Plant Cell Tracking Using Kalman Filter Based Local Graph Matching

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***Abstract*—**Automated tracking of cells in time lapse live-imaging datasets of developing multicellular tissues is required for high throughput spatio-temporal quantitative measurements of a range of cell behaviors, such as cell division, migration and cell growth. In this paper, a Kalman filter based local graph matching method is proposed to track the plant cells, by exploiting the tight spatial topology of neighboring cells in a multicellular field as contextual information. The Kalman filter is used to predict the movement of the cells, and then the local graph matching approach is used to search the target cells in the neighborhood of the predicted position. The combination of the Kalman filter and local graph matching greatly reduces the size of the searching region in the matching process and enhances the tracking stability as well. Furthermore, the cells' lineage tracklets could be associated by using the cells' spatial-temporal contextual information to obtain long-term lineages. Finally, we proposed a graph evolution method to enhance the association robustness by considering the statistical properties of individual cell tracklets. The effectiveness and efficiency of the proposed tracking method are validated by experiments on real datasets.

***Keywords*—**Cell tracking, Kalman filter, Local graph matching, Tracklets association, Tracklets adaptation

1. Introduction

In developmental biology, the causal relationship between cell growth patterns and gene expression dynamics has been one of the major topics of interest. A proper quantitative analysis of the cell growth and cell division patterns has remained mostly elusive so far. For high-throughput analysis of large volumes of image data (as shown in Fig. 1 (A)), the development of fully automated image analysis pipelines is becoming necessity.

This paper mainly deals with plant shoot apical meristem (SAM) cells. Fig. 1 (A) is an example of SAM cell images taken by Confocal Laser Scanning Microscopy at different time instances (T direction) and different spatial slices (Z direction). We can see that the low contrast of cellular image quality, deformation of cell shapes, frequent cell divisions, and highly clustered cell structure all pose significant challenges to the efficient and robust cell tracking in such cellular images.

There has been some work on automated tracking of cells in time-lapse images for both plants and animals or other objects [1-12]. But those methods are not suitable for tracking plant SAM cells, which are in close contact with each other and share very similar physical features. Fernandez et al. [13] developed an automated image processing pipeline for SAM cell images, but their image data are different from ours. Because their images are acquired from multiple angles, it imposes a limitation on the temporal resolution. Neighborhood structure based methods are widely used to solve recognition, classification and tracking problems [14-15]. In the earlier studies, we can track most of the cells when the images are not highly noised. A local graph matching method was proposed in [16-18] to track SAM cells. In the framework proposed in [18], a vertex in the graph represents every cell and neighboring vertices are connected by an edge. The graph structure automatically includes the relative position information of the cells, such as the relative distance between two neighboring cells (edge length) and edge orientation.

As described in the previous local graph matching scheme [17, 18], we can find the most similar cell pair (known as the "Seed Pair") by matching the relative positions of cells with respect to their nearest neighbors through the local graph for any two consecutive time points. Starting from this seed pair, we grow the number of matched cells by computing the similarities between local regions in the graph. However, this method employs an iterative search strategy by growing correspondence from a seed cell pair which tends to accumulate error and can throw the tracker off for cells spatially distant from the seed.

Besides the aforementioned approaches, tracking based on Kalman filter has shown good performance on time-lapse images [19]. In this paper, we combined the advantages of Kalman filter and local graph matching method, the pipeline of which is shown in Fig. 1. The Kalman filter greatly reduces the size of the searching region for the local graph matching approach and enhances the tracking stability, because the overall tracking algorithm does not require the identification of "tracking seeds" as in the previous local graph matching method and it can track all cells simultaneously. During the tracking procedure, the neighborhood of each cell's predicted position by Kalman filter is considered as the searching region of the local graph matching algorithm. And the matching problem is solved by obtaining correspondences from local graphs generated at different time instants. The local geometrical and topological features of cells are exploited to generate graphs of the local neighborhood of each cell. This process is followed by matching of the relative positional information of cells, such as the length and orientation of the edges with respect to their nearest neighbors. Moreover, the cell lineage tracklets (which are separated due to noise or cell growth or segmentation error) are associated by using the spatial-temporal contextual information from the initial

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