TOWARDS UNSUPERVISED SEGMENTATION IN HIGH-RESOLUTION MEDICAL NANO-IMAGING

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INTRODUCTION

Recent advances in cellular and subcellular microscopy demonstrated its potential towards unraveling the mechanisms of various diseases at the molecular level. From a computer vision perspective nano-imaging is an inherently complex environment as can for example be seen from Fig.1(a,c). For the image analysis of intracellular organisms in high-resolution microscopy, new techniques which are capable of handling high-throughput data in a single pass and real time are of special interest. The additional emphasis is put therein on automated solutions which can provide the *objective* quantitative information in a reasonable time frame. The state-of-the-art is dominated by manual data annotation[1] and the early attempts to automate the segmentation are based on statistical machine-learning techniques[4].

MATERIALS AND METHODS

We are developing our segmentation approach within the framework of spectral clustering (SC) which is a unsupervised machine learning method and as such requires a minimal number of training sequences. In addition, SC excels in flexibility towards defining segmentation objectives and accuracy. We have designed two novel similarity models for the purpose of localization and outer contour extraction of mitochondria for the provided datasets. We also applied the modified two-way graph-theoretic ***Ncut*** algorithm[3] for membrane and contour segmentation.

RESULTS

Our work aims to provide the applied solution to the datasets provided by our clinical collaborators and therefore primarily has been focused on the localization and segmentation of mitochondria of lamellar and tubular morphology (DU-145 cells). For the localization we incorporated the SC-based grouping with low-level primitives which represent the characteristic lamellar texture of an organelle. For the membrane segmentation we have applied combined distance, intensity[2] and the intervening contour similarity models[3]. We verify that our segmentation works well on small-scale images containing a small number of mitochondria as can be seen in Fig.1(b). In order to scale the segmentation to the very large image sizes we will consider a parallel implementation on our NBIPI-funded HPC cluster.

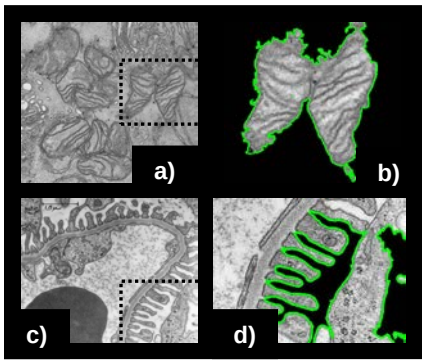

Figure 1 Example of SC-based segmentation (for marked regions) based on the intervening contour similarities model[3]. (a) 645 x 645 TEM image of clustered mitochondria in a human DU-145 cell treated with apoptosis inducer STS (image source: courtesy of RCSI) (b) Segmentation result. (c) 4800 x 4170 TEM image of a rat kidney cell showing various subcellular structures (image source: courtesy of ASCB). (d) Segmentation result.

DISCUSSION

While the preliminary medium-scale results look promising, algorithm validation will require manually annotated ground truth data sets in the order of >100 images. In addition, our future work will concentrate on the adaptation of the method to the very large scale problems and incorporation of membrane gap completion constraints[2].

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