Cell Segmentation in Whole Slide Images in Digital Pathology

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The advent of whole slide images (i.e. digitally scanning pathology slides can help usher in a new era of quantitative analysis of tissue samples. Whereas traditional judgments are made subjectively by a pathologist, image processing and computer vision algorithms can help determine cell densities in neoplasmic tissues, quantify the amount of Her2 in breast cancer, and much more.

One of the largest challenges in digital pathology is accurate cell segmentation. In tissue samples, cells are closely packed, and sometimes overlap since the tissue being imaged is actually a 3D specimen, of which we are taking a 2D image.



We propose to develop an image processing algorithm for segmenting distinct cells in tissue samples. A number of algorithms have already been proposed for this, including Euclidean distance transform, watershed segmentation, a combination of morphology operators, Laplacian of Gaussian filters, MSER detectors, and Hough transforms.

We will experiment with up to three of these different algorithms, compare the results for a set of 10 images from the Iowa State Virtual Slidebox, which is a large database of histopathology slides. Then, we will analyze why they did or did not perform well.

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