Abstract

The current research work aims to propose an improved clump splitting approach to classify breast cancer lesion based on extracting shape features. Identifying the number of benign and malignant nuclei in a given area of histopathological tissue is very important for the automated grading system. This process becomes difficult due to irregular size and shape of the nuclei leading to clump formation. Therefore, a major challenge lies in accurately separating these nuclei for further processing. Towards this end, there has been a well-focused research on accurate identification and extraction of nuclei based on concavity analysis. From exhaustive experimentations, it is observed that concavity based approaches pose several limitations: like identifying the concave point pair and selecting the valid split lines. Further, it is also observed from the literature that either region or edge based segmentation is the most commonly used method for segmenting nuclei. Experimental analysis showed that under or over-segmentation is the common problem with region-based methods. Since poor, unclear edges, noise and other artefacts are inevitable in histopathological images, the edge based method does not perform well. Therefore in this research work, a combination of both edge and region-based nuclei
segmentation is proposed. The performance measure of the proposed method is evaluated on a dataset consisting of 1820 histopathological images. Further, in comparison with the existing methods, the proposed method showed the improved accuracy of 86%. Also, it is clearly seen from the ROC curve that the non-linear SVM outperforms other classifying methods.

References


32. E. Cosatto, M. Miller, H. P. Graf, and J. S. Meyer, “Grading nuclear pleomorphism on


Index Terms
Keywords

Histopathological Images, clumps, Shape features, nuclei extraction, Digital Pathology