GLOBAL JOURNAL OF ENGINEERING SCIENCE AND RESEARCHES

A SURVEY ON METHODS FOR NUCLEI DETECTION, ADAPTIVE SEGMENTATION, AND CLASSIFICATION IN DIGITAL HISTOPATHOLOGY

Bharathi Philomina.D[*1] and P.N.Sundar Rajan M.E.,(Ph.D)[2]

PG Scholar, Department of Electronics and Communication Engineering, PSNA college of Engineering and Technology,Dindigul -624622, India[*1]

Associate Professor, Department of Electronics and Communication Engineering, PSNA college of Engineering and Technology, Dindigul -624622, India[2]

Abstract

Digital pathology represents one of the major evolution's in modern medicine. Pathological examinations constitute the gold standard in many medical protocols, and also play a critical and legal role in the diagnosis process. In the conventional cancer diagnosis, pathologists analyze biopsies to make diagnostic and prognostic assessments, mainly based on the cell morphology and architecture distribution. Recently, computerized methods have been rapidly evolving in the area of digital pathology, with growing applications related to nuclei detection, segmentation, and classification. Each hidden node represents a cluster used as a template to provide faster and more accurate nuclei detection and segmentation. In this paper, we present a fully automated method for annotating fluorescent confocal microscopy images in highly complex conditions. The second layer is comprised of two probabilistic classifiers, responsible for determining how many components may constitute each segmented region. Our results indicate that the proposed method is able to perform the identification and annotation process on par with an expert human subject, thus presenting itself.

Keywords: Pathology, Morphology, Segmentation, Detection, Microscopy image

I. INTRODUCTION

Pathology is the microscopic study of the cell morphology supplemented with in situ molecular information. The tissue sample is removed from the body and then prepared for viewing under the microscope by placing it in a fixative, which stabilizes the tissue to prevent decay. For the sake of visualizing under the microscope, different components of the tissue are dyed with different stains. Then, different staining techniques are applied to reveal specific tissue components under the microscope. Researchers in pathology have been familiar with the importance of quantitative analysis of pathological images. Quantitative analysis can be used to support pathologists decision about the presence or the absence of a disease, and also to help in disease progression evaluation. In addition, quantitative characterization is important, not only for clinical usage (e.g., to increase the diagnostic reliability), but also for research applications (e.g., drug discovery and biological mechanisms of disease). As a consequence, the use of computer-aided diagnosis (CAD) in pathology can substantially enhance the efficiency and accuracy of pathologists decisions, and overall benefit the patient. A review on automated cancer diagnosis based on histopathological images This paper is intended as a comprehensive state of the art survey on the particular issues of nuclei detection, segmentation and classification methods restricted to two widely available types of image modalities: hematoxylin-eosin (H&E) and immuno histo chemical (IHC).

II. RELATED WORKS

Nicolas Lerme, Florence Rossant, Isabelle Blochy, Michel Paquesz and Edouard Kochz, [1] presented a method for automatically segmenting the walls of retinal arteries in adaptive optics images. This is the first method addressing this problem in such images. To achieve this goal, they propose to model these walls as four curves approximately parallel to a common reference line located near the center of vessels. Then, their positioning is refined using a deformable model embedding a parallelism constraint. Such an approach enables us to control the distance of the curves to their reference line and improve the robustness to image noise. This model was evaluated on healthy subjects by comparing the results against segmentations from physicians.

Hema N. Agrawal, Smriti H. Bhandari, [2] Automated image analysis of histopathology specimens could potentially provide support for early detection and improved characterization of breast cancer.In this analysis Automated segmentation of the cells in histopathological image is a prerequisite for any subsequent quantitative analysis. This paper also presents summary of many of sequential methods and describes some parallel algorithms for cell segmentation. The aim of this paper is to review some prominent methods for cell segmentation developed in last few years. The need for developing parallel algorithm is because of time complexity of sequential algorithms.

Dzung L. Pham, Chenyang Xu, Jerry L. Prince, [3] presented a critical appraisal of the current status of semi-automated and automated methods for the segmentation of anatomical medical images. The use of image segmentation in different imaging modalities is also described along with the difficulties encountered in each modality. For increasing computational efficiency, multiscale processing and parallelizable methods such as neural network is used. Computerized segmentation methods are used for computer aided diagnosis and radiotherapy planning.

Chanho Jung, Changick Kim, Seoung Wan Chae, and Sukjoong Oh, [4] presented an unsupervised Bayesian classification scheme for separating overlapped nuclei. Their proposed approach first involves applying the distance transform to overlapped nuclei. In order to learn the distribution of the topographic surface, the parametric expectation-maximization (EM) algorithm is employed. They used Cluster validation is performed to determine how many nuclei are overlapped. A priori knowledge for the overlapped nuclei was incorporated to obtain separation line without jaggedness, as well as to reconstruct occluded contours in overlapped region

Yousef Al-Kofahi, Wiem Lassoued, William Lee and Badrinath Roysam, [5] used Automatic segmentation of cell nuclei for image cytometry and histometry. The image foreground is extracted automatically using a graph-cuts-based binarization. By using a novel method combining multiscale Laplacian-of-Gaussian filter the nuclear seed points are

detected. These points are used to perform an initial segmentation that is refined using a second graph-cuts-based algorithm. The expected range of sizes of the nuclei can be defined by provide to the software include the minimum scale for the LoG filter σ_{min}, the maximum scale value σ_{max}.

J. Macqueen [6] described a process for partitioning an N-dimensional population into k sets on the basis of a sample. The process, which is called 'k-means,' appears to give partitions which are reasonably efficient in the sense of within-class variance. They used k-means procedure because it is easily programmed and is computationally economical. They noted the possible applications such as similarity grouping, nonlinear prediction, approximating multivariate distributions, and nonparametric tests for independence among several variables. The k-means concept represents a generalization of the ordinary sample mean. They described a procedure called "adaptive sample set construction," which involves the use of what amounts to the k-means process.

Stephan Wienert, Daniel Heim, Kai Saeger, Albrecht Stenzinger, Michael Beil, Peter Hufnagl, Manfred Dietel, Carsten Denkert & Frederick Klauschen [7] approach a system to avoid a segmentation bias with respect to shape features and allows for an accurate segmentation of a broad spectrum of normal and disease-related morphological features without the requirement of prior training.

Humayun Irshad, Antoine Veillard, Ludovic Roux, and Daniel Racoceanu, [8] presents, discusses, and extracts the major trends from an exhaustive overview of various nuclei detection, segmentation, feature computation, and classification techniques used in histopathology imagery, specifically in hematoxylin–eosin and immunohistochemical staining protocols. And also states to measure the challenges to reach robust analysis of whole slide images, essential high content imaging with diagnostic biomarkers and prognosis support in digital pathology.

III. RESULTS AND DISCUSSION

So far, in this survey various algorithms were used to analyze the cancer diagnosis in which better approach are parametric expectation-maximization (EM) algorithm it plays an important role of distribution of the topographic surface for diagnosis and some approach enables us to control the distance of the curves to their reference line and improve the robustness to image noise and this scheme was evaluated on healthy subjects by comparing the results against segmentation's from physicians.

IV. CONCLUSION

In this survey, it has been concluded that there several methods exposed for diagnosis of Cancer. Since, I concluded that an algorithm for accurately segmenting the individual cytoplasm and nuclei from a clump of overlapping cervical cells for that some approaches will be used such as Nuclei Detection, Adaptive Segmentation, Classification is proposed in my future work.

V.   REFERENCES

[1]. Nicolas Lerme, Florence Rossant, Isabelle Blochy, Michel Paquesz and Edouard Kochz, "Segmentation of Retinal Arteries in Adaptive Optics Images", version 5 – 23, Apr 2014.

[2]. Hema N. Agrawal, Smriti H. Bhandari, "Review on Methods for Cell Segmentation of Histopathological Images of Breast Carcinoma", IEEE Sponsored International Conference On Empowering Emerging Trends In Computer, ISSN: 2278-7593, Volume-2.

[3]. Dzung L. Pham, Chenyang Xu, Jerry L. Prince, "A Survey of Current Methods in Medical Image Segmentation", MD 21224.

[4]. Chanho Jung, Changick Kim, Senior Member, IEEE, Seoung Wan Chae, and Sukjoong Oh, "Unsupervised Segmentation of Overlapped Nuclei Using Bayesian Classification", IEEE TRANSACTIONS ON BIOMEDICAL ENGINEERING, VOL. 57, NO. 12, DECEMBER 2010.

[5]. Yousef Al-Kofahi, Wiem Lassoued, William Lee, and Badrinath Roysam, Senior Member, IEEE, "Improved Automatic Detection and Segmentation of Cell Nuclei in Histopathology Images", IEEE TRANSACTIONS ON BIOMEDICAL ENGINEERING, VOL. 57, NO. 4, APRIL 2010.

[6]. J. Macqueen, "SOME METHODS FOR CLASSIFICATION AND ANALYSIS OF MULTIVARIATE OBSERVATIONS", FIFTH BERKELEY SYMPOSIUM: MAC QUEEN, pg 281-297.

[7]. Stephan Wienert, Daniel Heim, Kai Saeger, Albrecht Stenzinger, Michael Beil, Peter Hufnagl, Manfred Dietel, Carsten Denkert & Frederick Klauschen, "Detection and Segmentation of Cell Nuclei in Virtual Microscopy Images: A Minimum-Model Approach", Bioinformatics Software Medical Research Imaging, 11 July 2012.

[8]. Humayun Irshad, Student Member, IEEE, Antoine Veillard, Ludovic Roux, and Daniel Racoceanu, Member, IEEE, " Methods for Nuclei Detection, Segmentation, and Classification in Digital Histopathology: A ReviewCurrent Status and Future Potential", IEEE REVIEWS IN BIOMEDICAL ENGINEERING, VOL. 7, 2014.