

Automated Analysis of Histological Images by Computational Algorithms

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The study of cellular tissues provides an incontestable source of information and comprehension about the human body and the surrounding environment. Accessing this information is, therefore, crucial to determine and diagnose a wide variety of pathologies detectable only at a microscopic scale. Hence, histology plays an important role in the clinical diagnosis of pathologies involving abnormal cellular conformation. In histological images, semi- or automated segmentation algorithms are able to separate and identify cellular structures according to morphological differences. The segmentation is usually the first task in computational vision systems and, concerning histopathology, for the automated analysis of histological images. Since the histological samples are thin, the volumetric features are almost unnoticeable, corresponding to losses of valuable information, mainly topographical and volumetric data, critical for a correct analysis. Hence, the combination of segmentation and 3D reconstruction algorithms applied to histological image datasets provides more information about the analyzed pathology and microscopic structures, highlighting abnormal areas [1].

In order to provide insights on pathological volumetric data, the present work focused on developing an automatic computational solution for performing the 3D surface reconstruction of relevant tissue structures presented in 2D histological slices. A state of the art technique, called stain deconvolution, was implemented to achieve color image segmentation providing an accurate segmentation of two different stains present in the histological data: Hematoxylin and Eosin tissues. To register, i.e. align, the image slices presented in the input datasets, an intensity based registration method was implemented, being the alignment performed between each slice in the input dataset and the reference slice (middle slice of the dataset). The dataset chosen for the previous alignment operation was the set of images obtained through the stain deconvolution method for the hematoxylin stain. The transformation matrix obtained for each slice was then applied to the eosin stained images. The 3D reconstruction was implemented based on the Marching Cubes algorithm.

Thus, combining algorithms of image segmentation and registration with of 3D surface reconstruction, it was possible to obtain a volumetric representation of the pertinent tissue structures from the input image datasets. The experiments conducted revealed accurate and fast surface reconstructions of the different stained tissues under study, highlighting the interesting structures and their volumetric interactions with the surrounding healthy tissues.

Keywords: Image pre-processing, Image segmentation, Image registration, Biomedical imaging

References

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