Chapter 1
A High-Speed Architecture for Lung Cancer Diagnosis

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ABSTRACT

Here the authors propose a simplified technique and its architecture for blind segmentation of histopathological images of lung cancer, combining the K-Means and Histogram analysis. An improved version of Otsu's algorithm is introduced for performing histogram analysis to determine the number of clusters for executing the automatic segmentation of histopathological images. The architecture is input with Biopsy images of cancer patients suffering from different stages of Lung cancer, procured from standard hospital databases to evaluate the performance. The results obtained are compared with the existing works from the literature showing considerable improvement in the overall efficiency of the image segmentation process. Segmentation output in terms of quantitative parameters like PSNR, SSIM, time of execution, etc., as well as qualitative analysis, clearly reveals the usefulness of this technique in high-speed cytological evaluation. The proposed architecture gives promising results in terms of its performance with a time of execution of 192.25ms.

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INTRODUCTION

In the recent years, due to the tremendous growth in computation power combined with the exponential increase in the number of 'Image/video analysis algorithms', powerful computer assisted analytic approaches have been introduced (Fatakdawala et al., 2010; Kim et al., 2006; Sont et al., 2003). The quality of diagnosis and prognosis results have been exponentially rising as the quantity of data available from the smart sensors, endoscopic gadgets and diagnostic tools developed, are rapidly increasing day by day. This has led to the evolution of very successful and powerful Computer Aided Diagnosis (CAD) tools in the field of Biomedical image processing (Ancin et al., 1996; Bilgin et al., 2007; Ortiz de Solorzano et al., 1999). One of the most challenging problems in Biomedical image processing is to segment, classify and recognize the objects as per their characteristics without having any prior medical knowledge about the characteristics (Bartels et al., 1989; Belien et al., 1997; Cillekens et al., 2000; Markiewicz et al., 2006). Diagnosis through Biopsy images are often considered as a gold standard in many cytological evaluations. Modern histopathological diagnosis techniques are quite slow to detect cells, tumors, malignant tissues and other disease specific factors from Biopsy images. The main motivation for detecting, segmenting and recognizing pathological image structures is to automatically count, measure and analyze the objects- generally nuclei or lymphocyte cells etc. which itself have good diagnostic significance for certain conditions of cancer and many other diseases like tuberculosis, and some serious pulmonary infections like Nipah, COVID-19 (SARS Cov-2) etc. Segmentation of specific blood cells, capillaries, cell structures etc. using manual inspection is tremendously difficult and demands huge computation power, time and patience along with medical expertise. Here we propose a simplified technique and architecture for blind segmentation of histopathological images of lung cancer, combining the K-Means algorithm and Histogram analysis. Even after six decades of its existence K-Means algorithm is still used in multi-disciplinary arenas and applications like recognition (Agarwal et al., 2015; Hedberg et al., 2007; Rupanagudi et al., 2015), object identification and tracking etc. because of its simplicity and versatility. Their special ability to parallelize conventional optimization techniques has made them exceptional in the field of optimization techniques (Cai & Wang, 2019; Ratnakumar & Nanda, 2021a; Ratnakumar & Nanda, 2021b; Wang et al., 2009; Yadav et al., 2021). Many of its performance on the benchmark databases have reflected the same truth. The main cons of this algorithm are (i) needs number of clusters as input, (ii) captures spherical clusters easily but performs poorly with other distributions, (iii) hardware implementation requires a divider. One of the central problems conventional clustering is to presume the exact number of clusters within the biomedical image. We use an improved version of Otsu's thresholding method to automatically find the