Section A-Research paper

Performance Visualization of a Deep Neural Network Model for Mitotic Cell Detection in Histopathological Images for Breast Cancer Diagnosis

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Abstract

Breast cancer primarily affects women and is the second leading cause of mortality worldwide after lung cancer. Early detection of the mitotic stage at the cellular level can be a possible solution for timely curing it, as detection and counting of mitosis aid in determining how aggressive or malignant the cancer can spread. In the present research work, the author has proposed a deep neural network model for its performance visualization in classifying mitotic cells in histopathological images for breast cancer diagnosis. For this classification assessment, a dataset comprising 749 mitotic cells in the dataset's 1200 high-resolution histopathology images has been used. A transfer learning-based deep neural network model called squeezenet has been employed for this experimentation, which is a well-known pertained model that builds a solution for the current problem using the frozen weights stored in it while learning similar imagenet problems. In comparison to manual methods, deep learning findings produced better accuracy, recall, precision, and F-measure values of 86.84%, 85%, 93%, and 89%.

Keyword: Breast cancer, Mitotic, Histopathological images, Deep neural network model and Squeezenet

1. Introduction

Breast cancer primarily affects women and is the second leading cause of mortality worldwide after lung cancer [1]. In American women, breast cancer accounts for thirty percent of the total number of cancer diagnoses, making it the most widespread form of cancer among them [2]. Tissue from the breast biopsies gives pathologists the chance to histologically evaluate the tissue's micro components and texture. Histopathology tries to differentiate between healthy tissue, benign and malignant lesions (carcinomas), as well as to provide a prognosis assessment [3]. The main stain of tissue samples for standard histopathological diagnoses is a mixture of eosin and hematoxylin (H&E). There are numerous breast cancer forms that exhibit distinctive tissue morphology. Typical forms of breast cancer include ductal carcinoma in situ (DCIS), which has not yet migrated into additional tissues and is present in breastmilk ducts; although it similarly affects milk ducts, invasive ductal carcinoma (IDC) has migrated to nearby tissues. A

form of IDC that is tubular in shape is tubular carcinoma; a fleshy lump is known as a medullary carcinoma; milk-producing lobules are the origin of invasive lobular cancer (ILC). At the end of 2012, 1.68 million women worldwide received a breast cancer diagnosis, and of those, 0.5 million succumbed to the fatal condition [4].

Previously, experts most frequently utilized the clinical and pathological diagnostic procedures to identify breast cancer. Usually, tissue samples acquired from patients using pathological techniques are examined to detect the presence of tumor's formations. This condition is diagnosed using a variety of methods, including ultrasound, magnetic resonance imaging (MRI), mammography, and biopsy. In a biopsy, a sample of tissue from the diseased area is removed surgically or by some of another technique, such as fine needle aspiration (FNA), and is then used to make a slide. When hematoxylin and eosin (H&E) stains [5] are applied to the tissue, the cytoplasm turns pink from eosin and the nuclei turn blue from hematoxylin. Entire slide scanning scanners are used to integrate each High Power Field (HPF) picture of the tissue beneath the microscope into one picture known as a Whole Slide Image (WSI) [6]. These pictures can then be stored and transmitted simply over the internet and used for additional analysis using methods for image processing and gives histopathology images. In histopathology images, a crucial element in the detection of cancer is the mitotic count, which reveals how quickly cells are growing. Different methods are employed to make diagnoses using mitotic count on these histopathology images. All of such methods effectiveness of estimated the mitotic count highly depended on the segmentation of the mitotic cell in histopathology images. For mitotic cell's nucleus segmentation, a number of approaches have been published in the literature [7], and sometimes more than one method is combined for this purpose. These techniques include clustering, erosion, dilation, opening and closing, region growth, active contour modeling, thresholding, and graph cutting, among others [8-13]. However, using such a technique doesn't give satisfactory results because the precise segmentation is crucial for the diagnosis of the cancer. For this, a deep neural network, which is made up of an order of consecutive convolutional and pooling (subsampling) layers, can be viewed as an effective solution, as they are capable of extracting features from a given picture patch without the requirement of precisely separated nuclei. In terms of recognizing objects, recognition of speech, and image classification, neural network models have achieved impressive results [14-19]. The present research has been-focused on the same to classify the image mitotic cells in the dataset's 1200 high-resolution histopathology images using deep neural network [22][23].

Deep neural network models are of two types based on model's training such as transfer learning models and self designed models. Transfer learning models are deep learning models that have been pre-trained on problems with similar context to the current problem to build a solution. In contrast to this, CNN models have been built from scratch for a given problem. The pre-trained model in comparison to self-designed model gives numerous advantages such as the use of frozen weights and a minimum time of learning. Hence in the present work, squeezenet has been employed for mitotic cell detection in histopathological images for breast cancer diagnosis. The

major contribution of the present research work in term of novelty has been enlisted below [20][21].

1. A sizing collection of histopathological images has been retrieved from publically available platform https://rdm.inesctec.pt/dataset/nis-2017-003.
2. Effective visualization of histopathological images for mitotic cell detection has been done using different types of deep neural network without the segmentation of nuclei.
3. The effectiveness of the deep neural network model for mitotic cell detection in histopathological images for breast cancer diagnosis has been done based on recall, precision, and F-measure values.
4. The proposed method has shown an effective results in comparison to other CAD tool used for breast cancer diagnosis [24][25].

2. Material and Methodology

In this section, details of the dataset used for the present research and the proposed methodology have been described [26][27].

2.1 Dataset

The dataset used in this work is composed of 1200 high-resolution histopathology images. The dataset consists of 1200 images with an expansion of 2048 x 1536 pixels. The acquisition circumstances that have been used for all of the photos during their digitization include a 200x magnification and 0.42mm x 0.42mm pixel sizes. Normal and mitotic cells are the two balanced classes assigned to each image. The challenge's objective is to automatically classify each input image. Figure 1, shows sample image in the dataset [28][29][30].

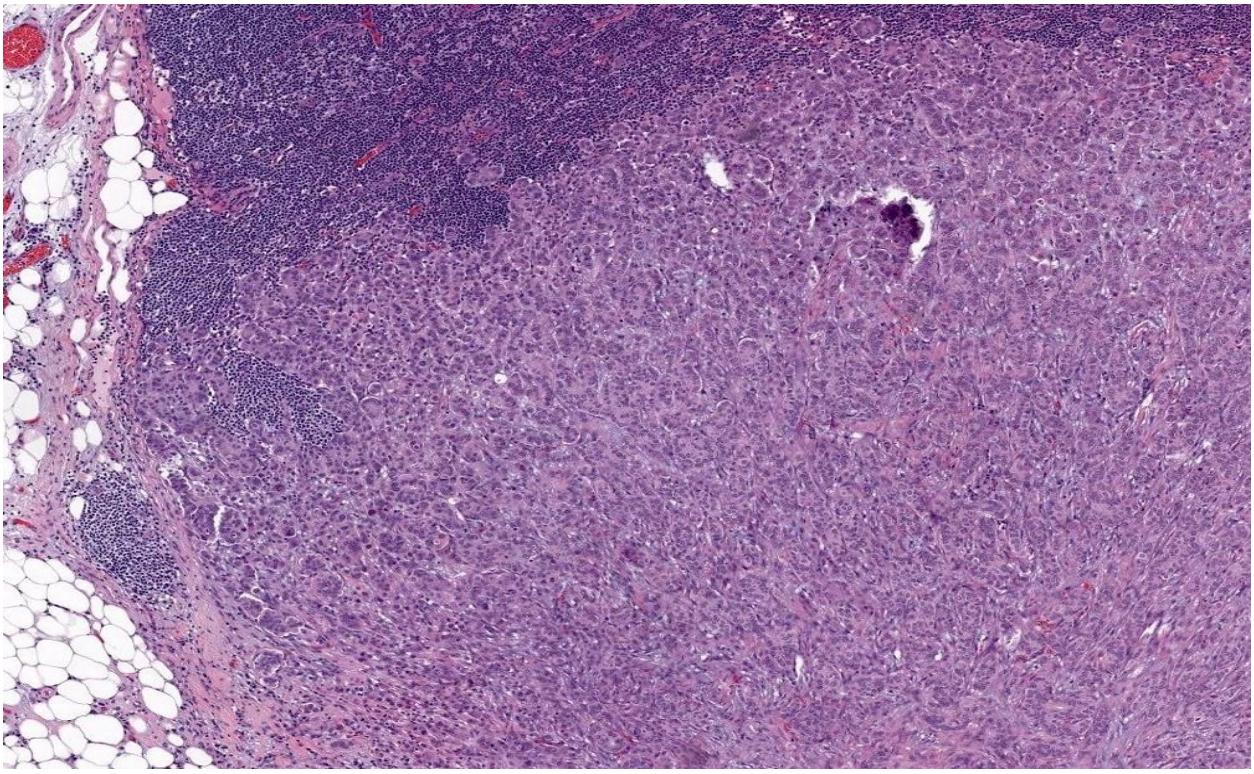

Figure 1: Sample image in dataset

2.2 Pre-processing

Before being used for diagnosis, the histopathological images are preprocessed with a median filter in size of 9 × 9 of contour size. Preprocessing, which is used to improve particular elements of images or remove undesired distortions, is one of the most important stages of the image processing procedure. A key step in the development of stronger features in histopathology images is preprocessing. The boundaries of cellular structures should be maintained and precisely defined, especially during the preprocessing stage. In the preliminary processing stage of the proposed study, investigations are conducted on noise reduction using median filtering and proper cell structure selection. Noise may arise while haphazardly scanning high-quality histopathological images. Noise should be minimized as much as possible for identification while retaining the boundaries of cellular structures [31].

2.3 Data augmentation

It is a technique was used to boost the number of images in the dataset. Various approaches including rotation, shifting, shearing, and zooming, were employed to supplement existing data. The dataset originally contained 1200 images, which is very less for training the DL model, but after data augmentation, it has grown to 48000 images.

2.4 Normalization

To maintain numerical stability for CNN designs, normalization of the image is used. The RGB representation of histopathological images is used at first, and each pixel's value has been normalized to fall between the range of 0 and 1 by multiplying it by 1/255. A model is anticipated to learn with less computation time when normalization has been used.

2.5 Deep learning model

The proposed model for this experimentation is SqueezeNet. SqueezeNet is a transfer learning model. Transfer learning models are deep learning models that have been pre-trained on problems with similar context to the current problem to build a solution. In contrast to this, CNN models have been built from scratch for a given problem. However, a pre-trained model gives numerous advantages over a self-designed model, such as the use of frozen weights and a minimum time of learning, and gives an effective solution in terms of identity and clear boundaries among given classes of the dataset for making the final decisions.

A SqueezeNet is an 18-layer deep CNN network. The ImageNet repository contains a pretrained version of the neural network that has been trained on over one million pictures. The pretrained network named as SqueezeNet can categories images into a thousand distinct categories of objects, including several animals, a mouse, a keyboard, and a pencil. The network has therefore acquired rich feature representations for a variety of images. In comparison to other machine learning models, it has high accuracy and requires fewer floating-point computations per prediction.

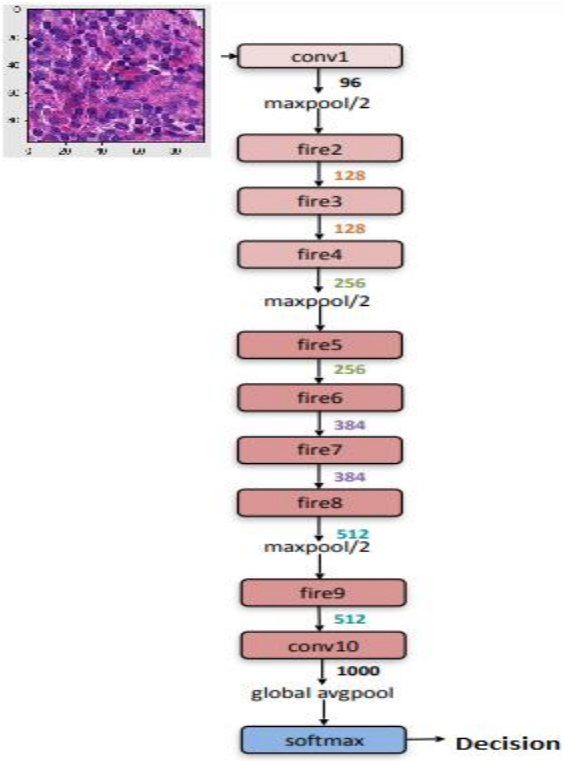

Figure 2: SqueezeNet testing on histopathological images

2.6 Simulation parameters

The various parameters for SqueezeNet model simulation on given dataset have been given below.

Table 2: Simulation Parameters of the SqueezeNe

Parameters	Value
Input Shape	2048 x 1536 pixels
Model	Sequential
Layers	18
Activation Function for Dense Layer	Softmax
Loss Function	Sparse categorical crossentropy
Optimizer	Adam
Metrics	Accuracy
Epochs	4

2.6 Experimental Setup

An experiment has been conducted utilizing a Tesla K80 GPU, which is virtually available on Google Colab, under the restriction of its limited use to a max of 12 hours for continuous training, in order to acquire the results of simulation using an estimated dataset. Along with this, the memory of other hardware RAM and ROM used for this experiment will be 12.69 GB and 107.72 GB, respectively. The maximum limit to use the GPU also fluctuates depending on the

traffic on GPU at that moment. The precision, sensitivity, accuracy and F1 Score has been the used to evaluate the model.

3. Results and analysis

This section has gives detailed analysis of the results for the experiment performed to detect mitotic cell in histopathological images for breast cancer diagnosis.

3.1 Results of classification

The spatial feature extraction algorithms' output feature vectors are used for categorization in this phase of the investigation. 1200 pictures selected from ten whole slides yielded approximately 180,000 non-mitotic and 749 mitotic cells. The suggested study's accuracy is assessed. The results of accuracy for the training images have been shown below.

epoch	train_loss	valid_loss	accuracy	time
0	0.400638	0.361613	0.843921	16:40
1	0.361891	0.329866	0.861596	16:15
2	0.347648	0.316130	0.858407	15:58
3	0.325453	0.307718	0.871036	16:11
4	0.330143	0.305901	0.868460	16:05

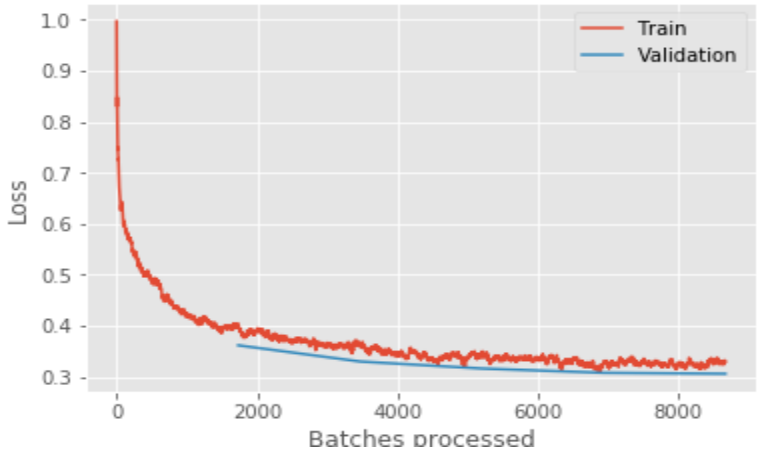

Figure 3: Training accuracy results

As per the loss curve in figure 3, the pretrained model SqueezeNet classified the images with 86.84% at 4 epochs while training on the dataset. The sample image of classification is shown in figure 4.

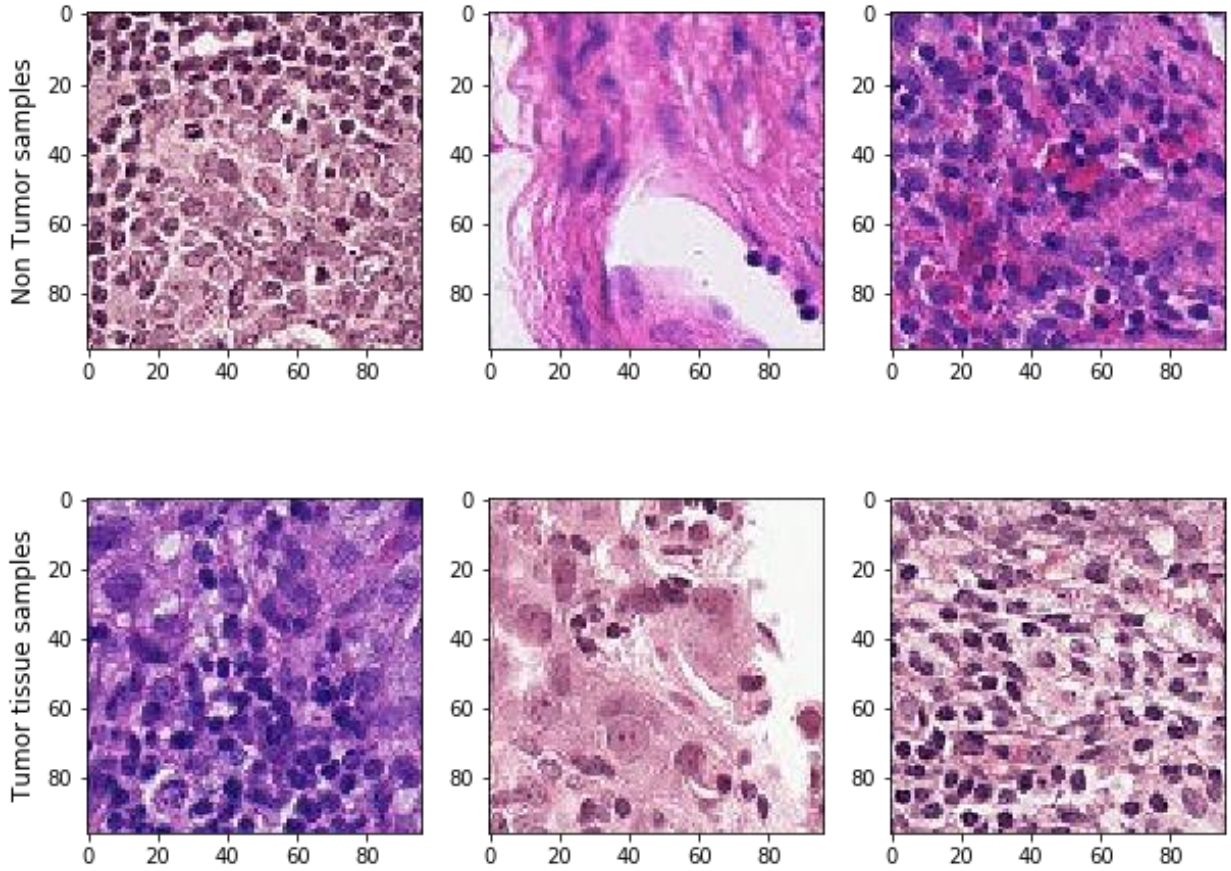

Figure 4: Classification results of non tumor sample and tumor samples

3.2 Confusion matrix results

Other than accuracy, the Confusion matrix results of the present experiment have been shown below in figure 5.

[INFO] evaluating network...

	precision	recall	f1-score	support
0	0.93	0.85	0.89	39808
1	0.69	0.85	0.76	15697
micro avg	0.85	0.85	0.85	55505
macro avg	0.81	0.85	0.83	55505
weighted avg	0.86	0.85	0.85	55505

Figure 5: Confusion matrix results

The proposed deep learning model's findings produced better accuracy, recall, precision, and F-measure values of 86.84%, 85%, 93%, and 89%.

4. Conclusion

In this article, the author presents a quick and efficient technique for categorizing histological breast cancer images when there are only a few hundred training samples available. The authors leverage deep convolutional features retrieved at various sizes with publicly accessible CNNs pretrained on ImageNet to improve the classifier's resilience. On top of that, the author provides significant techniques to pre-process the dataset for better results. To avoid less-than-ideal generalization, Author purposefully forgoes training neural networks on this volume of data, unlike some earlier research. Finally, deep learning model's findings produced better accuracy, recall, precision, and F-measure values of 86.84%, 85%, 93%, and 89%.

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