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Automatic tracking of neural stem cells in sequential digital images

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ABSTRACT

Neural stem cells are the cells that give rise to the main cell types of the nervous system. Due to their varying size and shape, and random movement, the tracking of these cells in suspension in video sequences is challenging. This paper develops an automatic tracking system for neural stem cells. The system first detects and localizes cells in the image sequence, followed by a feature extraction step for the subsequent cell tracking. Then, the system tracks inactive cells using an improved mean shift algorithm, divisive cells through a context-based technique, and active cells by means of dynamic local prediction (DLP) and gray prediction (GP) algorithms. Experimental results show that the proposed system not only improves the accuracy of fast moving tracking, but also constructs accurately the trajectories of the cell movement and reduces the iterations during the center searching.

1. Introduction

The discovery of neural stem cells is a significant progress in the field of bioscience at the end of the last century. Neural stem cells hide in certain parts of nervous system. Some of these cells stay in original state, some have the potential to divide with multi-aspect, and others have regeneration ability [1,2]. Due to the good plasticity of neural stem cells, we can make it as a therapy tool of nerve damage through genetic or cell engineering. Researchers have observed that new nerve cells are produced by neural stem cells in the brain of adult humans and animals [2,3]. However, people know little about the basic development mechanism of neural stem cells. In order to achieve further understanding on regeneration of brain cells, through the research on cultivated cells, scientists hope to get more germiparity characteristics in a certain period of cells. Therefore, specialized image processing techniques for segmentation, object detection and object tracking are required.

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In pharmaceutical process, traditional artificial methods not only depend on a large number of tediously manual labor, but also use dyeing and other chemical technology, whereas these operations influence the motion mode of the cells [4]. Therefore, the traditional cell movement research methods are no longer applicable, and it appears that computer vision technology is an approach for studying cell movement. Moreover, this technology lends itself well to systematization and equipment integration [5]. All that led us to propose a vision-based cell tracking system in this paper, and we also wish to provide a new technical support for biological cell researches.

Cell segmentation is an important step in cell tracking. Segmentation is the process of dividing an image into meaningful parts, resulting in a new image containing for each pixel a label indicating to which segment it belongs (such as ''foreground'' versus ''background''). In the category of segmentation driven methods, cells are first detected in each frame based on their intensity, texture, or gradient, and then the detected cells are associated in two or more consecutive frames. Korzynska et al. [30] described a segmentation method combining a texture based approach with a contour based approach. The technique is designed to enable the study of cell behavior over time by segmenting bright-field microscope image sequences. However, the performance gains of the method are derived from the initialization procedure performed by the human operator on the first image of the sequence. Iwanowski et al. [31] and Korzynska et al. [32] described a multistage morphological segmentation method (MSMA) for microscopic cell images. The proposed method is based on two types of information, i.e., the cell texture coming from the bright field images and the intensity of light emission. Warowny and Markiewicz [33] presented two methods of texture feature generation for recognizing neoplasm and non-neoplasm cells in cancer diagnosis. The proposed methods have proved to be useful in practice for diagnosing cancer. Koprowski et al. [34] presented an attempt to segmentation of cell structures images. With the employment of the presented decision trees algorithm, biological diagnostic support goes fully automatically. Korzynska [35] improved the neutrophils' movement quantification by extending the cell's activity description to two stages of classification. The proposed new method has been used to describe the differences between normal children and the Chediak-Higashi syndrome patients. Korzynska [36] also examined and compared three microscopic image segmentation methods (reference method, morphological flattening method and watershed method), and showed that the watershed method detects cells' area more precisely than others.

More recent examples of cell tracking algorithms include affine transformation invariance [6] and a biological global positioning system [7]. Several different nowcasting algorithms were compared from 2003 to 2011. The computer vision technology provided a way of investigating cell tracking algorithm in a wide variety of applications, such as quantitative motion analysis algorithm [25], epidermal Langerhans cells tracking [8], real-time tumor tracking [9], embryo cell motion tracking [13], tracking fluorescent cells with coupled active surfaces [10], automatic tracking of biological cells in time-lapse microscopy [14], cell tracking using level sets [11], and cancer cell tracking [15]. Li et al. [12] exploited a fast topology-constrained level-set method in conjunction with a stochastic motion filter with a higher accuration, making it suitable for some specific application. However, the application of these algorithms is limited by their assumptions and constraints. Most existing tracking methods have high computational complexity, and are only effective in limited applications. Hence, there is a great demand for developing automatic cell tracking system, which has attracted increasing research attention.

In this paper, based on the characteristics of neural stem cells [1–3], cells are classified into three types, and different tracking techniques are developed to handle cells with different characteristic. These types are (1) the inactive cells that produce only small inter-frame movement, (2) the active cells that do random, large hop movement between frames, and (3) the divisive cells that are in division. Different tracking techniques are developed to address the challenges that each type of cells have. To overcome the adhesion problem of adhesive cells so as to locate them properly, a context-based adhesive cell separation method is proposed. To track inactive cells, we propose an improved mean shift algorithm. To track active cells, we propose a dynamic local prediction (DLP) algorithm to adjust the central position of the candidate movement region, and a new gray prediction (GP) model is also established. When dealing with divisive cells, we firstly track one of the sub-cells by using our improved mean shift algorithm, and then search the other sub-cells using other features.

The rest of the paper is organized as follows. Section 2 details the cell tracking methodology. The experimental results of cell tracking are described in Section 3. Section 4 gives some dicussions and analysis. Finally, Section 5 highlights the achieved results.

2. The proposed method

The proposed method for automatic cell tracking consists of two main modules: i.e., the detection module and the tracking module, as shown in Fig. 1.

The detection module mainly detects and localizes cells in the image sequence, and extracts features for the tracking module. The tracking module consists of tracking inactive cells using our improved mean shift algorithm, tracking divisive cells through a context-based technology, and tracking active cells by means of DLP and GP algorithms.

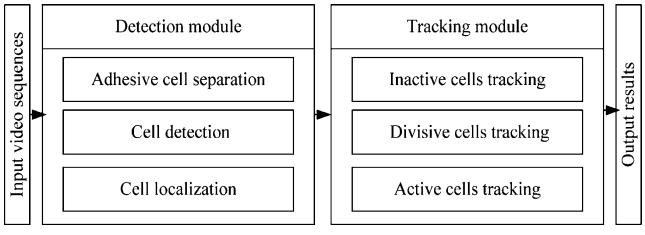

Fig. 1 – The framework of the proposed method.