Breast Cancer Classsification

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Abstract— **Breast Cancer is a serious danger and one of the biggest reasons of demise of women at some stage in the world. The identity of most cancers largely depends on digital biomedical photography evaluation together with histopathological photographs by doctors and physicians. Analyzing histopathological images is not trivial task, and decisions from investigation of these sorts of pictures always require specialized knowledge. However, Computer Aided Diagnosis (CAD) techniques can assist the medical doctor make extra reliable selections. Deep Neural Network (DNN) has been recently introduced for biomedical image evaluation. A method for the classification stained breast biopsy images using Convolutional Neural Networks (CNNs) is proposed. Images are classified in two classes. The architecture of the network is designed to be deeply layered to diagnose cancer. Accuracies of 77.8% for two class. The sensitivity of our method for cancer cases is 95.6%.**

Keywords— Computer Aided Diagnosis (CAD), Deep Neural Network (DNN), Convolutional Neural Network (CNN)

I. INTRODUCTION

According to the International Agency for Research on Cancer, breast cancer accounts for 22:9% of invasive cancers and 13:7% of cancer-related deaths in women worldwide. [1] The unwanted growth of cells causes cancer which is a serious threat to humans. Statistics show that millions of people all over the world suffer various cancer diseases. [2] The number of mitotic figures visible in histology sections is an important indicator for cancer screening and assessment. Normally, the count is performed manually by histologists, but automating the process could reduce its time and costs (thus making it more accessible), minimize errors, and improve the comparability of results obtained in different labs. Mitosis detection is very hard. In fact, mitosis is a complex process during which a cell nucleus undergoes various transformations. In addition, different image areas are characterized by different tissue types, which exhibit highly variable appearance. A large amount of different structures can be observed in histology images stained with Hematosin & Eosin, most of which correspond to cell nuclei. Only a subset of them is in a mitotic phase and must be detected. [3] The tissue collected during the biopsy is commonly stained with hematoxylin and eosin (H&E) prior to the visual analysis performed by the specialists. During this procedure, relevant regions of whole-slide tissue scans are assessed. Fig 1 shows an example of patches from whole slide images stained with H&E for each of the classes mentioned. [4] The staining enhances nuclei (purple) and cytoplasm (pinkish), as well as other structures of interest. During the analysis of the stained tissue, pathologists analyze overall tissue architecture, along with nuclei organization, density and variability. For instance, tissues with invasive carcinoma show a distortion of the architecture as well as higher nuclei density and variability (Fig 1-B), whereas in normal tissue the architecture is maintained and the nuclei are well organized (Fig 1-A). The diagnosis process using H&E stained biopsies is not trivial, and the average diagnostic concordance between specialists is approximately 75%. [4]

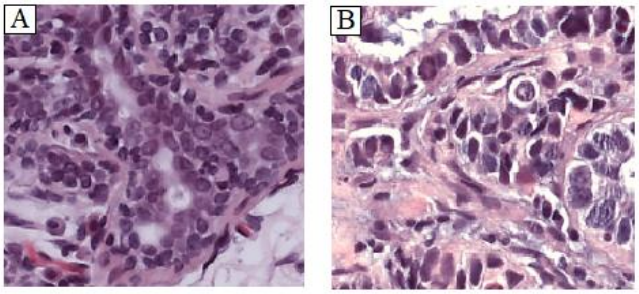

Fig 1. *Examples of microscopy image [4]*

Convolutional Neural Networks (CNN) have achieved impressive results on computer visions tasks spanning classification, object detection, and segmentation. [1] Our approach is conceptually very simple. We use a supervised Convolutional Neural Network (CNN) as a powerful pixel classifier. The CNN is a max-pooling (MP) deep neural network (DNN). It directly operates on raw RGB data sampled from a square patch of the source image, centered on the pixel itself. The DNN is trained to differentiate patches with a mitotic nucleus close to the center from all other windows. Mitosis in unseen images are detected by applying the classifier on a sliding window, and postprocessing its outputs with simple techniques. Because the CNN operates on raw pixel values, no human input is needed : on the contrary, the CNN automatically learns a set of visual features from the training data. Our main contribution is a new, important, practical application of CNN, which recently produced outstanding results in image classification, segmentation, and detection. Our approach is tested on a publicly available dataset. It significantly outperforms all competing techniques, with manageable computational effort: processing a 4MPixel image requires few minutes on a standard laptop. [3]

II. METHOD

A. Dataset

Invasive Ductal Carcinoma (IDC) is the most common subtype of all breast cancers. The original dataset consisted of 162 whole mount slide images of Breast Cancer (BCa)

specimens scanned at 40x. Table 1 shows the file name format of each patch.

Format	File Name
uxXyYclassC.png	10253idx5x1351y1101class0.png

Table 1. *Each Patch's File Name*

Where u is the patient ID (10253idx5), X is the x-coordinate of where this patch was cropped from, Y is the y-coordinate of where this patch was cropped from, and C indicates the class where 0 is non-IDC and 1 is IDC. The datasets are publicly available at https://www.kaggle.com/paultimothymooney/breast-histopathology-images/.

We partition the 92000 images into three subsets: Training(70000 images), Validation(11000 images), and Testing(11000 images). The number of these data are shown in table 2.

Data Sets	Negative	Positive
Training	35000	35000
Validation	6000	5000
Testing	6000	5000

Table 2. *The Number of Data Used*

B. Convolutional Neural Network (CNN)

CNNs are used for classifying the 48 × 48 histology image patches into the two classes. CNNs are feed-forward neural networks that are specialized in visual pattern recognition. Neurons are connected to overlapping local image patches (receptive fields), and arranged in convolutional maps with all the neurons sharing the same weights. This allows the convolutional maps to act as local image filters, detecting the same patterns at all the image positions, and to reduce the total number of parameters to be trained. The network is organized in a hierarchical layer structure that, at each level, combines the lower level features into higher level ones, until the image class label is obtained. The proposed network architecture follows the common trends in previous successful applications of CNNs for image classification, with several convolutional-pooling layer pairs, followed by a fully-connected network. [4] The architecture providing the best results in our experiments is illustrated in Fig 2, and summarized in Table 3, and resulted from the following design considerations:

Layer Type	Image Shape
Input Layer	(48, 48, 3)
SeparableConv2D	(48, 48, 32)
BatchNormalization	(48, 48, 32)
MaxPooling2D	(24, 24, 32)
Dropout	(24, 24, 32)
SeparableConv2D	(24, 24, 64)
BatchNormalization	(24, 24, 64)
SeparableConv2D	(24, 24, 64)
BatchNormalization	(24, 24, 64)
MaxPooling2D	(12, 12, 64)
Dropout	(12, 12, 64)
SeparableConv2D	(12, 12, 128)
BatchNormalization	(12, 12, 128)
SeparableConv2D	(12, 12, 128)
BatchNormalization	(12, 12, 128)
SeparableConv2D	(12, 12, 128)
BatchNormalization	(12, 12, 128)
MaxPooling2D	(6, 6, 128)
Dropout	(6, 6, 128)
Flatten	(4608)
Dense	256
BatchNormalization	256
Dropout	256
Dense(Output Layer)	2

Table 3. *Proposed CNN Architecture*

- Input Layer: this layer loads whole breast cancer histopathological images and produces outputs that feed to the first convolutional layer. The input layer is designed to resize the histopathological images as 48 × 48 with mean subtraction. The input images are composed of three 2D arrays in the 8-bit depth of red-green-blue channels.[5]
- Convolutional Layer: this layer extracts features by computing the output of neurons that connect to local regions of the input layer or previous layer. The set of weights which is convolved with the input is called filter or kernel. The size of every filter is 3 × 3. Each neuron is sparsely connected to the area in the previous layer. The distance between the applications of filters is called stride. The stride is set to 2 that is smaller than the filter size. The values of all local weights are passed through ReLU (rectified linear activation).[5]
- MaxPooling Layer: the role of the pooling layer is to down-sample feature map by reducing similar feature points into one. The purposes of the pooling layers are dimension reduction, noise drop, and receptive field amplification. The outputs of pooling layers keep scale-invariance and reduce the number of parameters.
- Output Layer: The output is composed of four neurons, corresponding to each of the two classes, that are normalized with a softmax activation function.[4]

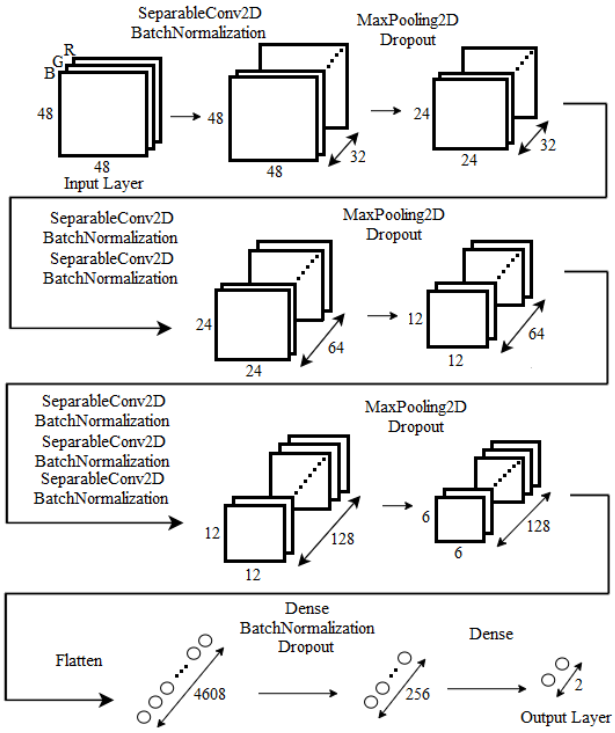

Fig 2. *CNN Architecture*

We describe the steps after CNN model as follows:

- Training stage: the goal of the training stage is to learn the sufficient feature representation and optimize the distance of different classes' feature space. After importing two breast cancer histopathological images at the same time, the CNN first learns the hierarchical feature representation during training and share the same parameters of weights and biases.
- Validation stage: the validation stage aims to fine-tune hyperparameters, avoid overfitting, and select the best model between each epoch for testing.
- Testing stage: the testing stage aims to evaluate the performance of the CNN. Feature learning process of CNN is shown in the testing. After the first step of the input layer, low-level features that include colors, textures, shape can be learned by the former layers. Via repeated iterations of high-level layers, discriminative semantic features can be extracted and inserted into a trainable classifier. [5]

III. Experimental Study

We first present empirical analysis of our model design using the CNN base architecture, then show quantitative results of our best models. Finally we use techniques for visualizing saliency maps to provide interpretability of the model. All results are presented on the validation and test sets, respectively. [1] We have utilised the BreakHis breast image dataset for our experiment. All the images of this dataset have been collected from 162 whole mount slide images. This dataset contains two groups of images depending on the magnification factor 40x. Each of the images of this dataset are RGB in nature and 48×48 pixels in size and they are elements of a particular set. [2] CNN - based image representations learned on large-scale annotated datasets have proven to to be a useful form of pre-training that can be effectively transferred to other computer vision tasks with limited training data. More recently, low-level features learned from natural images have shown to be effective for medical image classification. [1]

A. Accuracy Performance

- Training acc: means accuracy obtained over train data. In other words, putting the training data on the learned model to get results.
- Validation acc: Some of the data is the data reserved for testing the system. You determine it yourself. Sometimes keras reserves some of the train data for testing.

Performance results on the testing dataset are reported in Fig 3. [3] Our validation performance has fluctuated. If you pay attention, the 25th epoch gave the best results.

When saving the model, we should record it according to the best result. The other is the loss function. But it means an error when doing classification. We can gets better performance by changing the learning rate or epoch.

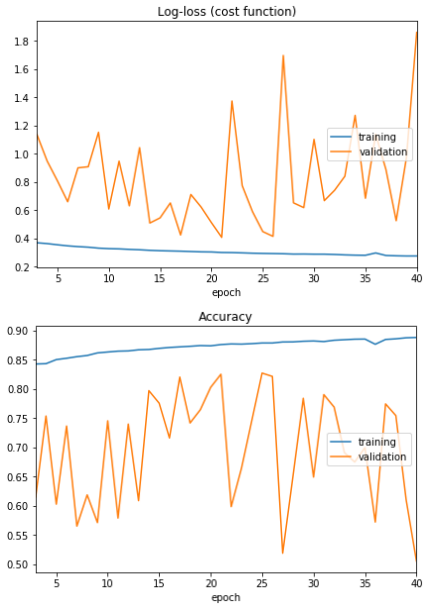

Fig 3. *Accuracy Cost Curves*

IV. Conclusion

In this work, we propose an end-to-end deep learning model to classify pre-detected breast masses from H&E stained histological breast cancer images.[1] We show additionally provide a method to give more interpretability to network predictions. All relevant features are learned by the network, reducing the need of field knowledge. For this, the architecture of the network is designed to extract information from different relevant scales, including nuclei and overall tissue organization. The network is trained on an augmented patch dataset and tested on a separate set of images. Both dataset augmentation and scale-based network design have been shown important for the success of the approach. The proposed classification scheme allows to obtain high sensitivity for carcinoma cases, which is of interest for pathologists. The performance of our system is similar or superior to the state-of-the-art methods, even though a smaller and more challenging dataset is used. Finally, since the network is designed to consider multiple biological scales, the proposed system can be extended for whole-slide breast histology image classification relevant for clinical settings.[4]

References

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