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CLASSIFICATION OF BREAST CANCER MEDICAL IMAGES USING RESIDUAL

LEARNING BASED U-NET CLASSIFIER

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Abstract

Breast cancer is one of the most prevalent types of cancer among women. This disease affects more than one-third of the world's female population. Radiologists utilize a variety of clinical techniques, such as mammography and biopsies, in order to accurately diagnose breast cancer in patients. The objective of this work is to enhance the imaging-based method used to accurately diagnose breast cancer. This research makes extensive use of multimodality MRI breast images. This study applies data processing to the unprocessed breast MRI images in order to make them more network-friendly. As a result of its utilization of the unified design, the ResU-Net network is able to produce more accurate and consistent classification results. We have evaluated the efficacy of our pre-trained DNNs by measuring their accuracy, precision, sensitivity, and specificity. The results indicate that feature extraction and feature

https://musikinbayern.com DOI https://doi.org/10.15463/gfbm-mib-2023-239 restoration play a larger role in increasing the classification accuracy of the Resu-Net classifier, which has higher accuracy rates than CNN, ResNet, and Transfer learning.

Keywords

Deep Learning, Classification, Residual Layers, U-Net classifier, Cancer, Images

1. Introduction

Research conducted in clinical settings has demonstrated that detection of cancer around breast regions that significantly enhances the patient chance of surviving the disease. Radiologists have used a broad variety of imaging modalities to screen for breast cancer. These imaging modalities range from those that are more traditional to those that are more cutting-edge [1].

Imaging techniques such as these have made it possible to detect the abnormalities in breast such as masses, microcalcifications, architectural deformities, and bilateral asymmetry, to name just a few examples of these types of abnormalities. On the other hand, they have problems such as overlap of breast tissue, which covers breast information and makes it difficult to discover harmful cancers. This makes it more difficult for women to get mammograms [2].

It is possible to diagnose breast cancer in its earliest stages by doing screening checks, paying attention to any internal pain, and maintaining frequent appointments with a doctor, to name just a few of the available options. As a result of these activities, mortality rates will decrease, and a greater number of individuals will have access to medical care that has the potential to save their lives [3].

In order to make an accurate diagnosis of breast cancer in patients, radiologists make use of a wide range of clinical techniques, such as mammography and biopsies. If radiologists are able to collect images of breast cancer in its earliest stages, they would be better equipped to enhance their patient chances of survival, according to a study that was published not too long ago [4].

Pathologists frequently perform a technique known as a biopsy. The area of the breast that is afflicted is sampled for its breast tissue, and this sample is then examined under a microscope

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to detect the particular type of tumor that is present. Because of this, the approach that we take to detect and categorize people suffering from breast cancer has a high rate of success [5]-[6].

There have been previous attempts made by scientists and technology to diagnose breast cancer through the use of cellular analysis. They performed an analysis on the nucleus of the cells, and depending on what they discovered, they categorized the cells as either benign or malignant [7]. There have been a variety of noise-efficient algorithms created for interest region recognition and classification in the field of medical image processing. These algorithms have been used to process images. Image analysis can be accomplished with the help of these procedures[8].

It would be useful to have a system or a framework that is capable of recognizing and classifying breast cancer patients with an extremely high degree of precision. As a result of the deterioration in performance, the question of how to improve the speed and precision of medical diagnostics is still one for which there is no satisfactory response. There is a need of an automated system that determine the type of illness in locations that have limited resources and/or a shortage of personnel. Qualified medical personnel can now initiate the administration of the appropriate drug [9].

The process of medical diagnosis is currently going through a phase in which there is a significant increase in the use of technological advancements. Computer-aided design, often known as CAD, has amassed a significant amount of popularity all over the world as a direct result of its remarkable precision and practicality. Machine learning and deep learning are two subfields of artificial intelligence that are making significant contributions to the field. Images of breast cancer can now be further categorized into the categories of benign and malignant tumors, which was previously only possible with the use of CAD software technology [10].

Within the realm of machine learning, one can choose from a wide selection of methods that have been validated by prior research. These techniques also make use of classifiers such as Naive Bayes (NBs), support vector machines (SVMs), convolutional neural networks (CNNs), and a variety of other similar methods. CNN is nonetheless among the most remarkable classifiers because of the remarkable classification and feature extraction

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accuracy [11] that it possesses. This makes CNN one of the most spectacular sources of information. It does pattern matching on images collected from large datasets in order to achieve the objective of classification. Deep learning is very significant in the medical image processing because of the complex nature of the interconnected systems that are used in this field.

For the goal of breast cancer classification, DL makes use of a technique known as U-Net. In order for these networks to successfully execute the task at hand, it is necessary for them to be composed of numerous layers. The architecture of U-Netis comprised of several distinct kinds of layers, each of which is of a different kind. Input layers, hidden layers, and output layers are all examples of these different kinds of layers. It is possible for images to learn from one another in order to acquire features; this is something that can even be done on layers that have been obscured.

2. Related works

George et al. [11] classified the breast cancer using support vector machines (SVM) and probabilistic neural networks. Breast cytological images are utilized in order to carry out investigations and analyze the mistake rate, correct detection rate, sensitivity, and specificity of various diagnostic methods. Both schools of thought argue that the outcomes that may be obtained using their respective methodologies produce superior results that can be utilized in a broad range of settings.

A comprehensive analysis of DL software for the detection of breast cancer was presented by Chugh et al. [12]. Both the outcomes of the investigation and the literature evaluation on the classification of breast cancer are discussed in considerable depth. It was emphasized that utilizing these tactics brings with it a number of benefits as well as drawbacks to consider. The researchers who carried out this study came to the conclusion that DL is always used for the classification task. This was their conclusion after finding that DLs are superior when it comes to dealing with large breast cancer image sets.

Houssein et al. [13] conducted a thorough and in-depth investigation of DL and ML strategies with the intention of recognizing breast cancer from medical images. They underlined the

https://musikinbayern.com DOI https://doi.org/10.15463/gfbm-mib-2023-239 increasing acceptance of DL and ML and demonstrated a number of cutting-edge diagnostic applications.

Hamed et al., [14] developed employing models that are based on ML in order to get around the difficulties of identifying breast cancer. They stated that the model had 91% accuracy compared to the 79% accuracy gained by physicians in detecting and diagnosing breast cancer.

Ragab et al. [15] came up with the concept of classifying breast cancer using a multi-deep convolutional neural network (CNN). They are able to extract the information from the images by using CNN that had already been trained before they are applied to the problem. The SVM is utilized these features, but it did so by combining them with a variety of other kernel functions in order to achieve the desired results. The researchers turned to principal component analysis in order to accomplish another level of success in terms of the size reduction of the feature vector. They claimed that their outcomes are of a higher quality than those generated by other cutting-edge CAD systems.

Khan et al. [16] applied DL in addition to transfer learning in order to identify benign and malignant tumors that are identified in pictures of breast cancer. They used pre-trained versions of the architectural frameworks GoogLeNet, VGGNet, and ResNet in order to collect the features. In addition, these benefits are brought to the completely by employing average pooling, which allowed the layering structure to function more efficiently. They employed a dataset that had 8,000 images, of which 6,000 are used for training the network and 2000 are used for testing the network performance. The dataset was utilized for both the training and testing of deep neural networks.

In order to supply clinical data for individuals who had been given a breast cancer diagnosis, Zhang et al. [17] made use of bidirectional encoder representations (BER). After that, in order to extract the characteristics or features, scientists used DL models on pictures of breast cancer patients who already had the disease. They claimed that by utilizing their strategies, one could attain a success rate of up to 96.73%.

An intuitive method for detecting cell nuclei was developed by Krithiga et al.[18], which took advantage of some of the qualities that are associated with systems that use fuzzy logic. The

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detection of cell nuclei was suggested using this technology. Both the segmentation and classification of breast cancer are carried out with the assistance of deep convolutional neural networks. Their method represents a considerable leap forward in contrast to other methods in terms of both its accuracy and its speed. As part of the efforts that are taken to assure the accuracy of the classifications, a process known as cross-validation was carried out ten times. They achieved an accuracy of 98.62% in the research that they had planned.

This section of the paper indicates, after conducting an examination of the research that is relevant to the subject at hand, that there is a significant gap in our existing capability to accurately identify cancer at an earlier stage by making use of DL and transfer learning. The fact that these works have been acknowledged demonstrates that this could be a difficult endeavor because there are not sufficient resources or enough individuals who are qualified. The conclusions of the researchers on this subject have a number of flaws, despite the fact that a large amount of research has been carried out in this area by certified medical professionals. By making use of the ideas of DL and transfer learning, we have made an effort to improve the approach that is used to accurately diagnose breast cancer through the use of images. Our objective is to detect breast cancer in its earliest stages with a high degree of precision and encouraging outcomes. In order for us to achieve this goal, we have been working hard to improve the strategy that is now being implemented.

3. Proposed Method

In this section, the entire process of breast cancer classification is given and the details of which are described below:

Pre-processing

The classification of breast cancer using pre-processed magnetic resonance images (MRI) is a significant difficulty in medical analysis. Processing the data is still crucial for producing reliable breast cancer classifications, despite the fact that models based on deep learning might be able to deal with background noise pretty effectively.

The study uses data processing on the raw breast MRI in order to make them more suitable for the network. This is done in order to make the images as accurate as possible. First, the

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great majority of inaccurate pixels are deleted from the raw data of the 3D breast image, and then the data is refined by breaking it up into a number of different 2D images.

The next step in the process is to reconstruct the 3D breast image. After several 128x128 pixel patches have been recovered from 2D image using the process of z-score normalization or zero-mean normalization, is conducted on each patch. This is done in order to normalize the scores of the patches relative to one another.

$$z'=(z-\mu)/\delta,$$
 (1)

where

z -input image

- z' normalized output image.
- μ mean input value, and
- δ standard deviation.

The study will be able to normalize images that exhibit intensity heterogeneity that is distributed throughout multiple centers. An algorithm for the elimination of Gaussian noise is applied to each normalized patch as the very last stage in the process. After that, the output of this algorithm is sent into the classification network as an input in an effort to reduce the detrimental impacts of the overfitting problem.

Residual U-Net Classifier

U-Net architecture is an end-to-end breast cancer classification network that was developed by residual blocks. This is due to the fact that the ResU-Net model is a breast cancer classification network that goes from beginning to end. ResU-Net was successful in achieving its goal of multi-modal pixel-level classification thanks to the assistance of a 2D convolutional neural network that was trained with the use of a gradient descent algorithm. The amount of data associated with the image that is uploaded to the network has a size of 128×128×4, where 128 and 128 refer to the dimensions of the image and 4 refers to the number of channels.



Figure 1. Overall architecture ResU-Net

A complete representation of the residual U-Net (ResU-Net) can be seen in Figure 1. It is primarily composed: contextual fusion, feature recovery, and feature learning. These three modules work together to form the entirety of the system. This is done in the feature-learning module.

As can be seen in Figure 1, by mixing shallow features with deep features, our breast cancer classification network is a encoder-decoder structure with high-level information and it is been stored inside the deep layers. This is possible because of the combination of shallow features with deep features. The combination of shallow features with deep features. The combination of shallow features with deep features enables this to be accomplished. For the purposes of pinpoint placement and feature recovery, the decoder module makes use of three up-sampling residual (SRes) blocks that are exactly the same.

Attention and Squeeze Excitation (ASE) block can be done by successfully improving the representation of the feature information. This paves the way for the accumulation of more detailed data at both low and high levels. After the softmax layer has been added, the results of the multi-class classification will be able to be viewed in their completed state. The ResU-Net network is able to generate more accurate and consistent classification results as a result of its utilization of a unified design.

Feature Learning

This module uses a downsampling method, which is carried out by a number of residual (Res) blocks. Aconnecting element-wise shortcut addition operation may be used to generate a residual block, which in turn considerably accelerates training without sacrificing accuracy. This can be accomplished without compromising the integrity of the training. A total of three levels are contained within each encoder block.

These levels are comprised of one pooling and two convolution layers. We rely on ResNet-34, which incorporates regularization, activation functions, and identical twin units as part of

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the architecture of its feature learning module. In addition to that, it features a convolutional layer that is 3x3. The mapping function for the residual path can be expressed as:

$$y=F(x,Wi)+x,$$

where

x-input vector of the related layers, and

y – output vector of the related layers,

F(x,Wi) - mapping function for the residual path.

It is necessary that the dimensions of x and the output of F(x,Wi) match one another exactly. By combining rough information from both local and global sources, residual blocks provide a short-cut that is both efficient and effective in preventing the disappearance of gradients and driving network convergence. We make use of three different down-sampling units in order to produce a feature map, and the size of the output image is 16×16 high. This is done while taking into account the size of the breast cancer in the patient.

Algorithm 1. Finding ROI Regions

- (1) Find the scanning area from the breast images for the estimated cancer mask
- (2) Find the ROI points in the range of the scanning area

(3) While

- (a) Find the possible distance estimation between the points
- (b) Obtain the maximum distance between the points
- (c) Develop a set that consists of a distance values
- (4) Apply feature extraction and recovery

(5) Recover the saliency points for the process of classification

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Contextual Fusion Module

By fusing the attention mechanism, the research is able to build a fusion module. In place of the direct link provided by the first iteration of the U-Net architecture, this paves the way for us to develop an innovative contextual fusion module. The contextual fusion component makes use of the fact that transferring over even tiny quantities of data from encoder to decoder can assist in the retrieval of feature information that would have otherwise been lost. Taking use of the fact that data is transmitted from encoder to decoder allows this to be accomplished.

Encoding the channel dependencies and the spatial global information is embedded into the channel vectors and it is found to be the operation of the ASE block. The connection between these encoding methods is complete.

It is possible that the ASE block of the network will assign higher priority to some channels than it does to others, and this will be determined by the information that is stored in feature maps. To begin, in order to gather feature information that is more accurate, we make use of regularization, 1x1 convolution layer, PReLU activation, and a sum operator on an input map.

$$Ftr = F(\beta, \theta, x) + x,$$

where

x - input of the related layer

Ftr- related layersoutput.

 $\theta\text{-}$ PReLU activation function, and

 β - normalized parameter

A global average pooling layer will combine all of the image channels into a single one while simultaneously compressing the information about the important output features Ftr. From the squeeze operation, the feature maps'output are given as input to the excitation operation to capture the channel-wise relationships. This is done in order to maximize accuracy. This excitation operation consists of two layers that are completely linked together and are centered around the interaction between channels that the non-linearity operations have with

https://musikinbayern.com DOI https://doi.org/10.15463/gfbm-mib-2023-239 one another. Both of these levels are connected in their entirety. The sigmoid activation and ReLU function are the two layers present in this layer.

The channel dimension of the transformed output Fscale(Ftr,Feq) is returned by a multiplication operation that is applied to the weight vector of each feature map(1,1,1,C), where C - feature maps. This operation is carried out after the transformed output Fscale(Ftr,Feq) has been transformed. The name of this particular operation is the Fscale(Ftr,Feq) transform. In regard to the pertinent procedure, the following are some key points:

 $Fsq(Ftr) = (H \times W)^{-1} \sum Ftr(i,j),$ $Feq(Fsq,W,r) = \rho(W_2\sigma(W1,Fsqr)),$

 $Fscale(Ftr, Feq) = Ftr \cdot Feq.$

Feq- channel-wise dependency

Fsq- squeeze global spatial information

W1 - dimensionality-reduction layer and

Fscale - output vectors of related layers.

W2 - dimensionality-increasing layer.

 ρ and $\sigma\text{-}$ non-linearity activation parameters.

r - reduction ratio,

H and W - spatial dimensions.

The ASE block gives priority to the components of the system that are the most significant while at the same time minimizing the quantity of background noise by employing various weights that are received from the attention mechanism. The contextual fusion module is able to make effective use of the attention layer, since it combines many diverse ASE building components into a single entity. It is able to place its attention solely on the feature maps that are of the utmost significance.

Feature Recovery

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It is possible to restore access to high-level features of an image that had previously been extracted using feature recovery module. Two common operations that are performed by decoder architectures are called bilinear interpolation and deconvolution. Even though they both enlarge the image, they do it in very different ways (linear interpolation for bilinear interpolation and convolution for deconvolution, respectively). These two methods are used in conjunction with one another to enlarge the image size. The spatial residual (SRes) block, which is the block that we use to boost the efficiency of the decoding process. This structure is exactly the same as the structure of the residue.

A 1×1 -convolution concatenation that leverages the feature maps in the form of a shortcut connections, which builds on the Res block two convolutional units. The SRes block builds on the Res block two convolutional units. These two processes are carried out simultaneously one after the other. The task of producing a mask with the same dimensions as the input falls on the feature decoder module of the SRes block. By utilizing deconvolution, which is founded on the combination of a large number of SRES blocks, we are able to reclaim additional information about the features that is more specific.

Loss Function

Class imbalance is a problem that usually develops while attempting to solve the challenge of classifying breast cancer using MRI. Even though data preprocessing helps to ease this problem to some degree, it is still one that has a substantial influence on classification accuracy. Even if this problem is alleviated to some degree, it still has a significant influence on classification accuracy. We use a loss function that, as will be demonstrated in further detail below, takes into consideration generalized dice loss (GDL) and weight cross-entropy (WCE). This allows us to address the issue with the class balance.

Loss=LGDL+LWCE,

where

LGDL- generalized dice loss

LWCE- weighted cross entropy loss.

 $LGDL=1-2(\sum w_i g_i p_i / \sum w_i (g_i + p_i))$

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LWCE = -\sum w_i g_i \log(p_i),
```

where

L - total labels, and

wi- weight of labeli.

pi- value of the pixel from a classified image

gi- ground truth value.

4. Results and Discussions

It is necessary to conduct testing and evaluation in order to determine the efficacy of the classifiers that are employed in this study to evaluate images of breast cancer. The efficiency of our pre-trained DNNs has been evaluated by measuring their accuracy, precision, sensitivity, and specificity. The results of this evaluation have been determined. In addition to this, there will be sets of observations and forecasts that are accurate in the positive, accurate the negative. false the positive. in in and inaccurate in the negative respectively. Implementation is conducted in python framework that runs on a computing engine with 16 GB of RAM with 16 GB of GPU on an intel i7 processor.Imaging is one of the two methods that can be used to classify the cancer images. There are two distinct ways that things can be categorized. It is only possible to collect data in the form of images from one cancer patient at a time when employing an imaging-based technique. These images can then be used for additional training and testing.

Dataset

These databases have been utilized for the majority of the time when breast cancer image analysis has been undertaken. Because of its usefulness, the database maintained by the Mammography Image Analysis Society (MIAS) is referred to by a significant number of researchers. There are a total of 322 samples, 208 of which are indicative of normal conditions, and 114 of which are representative of aberrant conditions (63 benign and 51 malignant). Normal conditions are represented by 208 of the samples. Aberrant conditions are represented by 114 of the samples.

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Figure 2: Accuracy

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Figure 3: Precision

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Figure 4: Recall

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Figure 5: F-Measure

As can be seen from the data in Figure 2-5, ResU-Net achieves the greatest classification results out of all of the pre-trained DNNs. From the results, it is found that the utilization of feature extraction and feature restoration enables a greater role in improving the classification accuracy of the ResU-Net classifier, which has higher accuracy rates than the existing CNN, ResNet and Transfer learning methods.

5. Conclusions

In this paper, the drawbacks of employing a deep convolutional neural network (DNN) to classify breast cancer in its early stages in this research. Because of the unified design, the ResU-Net classifier is capable of producing more accurate results. The accuracy, precision, sensitivity, and specificity of our pre-trained DNNs are measured to determine their efficiency. According to the findings, the use of feature extraction and feature restoration has a larger role in boosting the classification accuracy of the ResUnet classifier, which outperforms the existing CNN, ResNet, and Transfer learning methods. After performing an

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evaluation of the relevant literature, the findings reveal that there are major gaps in our current capability to effectively identify cancer at an earlier stage by utilizing the notions of DL and transfer learning.

There are still considerable gaps in the coverage of DL-based medical image analysis that need to be filled. The first thing that needs to be done is to collect a sizeable quantity of medical images and make them available to researchers. This is a prerequisite for any subsequent steps. The researchers have the option of picking one of several distinct pre-trained models that have previously been instructed on how to analyze medical images.

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