AN ESTIMATION METHOD FOR CELL COUNTING IN 3-D USING BAYESIAN CLASSIFICATION

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ABSTRACT

Biomedical image analysis has always been difficult due to the non-homogeneity of biological samples. Overly specific algorithms can often only be applied to one special case and high computational requirements for more complex methods also mean that large image stacks cannot be processed efficiently. We have designed a statistical method to count the number of objects in a 3-D dataset. In our approach, objects were identified in each image with an adaptive Bayesian classifier based on their area and perimeter. The total number of objects was estimated by summing all objects found in the image stack, then dividing by the average number of times they appear. The algorithm was tested with computer rendered test images as well as real images of cytochrome P450 expression within encapsulated rat hepatocytes. Rendered images were used to gauge the accuracy of the method since parameters like object size, number of objects and sectioning interval can be precisely controlled. P450 expression was chosen as a test case because it possesses the typical non-homogenous characteristics of biological images. Quantification is usually inaccurate using traditional edge detection and watershed methods since P450 is not a nuclear stain and cell overlapping is extensive. The advantages of this estimation method are that it is fast and fairly accurate. It can be easily adapted to count cells of widely differing characteristics once the system has been trained.

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