2: Dataset1 Jaccard Score

	0.5	**0.4**	**0.3**	**0.1**	**0.05**
UNet	0.740	0.743	0.746	0.752	0.753
UNet++	0.722	0.726	0.729	0.734	0.734
SegNet	0.745	0.748	0.750	0.750	0.750
Proposed Architecture	*0.761*	*0.763*	*0.765*	*0.769*	*0.770*

4.1.4. Jaccard Scores over Dataset2

Table 3: Dataset2 Jaccard Score

	0.5	**0.4**	**0.3**	**0.2**	**0.1**	**0.01**
UNet	0.694	0.696	0.698	0.700	0.703	0.708
UNet++	0.715	0.714	0.714	0.712	0.709	0.697
SegNet	*0.774*	*0.777*	*0.775*	*0.770*	*0.762*	0.725
Proposed Architecture	0.744	0.744	0.745	0.746	0.747	*0.748*

4.2. Discussion:

To compare the four deep segmentation architectures' predictions from Datasets 1 and 2, we may see their Jaccard Scores in the tables up top. Determine the Jaccard score by thresholding the final prediction from each of the four architectures at different levels, in order to look at genuine positives and false positives. Our new design outperformed the three previous designs using Dataset 1 to the tune of 0.77 on the Jaccard scale. In contrast, our proposed architecture achieved second-best results on Dataset2, whereas SegNet generated the best predictions (i.e., from 0.1 to 0.5), albeit with a higher number of false positives. The 0.01 cutoff was where our suggested design really shone. The proposed architecture outperforms UNet++ and SegNet in terms of computational efficiency without sacrificing performance.

5. Conclusion

The application of artificial intelligence in medicine has transformed it. It is difficult to detect some fatal diseases by manually examining and properly interpreting numerous medical datasets (e.g., medical pictures, medical reports). Manual diagnosis is fraught with subjectivity and misinterpretation. Because of their similarity in characteristics, precise interpretation and distinction of tumors (i.e. benign and malignant) by manual study is a difficult task. Deep learning may be used to overcome these problems because to its ability to learn thousands of high-level and low-level features. A lot of work has been done in recent years to automate the identification of breast cancer using breast imaging datasets from several modalities. The majority of the work, however, has been done with X-Ray mammogram datasets. The absence of large-scale publicly available quality datasets is a critical concern while developing such systems. The bulk of publicly available datasets are either tiny in size or have a lot of noise in them. We used a recently available breast ultrasound imaging dataset to detect aberrations in this study. A unique deep CNN was presented for semantic segmentation of these images. The model is trained on 70% of the available data, confirmed on 20%, and tested on 10%. Furthermore, another publicly available small size dataset was utilized to assess the proposed approach. Our proposed model earned a Jaccard score of 0.77 when tested on Dataset1 and 0.748 when tested on Dataset2. We want to improve the outcomes of our proposed model in the future by using alternative regularization procedures, as the model performed better on training data than on testing data.

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