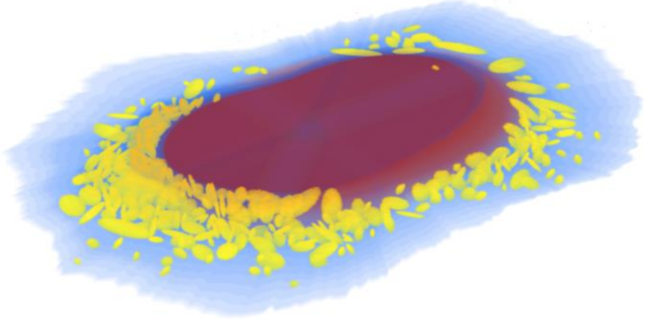
Major New Release of CellOrganizer 2.0 Published



Example cell image generated by CellOrganizer showing the nuclear membrane (red), cell boundary (blue) and individual lysosomes (yellow).

A major new release of the CellOrganizer system for creating image-derived models of cell shape and organization has just been published. The software is a major focus of research supported by the NIH through the National Center for Multiscale Modeling of Biological Systems (MMBioS). It creates statistical, generative models of cell and nuclear shape, microtubule patterns, and vesicular organelles that can be used as the basis for cell simulations (another focus of MMBioS). Generative models capture not just a description of a pattern but the ability to produce new examples of that pattern (analogously to the way in which humans capture models of letters or spoken words not just by describing them but by learning to produce new examples). Support for CellOrganizer has also come from NIH grants GM075205 and GM090033. Specific improvements or additions in the new release include:

Cell image synthesis

- Improved vesicular organelles model
  - Eliminate object/object and object/boundary overlap during generation
- Ability to combine models learned from images of different resolution, and synthesize images at desired resolution
- Ability to synthesis random walks in shape space from diffeomorphic models of cell and nuclear shape
  - Including directed random walks using Willmore energy and shape space density

Model training

- New capabilities for cell and nuclear shape model learning
  - Build nuclear models from images without nuclear marker
  - Build joint diffeomorphic models of cell and nuclear shape
- Per-cell representations for easy model building and comparison

Other

- Export to SBML-spatial and mesh formats for interfacing with tools such as CellBlender and VCell.
- Parallelization of model learning pipeline

- Reporter tools
    - assess learned models
    - compare models
    - compare per cell parameters within or across models