AUTOMATED ANALYSIS OF CELL MIGRATION IN TIME-LAPSE MICROSCOPY IMAGES

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INTRODUCTION

The process required to track cellular structures is a key task to quantitatively describe the biological implications associated with cell migration. With the advent of modern microscope that has vastly increased the volume of image data the development of automated tracking solutions is becoming a prerequisite for cellular analysis [1]. In this research we developed a fully automated framework that is able to track cell migration in time-lapse images and obtains the required measurements for the motility analysis.

MATERIALS AND METHODS

The core part of the proposed tracking framework is active particles that do not require prior knowledge about the motion model of cell or assumptions in regard to the image noise. A set of prominent cells are automatically detected to be tracked using a multi-stage segmentation approach that evaluates the relative intensity difference between the foreground (cellular structures) and background information. Each of the detected cells is represented by a set of active particles, where tracking process is driven by evolving these particles in subsequent frames by evaluating the similarity between the target candidate and the target model in an adaptive manner. The experimental tests have been performed on a large number of deconvolved (Autoquant X, Media Cybernetics, Bethesda, MD, USA) time-lapse florescence microscopy image sequences that record the in-vivo development of transgenic quail embryos where the nuclei of the endothelial (vascular) cells are labelled with a GFP (green fluorescent protein) variant. The spatial resolution of images is 1.3 µm/pixel where the time interval between two frames is ranging between 4 to 8 minutes.

RESULTS

Fig. 1 illustrates the visual tracking results obtained when the proposed framework is applied on quail images. Fig. 1(a) and 1(b) show the DIC and florescent images of a quail embryo, respectively. Lineages of tracked cells in Frames 78 and 80 are shown in Fig. 1(c) and 1(d), respectively (parts of the images are shown for better visualization). Fig. 1(e) shows the color coded full length trajectories of the tracked cells. These trajectories indicate the formation of a well-defined crescent-shaped field from which future endocardial cells are recruited. This can be verified by the corresponding DIC image shown in Fig. 1(f).

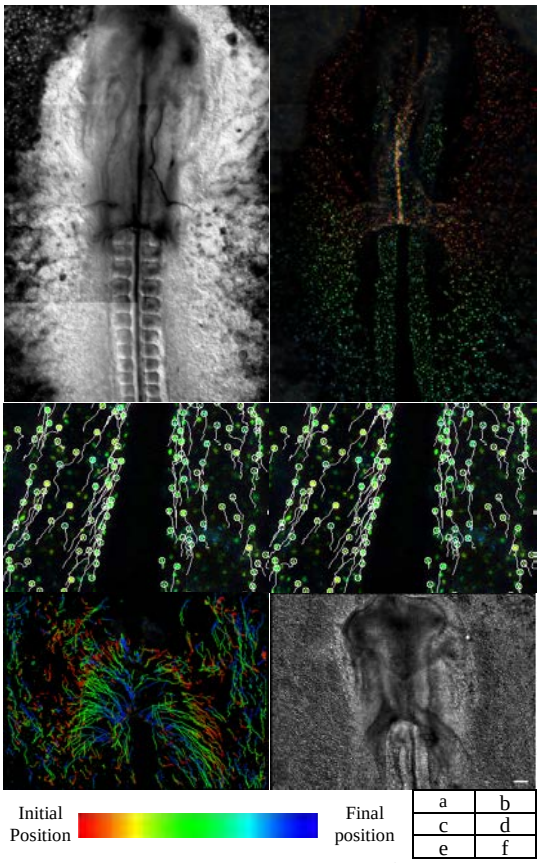

Figure 1: Tracking results. (a) DIC image of a quail embryo; (b) Fluorescent image; (c)-(d) Trajectories of the tracked cells at frames 78 and 80, respectively. (e) Full length trajectories of tracked cells. (f) Corresponding DIC image

DISCUSSION

The experimental results shown in Fig. 1 demonstrate the versatility and robustness of our cellular tracking algorithm when applied to challenging in-vivo data. The level of accuracy attained by our method allows a detailed analysis of biological implications associated with cellular migration and helps to understand the biological processes during embryonic development.

REFERENCES

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