Unsupervised segmentation of mitochondria using model-based spectral clustering

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Segmentation of mitochondria in microscopic images represents a significant challenge that is motivated by the wide morphological and structural variations that are characteristic for this category of membraneenclosed sub-cellular organelles. To address the drawbacks associated with manual mark-up procedures (which are common in current clinical evaluations), a recent direction of research investigate the application of statistical machine learning methods to mitochondria segmentation. Within this field of research the main issue was generated by the complexity of the training set that is able to describe the vast structural variation that is associated with mitochondria. To avoid this problem, in this paper we apply perceptual organization models such as Figure-Ground, Similarity, Proximity and Closure which target the identification of the closed membranes in EM images using multistage spectral clustering [1,2].



Fig 1. Mitochondria segmentation algorithm.

Our unsupervised mitochondria segmentation algorithm is outlined in Fig. 1. The first stage of the spectral clustering implements foreground segmentation with the similarity model S1 that aims to identify the dark contours that are given by the outer membrane of the mitochondrion. In the second stage, the foreground data is re-clustered with a different similarity model S2 to identify the inner membrane of the mitochondrion. The last stage involves a contour processing step that eliminates the pixels that are not consistent with the minimum distance between the inner and outer membranes of the mitochondrion.

The algorithm has been tested on a suite of EM images provided by the American Society of Cell Biology and a number of experimental results are presented in Fig. 2.



Fig. 2. Mitochondria segmentation results.

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