A Method of Automatically Calculating Vaginal Cleanliness Degree from Leukorrhoea's Microscope Images

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***Abstract*—Vaginal cleanliness degree is one of the most important diagnosis criteria in regular examination of leucorrhea. It can be used to judge whether inflammation occurs. The most common clinical way to obtain vaginal cleanliness degree is manual microscopic examination. In current research, some groups have already proposed some methods to automatically analyse images from microscopic examination of leucorrhea secretion. But none of these methods can recognize four important targets at the same time, so they can't obtain the vaginal cleanliness degree. This paper reports about a method that can automatically calculate the vaginal cleanliness degree of a microscopic examination image. This method includes a convolutional network similar to fully convolutional networks, and some morphological operations to extract contour of each cell and count their number. Experiments prove that our algorithm is simple, fast, efficient and accurate. It has good clinical potential.**

Keywords—vaginal cleanliness degree, fully convolutional networks, multi-target recognition, automatic calculation

I. INTRODUCTION

Bacterial Vaginosis and *Candidal Vaginosis* are the most common vaginitis in our daily life [1]. *Bacterial Vaginosis* a kind of mixed infection caused by *Gardnerella Vaginalis* and some anaerobes. It leads to imbalance of microecological environment in vagina, which causes the increase of vaginal secretions, fishy odour of leucorrhea and vulva itching and burning. If treatment is not in time, it may induce genital infection, pelvic infection, Periodontitis, sexual pain and so on [2]. It's also one of the factors that induce cervical carcinoma [3]. *Candidal Vaginosis* is caused by candidiasis, it's hard to be cured, recurrent, it may also cause premature delivery and fetal malformation [4].

Regular examination of leucorrhea is a necessary means for these two diseases. Vaginal cleanliness degree is one of the most important diagnosis criteria in regular examination of leucorrhea. It can be used to judge whether inflammation occurs. Furthermore, it figures out the causes of inflammation, which makes it able to provide direct basis for treatment. The judgement standard of vaginal cleanliness degree is described in Table I [5]. Degree I and II mean normal status, degree III and IV point out the existence of inflammation. Meanwhile, judged from the number of *Candida albicans* and *clue cell*, preliminary diagnosis of the type of inflammation is available.

Currently the most common clinical way to obtain vaginal cleanliness degree is manual microscopic examination. Doctors have to observe the smear of leucorrhea secretion under microscope and count the number of different cells so they can finally calculate the vaginal cleanliness degree. In current research, some groups have already proposed some methods to automatically analyse images come from microscopic examination of leucorrhea secretion. For example, in Youyi Song and his group's research, they used Superpixel [6] and CNN [7] to segment *Gardnerella Vaginalis* on *clue cell* [8]. They also proposed another recognition method of *lactobacilli* and *Gardnerella Vaginalis*, used markov random field and adaptive Boosting machine learning method to segment different bacteria [9]. Another research team led by Yolanda S. Baker tried to combine five feature selection methods, six search methods and three classifier algorithms of machine learning to recognize *Bacterial Vaginosis* [10]. But none of these methods can identify *epithelial cell*, *white blood cell*,

Candida albicans and *lactobacilli* at the same time, so they can ’ t obtain the vaginal cleanliness degree of the image.

TABLE I. VAGINAL CLEANLINESS DEGREE LOOKUP TABLE

Vaginal cleanliness degree	*lactobacilli*	*candida albicans*	*epithelial cell*	*white blood cell*
I	++++	-	++++	0~5
II	++	-	++	5~15
III	-	++	-	15~30
IV	-	++++	-	>30

We are the first to propose a method that can automatically calculate vaginal cleanliness degree from microscopic examination images of leucorrhea secretion. This method is similar to FCN (fully convolutional networks) [11]. It can recognize *epithelial cell*， *white blood cell*， *Candida albicans* and *lactobacilli* at the same time. Then with some morphological operations, we are able to count the number of each kind of cell. At last we export the vaginal cleanliness degree according to the vaginal cleanliness degree lookup table. In an experiment of 65 samples, the agreement rate of our result reached 96%, which proved that our method has good clinical potential.

II. METHODOLOGY

A. Materials

All of the data used in our research came from a database, which was founded by the Sixth People's Hospital of Shenzhen and school of Medicine, Shenzhen University. This database contained 50 patients’ microscopic examination images of leucorrhea secretion, provided by the Sixth People's Hospital of Shenzhen. All the images were collected in the same standard. First, we made a leucorrhea secretion smear, then we acquired images through an imaging system as shown in Fig. 1. This system included an OLYMPUS microscope, a scanning platform driven by a motor, and a CCD camera connected to a personal computer. The images collected are shown in Fig. 2 as example. They were all RGB images with the resolution 4080 x 3072. We collected 10 pictures for each sample, 500 in total. After that we invited some clinical professor to mark these images. They marked five types of cells (*epithelial cell*， *clue cell*, *white blood cell*，*Candida albicans* and *lactobacilli*) with different pixel values. Finally, we got the labels of these images, which had 6 kind of pixel values, in our research, we set the background as 0, *epithelial cell* as 5, *clue cell* as 10, *white blood cell* as 15, *Candida albicans* as 20, *lactobacilli* as 25. The cells could also be marked with other pixel values, as long as different cells were in different values. After image were marked we obtained a complete database.

We randomly picked 400 images and their labels as the training set, left the other 100 images as testing set. The original images were too large, we had to shrink them in equal ratio. After shrunken 4 times and added zero at the edge, we got images and labels with the resolution 1024×768.

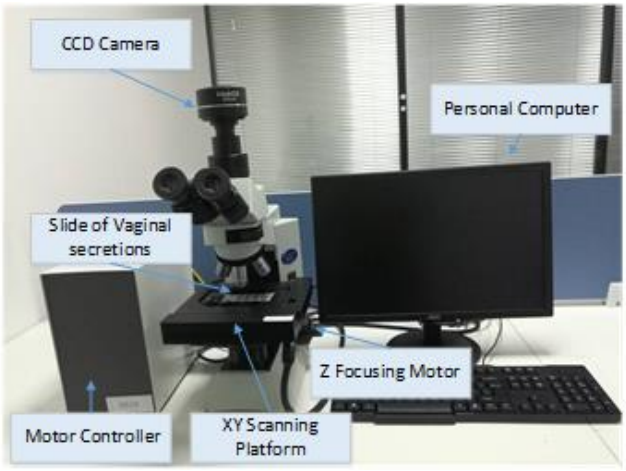
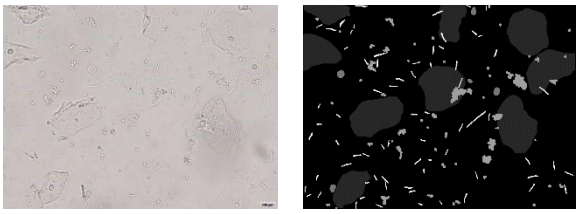


Fig. 1. Image acquisition system



(a) Collected image (b) Label

Fig. 2. Collected images and labels

Then we augmented the shrunk images and labels. The augmentation method included translation (-20~20 pixel, step 20 pixel), rotation (-20~20 degree, step 20 degree), noise adding (white Gaussian noise, energy range 0~0.0001, step 0.0001), brightness adjustment (range 0~0.10, 0.90~1.00, step 0.05), HSV (Hue，Saturation，Value) adjustment (range -0.2~0.2, step 0.2). After augmentation, the number of our images and labels increased to 200,000.

B. Methods

The flowchart of our method is presented in Fig. 3. First, a microscopic examination image of leucorrhea secretion was processed by our deep learning model, then the result went through morphological post-process, according to the result and vaginal cleanliness degree lookup table, we could finally calculate the vaginal cleanliness degree of the images.

1) Design neural network, train deep learning model

Our classification method in this paper belongs to Semantic Segmentation. There are many state-of-the-art Semantic Segmentation methods, including FCN, U-net [12], SegNet [13], DeconvNet [14], DeepLab [15] and so on. FCN is an original one, but it is complex to train, and the result is not fine, the details of the image are not sensitive enough. U-net is a network based on FCN, it fits medical image segmentation well, but it takes a bit long time to identify an image, usually more than 1s. SegNet is also based on FCN, it’s more efficient in memory usage than FCN, but the basic score it achieved in VOC2012 could not meet the practical needs. DeconvNet is a neural network with convolution-deconvolution structure, it’s similar to SegNet, but it has too many parameters, which slows down the training speed. DeepLab contains a well-designed

decoding module inside it's encoding-decoding structure, all the parts follow residual connection design. But with the usage of dilated convolution, the cost of calculation is relatively high. And the process of a large amount of high resolution characteristic maps takes up a lot of memory. In conclusion, none of the existed networks meet our requirement. So we designed a network based on FCN by ourselves. It has simple network structure, short training time, small memory footprint and fast recognition speed. It is very suitable for medical image, it is also able to recognize and classify different kind of targets at the same time. This network uses Caffe as framework, as shown in Fig. 4. It is divided into two stages according to function, which are feature extraction stage and feature map reconstruction stage. It also can be divided into 3 sub-network based on output size of each layer, they are 1/4 sub-network, 1/2 sub-network and 1/1 full-network.

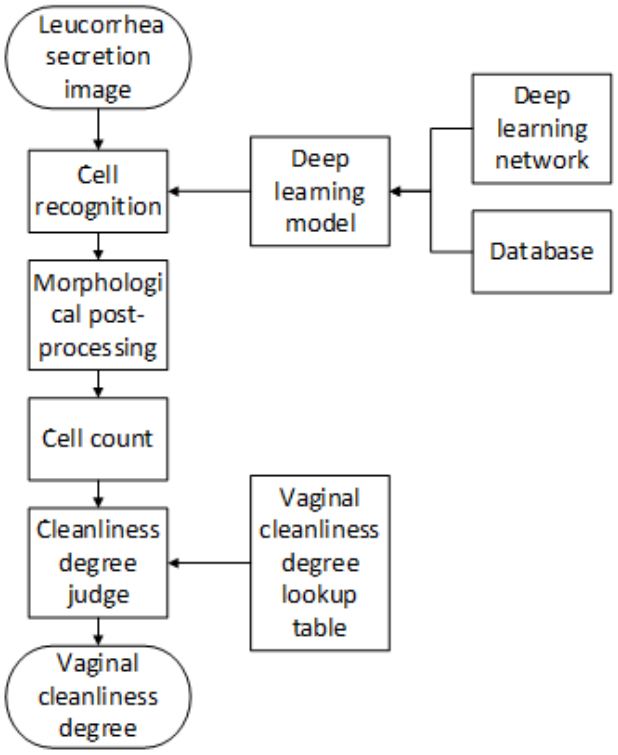


Fig. 3. Flowchart of our method

The feature extraction stage contained 5 convolution layers, 4 pooling layers and 5 ReLU layers. The first layer used a 3×3 filter to extract basic feature of data, followed by an ReLU function as activation function to increase convergence rate of gradient descent. Then we followed a down-sampling block formed by a pool-conv-ReLU layer, this layer contained 3 layers, a pooling layer, a convolution layer and a ReLU layer. We used 2×2 and 4×4 pooling layer in our down-sampling block, made it able to shrink the length and width of output map into 1/2 or 1/4. This block was meant to decrease the dimension of convolution feature corresponding to hidden nodes, gave the whole network shift invariance and more global information, so each local receptive field could extract more global features. The convolution layer after a pooling layer could combine the shrunk low-level feature maps into feature maps with more semantic information. After 4 down-sampling block, the feature map shrunk from 1024×768 to 16×12. After a conv-ReLU layer to combine this feature map, finally we got a scores map for next stage.

After continuous down-sampling operations during feature extraction stage, the dimension of the feature map decreased to 16×12 step by step, it was far smaller than the input image. In order to output scores-map at original image's size when training and testing, we needed to enlarge it to the original size. We added a feature map reconstruction stage, used interpolation to complete up-sampling operation. A deconvolution layer with a 4×4 kernel and 4 as stride could enlarge scores map to 4 times. Because the enlarged feature map had lost many local details, to overcome this, we connected the feature map obtained by deconvolution to the feature map obtained by the corresponding pooling layer. This kind of skip-layer operation added more multi-scale contextual information.

After 4 up-sampling, the scores map was reconstructed to 1024×768 resolution. Then we calculated loss according to the scores map obtained by forward propagation and the given ground-truth. Finally, through back propagation of gradient, we could make the parameters of front layers changing and iterating towards the right direction.

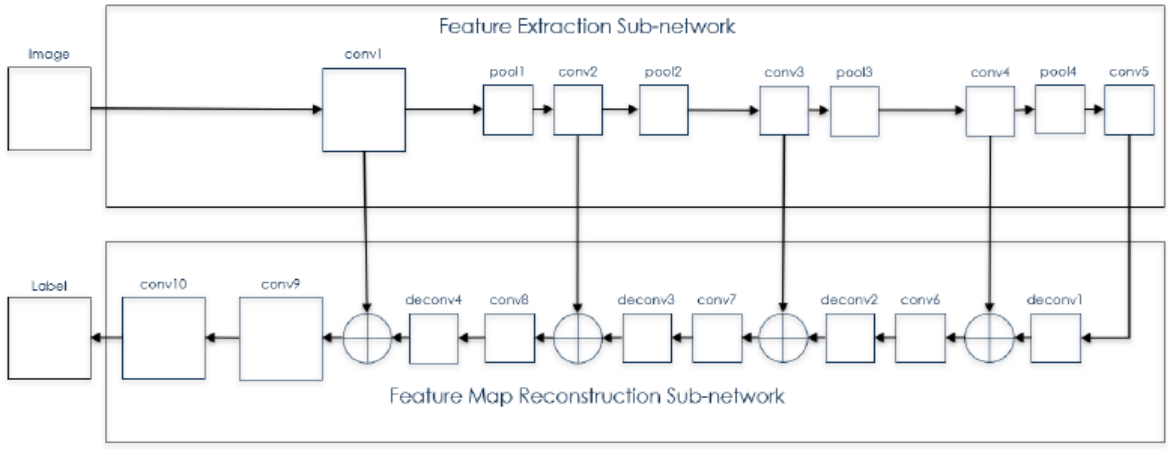


Fig. 4. Network Structure Diagram

We fulfilled our training in three steps corresponding to the three networks we mentioned. Firstly, we trained the 1/4 sub-network, it was extracted from the second construction step. This part exported an image at 1/4 size of original images, which was 256×192. Because the convergence difficulty was in direct proportion to the depth of network, we had to train this shallow sub-network to provide preparation conditions for deeper network. Secondly, we trained the 1/2 sub-network, it was extracted from the third construction step. This part exported an image at 1/2 size of original images, which was 512×384. This network added three layers on 1/4 sub-network, it was initialized by model trained out from 1/4 sub-network. Thirdly, we trained the 1/1 full-network, it was initialized by model trained out from 1/2 sub-network. This network exported images in the same size of original images, which was 1024×768. The model trained from 1/1 full-network was the deep learning model we need in our method.

2) Morphological process

The image processed by deep learning model was able to classify different kind of cells, but the edge of cells was not clear, and it contained much noise. So, we could not get the number of each type of cell. This was why we need morphological process [16]. The specific process information is shown in Fig. 5.

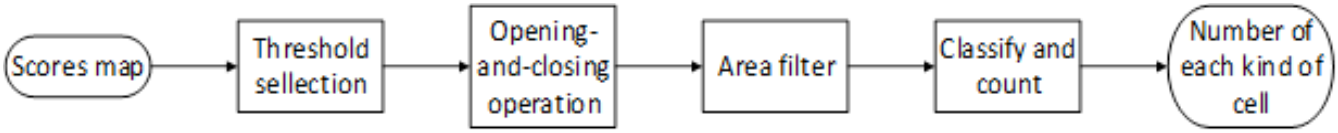


Fig. 5. Morphological process

First, we did threshold selection to images. According to the different pixel value we used when marking images, we could determine the threshold. The threshold here was 2.5. Then we determined the range. According to the pixels we used to mark images and the threshold we obtained in former step, we could get the range. In our research, it was 5±2.5(2.5~7.5) for *epithelial cell*, 10±2.5(7.5~12.5) for *clue cell*, 15±2.5(12.5~17.5) for *white blood cell*, 20±2.5(17.5~22.5) for *Candida albicans*, 25±2.5(22.5~27.5) for lactobacilli. Especially, the pixels greater than 27.5 or less than 2.5 were regarded as background. According to former step, we could convert the image into a special image with only 6 kinds of pixel values. *Epithelial cell* was 5, *clue cell* was 10, *white blood cell* was 15, *Candida albicans* was 20, *lactobacilli* was 25, background was 0.

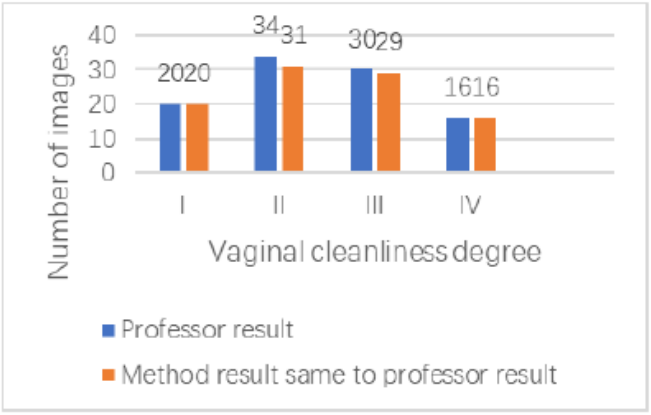
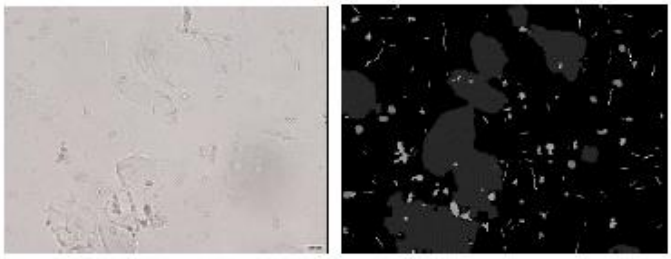


Fig. 6. Testing result

After the threshold operations, we added some opening-and-closing operation. First we did an opening operation to the image, following a closing operation, so we could divide each cell and smooth the edge. After that the image had to go through an area filter. This filter would delete the areas smaller than the area threshold (*epithelial cell* and *clue cell* as 1000, *white blood cell* as 200, *Candida albicans* as 25 and *lactobacilli* as 10). These area thresholds were determined by common areas of these cells. Then we calculated the number of each type of cells.



(a)Testing image (b) Result image

Fig. 7. Testing result images

3) Vaginal cleanliness degree calculation

After we got the number of each kind of cells, we could calculate this image's vaginal cleanliness degree according to the vaginal cleanliness degree lookup table.

III. Results

We evaluated our method by the agreement rate between the result of our method and the judgement made by professors. Agreement rate is another kind of accuracy [17], it is usually used in qualitative tests to compare two doctors' diagnostic results.

$$R = \frac{A}{B} \times 100\% \quad (1)$$

Equation (1) is the formula to calculate agreement rate. R is the agreement rate, A is the number of the images judged as the

same vaginal cleanliness degree by both our method and the professors, B is the total number of images used in our test.

TABLE II. MULTI TARGET RECOGNITION RESULT TABLE

Type of cell	Sum	Correct	Wrong	Lost	Accuracy	Sensitivity
epithelial cell	725	702	16	20	0.9683	0.9723
white blood	1299	1219	77	75	0.9384	0.942
candida albicans	2028	1963	35	70	0.9679	0.9656
lactobacilli	1360	1277	3	85	0.939	0.9376

TABLE III. RECOGNITION SPEED TABLE

Recognition method	Artificial	Our method (GPU)	Our method (CPU)
Average time	16.666667s	0.161651s	2.494755s

We picked the testing set and invited 3 professors to judge their vaginal cleanliness degree. Only when two or more professors got the same result, the result was regarded as true. Then we tested these images with our method. The result is presented in Fig. 6. According to the professors' result, there were 20 images of degree Ⅰ, 34 images of degree Ⅱ, 30 images of degree Ⅲ and 16 images of degree Ⅳ. Which meant the agreement rate of our method and professors' result reached 96%.

The image processed by deep learning model and morphological process is presented in Fig. 7. As we can see, (a) is the original image for testing, (b) is the testing result image. The result is good, *epithelial cell*, *white blood cell*, *Candida albicans* and *lactobacilli* are distinguished obviously from each other.

IV. DISCUSSION

In this research, we proposed a new method for auto detection of vaginal cleanliness degree. It could export vaginal cleanliness degree corresponding to the input microscopic examination image of leucorrhea secretion. In our test, it reached a 96% agreement rate with professional results. Meanwhile, this method had multiple advantages. The recognizing ability wasn't affected by the stacking of different kind of cells, or by hybrid bacterium or impurity. The recognition speed was 100 times faster than artificial identification.

This method could recognize different type of cells in an image at the same time, the recognition rate was high for every type. As shown in Table II, we can see that the recognition rate of these 4 kinds of cells reached over 93%.

As presented in Table III, it took a professor 16.66667 seconds to judge the vaginal cleanliness degree of a microscopic examination image of leucorrhea secretion. But it only took 0.161651s while using our method with GPU, and 2.494755s with CPU.

V. CONCLUSION

The method we presented can fulfill the recognition regardless of stacking of different cells, affection of hybrid bacterium and impurity. It reaches a 96% agreement rate with professional result. It has practical value in clinic, and will decrease doctors' repetitive work and increase the accuracy and speed of vaginal cleanliness degree diagnosing.

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