

AN APPROACH FOR OVERLAPPING CELL SEGMENTATION IN MULTI-LAYER CERVICAL CELL VOLUMES

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ABSTRACT

We propose a new method for detecting and segmenting overlapping cells in Pap smear images of multi-layer cervical cell volumes. This is a critical step in automating the analysis of cervical cells. This method first finds the nuclei inside the image using an iterative thresholding approach, then segment the location of overlapping cells, called cell clumps. The provided images from different focal are then used to segment the cytoplasm corresponding to each nucleus. The algorithm is evaluated using the dataset provided in the second overlapping cervical cytology image segmentation challenge at ISBI 2015. The results are presented based on two-fold cross validation on the training data which is provided with ground truth.

1. METHODS

The segmentation of overlapping cervical cells in each image is done in three steps: nuclei detection, cell clump segmentation and segmentation of individual cell's cytoplasm inside each cell clump.

For each multi-layer cell volume, an image obtained by a one-pass extended depth of field (EDF) algorithm [1] is also provided. The first two steps are performed on the provided EDF images and the last step is done using images of different depths. These steps are discussed in the following.

1.1. Nuclei Detection

Nuclei detection is done by processing the corresponding EDF image for each cervical cell volume (Fig. 1(a)). To do that a two-dimensional low-pass noise-removal filtering [2] is performed on the image. Then an iterative thresholding is performed to find the darkest pixels (usually corresponded to nuclei). Each found region can grow for a certain number of times in thresholding steps. The new regions which appear in each thresholding step, are bounded by other previously grown regions. The final regions represent the nuclei (Fig. 1(b)).

1.2. Cell Clump Segmentation

The cell clumps including overlapping cells (or isolated cells) are found as follows. A Gaussian mixture model with two components is learned based on pixel intensities. The two components will represent the foreground and background. Subsequently, the value of the background component's quantile function at 0.1 is used it as a threshold to binarize the image. Several morphological operations then follow to separate nearby cell clumps and remove too small cell clumps (Fig. 1(c)).

1.3. Cell's Cytoplasm Segmentation

Each EDF image is accompanied by 20 images of different focals. These images are used to segment the cytoplasm corresponding to each detected nucleus. If a cell clump has no segmented nucleus, it is rejected. If it has only one nucleus, then it is assigned as the cytoplasm of the nucleus. In case of existence of more than one nucleus inside a cell clump, we perform the following operation.

Each depth image is divided into square regions by a grid (each square is 8x8 pixel in this study). For each grid square, the standard deviation and average edge strength based on the Sobel operator are computed and used as a measure of sharpness. By a grid width of 8, each image is divided to 128×128 grid squares. For each EDF image, denote the depth images by I_1 through I_{20} . Also let $G_k^{i,j}$ and $S_k^{i,j}$ denote the average edge gradient and standard deviation of pixels intensities inside the (i, j) -th grid square of the k -th depth image respectively. We then put $T_k^{i,j} = S_k^{i,j} G_k^{i,j}$. For each grid square (i, j) , $T_k^{i,j}$ values are normalized to the interval $[0, 1]$. New values are denoted by $\bar{T}_k^{i,j}$. Moreover, suppose there are N nuclei inside a specific cell clump and suppose n -th nucleus overlaps with grid squares $(i_{n,1}, j_{n,1}), (i_{n,2}, j_{n,2}), \dots, (i_{n,s_n}, j_{n,s_n})$. For each two grid squares (i, j) and (i', j') we define

$$D_{i,j}^{i',j'} = \sqrt{\sum_{k=1}^{20} (\bar{T}_k^{i,j} - \bar{T}_k^{i',j'})^2}. \quad (1)$$

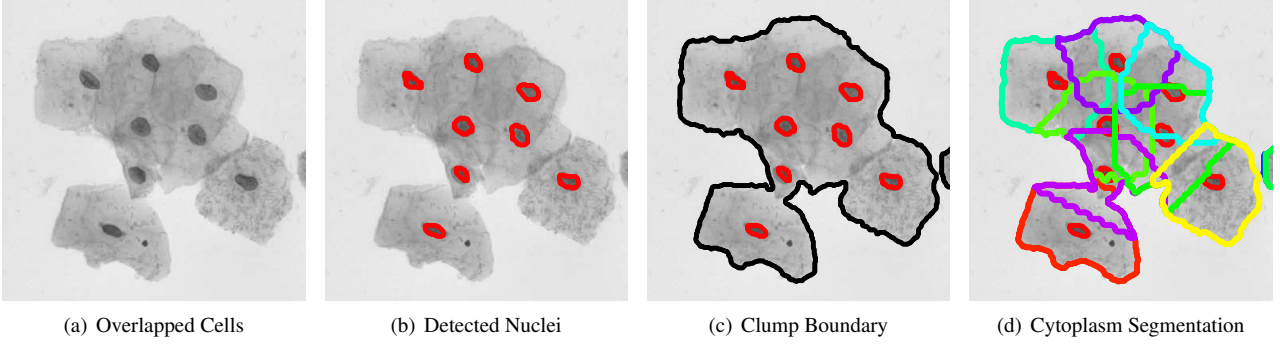


Fig. 1. A sample of overlapped cells segmentation inside a cell clump.

α, β	Dataset	DC	FNo	TPp	FPp
12, 2.8	Train on first four images	0.853 ± 0.079	0.326 ± 0.196	0.934 ± 0.076	0.002 ± 0.002
	Test on second four images	0.844 ± 0.071	0.183 ± 0.064	0.945 ± 0.076	0.003 ± 0.002
14, 1.8	Train on second four images	0.850 ± 0.069	0.197 ± 0.021	0.879 ± 0.117	0.002 ± 0.001
	Test on first four images	0.847 ± 0.078	0.236 ± 0.092	0.859 ± 0.117	0.001 ± 0.001

Table 1. Results over “good” cell segmentations

Finally, for each nucleus inside the cell clump, e.g. n -th nucleus, and each grid square (i, j) , we compute

$$F_n^{i,j} = \sum_{s=1}^{s_n} \exp \left(-\frac{D_{i_s, j_s}^{i,j}^2 + (i_s - i)^2 + (j_s - j)^2}{2\alpha^2} \right), \quad (2)$$

which measures how much the grid squares (i_s, j_s) and (i, j) are in focus in different depth images relatively and how close they are to each other.

For each cell clump, the corresponding $F_n^{i,j}$ is computed for all grid squares which are overlapped with it. After that, for each nucleus, n , inside the cell clump, we calculate

$$B_n^{i,j} = (N + \beta)F_n^{i,j} - \sum_{t=1}^N F_t^{i,j}. \quad (3)$$

Finally we classify grid square (i, j) as a part of the cytoplasm of cell with nucleus n if $B_n^{i,j} > 0$. Morphological operations are then performed to smooth the boundary and bound the cytoplasm inside the cell clump (Fig. 1(d)).

2. RESULTS AND CONCLUSION

Each image provided in the “The Second Overlapping Cervical Cytology Image Segmentation Challenge” (ISBI 2015) are 1024x1024 pixels. Eight multi-layer cervical cell volumes are provided for training, which include the ground truth, and eight others are used for testing the algorithms.

Because the test data has no provided ground truth, we divide the training data to two parts and perform a two-fold cross validation. We learn the two parameters α and β based

on each fold and test it on the other fold. The result is presented in terms of Dice Coefficient, False Negative (cell level), True Positive (pixel level) and False Positive (pixel level). Due to time constraint, the values of parameters are selected based on highest DC achieved amongst only six different values of α and four different values of β . The results are summarized in Table 1. The final values of α and β used to generate the segmentations of provided test images are 14 and 2.8.

The method can be improved further to include the edge information for cytoplasm segmentation. Moreover, the False Negative rate can be decreased potentially by using ground truth provided for nuclei in each image and improving the nuclei detection part of the method.

3. REFERENCES

- [1] Andrew P. Bradley and Pascal C. Bamford, “A one-pass extended depth of field algorithm based on the over-complete discrete wavelet transform,” *Image and Vision Computing (IVCNZ’04)*, November 2004.
- [2] Jae S. Lim, *Two-dimensional Signal and Image Processing*, Prentice-Hall, Inc., Upper Saddle River, NJ, USA, 1990.