CELL RECONSTRUCTION UNDER VORONOI AND ENCLOSING ELLIPSES FROM 3D MICROSCOPY

Geraldo L. B. Ramalho[1], Daniel S. Ferreira[1], Andrea G. C. Bianchi[2], Claudia M. Carneiro[2], Fátima N. S. Medeiros[3], Daniela M. Ushizima[4,5]
gramalho@ifce.edu.br, daniels@ifce.edu.br, andrea@iceb.ufop.br, carneiro@ef.ufop.br, fsombra@ufc.br, dushizima@lbl.gov,
[1]Federal Institute of Education, Science and Technology of Ceará, Maracanaú, Brazil
[2]Federal University of Ouro Preto, Ouro Preto, MG, Brazil
[3]Federal University of Ceará, Fortaleza, CE, Brazil
[4]Berkeley Institute of Data Sciences, University of California, Berkeley, CA, USA
[5]Lawrence Berkeley National Laboratory, Berkeley, CA, USA

ABSTRACT

Cell occlusion, staining variation, particulate forms and diversity of cervical cells are some of the challenges in automating cervical cytology. This paper tackles some of these issues, including the detection of nucleus and cytoplasm from a new standardization for specimen preparation through mono/thin-layer technology. Our approach consists of three main steps: (a) rough segmentation of subcellular compartments using super pixel combined to Voronoi diagrams, (b) structural refinement of the cytoplasm boundary through calculus of variations, and (c) morphological reconstruction combined to optimization methods to determine minimum enclosing ellipse. We test our implementation on real 3D cervical cell images, containing several cells at different occlusion levels and variable contrast. Our results show both qualitative and quantitative assessment of the datasets, using a completely automated computer program. The quantitative performance presents average Dice Coefficient higher than 87%.

Index Terms— Cervix cytology, Voronoi, Segmentation, Occlusion

1. INTRODUCTION

Cervical cancer is the fourth most common cancer among women, with about 527,000 new cases each year in the world, and nearly 80% of cases take place in low-income countries. This cancer was responsible for the deaths of 265,000 women in 2012, and 87% of these deaths occurred in developing countries [1, 2]. In Brazil, it is expected that 15.590 new cases of cervical cancer will occur every year, with an associated risk of about 15.33 cases per 100,000 women [3]. With the exception of skin cancer, this tumor has the greatest potential for prevention and cure when diagnosed early because it has a pre-cancerous condition that can be recognized and treated early. However, its incidence will continue to increase, especially in developing countries if preventive measures are not broadly applied. The examination of conventional Pap (Papanicolaou) smears is the main strategy of screening programs worldwide. However, the Pap test is based on human visual analysis, a procedure that is not accurate enough to ensure prevention. Therefore, the development of computational tools to ensure greater consistency in these analyzes and reduction mainly of false negative results is very important to ensure the quality of the Pap smear.

In order to address the digital images from Pap smears, this paper focuses on boundary extraction of individual cytoplasm and nuclei from overlapping cervical cytology images acquired at different focal planes (FOV). Our method differs from other approaches in the literature [4, 5] because it processes not only the extended-depth-of-field (EDF) image representation but also the FOV images to search for borders of overlapped cytoplasms. We combine intertwined algorithms to deliver an efficient pipeline for automated nucleus and cytoplasm segmentation: superpixel combined to Voronoi Diagrams or SPVD [5], followed by algorithms using calculus of variations to construct edge maps, processed using mathematical morphology methods, such as reconstruction allied to ellipse detectors and finally deliver a refined cytoplasm boundary.

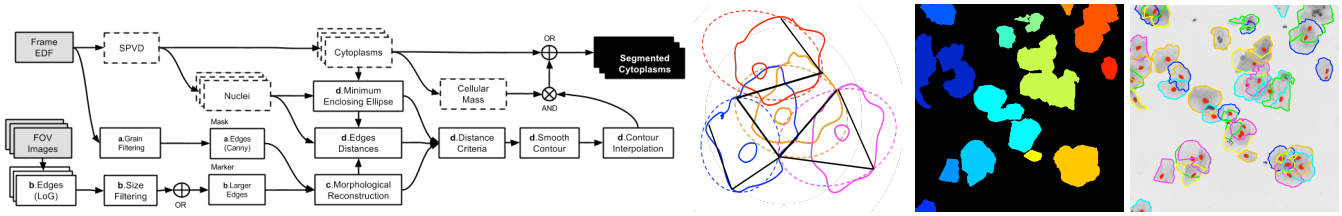

Fig. 1. (a) Cervical cell detection workflow for 3D cells. (b) Refinement of cytoplasm boundary through the combination of circumscribed ellipses to Voronoi combs. (c) Preliminary estimation of cell mass using SPVD; and (d) final result of SPVD+.

2. MATERIAL & METHODS

The datasets provided by the "Second Overlapping Cervical Cytology Image Segmentation Challenge" consists of 17 samples, which are collections of multi-layer cervical cell volumes. Each sample is composed of 20 images or layers, acquired at different focal planes (FOV), with each layer defined by a 1024x1024 8-bit PNG file - extended-depth-of-field (EDF) image representation were also provided. Each sample contains about 40 cells with different degrees of overlap, contrast, and texture. Among these images, only 8 samples are part of the training set, therefore they present ground truth for both nucleus and cytoplasm, which is fundamental for the development of quantitative analyses of segmentation procedures.

The proposed original algorithm, SPVD+, leverages an improved version of our previous implementation, SPVD [5], as the initial estimate of the cell compartment locations, which is input to a new algorithm that better outlines the cytoplasm regions. In order to detect and segment cervical cell regions of interest (ROI) into nuclei and cytoplasm, the SPVD+ algorithm relies upon a hybrid solution with three main steps to process EDF and FOV images: (*i*) preliminary estimation of two ROIs using SPVD segmentation under EDF images [4]; (*ii*) ROI around nuclei as constraint to Canny edge detection under EDF images, and (*iii*) ellipse area under Voronoi diagram of FOV images as constraint to Laplacian of Gaussian (LoG) border detection. Therefore the cytoplasm border detection results are an association of distance criteria from nuclei and a minimum-enclosing ellipse of Voronoi. Our hypothesis captures cell biological behavior since it reproduces the influence of cell nuclei for neighboring cytoplasm.

The border map extraction plays a major role in cytoplasm refinement since it contains most of the segments used to determine the cytoplasm boundary. Such an extraction includes two border maps: (a) LoG method applied to each sample layer (FOV) to retrieve a set of borders. SPVD+ combines these partial maps to represent the final border map, similarly to what the humans perform during visual analyses; (b) concurrently, the Canny algorithm extracts nearly noise-free contours from EDF images. These two border maps are combined as input to the morphological reconstruction, which uses the LoG of FOV as markers. This reconstruction improves the cytoplasm border connectivity, eliminating artifacts and inherent texture belonging to the intra-cytoplasmic regions.

3. RESULTS/CONCLUSION

We call SPVD+ the fusion of these new methods for cervical cell individualization and nucleus/cytoplasm separation. Table I summarizes our results according the metrics proposed by the challenge.

Table I: Results for training set.

Database	DC	FNo	TPp	FPp
Training_R1_ 01Dec2014	0. 862 ±0. 091	0. 400 ±0. 148	0.900 ±0.113	0.002 ±0.002
Training_R2_ Jan2015	0.888 ±0.073	0.528 ±0.222	0.924 ±0.104	0.001 ±0.001
Both Sets	0.875 ±0.083	0.472 ±0.182	0.912 ±0.109	0.002 ±0.001

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