IMM FILTER BASED LOCAL GRAPH MATCHING FOR PLANT CELL LINEAGE ESTIMATION

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ABSTRACT

In this paper, an interacting multiple models (IMM) motion 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 IMM 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 local neighborhood of the predicted position. The combination of the IMM 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' lineages are generated by using a maximum-a-posteriori (MAP) lineage association method. The effectiveness and efficiency of the proposed tracking method are validated by experiments on real plant cell datasets.

Index Terms—Cell tracking, IMM filter, local graph matching, tracklets association

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. The development of fully automated image analysis pipelines for high-throughput analysis of large volume image data is becoming necessity.

This paper mainly deals with plant shoot apical meristem (SAM) cells. Fig. 1 (a) is an example of SAM 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, 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 identification of cells in time-lapse images for both plants and animals or other objects [1-4]. 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. [5] developed an automated image processing pipeline for SAM cell images, but their image data are different from ours.

In the earlier studies [6-8], a local graph matching method was proposed to track SAM cells. In the framework proposed in [6], 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. The experimental results have confirmed the effectiveness of local graph matching approach.

Besides the aforementioned approaches, prediction based tracking methods have shown good performance on time-lapse cell images [9]. However, traditional motion filters, such as the Kalman filter, are bound to use only one motion model, which is inadequate for tracking biological cells because the cell dynamics vary with time. The IMM filter, instead, is capable of incorporating multiple motion models in parallel, and to select and switch to the model which is more accurate to represent the movement during a given period [10].

In this paper, we combine the advantages of local graph matching and IMM filter to propose an IMM filter based local graph matching approach for plant cell lineage estimation, the pipeline of which is shown in Fig. 1. During the tracking procedure, the neighborhood of each cell's predicted position by IMM filter is considered as the searching region of the local graph matching algorithm. The local geometrical and topological features of cells are exploited to generate graphs of the local neighborhood of each cell. The matching problem is solved by obtaining correspondences from local graphs generated at different time instants. 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 segmentation error) are associated by maximum-a-posteriori (MAP) lineage association method. Compared with the previous local graph matching method [8], the IMM filter based local graph matching approach greatly reduces the size of the searching region for

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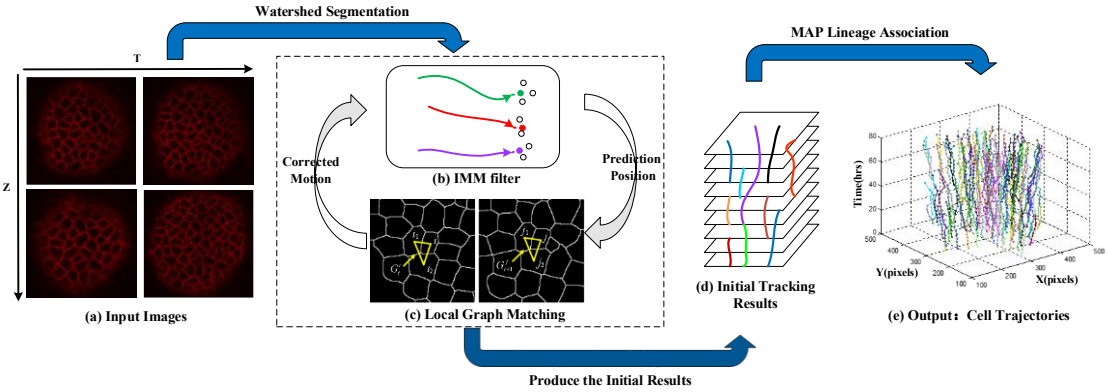

Fig. 1. The pipeline of the proposed IMM filter based local graph tracking approach for plant cells. (a) An example of the cell images at different time instances (T direction) and different spatial slices (Z direction); (b) Demonstration of the IMM filter tracking; (c) Local graph matching; (d) Illustration of tracklet association; (e) Cell trajectories obtained by our proposed tracking method.

the local graph matching algorithm, and it enhances the tracking stability, because the proposed tracking algorithm does not require the identification of "tracking seeds" [8].

2. DETAILED METHODOLOGY

2.1. Cell Segmentation and Local Graph Matching

The input to our cell tracking system is a series of image slices along multiple time points of observation. Watershed transformation is used to segment the plant cells from each image slice [11], and the experimental results confirmed its effectiveness in [6] [11], which is shown in Fig.1 (c).

Although the cells are growing and moving over time, their relative positions are not changed too much. The cells' stable position structure is the basic feature used in our tracking algorithm. In the local graph matching framework proposed in [6], 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 illustrated in Fig.1 (c). Every cell is related to a local graph, and then the cell matching problem could be solved by matching the local graphs. Meanwhile, we search the cell division events in the neighborhood of the cell which is matched already. The details of local graph matching method can be found in [6].

2.2. IMM Filter Based Local Graph Matching

In this paper, the plant cell motions are assumed to consist of a finite number of modes and each mode is described by a linear model with additive Gaussian noise [10]. The motion models and the measurement model are defined as

$$\begin{cases} \boldsymbol{s}_{\mathrm{k}} = \mathbf{A}^{i}\boldsymbol{s}_{k-1} + \boldsymbol{v}_{k-1}^{i}, \quad i \in \{1,...,M\} \\ \boldsymbol{o}_{\mathrm{k}} = \mathbf{H}\boldsymbol{s}_{k} + \boldsymbol{w}_{k} \end{cases} \tag{1}$$

Here, $\boldsymbol{s}_{\mathrm{k}}$ is the state vector of a cell in frame k, which consists of the centroid position, velocity, and acceleration of the cell, i.e. $\boldsymbol{s}_{\mathrm{k}} = (x_k, y_k, \dot{x}_k, \dot{y}_k, \ddot{x}_k, \ddot{y}_k)'$. The corresponding measurement vector $\boldsymbol{o}_{\mathrm{k}} = (x_k, y_k)'$ contains the measured cell centroid position. We have M Kalman filters in parallel, i is the model index. $\mathbf{A}^{i}$ is the state transition matrix of model i, and $\mathbf{H}$ is the measurement matrix that relates states to measurements. $\boldsymbol{v}_{k-1}^{i}$ and $\boldsymbol{w}_{k}$ are the process and measurement noise vectors, which are uncorrelated zero-mean Gaussian processes with covariances $\mathbf{Q}^{i}$ and $\mathbf{R}$, respectively.

The IMM filter assumes that the transition between models is regulated by a finite-state Markov chain, with probability p_{ij} of switching from model i to j in successive frames. The filtering recursion consists of two stages: prediction and correction, the details of which are as below.

Prediction: Starting from M weights ρ_{k-1}^{i}, states $\hat{\boldsymbol{s}}_{k-1}^{i}$ and covariances $\mathbf{P}_{k-1}^{i}$ from the previous iteration, the mixed initial condition is computed:

$$\begin{cases} \hat{\boldsymbol{s}}_{k-1}^{0j} = \sum_{i} \rho_{k-1}^{i|j} \hat{\boldsymbol{s}}_{k-1}^{i} \\ \mathbf{P}_{k-1}^{0j} = \sum_{i} \rho_{k-1}^{i|j} \left[\mathbf{P}_{k-1}^{i} + (\hat{\boldsymbol{s}}_{k-1}^{i} - \hat{\boldsymbol{s}}_{k-1}^{0j})(\hat{\boldsymbol{s}}_{k-1}^{i} - \hat{\boldsymbol{s}}_{k-1}^{0j})' \right] \end{cases} \tag{2}$$

where $\rho_{k-1}^{i|j} = p_{ij}\rho_{k-1}^{i} / \rho_{k|k-1}^{j}$, and $\rho_{k|k-1}^{j} = \sum_{i} p_{ij}\rho_{k-1}^{i}$.

These are input to M Kalman filters to compute the state prediction $\hat{\boldsymbol{s}}_{k|k-1}^{j}$ and covariance $\mathbf{P}_{k|k-1}^{j}$:

$$\begin{cases} \hat{\boldsymbol{s}}_{k|k-1}^{j} = \mathbf{A}^{j}\hat{\boldsymbol{s}}_{k-1}^{0j} \\ \mathbf{P}_{k|k-1}^{j} = \mathbf{A}^{j}\mathbf{P}_{k-1}^{0j}(\mathbf{A}^{j})' + \mathbf{Q}^{j} \end{cases} \tag{3}$$

The combined state and covariance predictions are

$$\begin{cases} \hat{\boldsymbol{s}}_{k|k-1} = \sum_{j} \rho_{k|k-1}^{j} \hat{\boldsymbol{s}}_{k|k-1}^{j} \\ \mathbf{P}_{k|k-1} = \sum_{j} \rho_{k|k-1}^{j} \left[\mathbf{P}_{k|k-1}^{j} + (\hat{\boldsymbol{s}}_{k|k-1}^{j} - \hat{\boldsymbol{s}}_{k|k-1})(\hat{\boldsymbol{s}}_{k|k-1}^{j} - \hat{\boldsymbol{s}}_{k|k-1})' \right] \end{cases} \tag{4}$$

The predicted centroid positions $\hat{\boldsymbol{o}}_{\mathrm{k|k-1}} = \mathbf{H}\hat{\boldsymbol{s}}_{k|k-1}$ of all cells are provided for the local graph matching based tracker in frame k to search their corresponding cells.

Correction: Given the predicted states, covariances, and measurement $\boldsymbol{o}_k$ from the output of the local graph matching based tracker, the Kalman filters are used to obtain the updated state $\hat{\boldsymbol{s}}_k^j$ and covariance $\mathbf{P}_k^j$:

$$\begin{cases} \hat{\boldsymbol{s}}_k^j = \hat{\boldsymbol{s}}_{k|k-1}^j + \mathbf{K}_k^j(\boldsymbol{o}_k - \mathbf{H}\hat{\boldsymbol{s}}_{k|k-1}^j) \\ \mathbf{P}_k^j = \hat{\mathbf{P}}_{k|k-1}^j - \mathbf{K}_k^j\mathbf{H}\hat{\mathbf{P}}_{k|k-1}^j \end{cases} \tag{5}$$

where $\mathbf{K}_k^j = \mathbf{P}_{k|k-1}^j\mathbf{H}'(\mathbf{H}\mathbf{P}_{k|k-1}^j\mathbf{H}' + \mathbf{R})^{-1}$ is the Kalman gain. The likelihood that model j is activated in frame k is

$$\lambda_k^j = \exp\left[-\frac{1}{2}(\mathbf{y}_k^j)'(\mathbf{S}_k^j)^{-1}\mathbf{y}_k^j\right] \Big/ \sqrt{2\pi\det(\mathbf{S}_k^j)} \tag{6}$$

where $\boldsymbol{y}_k^j = \boldsymbol{o}_k - \hat{\boldsymbol{o}}_{k|k-1}$ is the innovation of Kalman filter j, and $\mathbf{S}_k^j$ is the associated covariance. Then, the combined state $\hat{\boldsymbol{s}}_k$ and covariance $\mathbf{P}_k$ estimates can be computed by Eq. (4), with $\rho_{k|k-1}^j$ replaced by $\rho_k^j = \rho_{k|k-1}^j\lambda_k^j \big/ (\sum_i \rho_{k|k-1}^i \lambda_k^i)$.

Previously, the local graph matching based tracker is used to search the seed cell pair globally, which is time consuming and unstable if the seeds were chosen wrong. Now the IMM filter based local graph matching method takes advantage of IMM filter by predicting the cell's new position, and then we can search the target cell by local graph matching method in the neighborhood around the predicted position, as shown in Fig. 1.

2.3. Cell Tracklets Association

In the long-term tracking process, the cells may disappear shortly because they could be corrupted by noise or they are not correctly segmented at some time points. We propose to link the cell lineage tracklets by the MAP lineage association method. The process of linking cell tracklets into trajectories is performed using a global data association approach [12]. Linear programming is employed to solve the underlying maximum-a-posteriori problem.

Let us define $\mathbf{T} = \{T_k\}$ as the set of cell trajectories generated from plant cell tracklets $\mathbf{X}$. Similar to [12], the likelihood of a cell tracklet X_i is defined as

$$P(X_i \mid \mathbf{T}) = \begin{cases} P_{TP}(X_i) = \alpha^{\frac{|X_i|}{\beta}}, & \text{if } \exists \mathrm{T}_k \in \mathbf{T}, \mathrm{X}_i \in \mathrm{T}_k \\ P_{FP}(X_i) = 1 - \alpha^{\frac{|X_i|}{\beta}}, & \text{otherwise} \end{cases} \tag{7}$$

where $P_{TP}(X_i)$ is the probability of X_i being a true positive, $|X_i|$ is the number of detections, α corresponds to the miss detection rate, and β is a tuning parameter.

Under Bayes' rule, the MAP problem can be rewritten as a product of probabilities

$$\begin{aligned} \mathbf{T}^* &= \arg\max_{\mathbf{T}} P(\mathbf{T} \mid \mathbf{X}) \\ &= \arg\max_{\mathbf{T}} \prod_{X_i \in \mathbf{X}} P(X_i \mid \mathbf{T}) \prod_{T_k \in \mathbf{T}} P_{traj}(T_k) \end{aligned} \tag{8}$$

$P_{traj}(T_k)$ is the prior probability of a trajectory T_k consisting of $\{X_j^k\}_{j=1}^n$ tracklets, and defined as a Markov chain

$$P_{traj}(T_k) = \begin{cases} P_{init}(X_1^k)\left[\prod_{j=1}^{n-1} P_{link}(X_{j+1}^k \mid X_j^k)\right] P_{term}(X_n^k), & T_k \text{ broken} \\ P_{init|term}(X^k), & \text{otherwise} \end{cases} \tag{9}$$

Because the tracklet association is performed on each cell tracklet and all cells' initialization nodes and termination nodes are independent of each other, P_{init} and P_{term} can be set with a constant to simplify the computation, and P_{link} is the probability of linking two plant cell tracklets having distance $\Delta(X_i, X_j)$, defined as

$$P_{link}(X_i \mid X_j) = \begin{cases} D(X_i, X_j) & \text{if } \Delta(X_i, X_j) \le \delta_{max} \\ 0 & \text{otherwise} \end{cases} \tag{10}$$

The similarity $D(X_i, X_j)$ is learned using a binary neural net with Bayesian regularization. To this end, a set of spatio-temporal and visual features including the cell shape descriptor and spatial information which have been used in [6] are computed for pairs of cell tracklets. δ_{max} limits the gap size which is considered for bridging over frames with missing detections. Based on P_{link}, we define $P_{init|term}(X^k)$ as

$$\begin{aligned} &P_{init|term}(X^k) = 1 - \\ &\max\left\{P_{init}(X_1^k)\left[\prod_{j=1}^{n-1} P_{link}(X_{j+1}^k \mid X_j^k)\right] P_{term}(X_n^k)\right\} \end{aligned} \tag{11}$$

which means that the probability of a cell tracklet X_i not being linked to its most similar tracklet. This association approach is robust to errors of frame-by-frame cell segmentation component, because all hypotheses over all frames of the sequence are considered simultaneously, rather than propagating the results from frame to frame.

3. TRACKING RESULTS AND ANALYSIS

We have tested our method on multiple SAM datasets. The experimental results are shown on plant cell images which are captured by Confocal Laser Scanning Microscopy across consecutive time instants, with a time interval of 3 hours between two consecutive instants.

To adapt the IMM filter for cell tracking, cell motion models need to be defined by specifying the system matrices $\mathbf{A}^i$ and $\mathbf{H}$. In our experiment, we use three different models of dynamics: random walk (RW), constant-velocity (CV), constant acceleration (CA). The state-transition matrices corresponding to the RW, CV, and CA models are as below,

$$\mathbf{A}^1 = \begin{bmatrix} 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}, \quad \mathbf{A}^2 = \begin{bmatrix} 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & T_S & 0 & 0 & 0 \\ 0 & 0 & 0 & T_S & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix},$$

$$\mathbf{A}^3 = \begin{bmatrix} 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & T_S & 0 & 0 & 0 \\ 0 & 0 & 0 & T_S & 0 & 0 \\ 0 & 0 & 0 & 0 & \frac{T_S^2}{2} & 0 \\ 0 & 0 & 0 & 0 & 0 & \frac{T_S^2}{2} \end{bmatrix}, \quad \mathbf{H} = \begin{bmatrix} 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 \end{bmatrix}$$

where $T_S = 3$ is the time interval between the measurements. The proposed motion models share a common measurement matrix **H**. To initialize the IMM filter, the system tracks each cell without motion filtering in the first frame in which it appears. The measured cell centroid positions in this frame are used to initialize the cell state $\hat{\boldsymbol{s}}_0$ .The initial model weights ρ_0^i are set to equal $1/3 (i \in \{1,2,3\})$.

To illustrate the IMM filter's superiority to Kalman filter, the averaged mean-square error (MSE) of a few cells' trajectory from different models is shown in Fig. 2 (using Kalman filter and Kalman smoother [13]). From the comparison, we can see that the IMM filter achieves the least MSE, and exhibits appreciably smaller deviation with the plant cells' true trajectory.

The tracklet association method is demonstrated in Fig. 3, in which a few cell tracklets have been correctly linked into longer cell trajectories. By comparing the precision and time efficiency of the proposed lineage association method with the Markov Chain Monte Carlo (MCMC) method [8] in Table 1, we can clearly see the strength of the proposed MAP based cell lineage association method.

Table 1. Performance of Tracklet Association Methods

Dataset	Number of tacklets	Precision		Time(s)	
		Ours	MCMC [8]	Ours	MCMC [8]
A	32	12/12	10/12	3.1	144.3
B	138	56/60	51/60	42.5	2029.8
C	153	63/68	53/68	47.2	2364.8

In order to verify the overall improvement of the proposed tracking algorithm, we compared the cell tracking accuracy of our proposed method with that in the previous local graph matching method [8]. The number of correctly tracked cells obtained by tracking image sequences within a 72-hour period is listed in Table 2, from which we can see the improvement in the percentage of trajectory validity and the cell division detection accuracy by the proposed method.

The previous local graph matching based tracker employs an iterative search strategy by growing correspondence from a seed cell pair [8], while the IMM filter based local graph matching algorithm is able to track multiple cells simultaneously, so our proposed matching method has a better time efficiency. By implementing the algorithms using MATLAB on a PC with 3.60GHz CPU and 8GB memory, the time efficiency is improved from 15 minutes (Method in [8]) to about 8 minutes.

Moreover, the IMM filter based matching method does not require the identification of "seed cells", therefore it eliminates the risk that the overall tracking result could be nonsense if the seed pair were chosen wrong, which happens in the previous local graph matching approach [8], especially when the images are severely corrupted by noise.

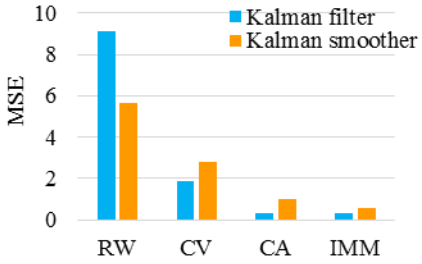

Fig. 2. Comparison of MSEs obtained by different filter models.

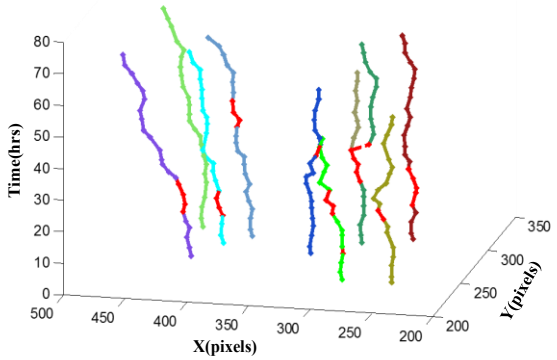

Fig. 3. The illustration of the MAP tracklet association algorithm. Cell tracklets have been correctly linked into longer cell trajectories.

Table 2. Tracking Accuracy Comparison

Dataset	Trajectory validity		Division detection accuracy	
	Ours	Previous [8]	Ours	Previous [8]
A	97.6%	90.4%	100%	90.0%
B	96.1%	94.2%	96.4%	92.9%
C	97.5%	92.5%	95.9%	90.9%

4. CONCLUSION

This paper presents an IMM filter based local graph matching method for plant cells' lineage estimation, by exploiting the tight spatial topology of neighboring cells in a multicellular field as contextual information. The IMM filter is used to predict the movement of the cells, and then the local graph matching approach can search the target cells in the neighborhood of the predicted position in a relatively small area. Furthermore, the cells' lineage tracklets are associated by a maximum-a-posteriori lineage association method. The experimental results confirmed the effectiveness of the proposed method.

5. REFERENCES

[1] F. Amat et al., "Fast, accurate reconstruction of cell lineages from large-scale fluorescence microscopy data," *Nature Methods*, vol. 11, no. 9, pp. 951–958, 2014.

[2] K. E. G. Magnusson, J. Jaldén, P. M. Gilbert, and H. M. Blau, "Global linking of cell tracks using the Viterbi algorithm," *IEEE transactions on medical imaging*, *v*ol. 34, no. 4, pp. 911–929, Apr. 2015.

[3] A. Santella, Z. Du, and Z. Bao, "A semi-local neighborhood-based framework for probabilistic cell lineage tracing," *BMC Bioinformatics*, vol. 15, pp. 217, 2014.

[4] H. Liu, J. Lu, J. Feng, and J. Zhou, "Learning deep sharable and structural detectors for face alignment," *IEEE Transactions on Image Processing*, vol. 26, no. 4, pp. 1666-1678, 2017.

[5] R. Fernandez, P. Das, V. Mirabet, E. Moscardi, J. Traas, and Jean-Luc Verdeil, G. Malandain, C. Godin, "Imaging plant growth in 4D: robust tissue reconstruction and lineaging at cell resolution," *Nature Methods*, vol. 7, no. 7, pp. 547-553, 2010.

[6] M. Liu, A. Chakraborty, D. Singh, R. K. Yadav, G. Meenakshisundaram, G. V. Reddy, and A. K. Roy-Chowdhury, "Adaptive cell segmentation and tracking for volumetric confocal microscopy images of a developing plant meristem," *Molecular Plant*, vol. 4, no. 5, pp. 922-931, 2011.

[7] M. Liu, A. K. Roy-Chowdhury, and G. V. Reddy, "Robust estimation of stem cell lineages using local graph matching," *Computer Vision and Pattern Recognition Workshops, 2009 IEEE Computer Society Conference on*, 2009, pp. 194-201.

[8] M. Liu, P. Xiang, and G. Liu, "Robust Plant Cell Tracking Using Local Spatial-Temporal Context," *Neurocomputing*, vol. 208, pp. 309-314, 2016.

[9] B. C. Arvind, S. K. Nagaraj, C. S. Seelamantula, and S. S. Gorthi, "Active-disc-based Kalman filter technique for tracking of blood cells in microfluidic channels," *Image Processing (ICIP), 2016 IEEE International Conference on*, 2016, pp. 3394-3398.

[10] K. Li, E. D. Miller, M. Chen, T. Kanade, L. E. Weiss, and P.G. Campbell. "Cell population tracking and lineage construction with spatiotemporal context," *Medical Image Analysis,* vol. 12, pp. 546–566, 2008.

[11] K. Mkrtchyan, D. Singh, M. Liu, G. Venugopala Reddy, and Amit K. Roy Chowdhury, and M. Gopi, "Efficient cell segmentation and tracking of developing plant meristem," *IEEE International Conference on Image Processing*, 2011, pp. 2165–2168.

[12] R. Bise, Z. Yin, and T. Kanade, "Reliable cell tracking by global data association," in *Biomedical Imaging: From Nano to Macro, 2011 IEEE International Symposium on*, 2011, pp. 1004–1010.

[13] L. S. Ong, M. H. A. Jr, and H. H. Asada, "Tracking of cell population from time lapse and end point confocal microscopy images with multiple hypothesis Kalman smoothing filters," *Computer Vision and Pattern Recognition Workshops, 2010 IEEE Computer Society Conference on*, 2010, pp. 71-78.