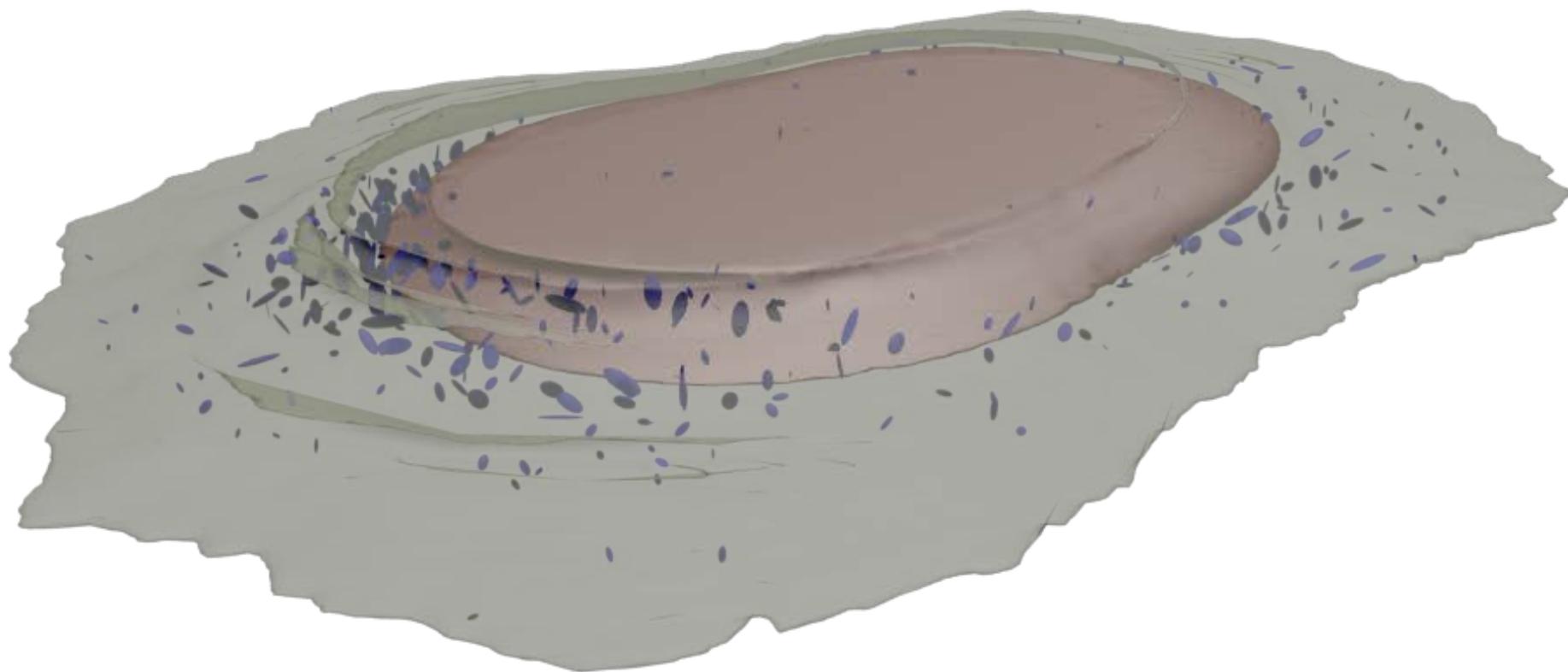
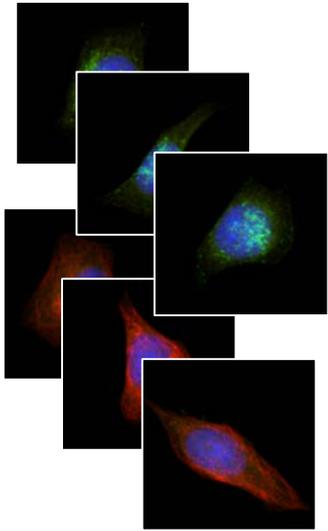


Training parametric models

Devin Sullivan



Training I/O



- Input

- Fluorescent microscopy images

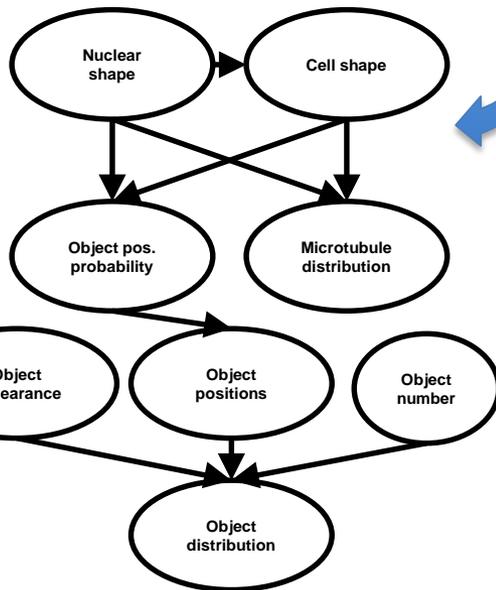
- Nuclear
- Cell marker
- Protein
- Crop

- Model parameters/options

- Protein type
- Resolution
- etc

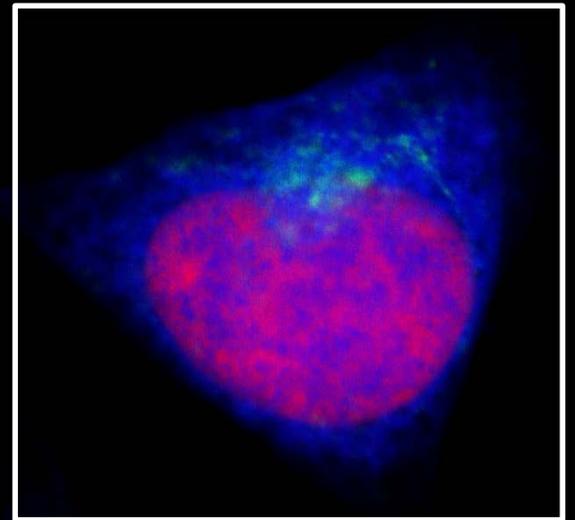
- Output

- Model with parameters that describe cell components



What's required

1. Nuclear – tagged or “hole-finding” (red)
2. Cell – cytoplasm or plasma membrane (blue)
3. Tagged protein/organelle of interest (green)
4. Cropped region (white box)



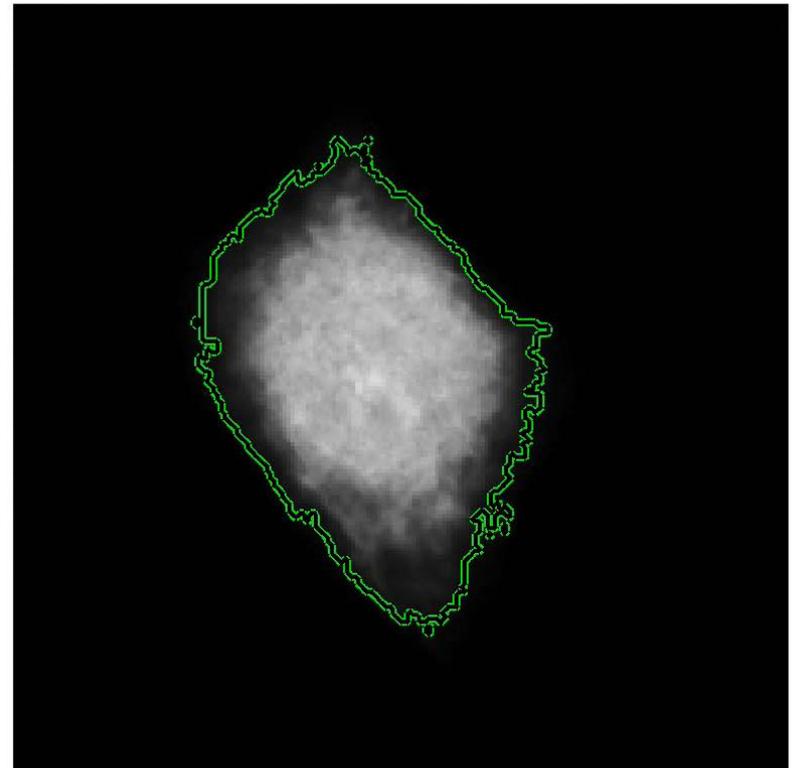
Microscopy image sources

- Experimental work
- <http://www.openmicroscopy.org/>
- www.cellimagelibrary.org
- <http://www.proteinatlas.org/>
- <http://murphylab.web.cmu.edu/data/>

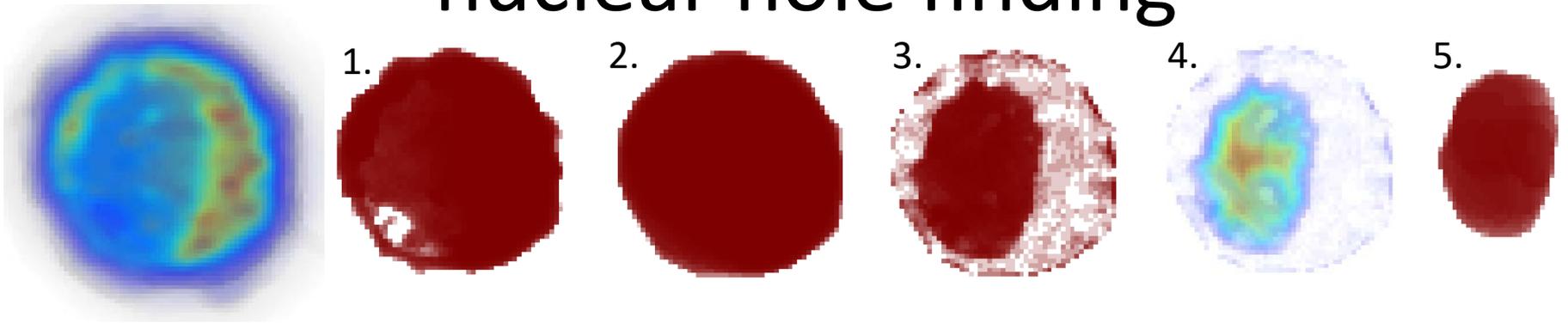
Step 1: Segmentation

- Built-in
 - Initialized using segmentation from previous slice
 - Active contour
- Pre-processed images

After 0 iterations



If no nuclear tag is present: nuclear hole finding

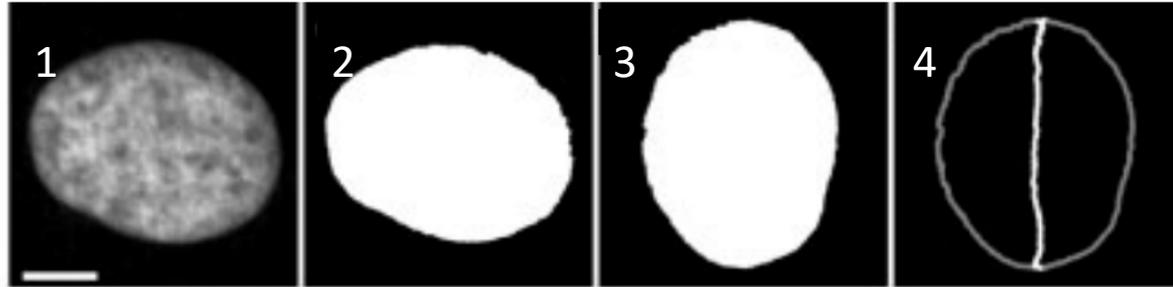


1. Threshold Image
2. Find Convex Hull
3. Nucleus is “Not Signal” within the Conv Hull
4. Distance Transform
5. Active Contour

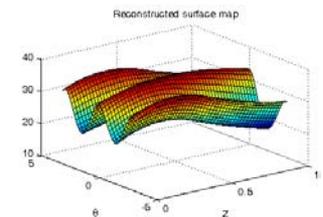
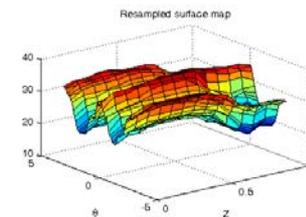
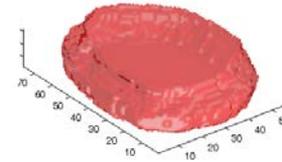


Training a nuclear model

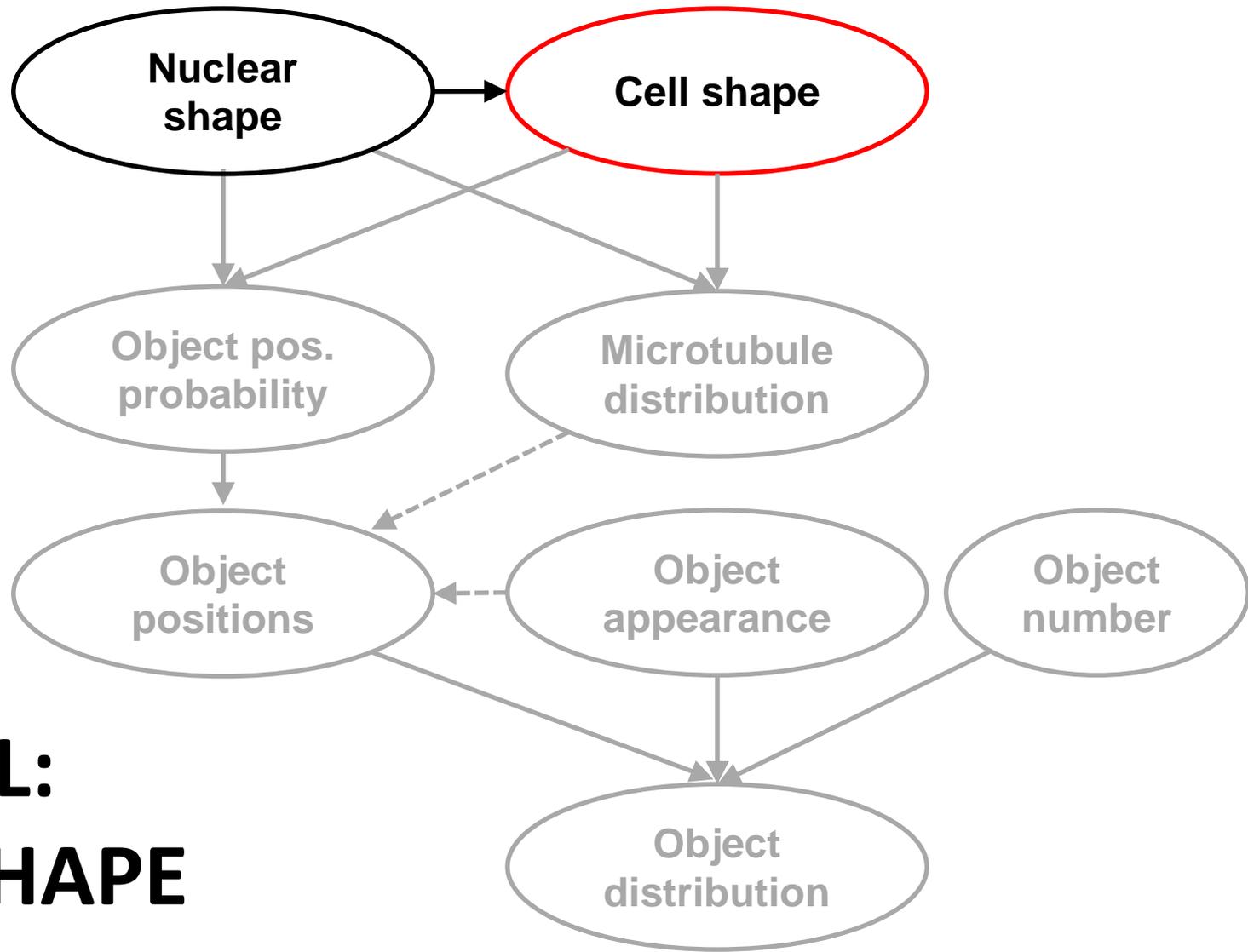
(2D) = medial axis



(3D) = spline
surface



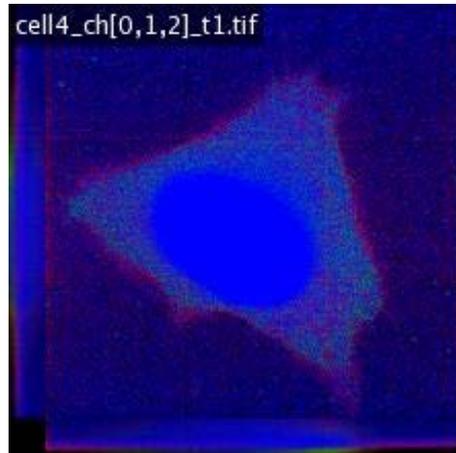
1. Read image
2. Segment nucleus
3. Orient along major axis
4. Fit medial axis or spline surface model



**MODEL:
CELL SHAPE**

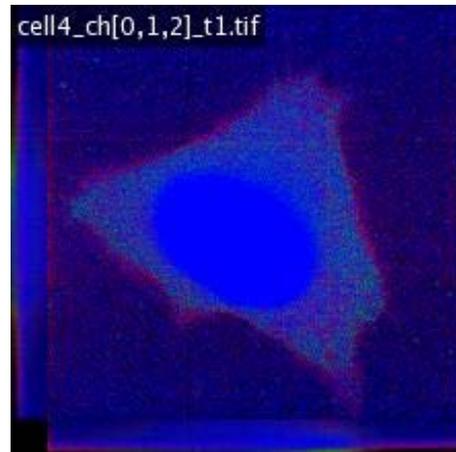
Cell segmentation

- Use active contour method for segmentation

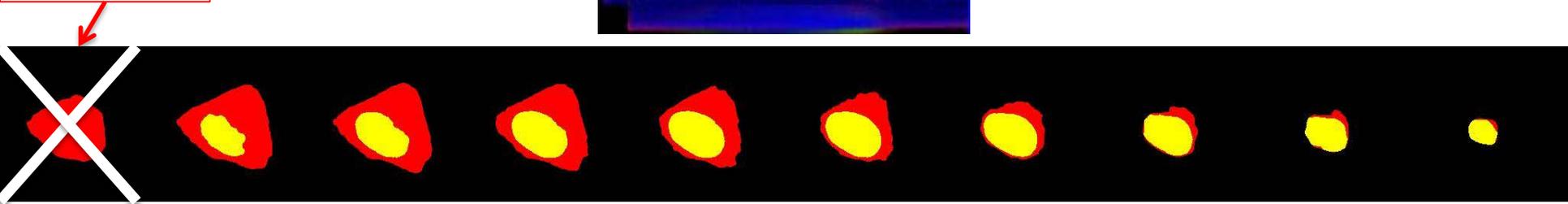


Cell segmentation

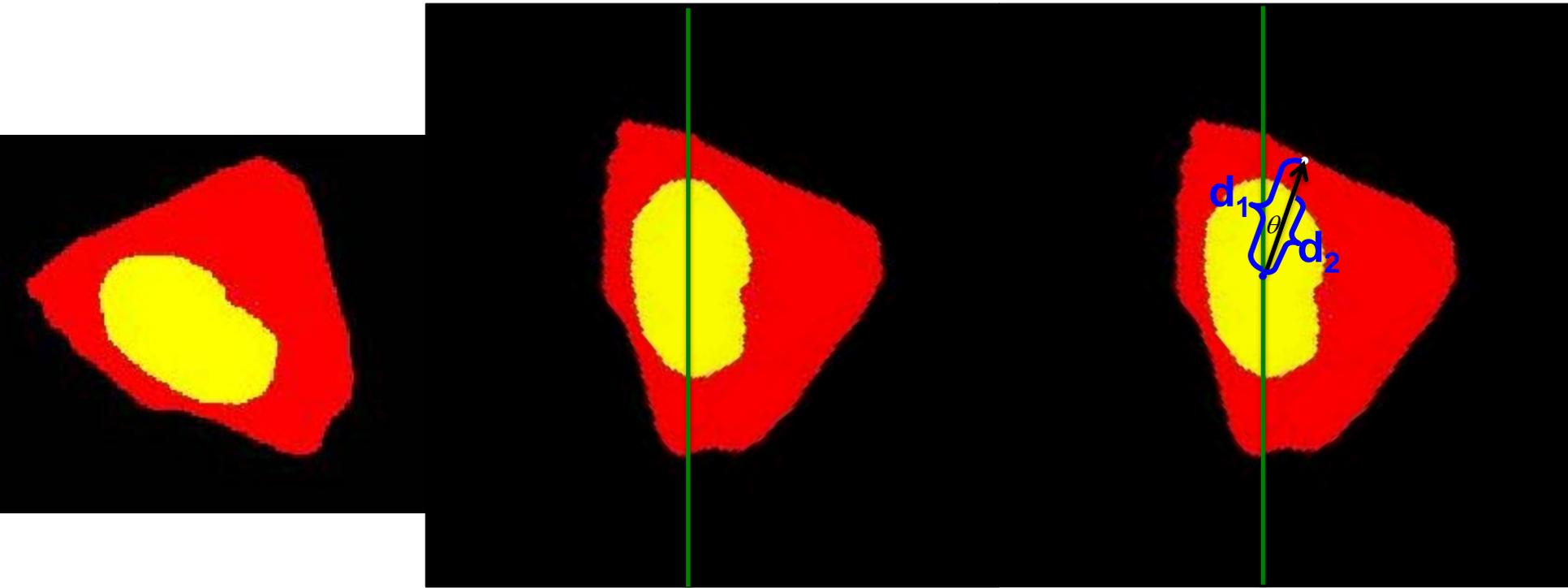
- Use active contour method for segmentation



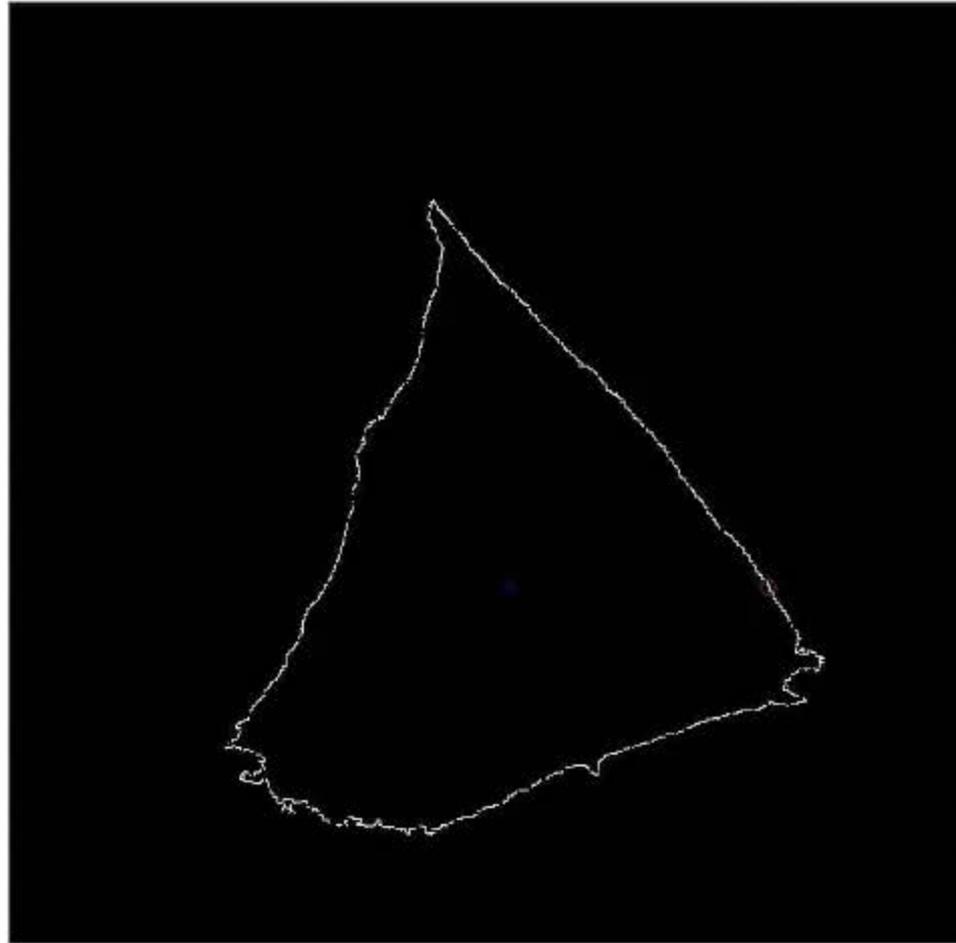
If adherent



Cell shape modeling

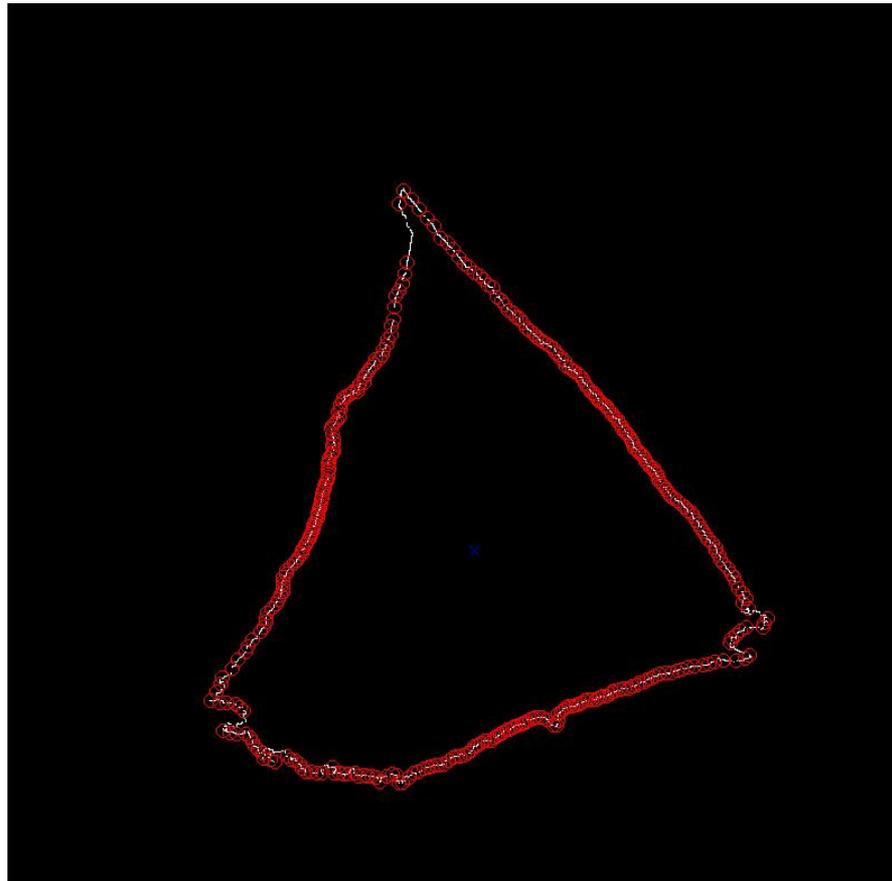


Cell “hit points”

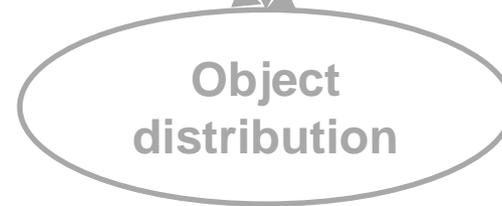
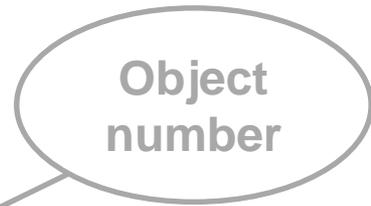
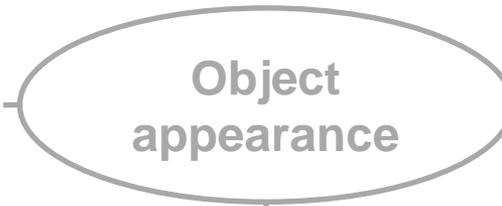
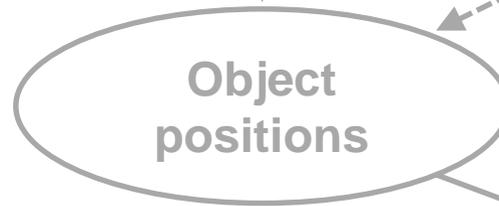
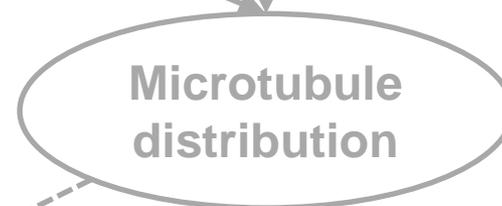
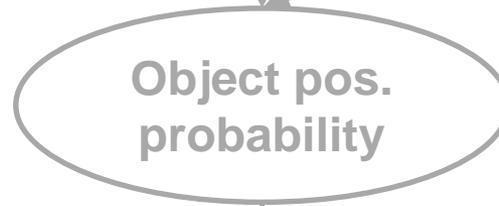
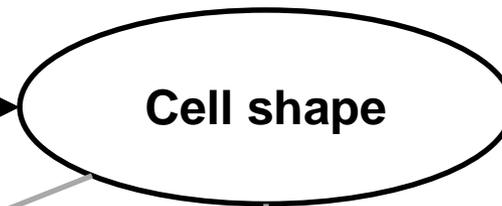
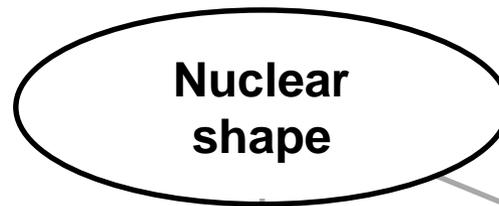


Cell “hit points”

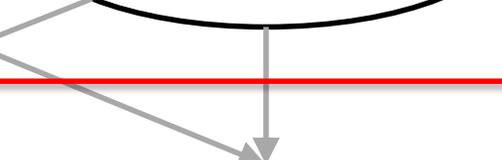
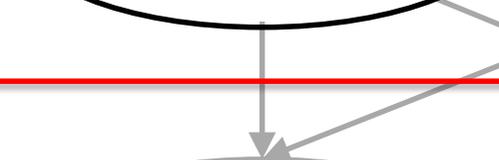
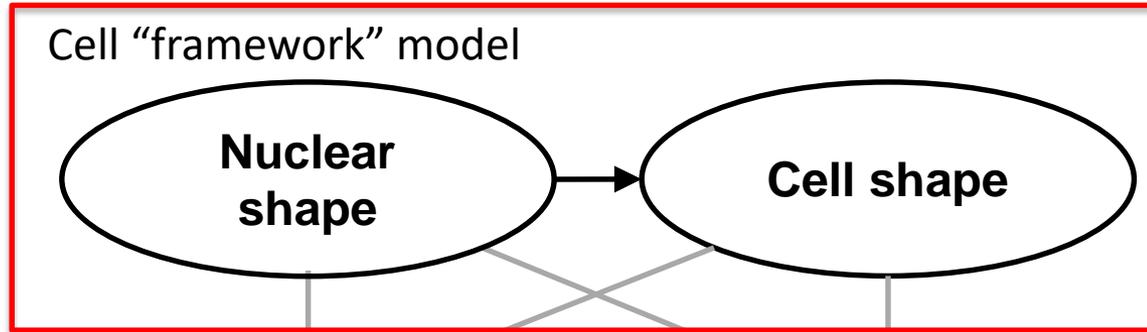
- d

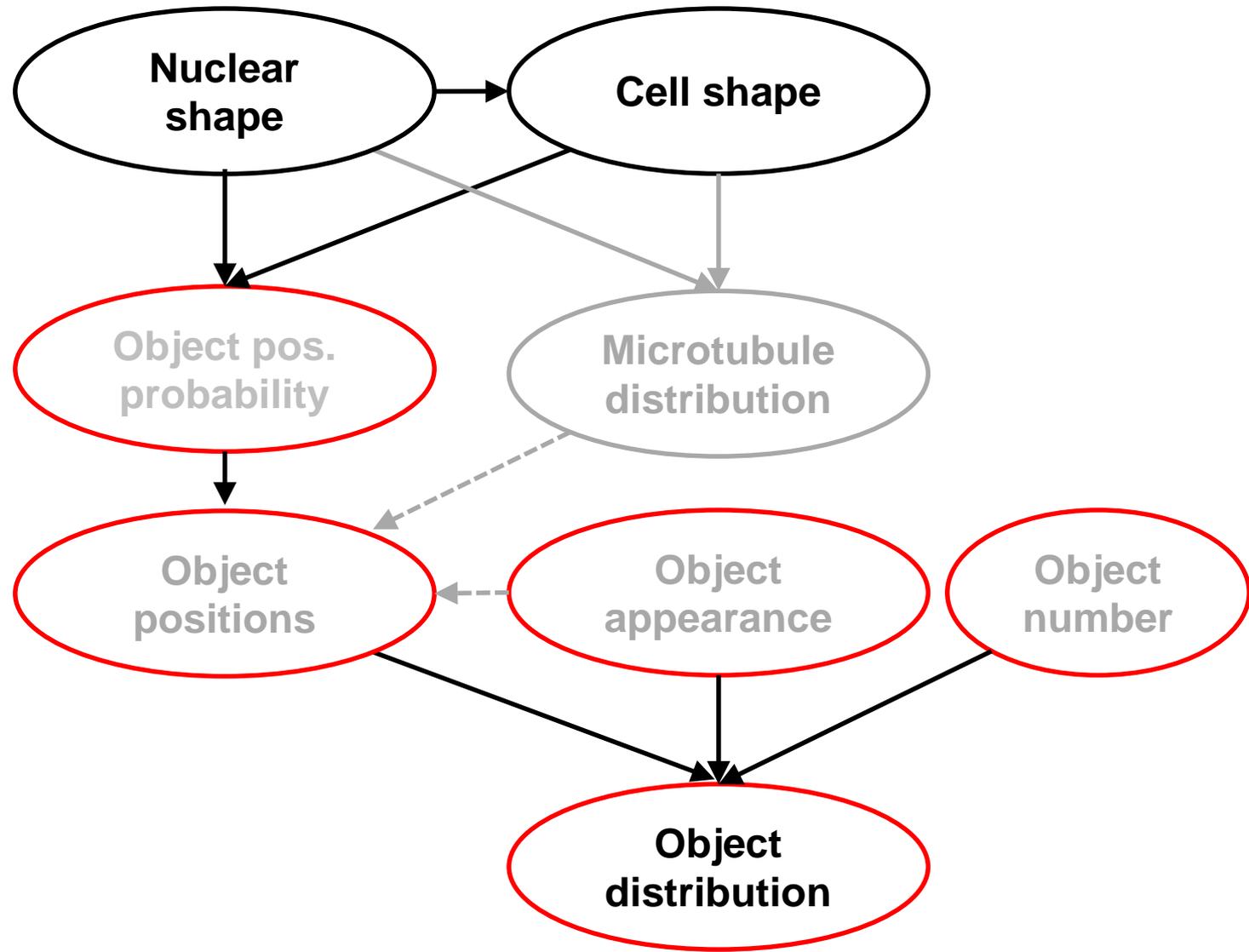


Cell "framework" model



**MODEL:
CELL SHAPE**

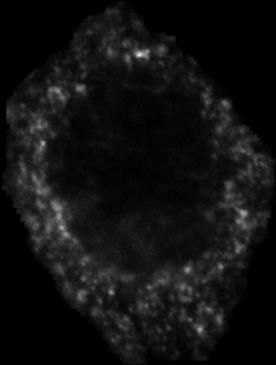




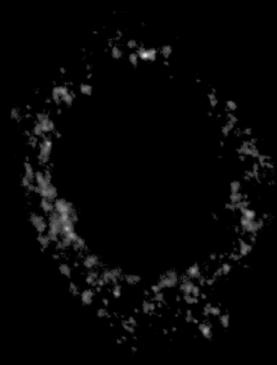
MODEL:
PROTEIN SIZE, NUMBER, LOCATION

Protein image processing

Original image



Processed image

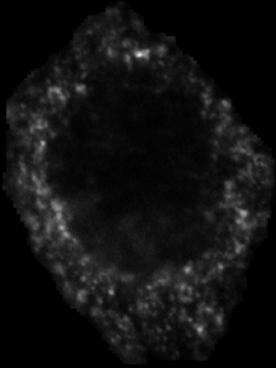


Masked objects

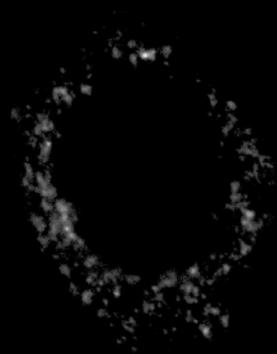


Protein image processing

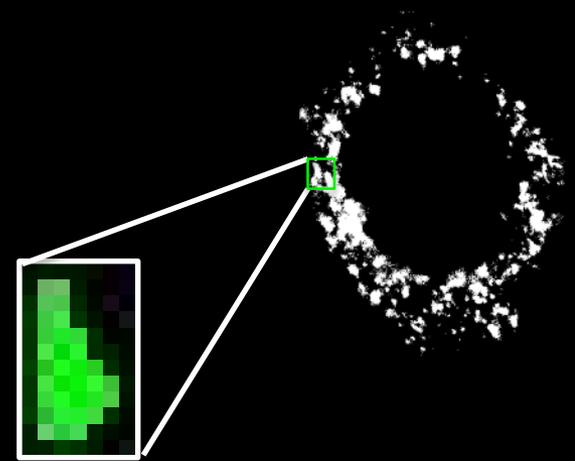
Original image



Processed image



Masked objects



Fitting Vesicular Organelles

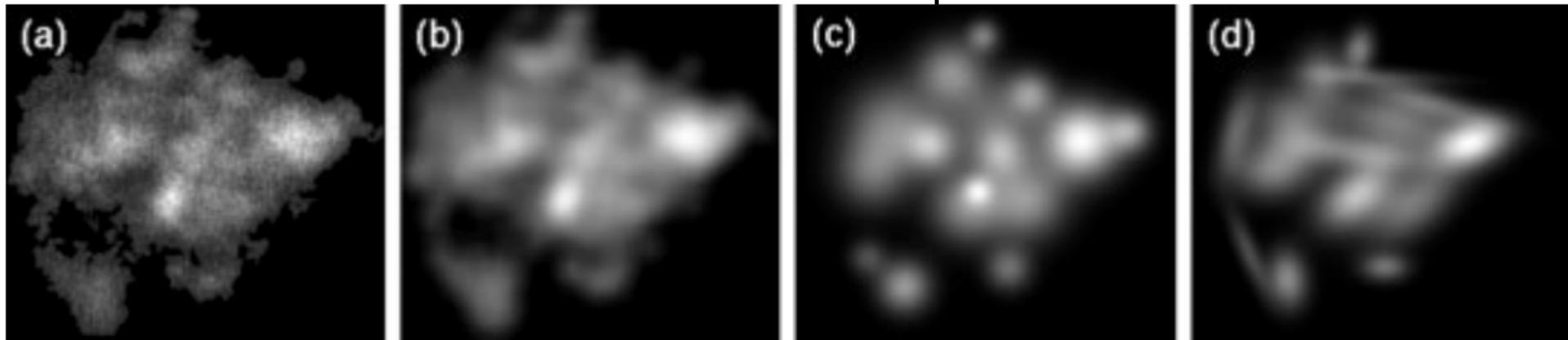
Fitted Gaussians

Original

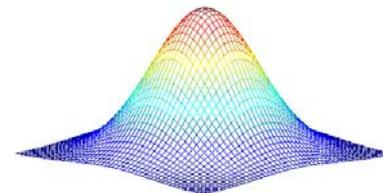
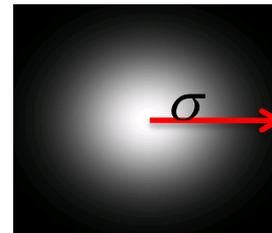
Filtered

Spherical

Full covariance



Example object



Gaussian object model parameters

Number of objects in a cell N

Object size σ_x σ_y σ_z

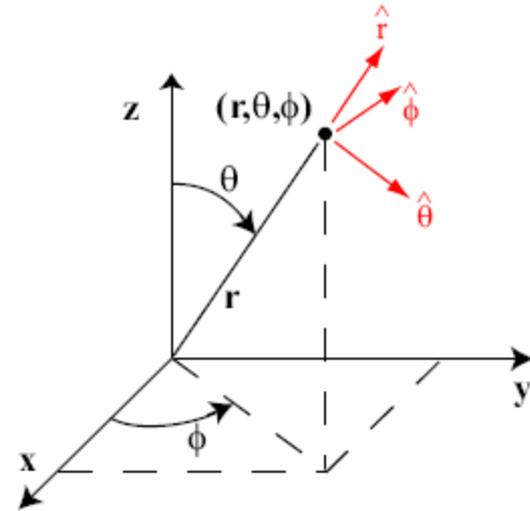
Single object fluorescence F

Protein Objects Model: Position

3D

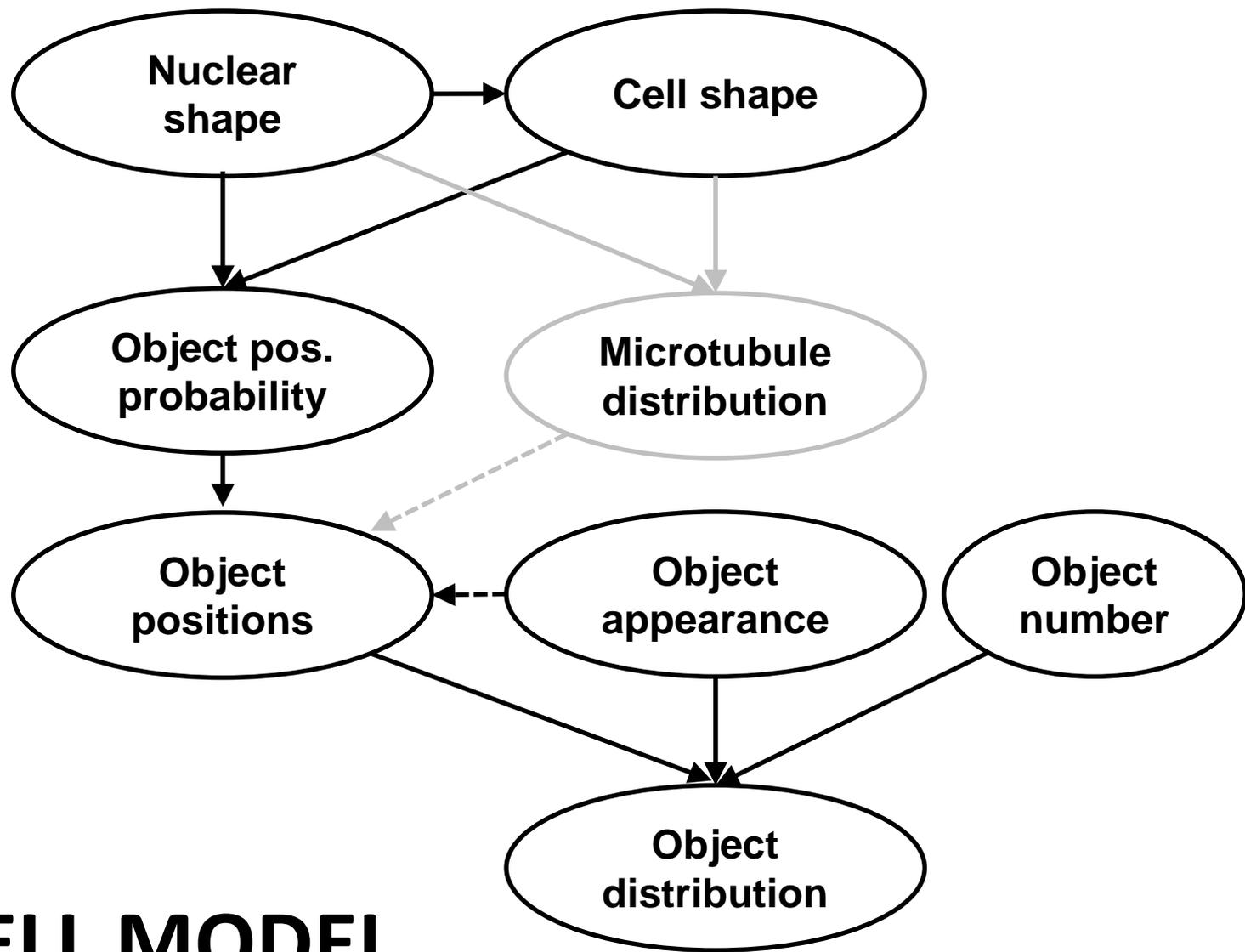
$$P(r, a) = \frac{e^{\tau(r, \theta, \phi)}}{1 + e^{\tau(r, \theta, \phi)}}$$

$$\tau(r, \theta, \phi) = \beta_0 + \beta_1 r + \beta_2 r^2 + \beta_3 \sin \theta \cos \phi + \beta_4 \sin \theta \sin \phi + \beta_5 \cos \theta$$



Radial
preference

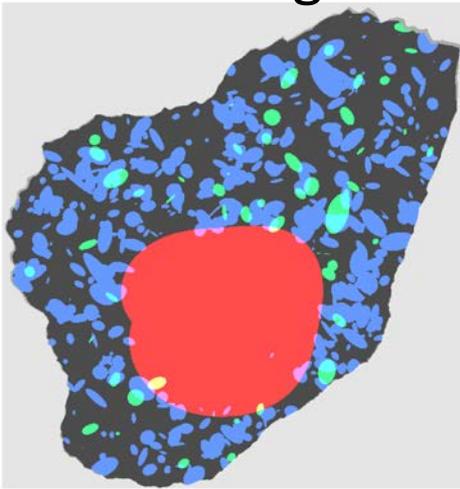
Angular
preference



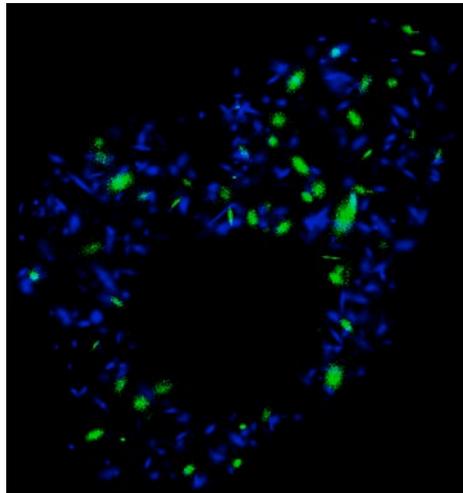
WHOLE CELL MODEL

Synthetic cells

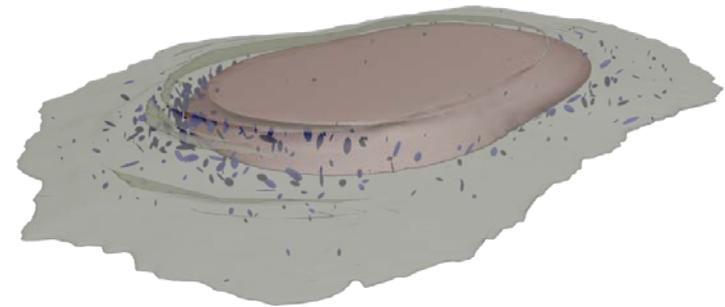
Tiff images



“Sampled” images



Idealized organelle meshes



CellOrganizer

Project Leaders



Robert F.
Murphy



Gustavo
Rohde

Major Collaborators



Klaus Palme



Christoph Wülfing



Jörn Dengjel



Hauke Busch



Melanie Boerries

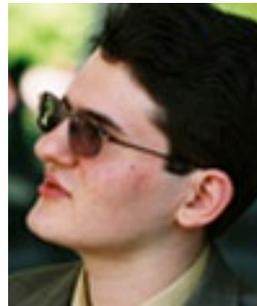


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Gregory R. Johnson



Ivan Cao-Berg

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Questions?