Abstract

Pap smear test plays an important role for the early diagnosis of cervical cancer in which human cells taken from the cervix of patient are analysed for pre-cancerous changes. The manual analysis of these cells by expert cytologist is labor intensive and time consuming job. The automatic and accurate detection of cervical cells are two critical preprocessing steps for automatic Pap smear image analysis and also for diagnosis of pre-cancerous changes in the uterine cervix. Similarly, the reliable segmentation of abnormal nuclei in cervical cytology is of utmost importance in automation-assisted screening techniques. This paper presents, the existing automated methods for the detection, segmentation and boundary determination of cells nuclei in conventional Pap stained cervical smear images. The majority of cytoplasm segmentation uses K-means algorithm, edge detection method, thresholding approach, graph cut and active contours technique. Most of existing work is done on images of isolated cells, especially for those which are in the Herlev data set. For segmentation of images which contains multiple cells, level set and thresholding techniques have been used. The nucleus segmentation varies as: single-nucleus segmentation, touching-nuclei splitting and
multiple-nuclei segmentation. However, many segmentation methods incorporates shape priors, usually enforcing elliptical shapes in order to overcome cell occlusion and noise. The main focus of this paper is comprehensive literature survey of various existing classification and segmentation techniques. The shortcomings and failures of the existing work are also provided for further enhancement and improvement of overall performance and accuracy.

References


Index Terms

Computer Science

Image Processing
Keywords

Cervical cell classification, Cervical cancer, Unsupervised segmentation, Radiating GVF Snake, Global and local scheme, Multiscale convolutional network