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A Computational Modeling Framework for the Arabidopsis Shoot Apical Meristem

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The computable plant project is developing an end-to-end research and modeling framework for the Arabidopsis shoot apical meristem with the goal of producing forward simulations that accurately predict and visualize meristem growth. We observe several cell type specific GFP-markers for growth and differentiation in real-time in live plants with a dedicated confocal laser scanning microscope. We are observing the spatial and temporal relationships between different genes and cell lineages in an effort to understand how primordial cells are progressively specified. Nuclear positions are inferred computationally via a gradient descent algorithm applied to image intensity. A watershed algorithm is used in combination with Voronoi diagrams for image segmentation: when cell membranes are visible, they are detected from the gradient of image data, and when the walls are not visible, they are inferred by the Voronoi diagram. Nearest neighbor interactions can be inferred via the corresponding Delaunay triangulation. The correspondence between cells at successive time points uses deterministic annealing and a softassign algorithm with clocked objectives to produce an optimizing network and a corresponding energy function. The energy function used for cell tracking determines cell correspondence while estimating the mapping functions such as affine and thin-plate spline transformations for cell growth and division history. Using a combination of computational modeling and image processing techniques we then infer specific signal transduction network (STN) data and fit mathematical models to produce two- and three-dimensional visualizations of the growing SAM. We are currently investigating several different areas: cell differentiation and meristem growth (based on CLV1/CLV3 and WUS); phyllotaxis (based on Auxin, PIN, and PIN1 concentrations and polarity); and SAM organ polarity(based on REV, MIR, KAN and other players). Cellerator is used to model STNs, taking as its input a set of known and/or hypothesized biochemical reactions and genetic regulatory interactions in an arrow based format, and translating them into a system of differential equations. An automated code generator links the ODEs to an efficient simulation engine and generates executable computer programs. With this infrastructure we then produce forward simulations and their corresponding 3D visualizations. The work described in this abstract was performed at Caltech and funded by NSF Grant 0330786.