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Advance Cell Detection in Histopathological Images using Convolutional Network

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ABSTRACT : Cell detection is often extremely important requirement for later cellular analysis in computer for histopathology images .It is challenging due to high cell density ,touching cells , low contrast ,version cell shapes and sizes ,weak borders and the use of different image learning ways of doing things. Existing methods are often struggling at tackling with the challenges at the same time. More importantly , the detection time efficiency, which is also extremely important for cell detection.

In this paper, a novel end to end cell detection pipeline based on convolutional moving backward Nerve-related networks to achieve competitive cell detection and better time efficiency at the same time.

KEYWORDS: cell detection, histopathology image, deep learning , feature extraction, etc.

I. INTRODUCTION

Strong and healthy cell detection plays an important role in the automatic analysis of histopathology images, which is an important tool for the disease-identifying, treatment result (statement about a possible future event),and medicine-based decision making in many cancer cases.

Detection of cells successfully is hindered by the extremely high cell density, touching cells, low contrast, version cell shapes and sizes, weak borders and the use of different image learning ways of doing things. Existing cell and centers detection methods include many sets of computer instructions: Image processing methods like graph-cuts, operations, Maximally Stable External Area detection, Radial Symmetry Based Voting, and supervised learning based methods like binary SVM classifier, Random forests, etc.

Due to the very high cell density and weak cell borders in histopathology images, most existing supervised learning, including CNN based methods can only get dot notes. Unlike the object detection in natural image, where the detection performance is often figured out by the intersection between the ground truth bounding boxes, the cell detection performance is often figured out by the distance between described a possible future event and the ground truth dots near the cell center.

Besides the efficiency of this method can be limited by GPU memory if the patch size is bigger and needs a much bigger output from the fully connected layer. This method assumes that given an image patch($27*27$ in experiments),the maximum cell numbers in this patch is M.However, this cannot be true when it is applied to the detection of tumor cells, which are often bigger and irregular in centers(of cells or atoms) sizes(which can be larger than $27*27$).

Breast cancer is the most common invasive cancer in women and the second main cause of cancer death in women, after lung cancer. According to International Agency for research on cancer the number of deaths caused by cancer in the year 2012 alone came to around 8.2 million. Breast cancer can be diagnosed using medical images testing, like



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histology and radiology images. The histology images allow us to distinguish the cell nuclei types and their architecture according to a specific pattern. If the histopathologists are not well-trained, this may lead to an incorrect diagnosis. With onset of pattern recognition and machine learning, many handcrafted (engineered) features-based studies are proposed for classifying breast cancer histology images. After selecting the region of interest, a set of features are extracted and fed into traditional classifiers to classify the breast histology images into either benign or malignant.

The convolutional neural networks are regarded as a variant of the standard neural networks. This variant introduces a new special network, which comprises convolution and pooling layers. To get final classification result, the patches results are combined for whole image.

II. MOTIVATION

The main approach of this method is detection of cell in histopathology images which is used for identification of sickness.

(quality of being very close to the truth or true number) of the image and time efficiency is the most important(feature/qualities) of this approach.

Using very less (math-based/ computer-based) efforts the optimization of results.

III. SYSTEM ARCHITECTURE

The client (record by a camera or computer) the image of cell using camera or import image of cell if present in system (computer file full of information). The histopathological image is passed as input to the software. The system works on that image and creates convolution layers moving backward layers for further work.

Convolution Layers:

The image is divided in smaller parts by using convolution layers. The smaller parts again divided into more smaller parts, the process goes on till the image is divided to the needed/demanded stage. for example: The input image is of size 600*600 then system divides the input image to 300*300 again the image divided, the divided image is broken into parts.

Classification:

For classification system use the SVM method SVM stands for Support Vector Machine it is supervised machine learning set of computer instructions which can be used for both classification or moving backward. SVM separates the classes. It finds out a line/ hyperplane (in multidimensional space that separate outs classes). By classification system gives output as the patient have any disease or not.

Histopathology image:

Histopathology is the study of the signs of the disease using tiny examination of a sample of living tissue for analysis or surgical medical sample that is processed and fixed onto glass slides. To see (in your mind) different parts/ pieces of the tissue under a microscope, the sections are dyed with one or more stains.

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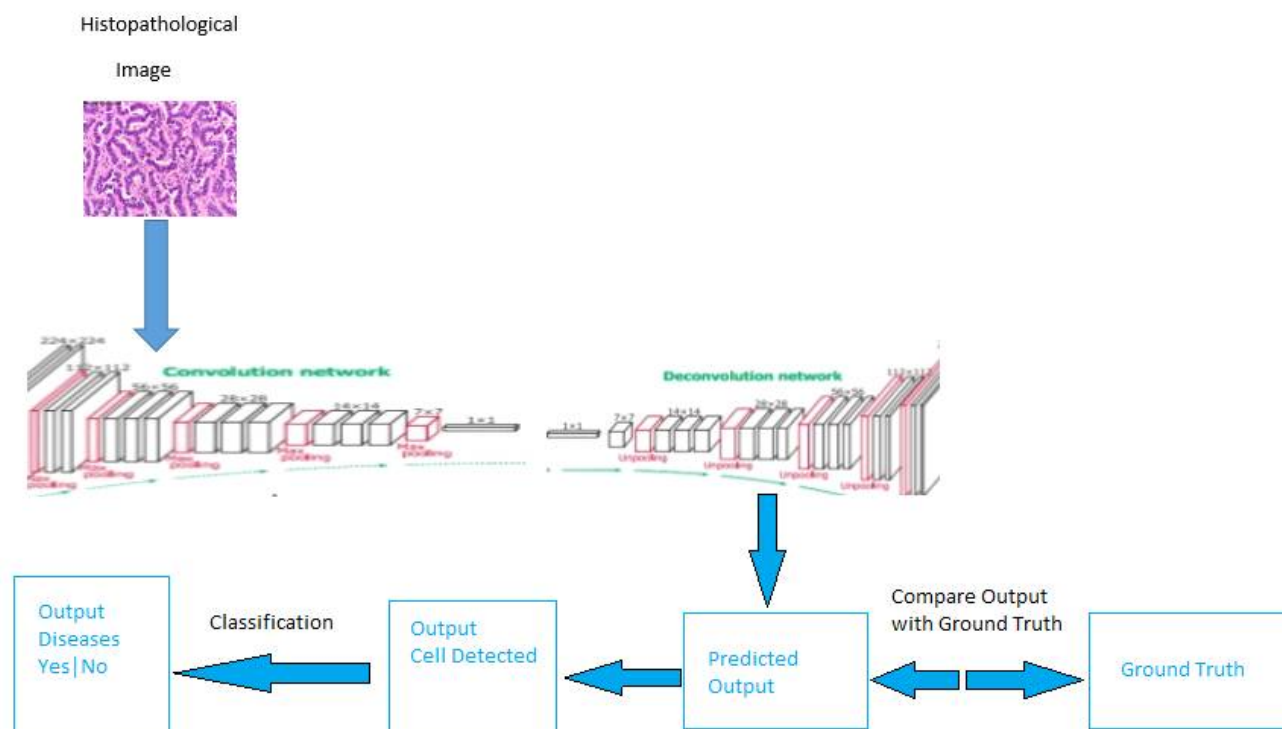


Fig. System Architecture

IV. EXISTING SYSTEM

Graph-Cut Method

It is used for solving low level computer vision problem such as smoothening, image (division of something into smaller parts).

In this method centers (of cells or atoms) seed points are detected and are used to perform initial (division of something into smaller parts) using second-cut graph based set of computer instructions which reduce (math-based/computer-based) complex difficulty.

Radial symmetry based voting

This method is used for shape detection, the different shapes can be (at the same time) located and classified. It is used by taking account of both voting (collections over time) and voting directions. It reduces false detection.

V. PROPOSED SYSTEM

- 1) Model is based on quite recent natural image processing: Convolutional networks.
- 2) Solves the image problem in end-to-end way by introducing convolution layers.



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- 3) Overall structure of our model would be passed into sequence of convolutional layers and de-convolution layers.

VI. RESULT EVALUATION AND DISCUSSION

To decide if a detection actually corresponds to a cell center, consider a threshold if the distance between a detection and a ground truth note is less or equal to threshold regard the decision as true positive (TP). If more than one detection falls into this area, assign the most confident one to the ground truth location and regard the others as false positive (FP), and all ground truth notes without any close detections are false negatives (FN). With these definitions it can be calculated the precisions, recalls and F1 scores of different methods besides, average Euclidean distance and standard deviation between TP and its correctly assigned ground truth location as well as the average complete and total difference and standard deviation between number of ground truth notes and detections.

VII. FEATURE EXTRACTION

Feature extraction is a crucial and challenging aspect in the computer-aided diagnosis of breast cancer with histopathological images. Here the features of the images are extracted and compared with the ground truth whether it is of malignant or benign. A novel nuclei-guided feature extraction method based on convolutional neural network is proposed for histopathological images stained by hematoxylin and eosin. The nuclei in the image are first detected. Considering the location information of the nuclei, a fine-designed neural network is trained to extract features regarding pattern of nuclei.

For extraction autoencoder and SVM classifier is used.

Autoencoder:

In general, cell detection and classification are separated and assigned into two different networks, resulting in increased computational complexity for training the deep network. A novel deep autoencoder structure for classification with detection is proposed.

This novel network uses one deep autoencoder to detect the positions of cells and classify types of cells simultaneously. In addition, the proposed network can efficiently detect the cells with irregular shape.

Classifier:

The objective of SVM (Support Vector Machine) is to find a hyperplane.

Hyperplane means a decision boundary separating the tuples of one class from another. It uses a non-Linear mapping to transform the original training data into a higher dimension. In SVM if the output of the linear function is greater than 1, it is defined as one class and if the output is -1 it is identified with another class.

VIII. EXPERIMENTS

Datasets

The dataset used consists of microscopic images of benign and malignant breast tumors.

The method is to evaluate on two histopathology image cell datasets. The BM dataset is provided which contains eleven 1200*1200 pixel images of healthy human bone (the deep insides of the bones) from eight different patients, with 4205 dot notes near the cell centers. The second dataset consist of twenty 100*100 pixel histopathology images of breast cancer tissue.

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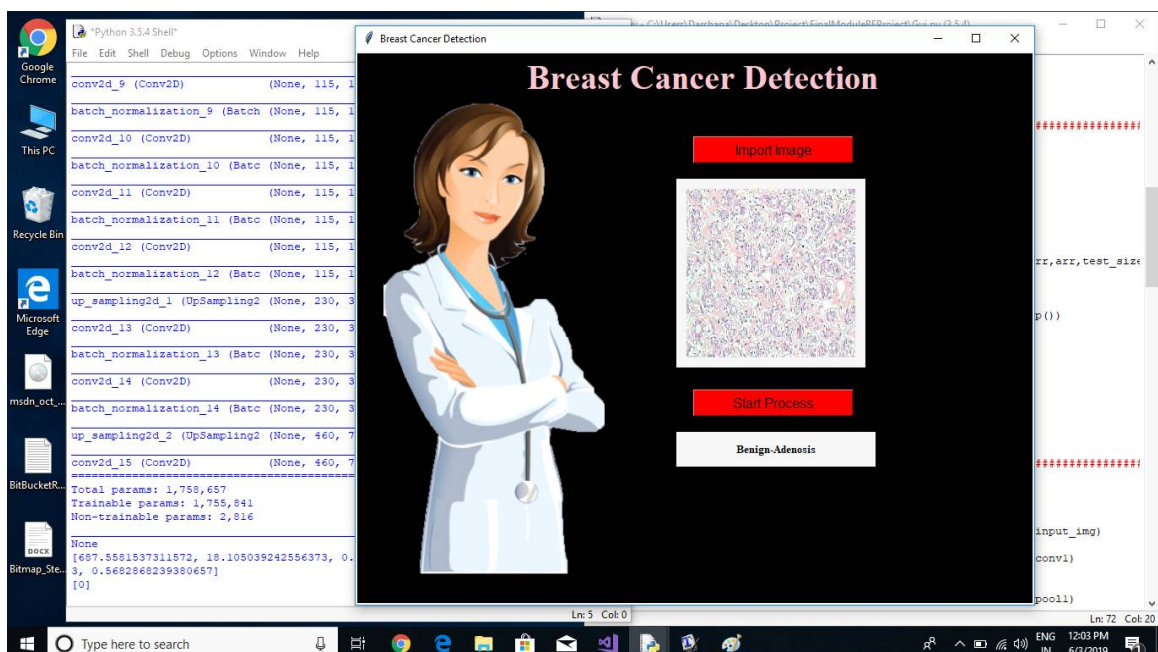
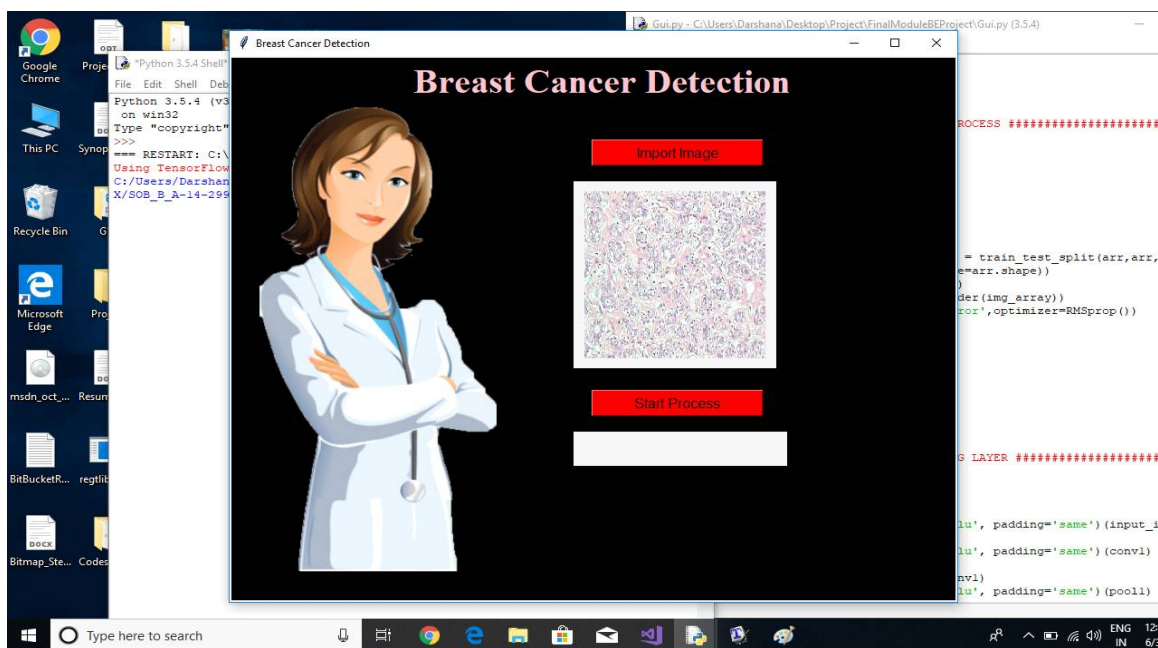
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Implementation

For the two datasets rotation, left and right operations are performed on all of the training samples for data enlargement purposes. At inference time, the test images are passed into the model. Then the final cell detection dots can be received by localizations of the local maximum values on the output density map.

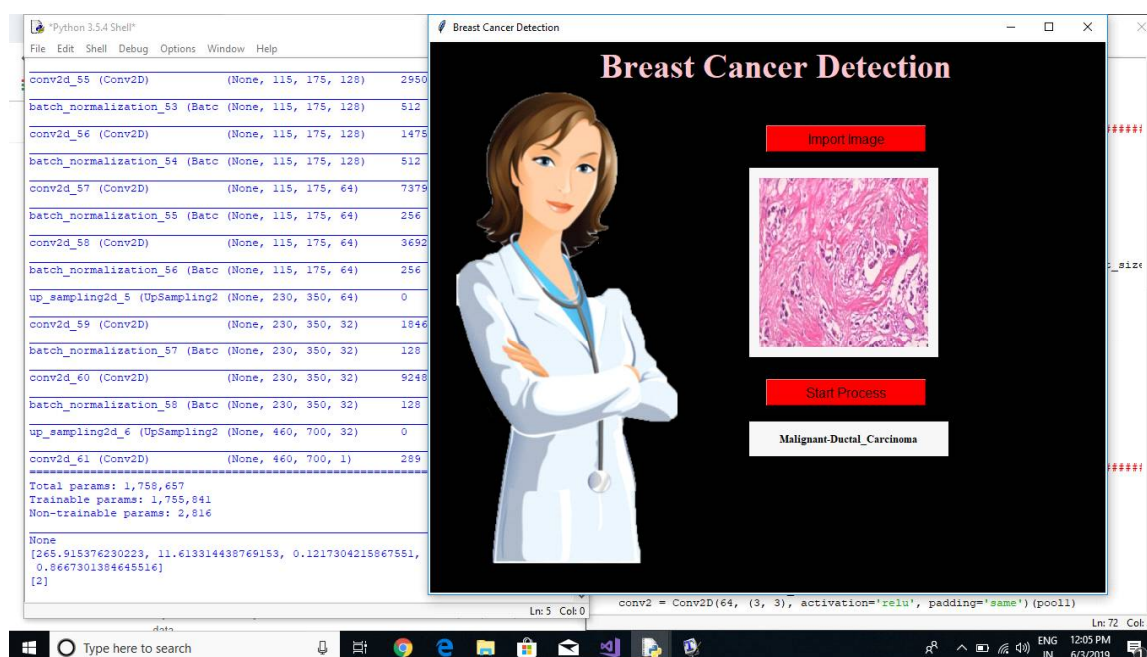


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IX. CONCLUSION

The main approach is to determine cell detection for histopathological images based on convolutional networks, which is more time efficient. Due to the huge size of the whole slide histopathology images, the method is related to whole slide level cell detection while keeping a balance between (quality of being very close to the truth or true number) and time efficiency.

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