

Computer-Guided Recognition of Mitochondria in Densely Cluttered Subcellular Environments

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Mitochondria are membrane enclosed organelles, on average approximately 300nm in diameter, which reside inside every living cell. Mitochondria play a central role in cellular bioenergetics and in the regulation of apoptotic (programmed) cell death. They contain a family of pro-apoptotic BCL-2 proteins that interact with anti-apoptotic proteins to induce apoptosis. The measurement of the morphological changes that mitochondria undergo during experimentally induced apoptosis is crucial to the understanding of apoptosis mechanisms and for the subsequent development of therapies targeting age and cancer-related

diseases. From a computer vision perspective, the Transmission Electron Microscope (TEM) images represent extremely complex and dynamic environments and pose considerable challenges on the automated localization and segmentation of mitochondria. This is due, in part, to the variety of subcellular organisms and the deformable nature of their shapes and textures. Furthermore, mitochondrial morphology depends on the type of biological tissue and undergo changes during induced or naturally occurring biochemical processes. TEM images of mitochondria are able to capture the intrinsic structural elements that are caused by the inner membrane folding. This evidence suggests the feasibility of a feature-driven recognition approach. Therefore, our work is focused on the quantitative analysis of mitochondrial morphology and on the development of algorithms that perform the localization and segmentation of mitochondria in TEM images. We report initial success on the extraction of specific localization markers for categories of mitochondria with *normal*, *lamellar* and *tubular* morphology. Future work will focus on the development of shape segmentation algorithms.

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