

Breast Cancer Classification from Histology Images using Dense Residual Capsule Network.

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Abstract – Breast cancer stands as a prominent form of cancer predominantly affecting women globally, with a concerning trend of rising incidence in developing nations. The detection and diagnosis of breast cancer can be achieved through non-invasive methods and biopsy. Non-invasive methods primarily include imaging procedures such as diagnostic mammograms, Magnetic Resonance Imaging (MRI) of the breast, breast ultrasound, and thermography. While imaging procedures are commonly used for cancer screening, biopsy remains the most reliable method to confirm the presence of cancer. Histopathological analysis, vital for diagnosing cancer, requires specialized expertise and is time-consuming. It heavily relies on the experience of pathologists and can be affected by factors like fatigue and decreased attention. Recent advancements in image processing have significantly improved the accuracy of diagnosis. An image can be analysed for classification of Malignant and normal cells in a different datasets of breast cancer. Several machine learning/deep learning based approaches are being applied for analysis of microscopic images. Early identification holds significant importance in detection and treating breast cancer, ultimately reducing mortality rates. Hence, this study presents an automated technique for detecting breast cancer through the application of deep learning on histopathological images. Proposed method employs breast histology images, which were categorized into different classes using the Attention Residual Dense Capsule Network. This innovative approach was developed and evaluated using the Python platform and the BreakHis dataset. Performance assessment was conducted using various metrics including f-measure, recall, specificity, precision, and accuracy to gauge the efficacy of the proposed methodology.

Keywords- Histopathological image, Breast Cancer, Dense Residual network, Capsule Network.

I-INTRODUCTION

Cancer is a challenging task for pathologists and doctors as its detection is dependent on the person who is examining the sample (subjective in nature) hence the opinion may differ from a person to person[1]. The computer vision based classification of microscopic biopsy images provides better and consistent results than subjective evaluation by an individual person. Since early detection and classification of cancer yields more chances of survival of the patient, the automatic diagnosis system has a very important role in this end-to-end histopathological diagnosis process[2]. There are two types of breast cancer found classify as Malignant and benign tumors . Malignant tumors pose a greater threat due to their rapid growth compared to benign ones.

. Thus, Promptly recognizing the specific type of tumor becomes crucial in selecting the most suitable therapy for individuals diagnosed with breast cancer [3] Assessing the malignancy of tissue biopsies is challenging due to its subjective nature reliant on observer analysis. Furthermore, histological pictures treated with hematoxylin and eosin stains, display significant variability in appearance. Utilizing histological images for breast cancer diagnosis involves categorizing the malignancy into four distinct levels: normal, benign, in situ, and invasive.[4] Various

machine learning classifications and computer vision models for pathological image use of breast cancer have been established. These models may automate certain of the tasks that a detection system's pathological workflow requires. Nevertheless, the use of an efficacious image processing technique is essential for use in the clinic. Therefore, researchers use deep learning models to solve these setbacks.

[5] These models offer potential for automating certain tasks involved in the pathological workflow of detection systems. However, for practical use in clinical settings, a strong and efficient image processing technique is indispensable. To overcome these problems deep learning models are used by researchers [6]. Deep learning employs a framework that can capture diverse non-linear patterns to represent essential features within data. Deep learning models typically require abundant training data, however, there is an insufficiency of available training data in medical imaging to overcome this problem. A new proposed deep learning technique used for classification of Breast cancer in this paper.

II - LITERATURE REVIEW

K. George et al [7] introduced a method for extracting nucleus-level features employing convolutional neural networks (CNNs). They conducted feature-level fusion and applied a support vector classifier to categorize cell images as cancerous or non-cancerous. The experimentation utilized the publicly accessible BreakHis dataset, resulting in an accuracy of 96.66%, with 100% specificity and 96.21% sensitivity achieved.

Siegel R L, K.D. Miller, A and Goding Sauer et al. [8] Colorectal cancer is a malignant tumor which resides on the internal wall of the large intestine (colon) or rectum. This type of cancer is most commonly affecting cancer and with 55% cases occurring in developed nations.

Alom et al. [9] have presented an approach based on Inception Recurrent Residual Convolution Neural Network with SGD optimization function. The IRRCNN network provides improved performance while having less number of parameters than CNN or Inception. This approach has an accuracy of 97.09% using BreakHis dataset.

Mohammed Abdullahi et al. [10] proposed the multi-classification of breast cancer was done using histopathological images from the BreakHis dataset by using Deep Neural Network (DNN) together with handcrafted feature extraction techniques which include

Hu moment, Haralick textures and color histogram. DNN classifiers were built using these features obtained through handcrafted methods by designing four dense layers with Softmax activation and data augmentation techniques were implemented to mitigate over fitting concerns.

Hayder A. Khikani et al [11] A refined capsule network has been developed to extract multi-scale features by incorporating the Res2Net model plus four additional convolutional layers. Additionally, the proposed method achieves parameter efficiency by employing smaller convolutional kernels and integrating the Res2Net block. The model was trained and tested on the publicly available BreakHis dataset, achieving an accuracy rate of 95.6% and a recall rate of 97.2%.

Asadulla Ashurov et al [12] proposed a novel approach for classifying breast cancer histopathological images, aiming to enhance interpretability and robustness through the integration of modified pre-trained CNN models and attention mechanisms. Our method focuses on capturing localized features to accurately discern complex cases. We employ transfer learning with well-known deep CNN models, including Xception, VGG16, ResNet50, MobileNet, and DenseNet121, augmented with the convolutional block attention module (CBAM). After fine-tuning the pre-trained models, we integrate two CBAM models at the end of each pre-trained model. To assess performance, we compare our models to existing state-of-the-art breast cancer diagnosis approaches, evaluating metrics such as accuracy, precision, recall, and F1 score. Furthermore, confusion matrices are utilized to visualize and evaluate the results of the compared models.

Ms. Su Myat Thwin et al [13] Proposed different augmentation techniques to enhance the size of the input data and ensemble technique that parallelly leverages modified SE-ResNet50 and InceptionV3 as a backbone for feature extraction, followed by Channel Attention (CA) and Spatial Attention (SA) modules in a series manner for more dominant feature selection.

III -METHODOLOGY

The following processes are included in the proposed technique: image filtering, image segmentation, feature extraction, feature selection, and classification. The deep learning model used in this methodology is used to classify breast cancer.

Histology Images as Input :

BreakHis dataset: This Data set have a total of 7,909 breast histopathological images.[18] which are Samples taken from breast tissue biopsy slides, stained with hematoxylin and eosin . The dataset contains four different class images based on the malignancy of the tissue: Benign, Ductal carcinoma in situ, Atypical ductal hyperplasia, ductal and Invasive ductal carcinoma. Images having different magnifications such as 40×, 100×, 200×, and 400×.

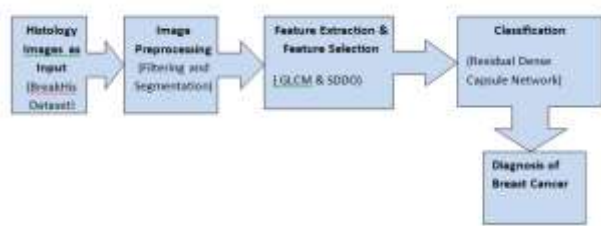


Fig. 1 Workflow of the proposed approach

3.2 Image filtering:

. The adaptive weighted mean filtering method [14] used for preprocessing to perform a weighted average filtering process after filtering the effects of noise so that only the target image is affected by the weighting. This method first perform noise detection and weight calculation is to improve the filtering effect.

Segmentation of Image:

Segmentation of image done by fuzzy C-means (FCM)[15] The template uses classical k-means depending on the breast image’s gray level intensity. But, in FCM, the membership function and Euclidean distance are changed by the features of an image. The centre part is provided as a classical k-means algorithm specified as the distance between each point and the cluster centre. Here, $C(y_i, z_j)$ resembles the coarse image, as well as the preferred template, U_{np} is template based window is presented in the below equation.

$$C(y_i, z_j) = \sum_{i=i+1}^N \sum_{j=j+1}^P Q(y_i, z_j) \times U_{np}$$

In FCM, the value of the membership function V_{ij} is updated with the Euclidean distance $e(y,w)$ depending on the features of the image like energy, contrast, entropy etc. The degree of fuzziness n , as well as the

feature centre, $W = w_1, w_2, w_3, \dots, w_i, \dots, w_d$ is calculated.

Feature Extraction:

Feature extraction is a computational technique aimed at distilling pertinent information from breast images, encompassing attributes such as color and texture. This process streamlines the representation of extensive datasets by condensing them into essential features, thereby minimizing resource consumption. By isolating and characterizing distinctive aspects like color variations and textural patterns, feature extraction facilitates efficient analysis and interpretation of breast imagery for diagnostic purposes. -GLCM model is used to extract the feature vectors. GLCM (Gray-Level Co-occurrence Matrix)[16] harnesses the power of pixel intensity correlations within an image area to capture intricate data. By computing the correlation between adjacent pixels and a reference pixel, GLCM systematically analyzes texture features across various directions and distances within the image. This second-order approach to texture calculation enables the replication of detailed information, enhancing our understanding of the underlying patterns and structures present in the image.

Feature Selection:

feature selection is performed using Stochastic Difusion Dynamic Optimization (SDDO). This algorithm is a type of pattern matching method that operates on a population level. In simpler terms, it involves comparing a pattern to various locations in a search space to find the best match. This process can be framed as an optimization task by defining an objective function, denoted as $F(x)$, where x represents a hypothesis about the optimal location for the solution. The objective function, $F(x)$, quantifies the similarity between the target pattern and the corresponding region at position x within the search space. The goal is to locate the position x that maximizes the value of $F(x)$, indicating the best-fit location for the solution.

The Dense residual network:

The dense residual community is built to combine deep capabilities. The dissimilarity between the traditional convolutional community and the residual community is that the residual community offers a skip residual operation. This operation minimizes the characteristics parameters in addition to eliminates the disappearance of

gradient and degradation instigated by using deep features. As Z suggests the output of the layer

$$Z = X_j \gamma(X_{j-1} Y_{j-1}) + Y$$

In each feature fusion, the dense network provides substantial prior information, offering features for deep feature extraction. Here, γ corresponds to the ReLU activation function, while X represents the weight matrix, and Y signifies the input to the current layer. This setup enables the mining of deep features by leveraging the dense network's prior knowledge, enhancing the fusion process.

Capsule Network:

The capsule network is introduced to maintain the object position and properties of the object in breast histology images. It encourages the vectorial output of equal size with different routings . The vector routings define the parameters of histology image . Scalar input activation functions used in a traditional neural network . The input activation functions are tangent, sigmoid, and ReLU . In contrast, the capsule network used the vectorial activation function also referred to as squashing. Known the attention mechanism as a probability weight distribution mechanism is the general term . The feature is calculated at several intervals, and any feature is given a weighting factor based on the information. By the same process, hidden layer features of high dimensions are better . In this mechanism, the researchers follow a method to decide the weighting factor dynamically, which is called the attention mechanism. enables the model to focus on specific features that are crucial for the task at hand and ignore irrelevant ones. denoted as Hj1, Hj2, Hj3, ..., Hnp, using a weighted sum to obtain a single local feature, represented as dj.

IV -RESULT & DISCUSSION

A comprehensive analysis of the proposed methods is conducted by utilizing various performance metrics such as accuracy, sensitivity, precision, and F1-score. These metrics provide a detailed understanding of the model's effectiveness in identifying breast cancer from images. Accuracy represents the ratio of correctly predicted breast cancer instances to all predictions made. Sensitivity, also known as recall, signifies the proportion of accurately identified abnormal samples, The F-score is a metric used to evaluate the performance of a classification model, particularly in the context of imbalanced data sets. It is commonly employed in

scenarios where one class dominates over the other, such as in the detection of rare diseases. The F-score combines the precision and recall of a model into a single value, providing a balanced measure of its effectiveness in identifying both true positives and minimizing false positives.. Lastly, specificity denotes the proportion of accurately identified normal classes, or instances not indicative of breast cancer, among all actual normal instances.

At the outset of the training procedure, the dataset is partitioned into three distinct sets: training, validation, and testing. In the case of the proposed Rapid Tri-Net model, the dataset allocation is as follows: 80% of the data is allocated for training, 10% for testing, and the remaining 10% for validation purposes.

The performance evaluation of the proposed technique for breast most cancers type utilizing histological images entails comparing its class outcomes with those achieved by established architectures such as ResNet combined with CNN [19]and ResNet with KWELM[20].

Table 1- Simulation results of proposed and existing approaches on BreakHis dataset

Methods	Magnifying factors	Accuracy (%)	Precision (%)	Recall (%)	F-measure (%)
ResNet and CNN	40X	85.9	94.1	87.9	90.9
	100X	83.3	91.8	89.5	90.5
	200X	85.6	93.2	93.6	93.4
	400X	81.6	90.8	88.9	89.7
ResNet and KWELM	40X	88.3	87.1	86.1	86.6
	100X	87.1	85.2	88	86
	200X	90	88.6	89.1	88.6
	400X	84.1	82.1	84.1	82.8
Proposed approach	40X	99.7	99.8	99.9	99.7
	100X	99.8	99.6	99.9	99.7
	200X	99.7	99.6	99.9	99.7
	400X	99.7	99.8	99.9	99.7

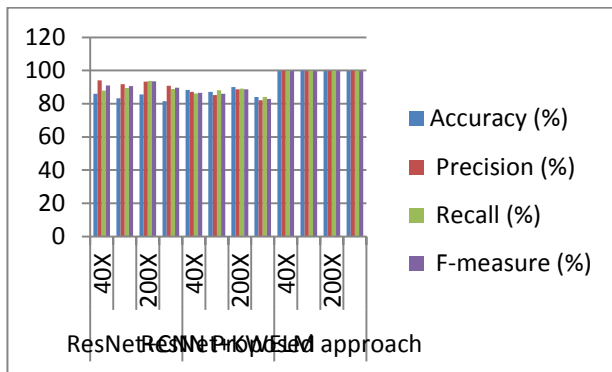


Fig. 2 Analysis of performance parameters with proposed and existing approaches

V- CONCLUSION

This paper introduces an easing breast cancer classification system deep learning algorithms applied to histopathology images. It utilizes a combination of residual dense network, capsule network, and softmax classifier to effectively categorize histopathology images into various classes. For proposed work the BreakHis dataset used, the proposed approach demonstrates superior overall performance compared to recent existing approaches. The Proposed method achieves remarkable accuracies of 99.7% for 40X magnification factor, 99.8% for 100X magnification factor, 99.7% for 200X magnification factor, and 99.7% for for 400X magnification factor. In the future try to develop a hybrid model using optimization techniques for real time application.

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