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## Segmentation of biomedical images by a computational topology framework

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The segmentation of patterns of cells in biomedical images constitutes a significant step towards the automated analysis of histological images. However, the presence of large numbers of cells and large cell patterns in whole slide images demands methods that are computationally tractable in addition to being efficient. This work presents a method for the robust segmentation of cell nuclei and cell patterns in histological whole slide images based on persistent homology. An abstract simplicial homology approach for image segmentation is established. The approach deals with the persistence of disconnected sets in the image thus identifying salient regions that express patterns of persistence. By introducing an image representation based on homological features, the task of segmentation is less dependent on variations in color and texture. This results in a novel approach that conceptualizes regions of interest (cell nuclei and cell group arrangements) pertinent to their topological features in a successful manner. The time cost of the proposed method is lower-bounded by an almost linear behavior and upper-bounded by  $O(n^2)$  in a worst-case scenario. Time complexity matches a quasilinear behavior which is  $O(n^{1+\epsilon})$  for  $\epsilon < 1$ . Images acquired from histological sections of liver tissue are used as a case study to demonstrate the effectiveness of the approach in cell nuclei segmentation. The histological landscape consists of hepatocytes and non-parenchymal cells. The accuracy of the proposed methodology is verified against an automated workflow created by the output of a conventional filter bank (validated by experts) and the supervised training of a random forest classifier. The results are obtained on a per-object basis. The proposed workflow successfully detected both hepatocyte and non-parenchymal cell nuclei with an accuracy of 84.6%, and hepatocyte cell nuclei only with an accuracy of 86.2%. A public histological dataset with supplied ground-truth data is also used for evaluating the performance of the proposed approach (accuracy: 94.5%). Further validations are carried out with a publicly available dataset, and ground-truth data from the Gland Segmentation in Colon Histology Images Challenge (GlaS) contest are used to demonstrate the effectiveness of the approach for the segmentation of cell structures. The proposed method is useful for obtaining unsupervised robust initial segmentations that can be further integrated into image/data processing and management pipelines.