Mytoe: Automatic analysis of mitochondrial dynamics

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ABSTRACT

Summary: We present Mytoe, a tool for analyzing mitochondrial morphology and dynamics from fluorescence microscope images. The tool provides automated quantitative analysis of mitochondrial motion by optical flow estimation and of morphology by segmentation of individual branches of the network-like structure of the organelles. Mytoe quantifies several features of individual branches, such as length, tortuosity, and speed, and of the macroscopic structure, such as mitochondrial area and degree of clustering. We validate the methods and apply them to the analysis of sequences of images of U2OS human cells with fluorescently labeled mitochondria.


Supplementary material: Supplementary file and User’s manual are available online.

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1 INTRODUCTION

Mitochondria play a key role in several cellular processes, from energy production to apoptosis and ageing. Malfunctioning in mitochondrial processes has been associated to several diseases (Westermark, 2010). Due to mitochondrial fusion and fission, the organelles form a highly dynamic structure that can change from fragmented to filamentous (Koopman et al., 2005). A better understanding of the dynamics of this structure and its relationship with complex cellular processes may provide much insight on mitochondrial functioning and their role on the well-being of cells.

Recent works addressed the problem of segmenting mitochondria from fluorescence microscope images. Koopman et al. (2005) presented a segmentation method along with descriptors for mitochondrial properties. Another method uses 3-dimensional imaging (Song et al., 2008). Mitochondrial motility has been assessed by the degree of coocalization between successive images and from the differences of subsequent image pairs (Koopman et al., 2005; Yi et al., 2004). These methods detect motion but do not yield data on directionality. Other methods to study motility include Optical Flow (OF) estimation (Gerencser et al., 2008) and distance transform (Beraud et al., 2009). Tracking methods for motility analysis exist, but rely heavily on human interaction (Saunter et al., 2009; Silberberg et al., 2008).

We present an easy-to-use software, Mytoe, for automated study of mitochondrial structural dynamics from temporal confocal images. It has a simple graphical user interface and requires only a few parameters from the user. Mytoe includes a novel segmentation method which identifies individual branches of the organelles' structure by thresholding and by morphological image processing. In contrast to previous methods, this allows quantifying properties of both single branches and the macroscopic structure formed by the mitochondria. OF is used for motion analysis. The output can be examined in Mytoe with branch-level data being visualized by color-coding individual branches based on the data, and motion vectors being visualized as quiver plots. The results are saved as MATLAB MAT-files and comma-separated values. We first describe the methods in Mytoe and results of the validation procedure. Finally, we use Mytoe to analyze time-lapse sequences of U2OS human osteosarcoma cells.

2 METHODS, APPLICABILITY, AND VALIDATION

Mytoe segments the nucleus and cell membrane from fluorescence microscope images. The outlines can be manually drawn if the automatic segmentation is unsatisfactory. The mitochondria are segmented in two steps. The first is similar to the method of Koopman et al. (2005) but uses morphological Top-Hat (TH) (Soille, 2003) instead of linear filtering. Each image of mitochondria is first denoised with a median filter, followed by TH, which enhances the separation of mitochondria from the background. The result is median filtered to remove noise enhanced by the TH. Finally, the denoised image is contrast stretched and binarized by Otsu’s method (Otsu, 1979) to produce a mask. The next step, developed here for our aims, extracts individual branches of the network by applying to the mask a two-iteration thinning procedure (Guo et al., 1989) and locating the branch points of the resulting skeleton.

Motion is analyzed by OF estimation, using a pyramidal implementation (Bouguet, 2000) of the method proposed in Lucas et al. (1981). OF yields the displacements of objects between each pair of subsequent frames in a movie, enabling the calculation of velocities. Results using this method are provided in the supplementary material. If desired, motion can also be analyzed by measuring the coocalization of mitochondria between successive images as proposed in Koopman et al. (2005).

Mytoe extracts various statistics. From individual branches it computes properties such as thickness, length and orientation. From the OF, the

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Table 1. Quantitative features from Mytoe. Cell-level features marked with (C).

<table>
<thead>
<tr>
<th>Feature</th>
<th>Description</th>
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<tbody>
<tr>
<td>Length</td>
<td>Distance to cell membrane</td>
</tr>
<tr>
<td>Thickness</td>
<td>Orientation relative to centroid</td>
</tr>
<tr>
<td>Tortuosity</td>
<td>Number of branches (C)</td>
</tr>
<tr>
<td>Intensity</td>
<td>Number of connected components (C)</td>
</tr>
<tr>
<td>Speed</td>
<td>Total mitochondrial area (C)</td>
</tr>
<tr>
<td>Orientation relative to x-axis</td>
<td>Degree of clustering (C)</td>
</tr>
<tr>
<td>Direction</td>
<td>Colocalization (C)</td>
</tr>
<tr>
<td>Wiggle Ratio (Gerencser et al., 2008)</td>
<td>Distance to nucleus membrane</td>
</tr>
<tr>
<td>Distance to centroid</td>
<td></td>
</tr>
<tr>
<td>Distance to cell membrane</td>
<td></td>
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<tr>
<td>Orientation relative to x-axis</td>
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Fig. 1. Original image (a) and cropped region (b). (c) The skeleton (grey), branch points (squares) and end points (circles) found from the mask. (d) Time series of mean mitochondrial speed in four cells.

3 DISCUSSION

Mytoe provides an easy means to study mitochondrial structure and kinetics by automated image analysis of temporal images of fluorescently labeled mitochondria. The structure analysis was found robust to noise and insensitive to saturation. Thus, the method can be used to obtain reliable measurements from saturated images, provided that the mitochondrial branches are separable.

So far, we tested Mytoe on one cell type. Its efficiency may depend on the shapes of cell type and mitochondria. Here we showed that it is accurate enough to, for example, distinguish the kinetics of the mitochondria structure from one cell to another.

In the future, this framework can be extended by including additional descriptors and adding other shape analysis techniques that can be chosen as a function of the cell type. Additionally, we aim to further develop Mytoe so as to automatically detect abnormalities in the mitochondria structure, due to chemicals (such as in drug screening) or disease.

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