3D Tracking of cell lineages from 4-D fluorescence imagery of stem-cell niche

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Shoot apical meristem (SAM) stem-cell niche, in plants, is a dynamic multilayered structure consisting of about 500 cells and it provides cells for all the above-ground plant structures. SAM has been divided into distinct functional domains based on differential gene expression patterns and growth patterns. The stable population of stem-cells are maintained through regulated patterns of cell division and differentiation, mediated by cell-cell communication machinery. Deciphering the underlying principles regulating stem-cell homeostasis within interconnected network of cells requires the development of computational models which incorporate growth dynamics. Understanding the growth dynamics requires the development of computational platforms which are capable of automatically tracking cell division patterns from fluorescent 4-D images acquired by using laser scanning confocal microscopy.

We are currently, utilizing 4-D fluorescence image stacks in which cell outlines are labeled with yellow fluorescent protein (YFP) marker to track cell division events. We are exploring algorithms for tracking the *3D structure of the cells as a single entity* and identifying the instants of cell division, which manifest themselves as changes of topology of the structure. This requires developing dynamical models for the describing cell growth, estimating the parameters of these models on-line, and computing the similarity between patterns in 3D. Global tracking methods relying on correlation methods, information theoretic methods or annealing-based methods are often sufficient to get the correspondences between the cells but they may fail to identify cell divisions which may happen only in a few isolated cells [1]. To identify such changes of topology, level set based approaches can be used, but they need to be robust to tracking the overall structure whose geometry can be quite complex.

Our approach is to use a combination of global tracking methods with the techniques that can model the changes of topology. We model the shape deformations in the multilayered cell structure using our previous work on this topic [3]. To this we add constraints to check for topology changes and identify the locations where such changes happen. All of this is done in 3D which allows us to look for correspondences in neighboring image stacks thus accounting for the changes in location due to the growth of the plant [2]. The final output is a set of tracked cells in 3D and the locations of the cells where there are divisions.

The first step in this process is segmentation of the cells in a way that is consistent across the layers. For example, a cell segmented in Layer n may have a corresponding part in a neighboring layer. This consistency across the layers must also be present at different time instants. That way, we will be able to use the consistently segmented layers as inputs to the tracker. This way, errors in segmentation in one layer will have minimal effect on the overall tracked output as a cell division may be identifiable at some other layer. To demonstrate this idea, we show some preliminary results on multi-layer cell segmentation at different time instances in Figure 1.

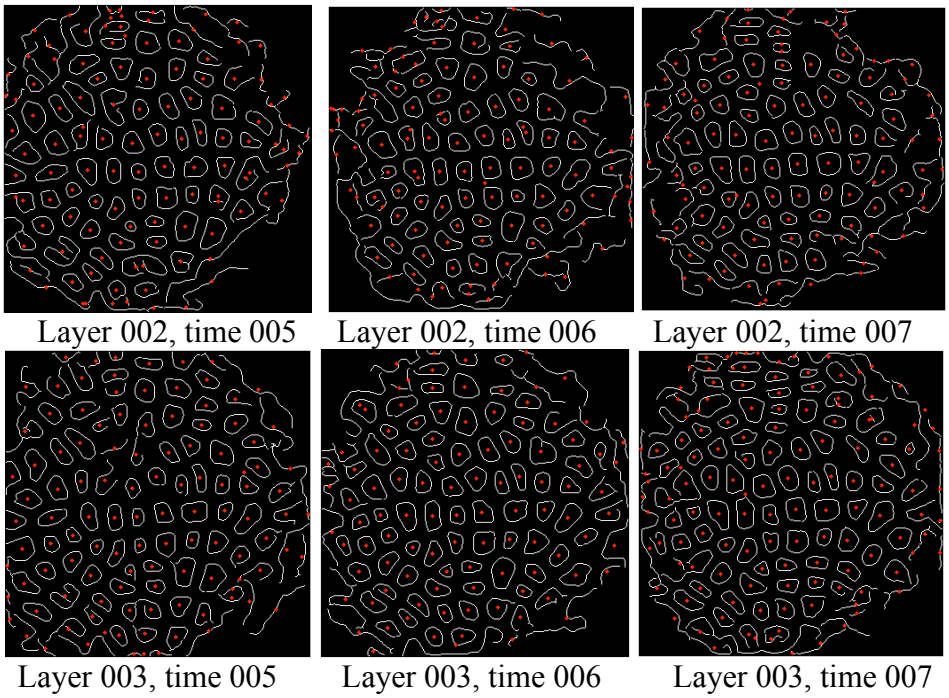

Figure 1: Segmentation results of a multi-layered structure. We show results for two segments and three time instants. Consistency in the segmentation across the layers will help in tracking and identifying cell divisions even if some of the segmentation results are erroneous.

The proposed work will lead to a computational environment to accomplish research tasks such as segmentation and representation of 3D cell shape, 3D tracking of cells and cell divisions, long-term tracking for identifying cell lineages. The segmentation and representation of 3D cell shapes will facilitate the quantification of cellular volumes and therefore can be used to get a measure of gene expression or protein concentrations. The 3D tracking of cells and cell divisions will lead to computational models to explain the causal relationships between cell deformation dynamics, cell growth and cell division patterns. The long-term tracking of cell lineage patterns would help in probing the effects of local control of cellular dynamics on morphogenesis and gene expression dynamics within the developing SAM stem-cell niche.

References:

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