



Multi-task ant system for multi-object parameter estimation and its application in cell tracking



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ABSTRACT

Inspired by ant's stochastic behavior in search for multiple food sources, we propose a cooperating multi-task ant system for tracking multiple synthetic objects as well as multiple real cells in a bio-medical field. In our framework, each ant colony is assumed and assigned to fulfill a given task to estimate the state of an object. Furthermore, two ant levels are used, i.e., ant individual level and ant cooperation level. In the ant individual level, ants within one colony perform independently, and the motion of each individual is probabilistically determined by both its intended motion modes and the likelihood function score. In the ant cooperation level, each ant adjusts individual state within its influence region according to heuristic information of all other ants within the same colony, while the global best template at current iteration is found among all ant colonies and utilized to update ant model probability, influence region, and probability of fulfilling task. Our algorithm is validated by comparing it to the state-of-art algorithms, and specifically the improved tracking performance in terms of false negative rate (up to 10.0%) and false negative rate (up to 2.1%) is achieved based on the studied three real cell image sequences.

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1. Introduction

The study of analysis of cellular behavior is rapidly becoming a requisite for describing biological processes and diagnosing diseases, and some promising research results on cellular image segmentation or tracking have been reported [1–10], ranging from single cell to multiple cells [3,4], from deterministic analysis method to Bayesian estimate technique [5–7], from phase-contrast microscopy cells to fluorescent image cells [8–10], and so on. Since the study of cellular behavior analysis involves many challenges, such as model uncertainty, morphological variance, and overlapping and colliding between cells, both conventional and manual techniques become tedious and time consuming processes for computing qualitative and quantitative features of a large number of cells. For efficiency and accuracy, the automated tracking methods that eliminate the bias and variability to a certain degree are of great importance.

Many efforts have been made in automated cell tracking over the past decades, and could be divided into three groups, i.e., model propagation based method, detection based method, and

Random Finite Sets (RFS) based method. As for the model propagation based method, snakes or active contours are parametric or nonparametric, closed or open curves that can capture object boundary and further track the object of interest [11–14], but it requires cells to be partially overlapping in adjacent frames; level set [15] is able to tackle the changes in object topology, but it will merge two contacting contours into a single one and it also requires cells to be partially overlapping in different frames; mean-shift algorithms [16] give a fast solution for object tracking in video sequences (e.g., vehicle tracking, closed loop video), but usually do not give object contours. In terms of the detection based method, also called “detect-before-track” technique [7,17–19], particle filter is usually adopted since it is able to cope with heavy clutter, and is very easy to implement. However, various accurate models, such as state transition model, observation model, object intensity model and shape model, are required to be formulated besides the detection segmentation module. Furthermore, this algorithm usually encounters some problems during the temporal data association stage especially in the case of cell division and cell high density, which lead to tracking failures. For instance, as reported in [19], although the segmentation accuracy is 99.5%, the tracking accuracy is only 90.0%. The last category of tracking algorithm is the RFS-based method, which has demonstrated that it is suitable for tackling the multi-object state estimate problem of spawn events, objects entering and leaving image region

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[20,21]. Therefore, RFS-based filters are naturally suitable for tracking multiple cells in various cases, such as *E. coli* bacteria tracking and T cell tracking [22–24]. Specifically, the multi-Bernoulli filtering algorithm used in [23] is very competitive and also called a “track-before-detect” method, which by-passes the detection module and exploits the spatiotemporal information directly from the image sequence, and yields better results in low contrast cell image sequences.

Ant colony optimization (ACO) is a population-based and meta-heuristic approach to model the behavior of almost blind ants in establishing the shortest path from their colony to their feeding sources and back by laying a chemical substance called pheromone. By virtue of the learning and searching power of an autocatalytic self-organization of an ant colony, ACO-based algorithms are receiving increasing attention and have enjoyed great success in the solution of traditionally difficult optimization problems [25,26]. To date, most of these algorithms are improved and extended to applications such as vehicle routing [27], scheduling [28], clustering [29–31], classification task [32], and target tracking [33–36], but the application to biological cell tracking is seldom reported. As we know, in addition to the aforementioned learning and searching power of ant colony, there are other salient features for the track of multiple biological cells, and they could be characterized as follows. First, there usually exist dynamic differences between tiny cells (such as cells 1 and 2 in Fig. 1), and we have to resort to well-designed motion models for acquiring better performance in the general tracking framework. However, through the use of all-orientation searching strategy of ant colony, the constraint of requiring accurate models for different tracking modes can be relaxed, i.e., we utilize the proposed ant decision of simple form to accommodate the differences in cell dynamics. Second, the number of cells varies over time, i.e., tiny cells leaving or entering the image (cell 3 in Fig. 1), and this requires the proposed approach could adaptively and jointly estimate the number of cells and its individual states. In the framework of ant colony, we define the mapping between colonies and cells, namely, some ant colonies are modeled to correspond to existing or new entering cells with a big value of colony existing probability, whereas some to disappearing cells with a small existing probability, which will be removed in the next frame. Finally, the variation in cell distribution density often happens (cells 1 and 2 in Fig. 1), and this easily leads to the “hijacking” problem for adjacent or interacting cells. However, for a group of ant colonies, the independent and cooperating mechanism is designed and expected to be suitable for solving the problem. The main contributions of our method can be summarized as follows: (1) introducing an idea of bio-inspired estimator, i.e., multi-task ant system, for estimating the states of multiple cells (objects), which opens another interesting research branch for both swarm intelligence and object tracking; (2) introducing a series of ant-related behavior variables, such as moving mode, influence region and ant colony existing probability, and the corresponding recursive forms are formulated as well; (3) considering two ant levels, namely, the ant individual level and the ant cooperation level. The ant individual level propels ants with the same task to move toward the location of the same interested cell, whereas in the ant cooperation level the cooperation mechanism among colonies is utilized to update and regulate ant-related behavior parameters for accurately locating the cells of interest in the following iterations as a whole.

Preliminary results have been announced in the conference paper [37]. This paper presents a more complete theoretic study and abundant experimental analysis. We first address the background on multi-Bernoulli filter for multi-object image tracking in Section 2. In Section 3, a multi-task ant system algorithm is then proposed to track multiple cells and determine the number of cells,

which utilizes the heuristic information and cooperation mechanism among ant colonies to find potentials in a recursive way. In Section 4, the experiment results on various cases are presented to demonstrate the effectiveness of our algorithm. Finally, conclusions are summarized in Section 5.

2. Background on multi-Bernoulli filter for multi-object image tracking

In the framework of multi-object tracking, our focus is to determine the posterior multi-object distribution given all history observations. With the assumption that each object follows Markov process, the Bayesian filtering algorithm offers a concise way to describe the multi-object tracking problem. Since both the states and measurements are represented as sets of random vectors, the concept of random finite set (RFS) is introduced to solve the multi-object estimation problem in the Bayesian framework. For tracking n objects at time k , the multi-object state is denoted by a RFS $\mathbf{X}_k = \{\mathbf{x}_{1,k}, \mathbf{x}_{2,k}, \dots, \mathbf{x}_{n,k}\}$, where $\mathbf{x}_{i,k}$ is the state vector of i -th object. Let $\mathbf{z}_k = [z_{1,k}, z_{2,k}, \dots, z_{\bar{m},k}]$ denote the image observation comprising an array of \bar{m} pixel values at time k , and $\mathbf{z}_{1:k}$ is defined as the cumulative image observations up to time k . Therefore, if the posterior multi-object density is denoted by $\hat{\pi}_{k|k}(\cdot|\mathbf{z}_{1:k})$, the recursive form of multi-object state estimation problem can be defined as

$$\begin{aligned} \hat{\pi}_{k|k-1}(\mathbf{X}_k|\mathbf{z}_{1:k-1}) &= \int \mathbf{f}(\mathbf{X}_k|\mathbf{X}) \hat{\pi}_{k-1|k-1}(\mathbf{X}|\mathbf{z}_{1:k-1}) \delta \mathbf{X} \\ \hat{\pi}_{k|k}(\mathbf{X}_k|\mathbf{z}_{1:k}) &= \frac{\mathbf{h}(\mathbf{z}_k|\mathbf{X}_k) \hat{\pi}_{k|k-1}(\mathbf{X}_k|\mathbf{z}_{1:k-1})}{\int \mathbf{h}(\mathbf{z}_k|\mathbf{X}) \hat{\pi}_{k|k-1}(\mathbf{X}|\mathbf{z}_{1:k-1}) \delta \mathbf{X}} \end{aligned} \quad (1)$$

where $\mathbf{f}(\cdot)$ is the multi-object transition density function, $\mathbf{h}(\cdot)$ denotes the observation likelihood function, and δ is an appropriate reference measure on some state space.

Observe that, due to the fact that there are multiple integrals implied in the above recursion, the estimate of posterior multi-object density is in essence an intractable problem in most cases. However, an approximated solution to this problem is the probability hypothesis density (PHD) recursion [20], in which the first order statistical moment of the posterior multiple-object state is propagated in time in the Bayesian recursion form, instead of propagating the multiple-object posterior density as a whole. More recently, the multi-Bernoulli filter developed from the RFS framework is proposed and utilized as a more effective visual tracking technique [22,23], and the salient features of the filter are that it operates in the single-target state space and in parallel. To give an intuitive understanding of the multi-Bernoulli filter, which will be discussed in Section 4 for performance comparison with our approach, we briefly introduce the principle and its notions. With the assumption of multi-object density being characterized by multi-Bernoulli parameters, the multi-Bernoulli filter for image sequences can be represented, respectively, by a prediction step and an update step.

In the prediction step, if the multi-Bernoulli parameters of \mathbf{X}_k is denoted by $\hat{\pi}_{k-1|k-1} = \{(r_{k-1}^{(i)}, p_{k-1}^{(i)}(\cdot))\}_{i=1}^{M_{k-1}}$, where the parameter $r_{k-1}^{(i)}$ is the existence probability of the i -th object and $p_{k-1}^{(i)}$ represents the probability density of the state conditioned on its existence, the predicted multi-object state is also a multi-Bernoulli RFS

$$\hat{\pi}_{k|k-1} = \{(r_{k|k-1}^{(i)}, p_{k|k-1}^{(i)}(\cdot))\}_{i=1}^{M_{k-1}} \cup \{(r_{\Gamma,k}^{(i)}, p_{\Gamma,k}^{(i)}(\cdot))\}_{i=1}^{M_{\Gamma,k}} \quad (2)$$

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