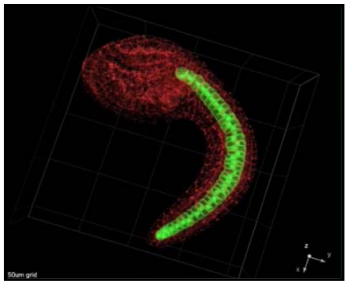
Short description of my research interests

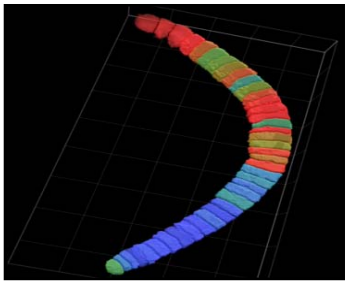
My interdisciplinary research focuses on advancing the state of the art in imaging, pattern recognition and data mining. I am currently developing new image analysis and processing technologies aimed at a better understanding of the complex biological processes which occur at the cellular and sub-cellular level. My work includes analyzing, processing and understanding the biological images obtained by confocal, scanning laser, atomic force, differential interface contrast, optical and polarized microscopy.

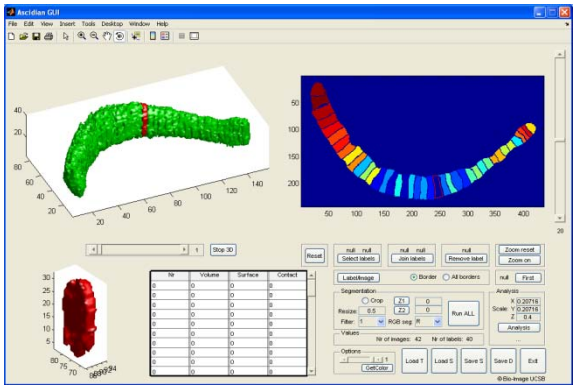
My current research is focused on development and application of image analysis and processing method in biology and medicine. I am working on following research projects:

Segmentation and analysis of notochord cells in 3D, observed using confocal microscopy.

The notochord is an embryonic structure that undergoes dramatic cell shape changes as it itself changes shape from a roughly isodiametric primordium of mesenchymal cells to a long extended rod. I developed an automated method for the 3D segmentation of individual notochord cells, and present our prelimary findings applying this method to a multi-gigabyte confocal image collection of phalloidin-stained ascidian embryos.





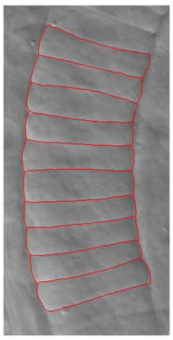


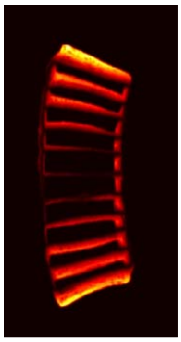
The proposed approach is based on mathematical morphology. The algorithm is able to reconstruct topological images and provide precise statistical data about the notochord cells. The proposed approach can be easily extended to any other tissues stained in a similar way.

Morphomic analysis of the sample chordate

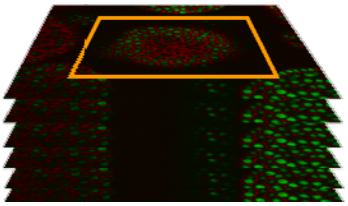
A quantities systems-level understanding of chordate morphogenesis will require the acquisition and analysis of extremely large multi-dimensional (3D+time) image sets with the challenging requirements of having sufficient resolution to capture the behavior of single cells while still encompassing entire developing tissue or organisms.

I am working on analysis and processing of DIC microscope images of chordate. A reasonable, albeit gappy, edge map is provided by convolution based on directional derivatives of Gaussian, and individual notochord cells. The cells are segmented using network snake, which is a modified parametric active contour that can be initialized as a network with a predefined topology. In addition to many standard parameters that can be derived from segmented data, a mapping of strictly local cell motility can be generated.

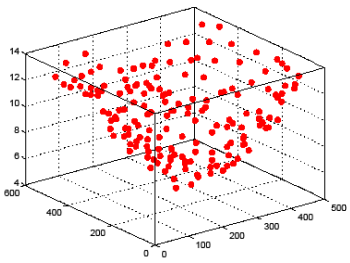


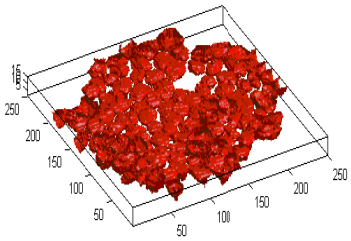


Automated detection of cell nuclei and membrane in 3D laser scanning confocal microscope images of the Arabidopsis



Identification of cell nuclei is a fundamental operation, nuclei centroids are used in a wide gamut of biological and medical analysis. Although, counting is usually done manually on 2-D images, it becomes extremely time consuming and practically impossible task with 3-D images. Furthermore, the scale difference between X-Y and Z dimensions might cause manual counting to be subjective and highly inconsistent, thus it's important to build robust and reliable automatic nuclei detector.





For my experiments whole mount Arabidopsis images are used. The proposed method uses Gaussian and the inverted Laplacian of Gaussian (LoG) 2-D and 3-D kernels for template matching. The nuclei are modeled as circular objects (although they are mostly ellipsoids) to achieve rotation invariance. In 3-D it is common that voxel size in the Z axis can be orders of magnitude larger than that of the X/Y axis. Therefore, to increase detection accuracy, the Z axis interpolation takes place prior to detection. Detected nuclei are used in the membrane segmentation procedure based on mathematical morphology.

Bio-Image Semantic Query User Environment

I am one of the core developers of the Bisque System (Bio-Image Semantic Query User Environment). Bisque is an ongoing project with the goal of providing an online platform for data exchange and exploration of biological images. The Bisque system supports several areas useful for imaging researchers, from image capture to image analysis and querying. The Bisque system is centered on a distributed database of images and metadata. Search and comparison of datasets by image data and content is supported. Novel semantic analyses are integrated into the system allowing high level semantic queries and comparison of image content.