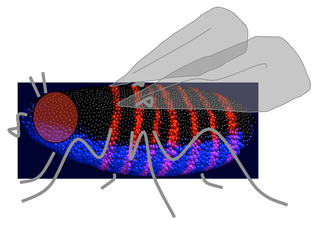
Visualization tools for three-dimensional gene expression data in *Drosophila*



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IDAV visualization and graphics research group

BDTNP Berkeley Drosophila Transcription Network Project

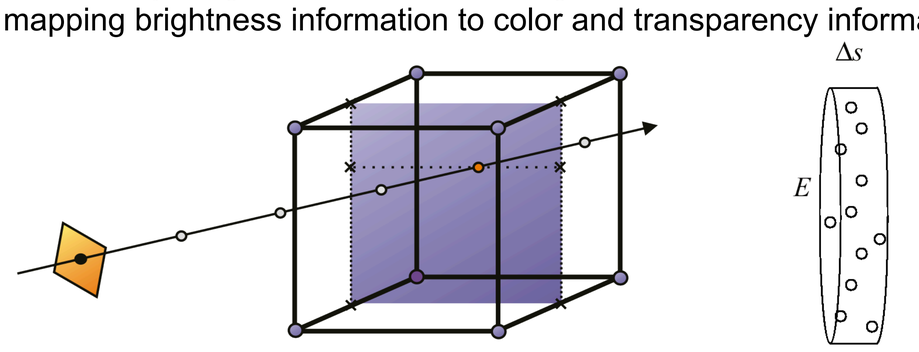
Introduction

It is intrinsically difficult to visualize complex gene expression patterns and morphology in three dimensions, especially at cellular resolution. As part of the Berkeley Drosophila Transcription Network Project (BDTNP), we are developing methods to overcome this challenge using images of whole *Drosophila* embryos. Specific tools under development permit

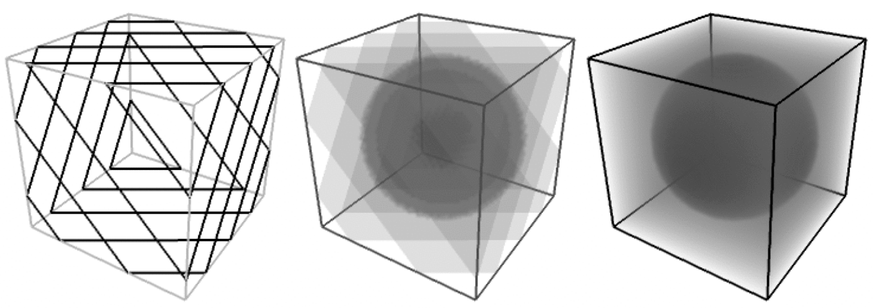
1) visualization of raw confocal microscopy data
2) interactive control and verification of the image processing algorithms and
3) visual analysis of complex gene expression patterns.

Visualization of raw confocal microscopy images

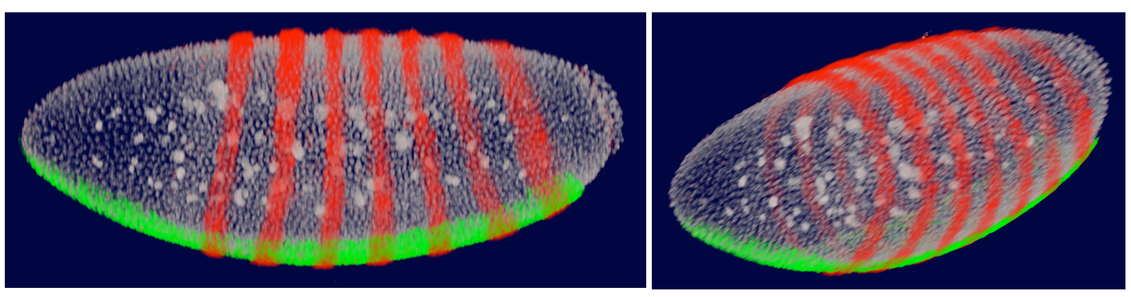
Confocal microscopy images acquired within the BDTNP typically consist of three channels, one channel that is stained for DNA using SytoxGreen™ and two channels that are stained for gene expression (e.g., ftz and sna). By adapting volume-rendering methods to multi-channel confocal microscopy data, every single channel of an image stack is rendered independently by mapping brightness information to color and transparency information.



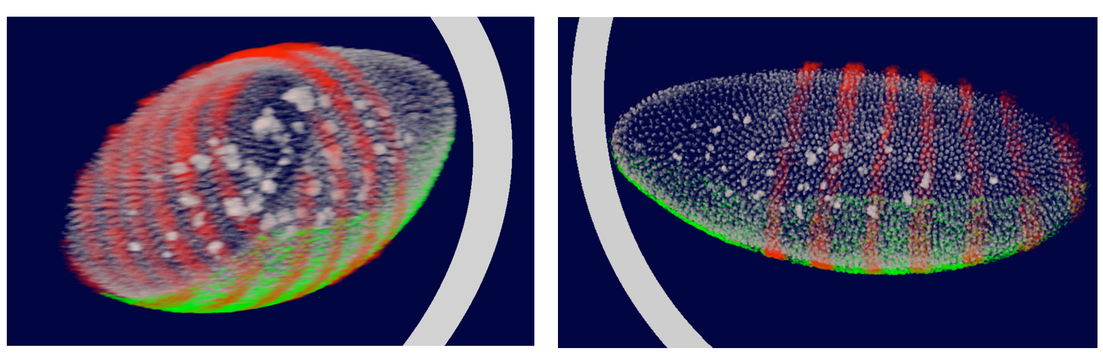
Using modern PC graphics boards, it is possible to generate volume rendered images at interactive frame rates.



Resulting colors are blended using user-specified weights, supporting seamless blending between channels, including the possibility to show all three channels simultaneously.

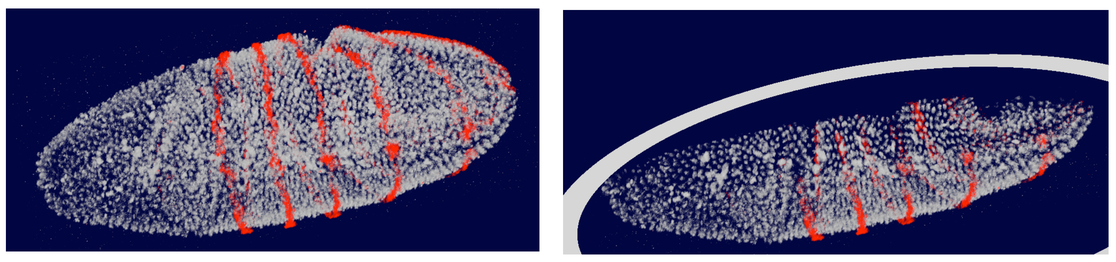


Three-dimensional slicing and rotation tools make it possible to visualize an arbitrary cross-section from an image stack, and to explore the interior of an embryo



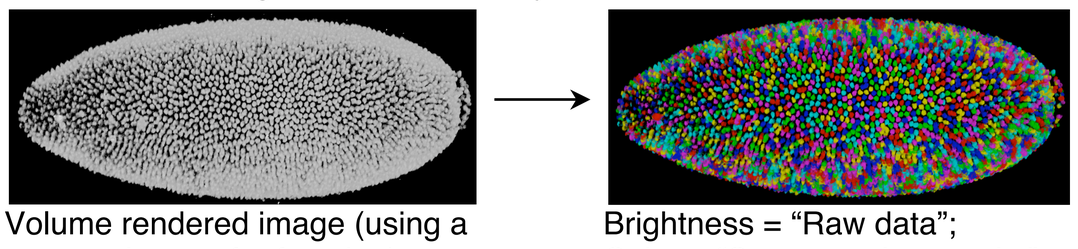
Visualization of later stage embryos

Our tools can also be used to visualize embryos in later developmental stages. The more complex morphology makes the slicing tool particularly useful.



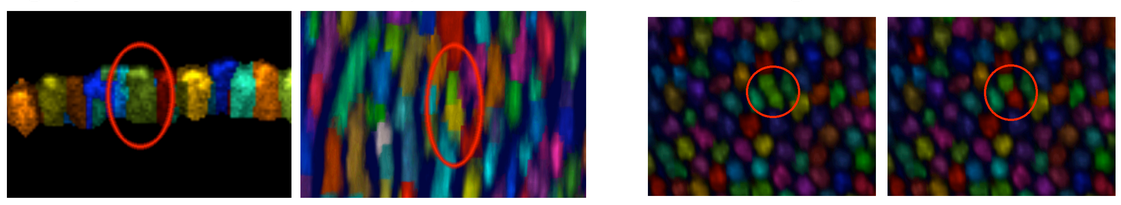
Interactive control and verification of image processing algorithms

Our volume visualization prototype has been combined with user interaction tools to support quantitative determination of the accuracy of the BDTNP's nuclear segmentation methods (see poster 358A by Luengo Hendriks et al.). Nuclei are rendered to include information obtained from a nuclear segmentation mask. It is possible to select individual nuclei interactively and identify falsely segmented objects. This work has already yielded significant improvements in segmentation accuracy.



Volume rendered image (using a gray scale transfer function)

Brightness = “Raw data”;
Color = “Segmentation results”

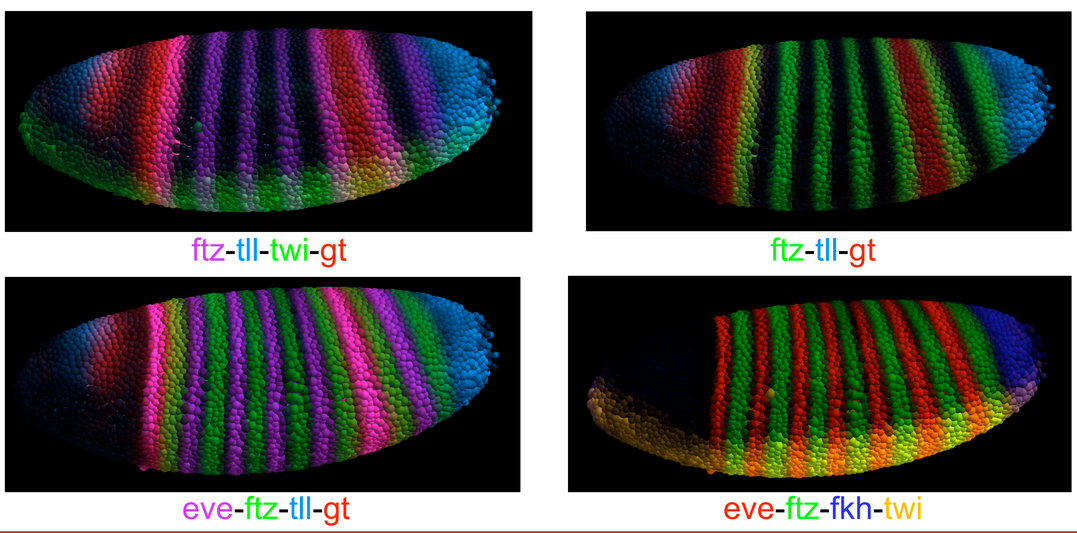


Detecting incorrectly segmented nuclei

Manual correction of segmentation results

Visualization of “point cloud” data

The BDTNP's final 3D gene expression data is in the form of matrices or "point clouds" that describe nuclear positions and their associated gene expression levels. The point cloud below describes the expression patterns for fourteen genes averaged from tens of embryos that have been registered using methods developed by Fowlkes et al. (see Poster 350B). We are developing a point cloud visualization tool that will be offered as an effective means for the fly community to access and analyze 3D expression data from the BDTNP.



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