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An ant-based stochastic searching behavior parameter estimate algorithm for multiple cells tracking

Benlian Xu [a,*], Mingli Lu [a,b]

[a] School of Electrical & Automatic Engineering, Changshu Institute of Technology, 215500 Changshu, China
[b] School of Automation, Nanjing University of Science & Technology, 210094 Nanjing, China

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ABSTRACT

This paper presents a novel ant-based parameter estimate algorithm to accurately track multiple cells in a series of low-contrast image sequences. Our proposed algorithm consists of three main blocks, i.e., priori colony distribution block, multi-colony reconstruction block, and cell labeling and state extraction block. Priori colony distribution block aims to directly distribute birth ants into regions where cells probably occur, which is implemented through kernel density probability estimate. Multi-colony reconstruction block is to move ants towards potential regions based on histogram similarity and place agent pheromone with appropriate introduction to evaporation and propagation models. Cell labeling and state extraction block is implemented by a fast ant clustering algorithm to determine the number of cells and their individual states, and the ratio of known identity ants to unknown ants in a cluster contributes to discriminate cell identity. Experiment results show that our algorithm could automatically track numerous cells in various scenarios, and furthermore, it is more accurate and robust than other popular tracking methods.

1. Introduction

The study of analysis of cellular behavior has been attracting more and more attention in the past ten years (Chicurel, 2002; Debeir et al., 2005; Mansfield et al., 2005; Chen et al., 2006; Yang et al., 2006). Its significance surges mainly due to its potential in achieving new and high-throughput way to conduct drug discovery and quantitative cellular studies. However, cellular analysis poses many challenges to those existing techniques because of severe image noise and clutter, cell shape deformation, and image contrast change. It is obvious that manual analysis of these images is a tedious process involving many efforts of human inspection. Sometimes, it becomes impossible for an expert to accurately follow many different events over a long sequence, especially when it requires tracking a large number of cells during long period of time in order to obtain robust results. Thus, the lack of an automated system becomes the bottleneck of studying the cell cycle process in a systematic and quantitative manner.

Recent literature reports mainly focus on the following three groups of automated or half-automated cell tracking techniques, i.e., model propagation based method, detection based method, and multi-object Bayesian probabilistic method. In terms of model propagation based methods, active contours (Zimmer and Olivo-Marin, 2005; Ray et al., 2002) can capture object boundary, but it usually requires cells to be partially overlapping in adjacent frames; Level set (Mukherjee et al., 2004) is able to tackle object topology changes, but it often merges two contacting contours into a single one and it also requires cells to be partially overlapping in different frames; Mean-shift algorithms (Debeir et al., 2005; Yang et al., 2006) give a fast solution for object tracking in video sequences, but usually do not give object contours. In the category of detection based method, often called “detect-before-track” technique (Wen et al., 2007; Smal et al., 2008), the typical advantage is computational efficiency with respect to segmentation, but the algorithms encounter problems during the temporal data association stage, which lead to tracking failures. The last category is the multi-object Bayesian probabilistic method, and most reports are recently presented using the probabilistic hypothesis density (PHD) filter, Gaussian mixture PHD (GM-PHD), and other variants (Wood et al., 2012; Vo and Ma 2006; Vo et al., 2010; Hoseinnezhad et al., 2012; Juang et al., 2009). Techniques used in Vo et al. (2010) and Hoseinnezhad et al. (2012) are also called “track-before-detect” methods, which by-pass the detection module and exploit the spatiotemporal information directly from the image sequence, and reported results have demonstrated that they are suitable for tackling multi-object state estimate problem of spawn events, objects entering and leaving image region (Vo et al., 2010), as well as multiple cells tracking (Hoseinnezhad et al., 2012).

It is well known that ant colony optimization (ACO) was first proposed by Dorigo, and such a population-based and meta-heuristic

* Corresponding author.
E-mail address: xu_benlian@cslg.cn (B. Xu).

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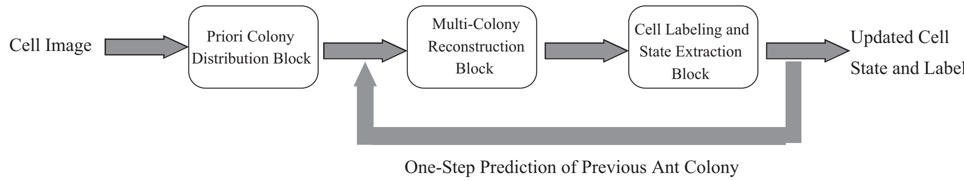

Fig. 1. Overview of our proposed algorithm.

approach has successfully solved various optimization problems (Dorigo et al., 1996; Chen et al., 2011; Loyola et al., 2012). Meanwhile, inspired by ants clustering corpses to form cemeteries and sort the larvae into several piles, another type of ant-related algorithm, i.e., ant-based clustering method, is also developed on the swarm level and promising results are achieved for various data sets (Deneubourg et al., 1991; Lumer and Faieta, 1994; Kanade and Hall, 2007). For instance, the ant behaviors of picking up and dropping items are modeled with a certain probability according to similarity or dissimilarity measure of local density of items (Deneubourg et al., 1991; Lumer and Faieta, 1994). In Kanade and Hall, (2007), Kanade et al. develop a fuzzy ants and clustering algorithm in which ants are combined with the fuzzy C-Means algorithm to find the cluster centers in feature space.

As we observe in natural ant colonies, the movement of each ant is usually stochastic and non-linear, and similarly, each cell also travels in an irregular way and exhibits non-linear dynamic behavior in cell image sequences. As a result, the paths of individual ants are somewhat analogous to the tracks of individual cells. Motivated by these similarities, a novel parameter estimate algorithm, which models ant stochastic searching behavior for effective clustering but differs from the optimization idea of tradition ACO algorithm, is proposed to track multi-cells in various scenarios. In contrast to aforementioned cell tracking approaches, our algorithm first uses the swarm intelligence, i.e., ant colony system, to deal with the problem of cell tracking, and moreover, it is expected that our approach could achieve better performance, since it belongs to the category of probabilistic method and is also characterized by "track-before-detect" technique. More specifically, to approximately locate cell distribution region in each frame, a kernel density estimation background subtraction technique is presented to generate the initial distribution of ant colonies; afterwards, to guide ants of the same interest to cluster together, the multi-colony reconstruction is proposed using heuristic information such as histogram similarity and pheromone field; finally, to jointly estimate the state of each cell and determine the identity of each colony, we develop a fast ant clustering algorithm for determining the number of cells and their individual locations, and then the cell label management strategy is proposed for ant colony correspondence between consecutive frames.

This paper is organized as follow. We first present the approximation description of multi-object posterior density in Section 2. In Section 3, our ant-based algorithm is then proposed, which utilizes priori colony distribution block, multi-colony reconstruction block, and cell labeling and state extraction block sequentially. The experiment results on various cases are presented to demonstrate the effectiveness of our algorithm, and discussions are detailed in Section 4. Finally, conclusions are summarized in Section 5.

2. The posterior multi-object density description

For tracking n objects, we denote the multi-object state by $\boldsymbol{X}(k)=\{\boldsymbol{x}_1(k),\boldsymbol{x}_2(k),\ldots,\boldsymbol{x}_n(k)\}$ at time k Let $\boldsymbol{z}(k)=[z_1(k),z_2(k),\ldots,z_{\overline{m}}(k)]$ denote the image observation comprising an array of $\overline{m}$ pixel values, and $\boldsymbol{z}(1:k)$ is defined as cumulative image sequences up to time k. With the assumption that each object follows Markov process, the Bayesian filter updates the posterior multi-object density (PMD) function over the joint state $\boldsymbol{X}(k)$ of all objects given all observations $\boldsymbol{z}(1:k)$ according to

$$\pi(\boldsymbol{X}(k)|\boldsymbol{z}(1:k))=c\boldsymbol{h}(\boldsymbol{z}(k)|\boldsymbol{X}(k)) \int \boldsymbol{f}(\boldsymbol{X}(k)|\boldsymbol{X}(k-1))\pi(\boldsymbol{X}(k-1)|\boldsymbol{z}(1:k-1))\,d\boldsymbol{X}(k-1) \quad (1)$$

where c is a normalized constant, $\boldsymbol{f}(\cdot)$ is the multi-object transition density function, $\boldsymbol{h}(\cdot)$ is the observation likelihood function. Note that, if multiple objects move in close proximity, multimodality is formed in the state space and this greatly complicates approximation of the posterior density function.

Although the PHD filter gives the approximation to PMD with satisfactory performance, it is usually based on many assumptions for implementation, and some are impractical in real tracking tasks. As such, we try to develop a general framework of multi-object tracking, which utilizes the searching behavior of ant colony level to approximately estimate the PMD in proportion, and the overview of our proposed algorithm is illustrated in Fig. 1. It can be observed that the initial approximation to PMD is the combination between the prior colony distribution obtained from current background subtraction and one-step prediction of previous colony distribution, whereas the updated colony distribution is formed by multi-colony reconstruction block followed by the cell labeling and state extraction, which eventually constitutes the approximation to PMD in proportion.

3. The ant-based parameter estimate algorithm for cells tracking

This section gives the details of our proposed algorithm. First, the priori colony distribution block is described in Section 3.1. Then, the multi-colony reconstruction block is illustrated in Section 3.2. Finally, the cell labeling and state extraction block is elaborated in Section 3.3.

3.1. Priori colony distribution with background subtraction

Background subtraction is an approach for discriminating the moving objects from the background scene (Elhabian et al., 2008), and it is recognized as a fundamental step for video surveillance (El Maadi and Maldague 2007), traffic monitoring (Mandellos et al., 2011), and human detection and tracking (Bhaskar et al., 2013), with two common forms, namely, recursive technique and non-recursive technique. In terms of the recursive form, approximated median filter recursively gives the estimate of the median through incrementing the median by one if the input pixel is larger than the estimate, and decreasing the median by one if smaller. This estimate eventually converges to a value for which half of the input pixels are larger than and half are smaller than this value. The drawback of this approach is that it adapts slowly toward a large change in background. Among the category of non-recursive techniques, the nonparametric kernel density estimation is widely used in various applications (Elgammal et al., 2002).