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A Super-Resolution Generative Adversarial Network with Siamese CNN Based on Low Quality for Breast Cancer Identification

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***Abstract*—Breast cancer is a chronic illness leading to the death of millions of people yearly. Despite the fact that successful identification of benign and malignant images is dependent on radiologists' long-term knowledge, specialists occasionally disagree with their decisions. An automatic system provides an alternative choice for the image diagnosis, thereby helping the expert to make more reliable decisions efficiently, less prone to errors and make diagnosis more scalable. Another issue based with the diagnosis of breast cancer identification is the poor quality of the image which poses a challenge in identification performance. An enhanced super-resolution generative adversarial network has been implemented in this paper to produce super-resolution images of breast cancer from a low-resolution counterpart with higher quality and finer details using an upscale factor of 4. Additionally, siamese convolutional neural network was utilized for the features extraction and classification of breast cancer. The proposed model provides an effective classification performance in terms of accuracy and ROC-AUC scores of 98.87% and 98.76% respectively as compared to other existing approaches.**

Keywords—breast cancer, deep learning, super-resolution, siamese network, generative adversarial network

I. Introduction

Breast cancer (BC) is one of the most widespread diseases for women all over the world [1]. Recognizing cancer early on and initiating therapy immediately increases the likelihood of cure and survival. The chances of treating a cancerous tumor at an early stage, before it extends to key organs are higher. Breast cancer arises from the breast tissue which is identified by the lump in the breast and alternations in normal conditions [2]. Methods such as mammography, biopsy, ultrasonography and others are utilized in clinical screening. However, the biopsy [3] has been accepted as the golden standard for the diagnose of breast cancer. In this scenario, the pathologists by the means of a visual inspection of histological slides under the microscope can determine the suspicious area being cancerous. With traditional manual diagnosis, intense effort is needed from a domain expert and diagnostic errors are prone to happen when carried out manually. To this fact, there is a need for an automated system for the identification of histopathological images and to also provide medical practitioners with more factual and accurate diagnostic results.

Currently, there have been research reports on the recognition of histopathology images mainly using small datasets leading to a huge limitation in improving the accuracy of the recognition task. The current release of the BreaKHis dataset [3] collected from more than 85 patients contains 7909 images from different four magnification factors which allows researchers to apply the aspect of deep learning for better results.

Recently, the state-of-the-art results of the BC recognition applied either of the two common ways: hand-crafted features or task-specific CNN methods. However, the latter achieves better recognition rates [4] than the former as the extraction of features [5] are carried out in small patches from the original images in training a specific CNN architecture but it requires a longer training period [6] and lots of expertise in tweaking the system for better results [7].

Siamese neural networks are made up of two identical networks sharing the same weights. They are commonly used for binary classification. This classification is carried out by identifying how similar or dissimilar two classes are. For this,

the commonly used loss function includes either contrastive or triplet loss[8], [9] .

From this view, our work will focus on using a siamese convolutional neural network with an enhanced super-resolution generative adversarial network called ESRGAN-SCNN for the recognition of BC histopathological images using the BreaKHis dataset. To achieve our main work, we introduced an enhanced-based super-resolution with a generative adversarial network to inculcate a connected nonlinear mapping feature from noise-contaminated low-resolution input images to produce deblurred and denoised high-resolution images, and then the high-resolution images are passed to a siamese network which extracts distinct features for breast cancer classification.

II. Related Work

Recently, numerous research studies are proposed for breast cancer classification in histopathological images focusing more on Whole-Slide Imaging (WSI) and other aspects of automatic pathology but insufficient productivity for high-rated clinical routines, high cost of producing, operating and maintaining the technology have been a challenge to the pathologists [10]. Another challenge is the limited dataset which is not available for the research community in developing new system for benchmark results. For bridging this gap, BreaKHis dataset [4] has been set as a public domain for the scientific community. This surgical biopsy dataset comprises of microscopic breast tumor images amounting to 7,909 images classified into malignant and benign tumors gotten from four distinctive magnification factors: 40x, 100x, 200x and 400x. The distinctive features between the benign and malignant tumor images is that the latter tumors are partially rounded shaped in an irregular outline whereas the former tumors are in round or oval shapes.

With the provision of the BreaKHis dataset, some researches have been proposed with different architectures and methodologies. In [4], the authors reported an evaluation using six different visual feature descriptors along with different classifiers and achieved accuracies from 80% to 85% all lies within the magnification factors. Bayramoglu et al. [11] presented a classification approach for the BC histopathology images but independent of the magnifications factors and yet have a similarly result like the authors in [4]. Results were presented by Spanhol et al. [12] using a random-patches trick consisting of extracts of sub-images at the training and testing phases. At the training stage, there is a purpose of increasing the train set via extracting patches positioned randomly. While at the test stage, patches are extracted from a grid, and after each patch classification, their classification results were put together. With this method, an increment of 84% to 91% in accuracy was achieved. Another work was published based on a similar model like AlexNet with different fusion techniques for patient and image-level classification of breast cancer. This paper presents average recognition accuracy with the max fusion method as 85.6% and 90% for patient and image-levels respectively [12]. Exploring the superior performance of deep learning models, another author achieved an average of 93.2% accuracy for patient-level breast cancer classification [13]. Different SMV-based techniques were incorporated for the recognition of breast cancer achieving their best accuracy of 94.97% for data with a 40x magnification factor [14]. Furthermore, an Inception Recurrent Residual CNN framework was proposed using the BreaKHis dataset and Breast Cancer Classification Challenge 2015. The best test accuracies were 99.05% and 98.59% for binary class and multi-class on the breast cancer classification challenge dataset [15].

Overall, the application of deep learning in BC classification has proven to provide better performance than other traditional machine learning methods in several tasks. Nevertheless, achieving better performance is dependent on the large size of dataset and long training time but there is a need to consider the quality of the image as it places difficulty in recognizing the full detail of an image. A solution in avoiding the issue of long training time and low image quality is by applying the use of ESRGAN and a simple siamese network as it improves the image resolution and trains the network for a short range respectively.

III. Methodology

This comprises of three phases. The first phase is the retrieval of the dataset used for this paper. Secondly, the improvement of the image quality using the enhanced super-resolution generative adversarial network and finally, we applied our simple siamese network for breast cancer identification.

A. Dataset

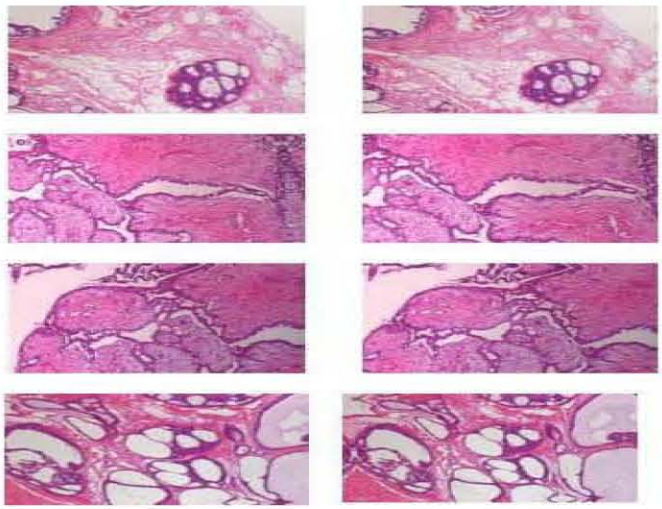

Fig. 1. Few samples of benign versus malignant augmented images.

For our experimental analysis, the BC dataset was gotten from the BreaKHis database [9] obtaining 7,909 microscopic images of benign and malignant breast tumors. Images are acquired in 3-channel (RGB) using magnifying factors of 40x, 100x, 200x, and 400x. Table I illustrates the distribution of the BreaKHis images. In resolving the imbalanced class problem in the BreaKHis dataset, we augmented the training dataset based on the ratios of the imbalanced classes and the testing sets are used as real-world scenarios. The different image augmentation techniques used include sequential rotation by 10 degrees, zooming range of 0.1, fill mode set as reflect, and rescaling

process. As we have considered only the binary classification of benign versus malignant images, Figure 1 illustrates just a few samples of the benign and malignant images been augmented. The dataset split is 80% for the training and 20 % for the testing sets.

TABLE I. IMAGE DISTRIBUTION BASED ON THE CLASS AND MAGNIFYING FACTOR

Magnification Factor	Benign	Malignant	Total
40x	625	1370	1995
100x	644	1437	2081
200x	623	1390	2013
400x	588	1232	1820
Sum Total	2480	5429	7909
No of Patients	24	58	82

B. *The Proposed ESRGAN-SCNN*

Our proposed model in Figure 2 illustrates a combined model of enhanced super-resolution generative adversarial network and siamese convolutional neural network in an end-to-end fashion. The major function of the generative adversarial network is to improve the image quality while the siamese convolutional neural network is to learn the features extracted for breast cancer identification.

- Super-Resolution Network

Several literatures have ignored the fact that in a real-life scenario, medical radiographs are generally low in quality and as such require a robust AI-based technique that will take into consideration an enhancement strategy in order to mitigate this bottleneck. Therefore, the goal of our proposed architecture is to improve the quality of breast cancer images adopted in this work using super-resolution technique which takes in the low quality images as input and generate them into a super resolution for better performance. In generating the super resolution images from low-resolution equivalent, our proposed model has shown excellent performance. As presented in Figure 2, the input images are upscaled to a factor of 4. The super-resolution network consists of a generative and discriminative neural network positioned against each other for the purpose of creating synthetic instances of images that are exactly genuine. The generative network generates $w^{k+1} = G_k(w^k)$ images where the feature maps are extracted for perceptual loss calculation before it is final passed to the activation function. It is important to mention that while the content loss is measuring the improvement of the pixel level quality of the generated image, the created images are passed to the discriminative network to verify the distinctive features of the original images $\hat{w}^{k+1}$ and the created image w^{k+1}. Since our purpose is to obtain super-resolution image, we utilize the discriminative loss to ensure the generation of super-resolution images that are realistic as compared to the original images. Finally, the adversarial loss is utilized to prompt the classifier to verify either the image is real or fake. This process continues until the discriminative network could no longer differentiate between the real and the generated images.

The mathematical expression for the summation of the super-resolution network is as follow:

$$L_{Totalloss} = L_{Gen}\left(L_{Perceptualloss} + \mu L_G^{Ra} + \eta L1\right) + L_{Dis}^{Ra} \quad (1)$$

where L_G^{Ra} is the adversarial loss and $L1$ is the content loss and μ **and** η are the coefficient to offsets the losses， respectively.

Whereas the perceptual loss is given as:

$$L_{Perceptualloss} = \sum_{x=1}^{F_{ij}} \sum_{y=1}^{H_{ij}} \left(\alpha_{ij}(\hat{w}^{k+1})_{xy} - \alpha_{ij}\left(G_k(w^k)\right)_{xy}\right)^2 \quad (2)$$

The enhancement of image quality can be seen in Figure 3 as compared to the original image.

- Siamese Convolutional Neural Network

In this study, we put two similar CNN in parallel to each other sharing the same weights to learn fixed-length representations. The vanishing gradient problem is common to most deep neural networks due to the complex networks. Therefore we built each identical CNN from scratch in our experiment as illustrated in Figure 2 in order to reduce the computational cost and model complexity. Irregular patterns in deep learning models during training could be a result of overfitting. To avoid this problem, we used 50% dropout for regularization. A nonlinearity activation function called rectified linear units (ReLU) and Adam optimizer was utilized with a learning rate of 10^4. The similarities between images were examined by the Euclidean distance and the contrastive loss function computes the loss margin. The numerical expression of the contrastive loss is presented in equation (3)

$$\mathcal{L}(W, I_1, I_2) = 1(L = 0)\frac{1}{2}D^2 + 1(L = 1)\frac{1}{2}[max(0, margin - D)]^2 \quad (3)$$

where I_1, and I_2 are similar images. $1(\cdot)$ is an indicator function that shows images with a similar name, where 0 indicates similarity and 1 indicates non-similarity. W indicates the shared parameter vector in neural networks, $f(I_1)$ and $f(I_2)$ represent the latent representation of the input I_1 and I_2 respectively. The distance, D, between $f(I_1)$and $f(I_2)$, is:

$$\| f(I_1) - f(I_2) \|^2 \quad (4)$$

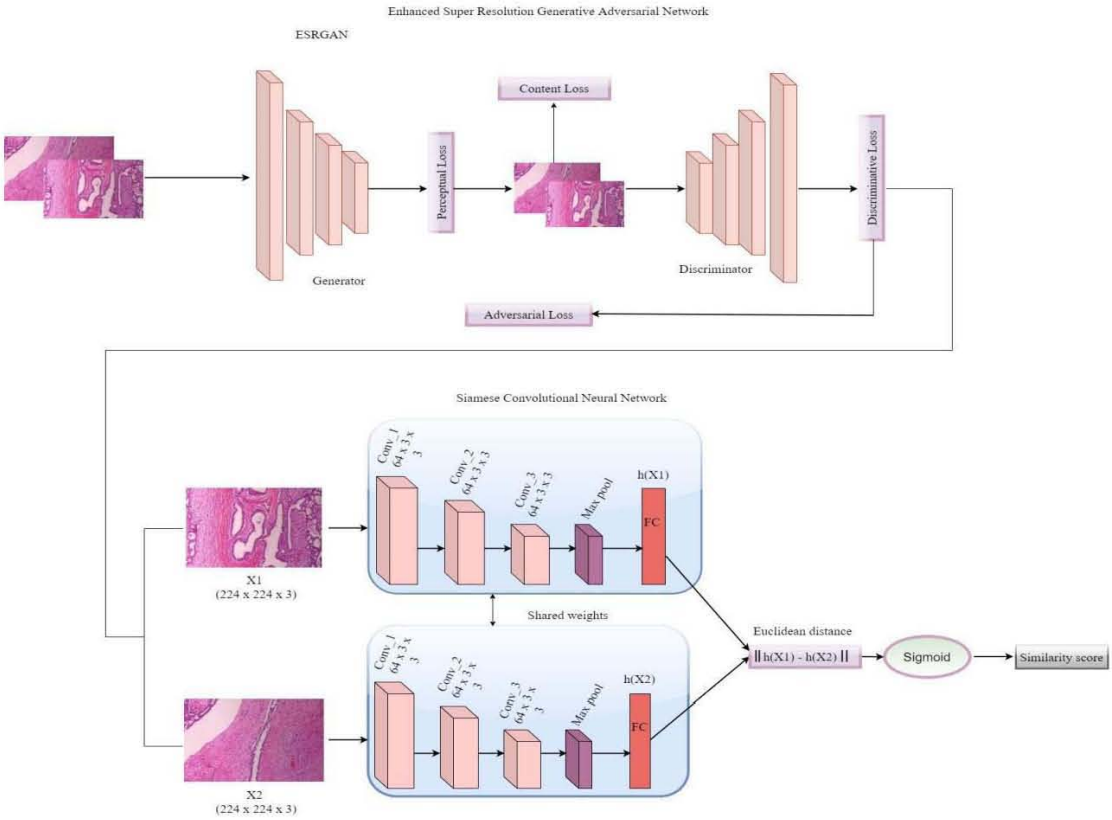

Fig. 2. Joint framework of ESRGAN and siamese convolutional neural network for the identification of breast cancer.

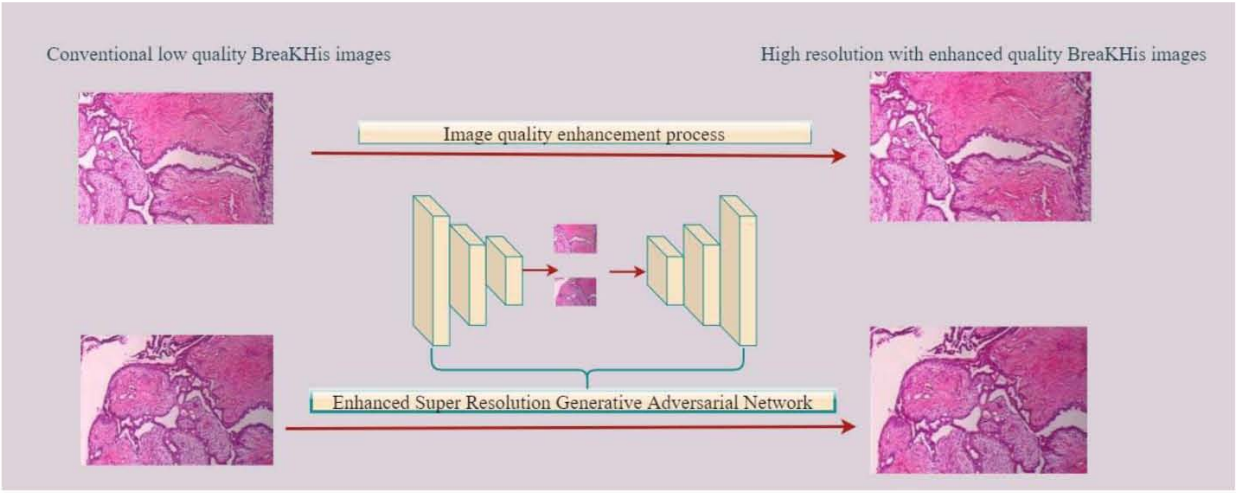

Fig. 3. Enhancing the BreaKHis dataset using ESRGAN.

IV. Experimental Results

A. Model Hyper-Parameters

In this study, we trained our model for breast cancer identification based on the siamese convolutional neural network using a data split of 80% for training and 20% for the testing set with an epoch of 10 and batch size of 32. A sigmoid classifier is used in this study since our task is a binary classification problem with a learning rate of 0.0001. It is worth mentioning that the dataset collected from public domains contains different resolution size, so we resized the images to a dimension of 224 × 224 before they are fed to the enhanced super-resolution generative adversarial network. The generated super-resolution images are then passed to the siamese convolutional neural network to either classify the output as malignant or benign. We executed and implemented our work using on Keras framework.

B. Evaluation Metrics

This paper reports the performance of our proposed model based on some core evaluation metrics for breast cancer

identification using pathological dataset. These metrics include accuracy, loss, and ROC AUC. For the identification of breast cancer, the equations for explaining the aforementioned metrics can be seen in equation (5), (6) and (7).

$$\text{Accuracy} = (TP + TN) / (TP - TN + FP + FN) \quad (5)$$

$$\text{True Positive Rate} = TP / (TP + FN) \quad (6)$$

$$\text{False Positive Rate} = FP / (TN + FP) \quad (7)$$

Where True Positives (TP) is the correctly identified malignant, False Negative (FN) is the incorrectly identified malignant, True Negative (TN) is the correctly identified benign instances and False Positive (FP) is the incorrectly identified benign instances.

Model Predicted score: For the scenario of the imbalance class in the BreaKHis dataset, we augmented our training set. With a split ratio of 80% for the training set and 20% for the testing set, our model achieved a loss of 0.0391, accuracy of 0.9887 and ROC AUC of 0.9876.

Figures 4, 5, and 6 show the performance metrics of the proposed model for the images in the test sets of the BreaKHis dataset. As we can see, our model provides better efficiency even when those images were more difficult to differentiate.

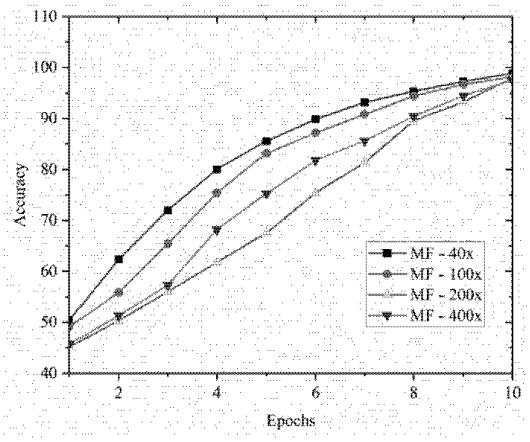

Fig. 4. The proposed model acccuracy.

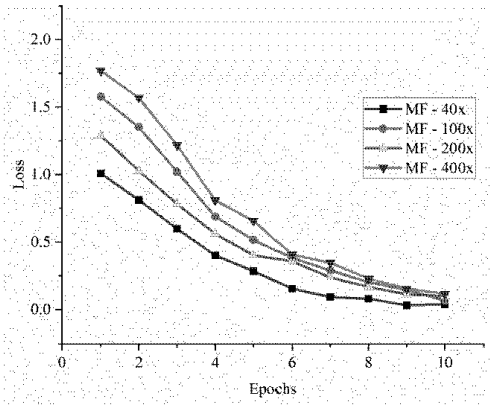

Fig. 5. The proposed model acccuracy.

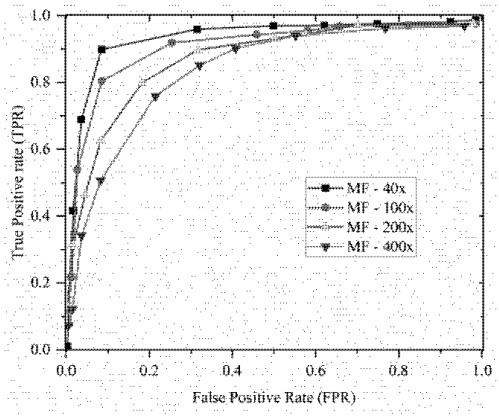

Fig. 6. The proposed ROC AUC.

In Table II, to prove the effectiveness of our proposed network, we compared our proposed framework with other states-of-the-art (SOTA) models using the implementation task of the identification of breast cancer from BreaKHis dataset. From all indications, our proposed model surpassed the SOTA models on the bases of accuracy with a margin of 0.92%, 0.58%, 0.006%, and 0.002% for the different magnifying factor of 40x, 100x, 200x and 400x respectively. To this, we can report that our model is a promising AI-based method for the identification of breast cancer.

TABLE II. COMPARISON RESULT FOR BREAST CANCER CLASSIFICATION USING BREAKHIS DATATSET

Authors	**Methods**	**Year**	**Classification Value at Different Magnification Factor**			
			40x	*100x*	*200x*	*400x*
Fabio et al. [4]	PFTAS + SVM	2016	81.6 ± 3.0	79.9 ± 5.4	85.1 ± 3.1	82.3 ± 3.8
Bayramoglu et al. [11]	Multi-task CNN	2016	81.87 ± 3.06	83.39 ± 5.17	82.56 ± 3.49	80.69 ± 4.23
Fabio et al. [12]	CNN + fusion	2016	85.6 ± 4.8	83.5 ± 3.9	83.6 ± 1.9	80.8 ± 3.0
Han et al. [13]	AlexNet + Aug	2017	85.6 ± 4.8	83.5 ± 3.9	83.1 ± 1.9	80.8 ± 3.0
	CSDCNN + Aug	2017	95.80 ± 3.1	96.9 ± 1.9	96.7 ± 2.0	94.90 ± 2.8
Kahya et al. [14]	ASSVM	2017	94.97	93.62	94.54	94.42
Alom et al. [15]	IRRCNN + w/o aug.	2018	97.16 ± 1.37	96.84 ±1.34	96.61 ± 1.31	95.78 ± 1.44
	IRRCNN + w. aug.	2018	97.95 ± 1.07	97.57 ± 1.05	97.32 ± 1.22	97.36 ± 1.02
Our proposed work	**ESRGAN + Aug + Siamese CNN**	**2021**	**98.87**	**98.15**	**97.92**	**97.53**

V. Conclusion

We presented a joint framework of an enhanced super-resolution generative adversarial network with a siamese convolutional neural network. We utilized dataset from BreaKHis in optimizing the performance of our proposed algorithm. We investigated a detailed experimental analysis to evaluate the performance of our algorithm using the evaluation metrics such as loss, accuracy, and ROC AUC. Thus, in all our result the BreaKHis dataset which is augmented for a balanced class achieved a better performance of 98.87% in identification accuracy, ROC AUC of 98.76% for the binary classification of benign versus malignant breast cancer.

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