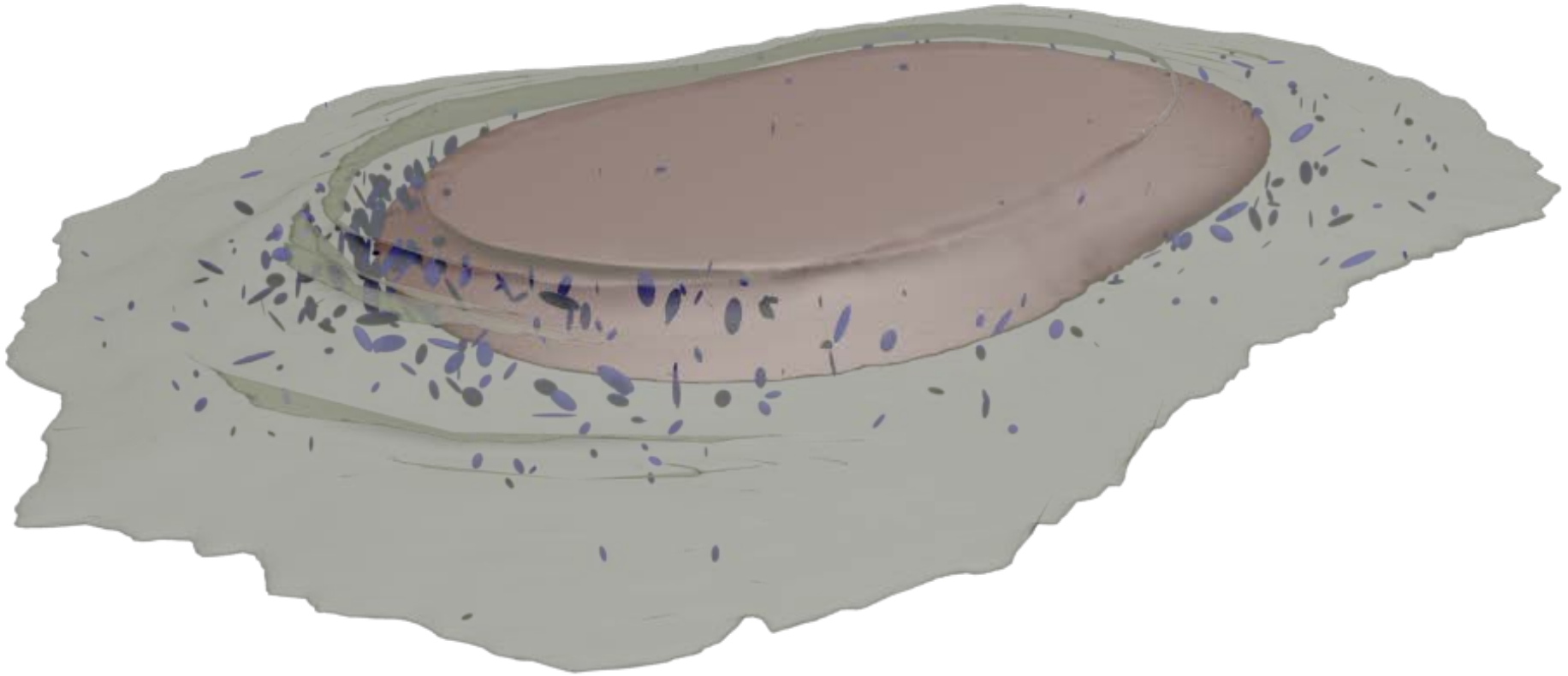
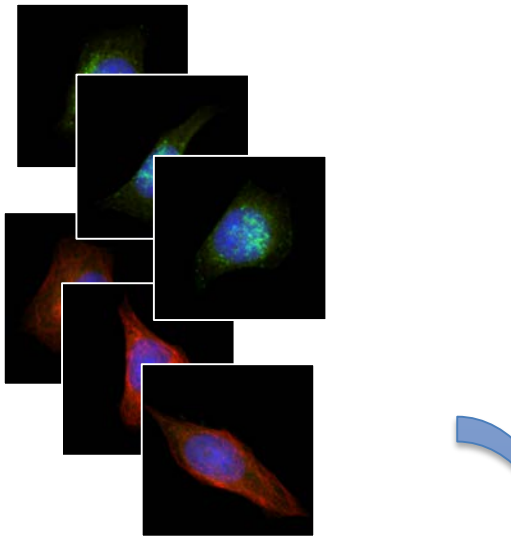
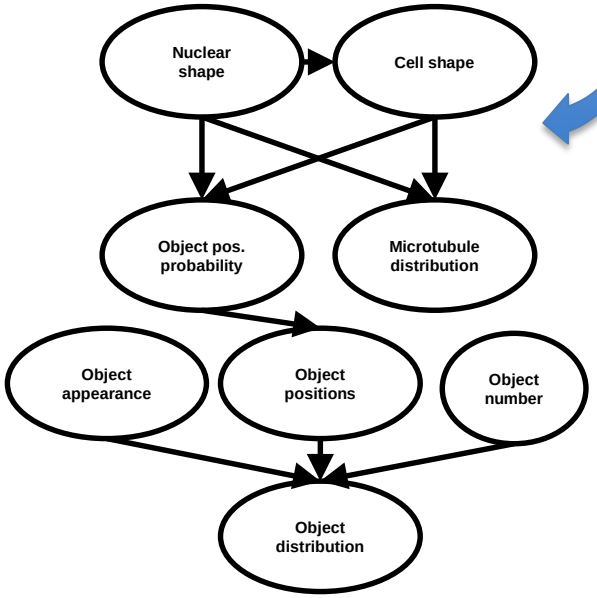
Training parametric models

Devin Sullivan



Training I/O

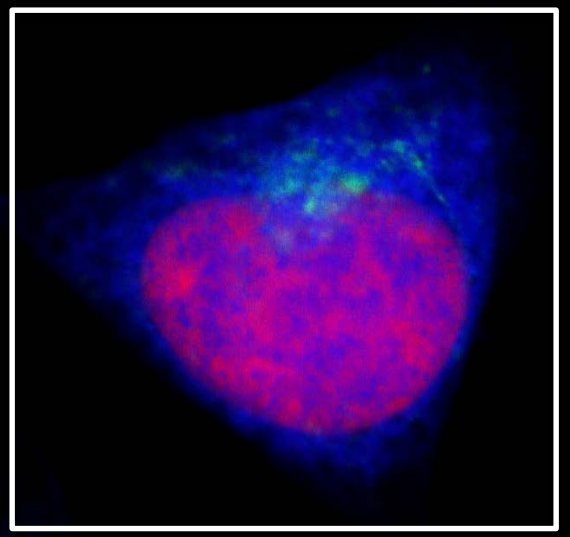




- Input
  - Fluorescent microscopy images
    - Nuclear
    - Cell marker
    - Protein
    - Crop
  - Model parameters/options
    - Protein type
    - Resolution
    - etc
- Output
  - Model with parameters that describe cell components

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)

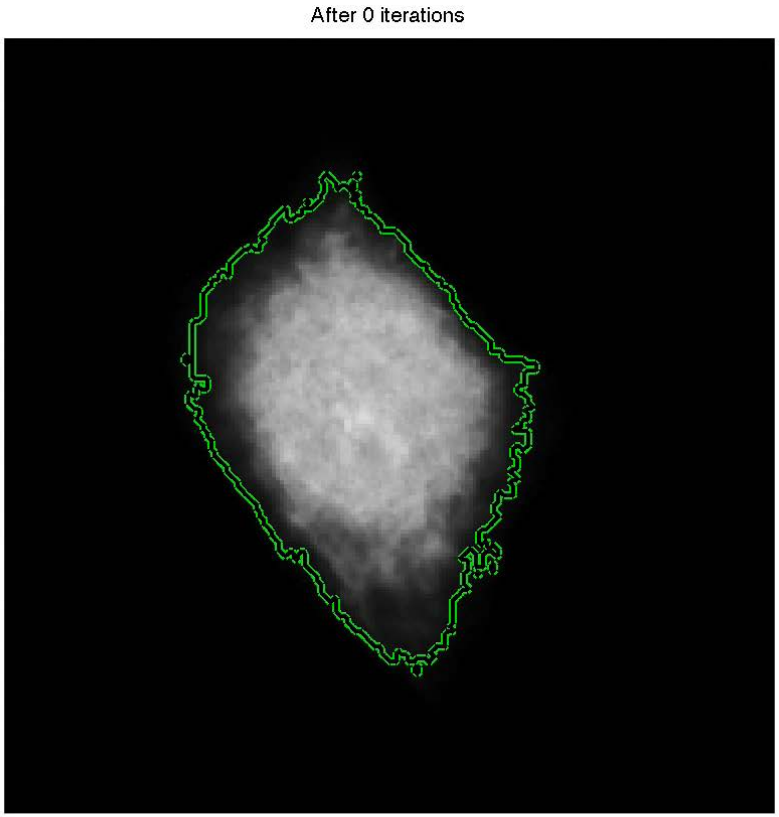


Microscopy image sources

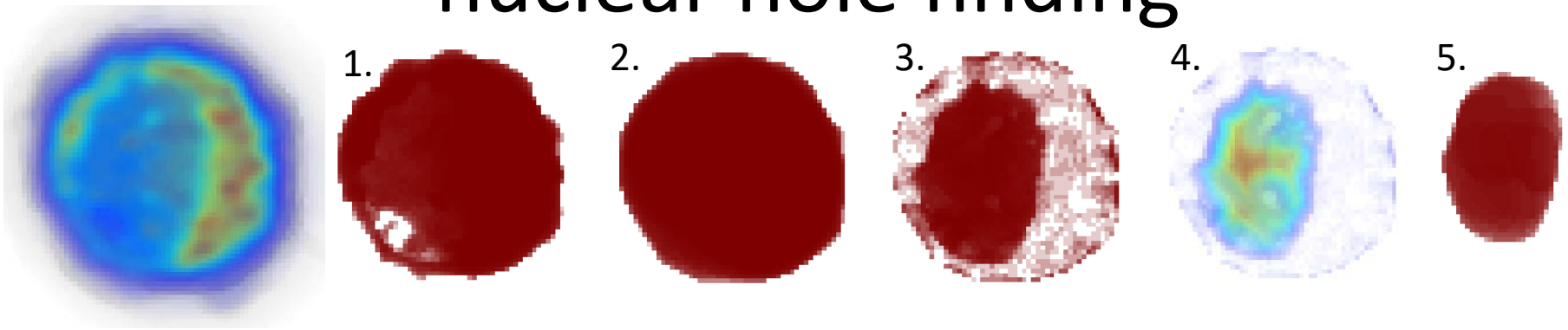
- Experimental work
- http://www.openmicroscopy.org/
- www.cellimagelibrary.org
- http://www.proteinatlas.org/
- http://murphylab.web.cmu.edu/data/

Step 1: Segmentation

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



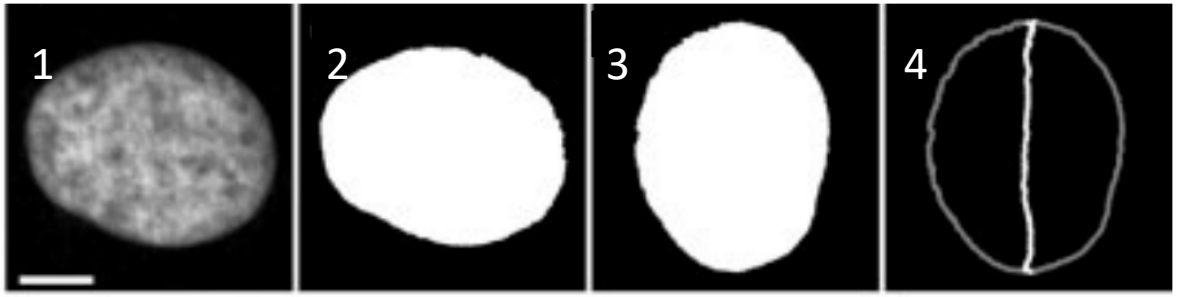
If no nuclear tag is present: nuclear hole finding



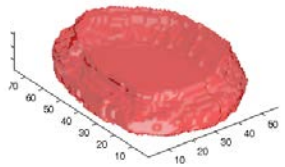
1. Threshold Image
2. Find Convex Hull
3. Nucleus is “Not Signal” within the Conv Hull
4. Distance Transform
5. Active Contour

Training a nuclear model

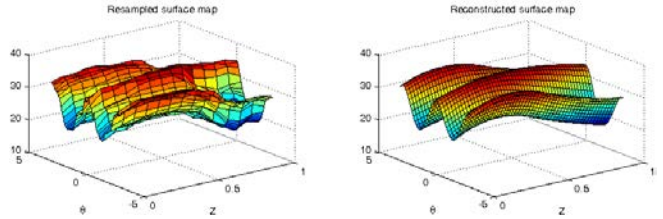
(2D) = medial axis

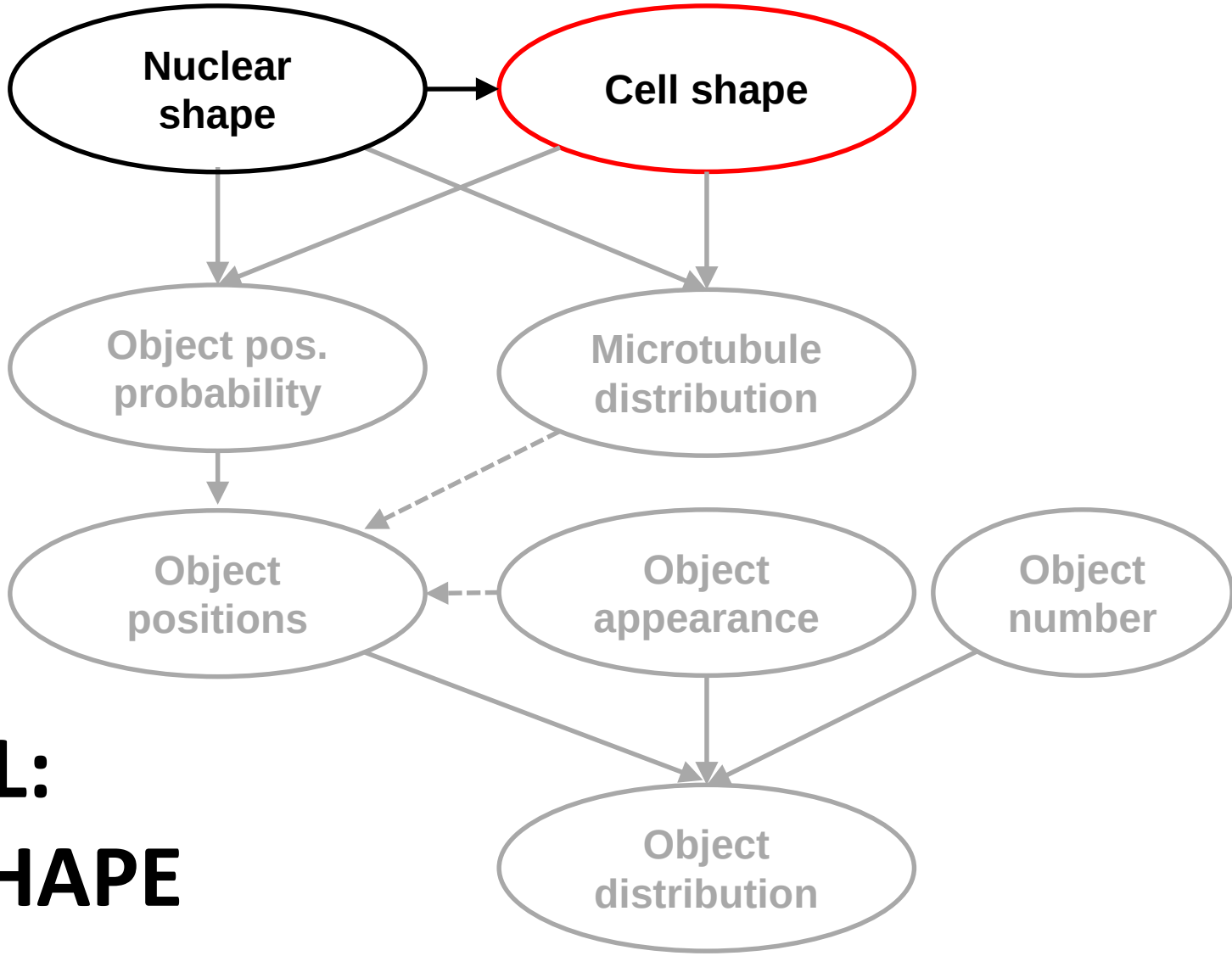


(3D) = spline surface



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

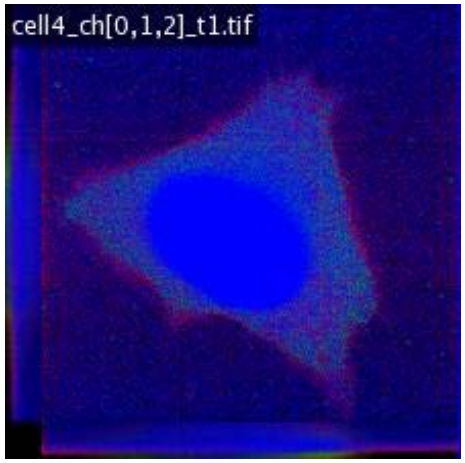


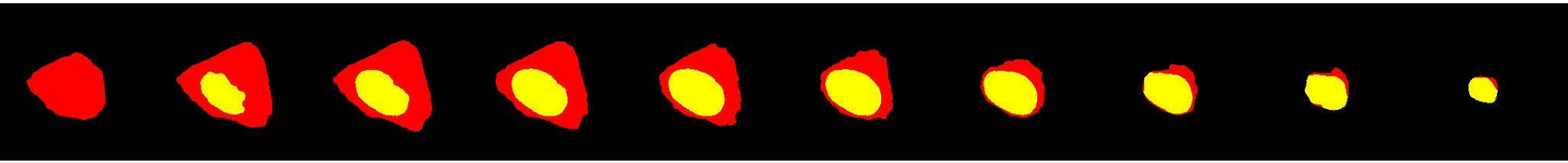


MODEL:
CELL SHAPE

Cell segmentation

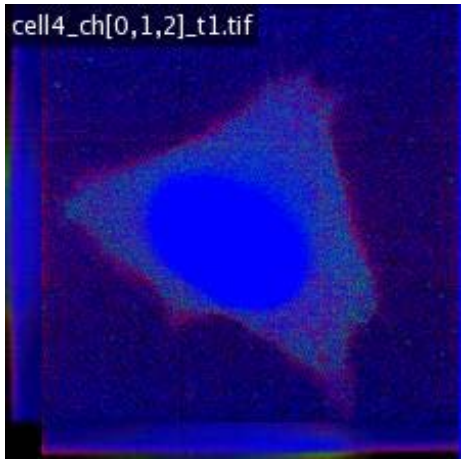
- Use active contour method for segmentation



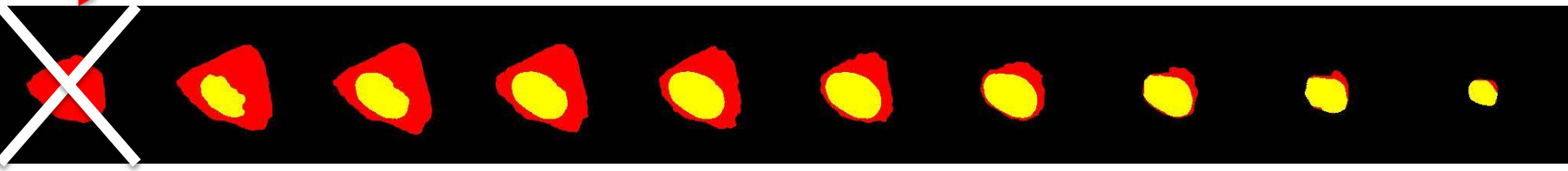


Cell segmentation

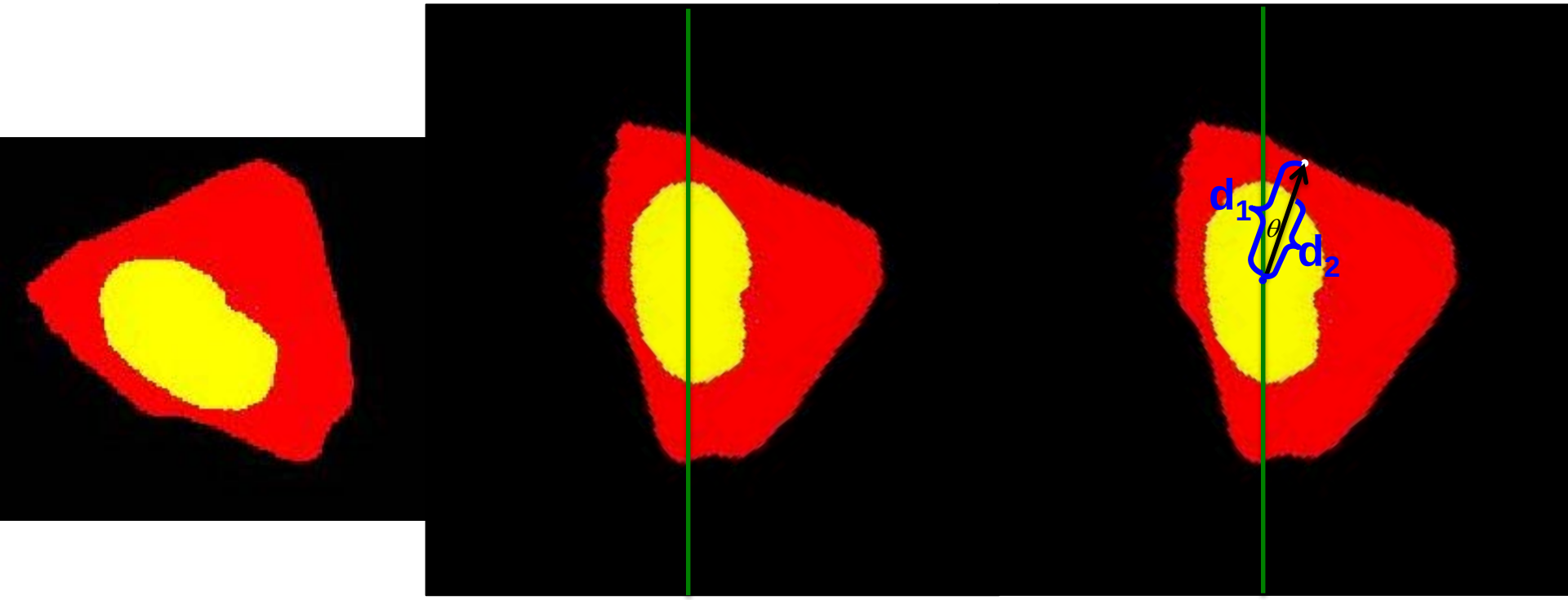
- Use active contour method for segmentation



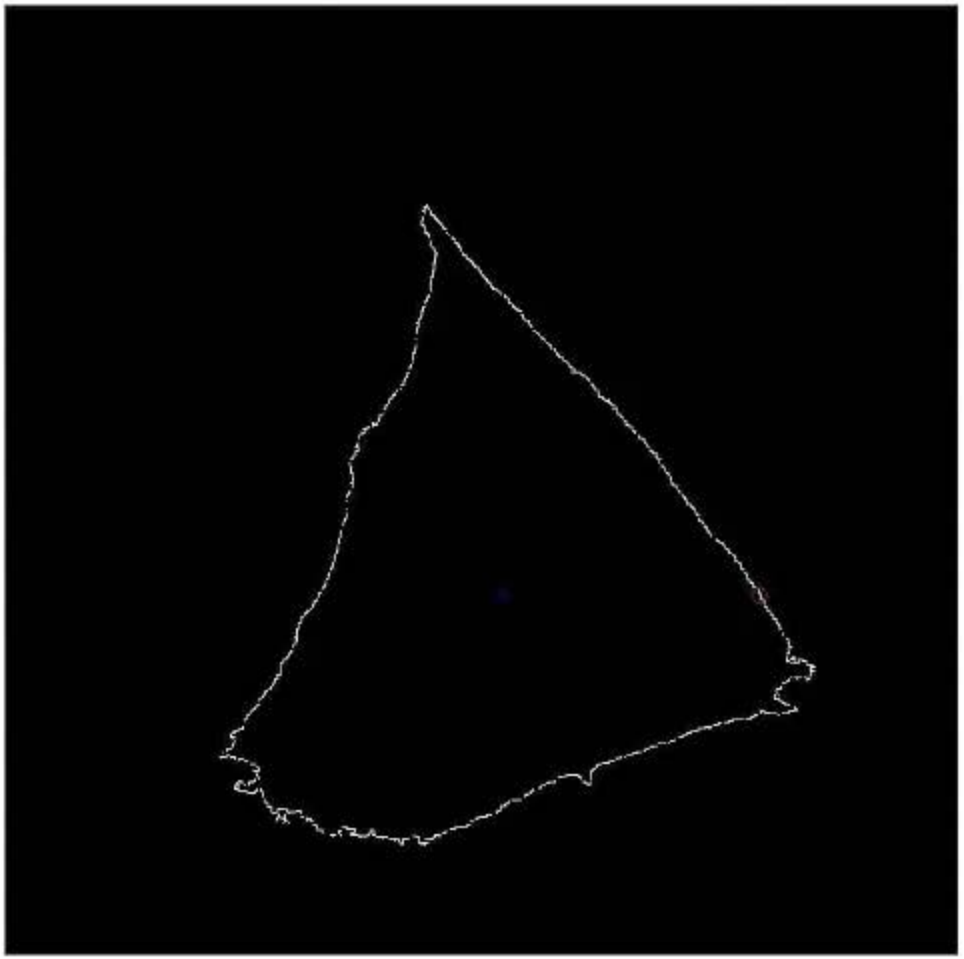
If adherent



Cell shape modeling

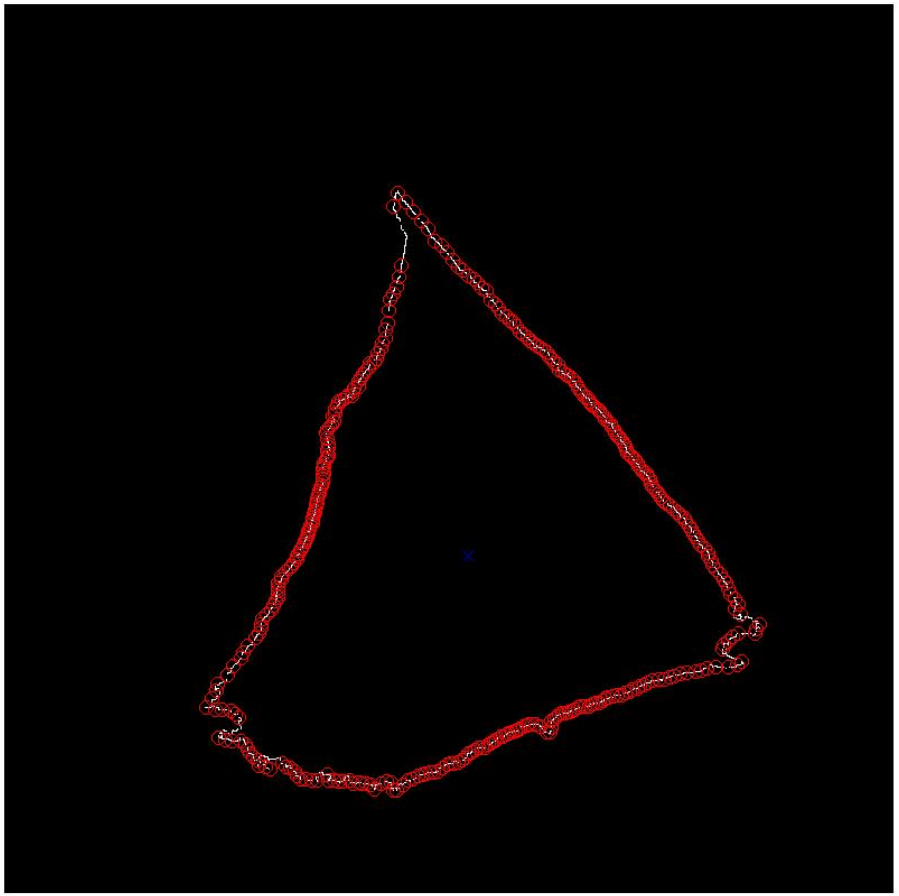


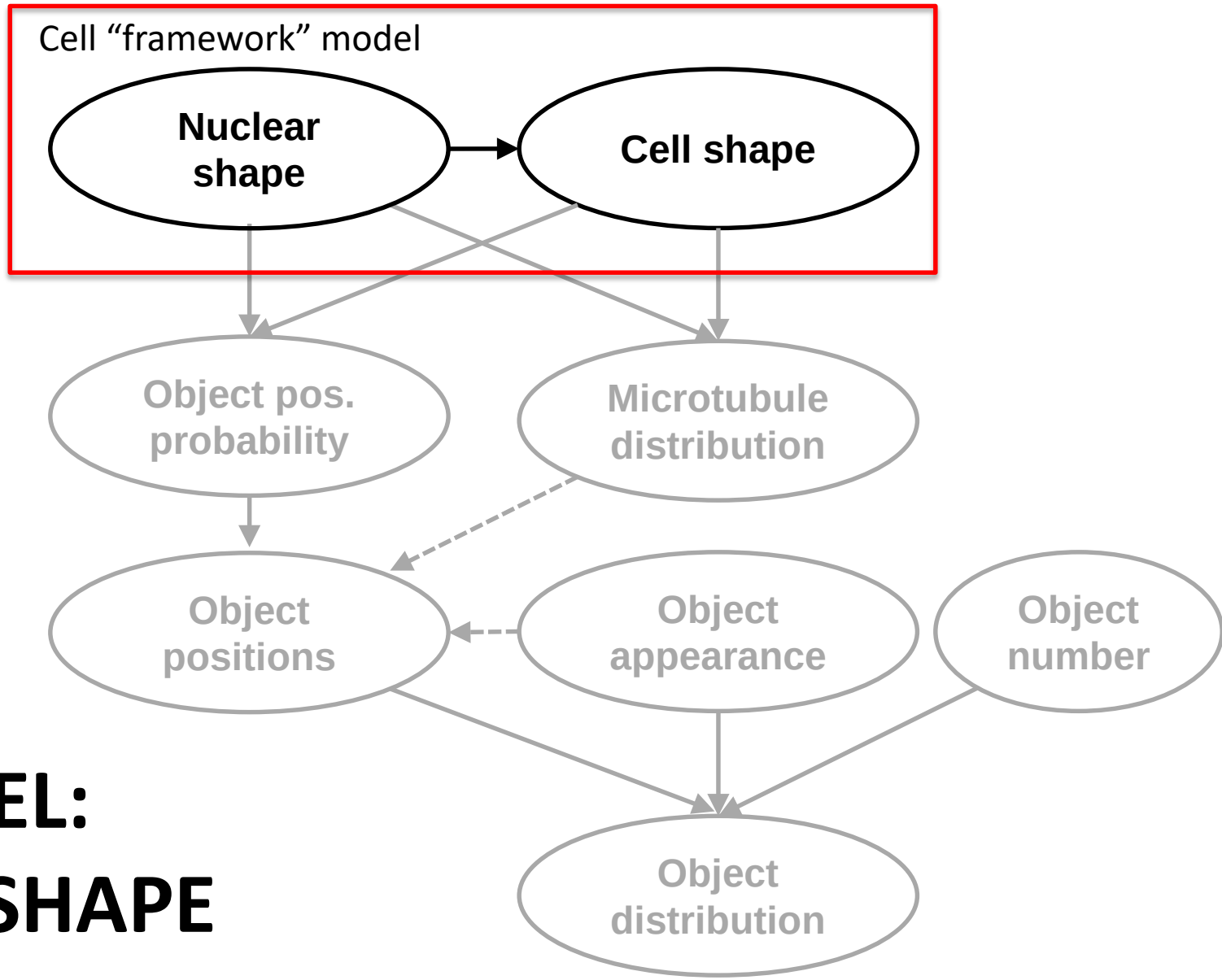
Cell “hit points”



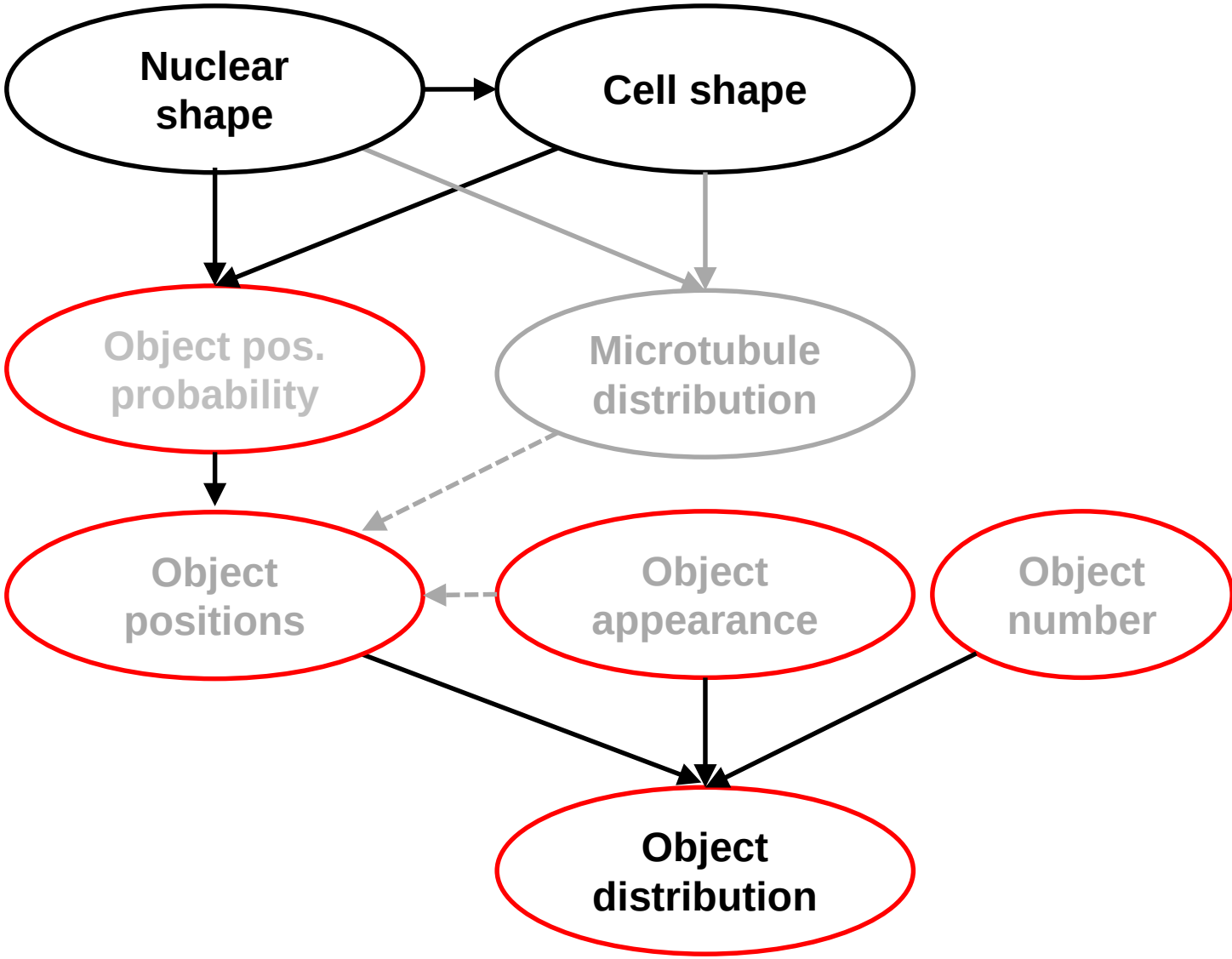
Cell “hit points”

- d





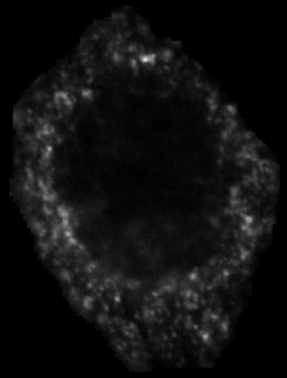
MODEL: CELL SHAPE



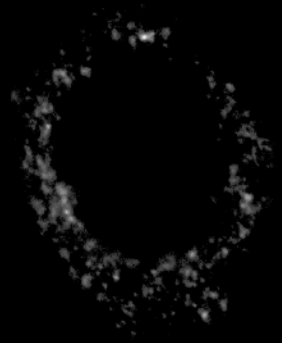
MODEL:
PROTEIN SIZE,NUMBER,LOCATION

Protein image processing

Original image

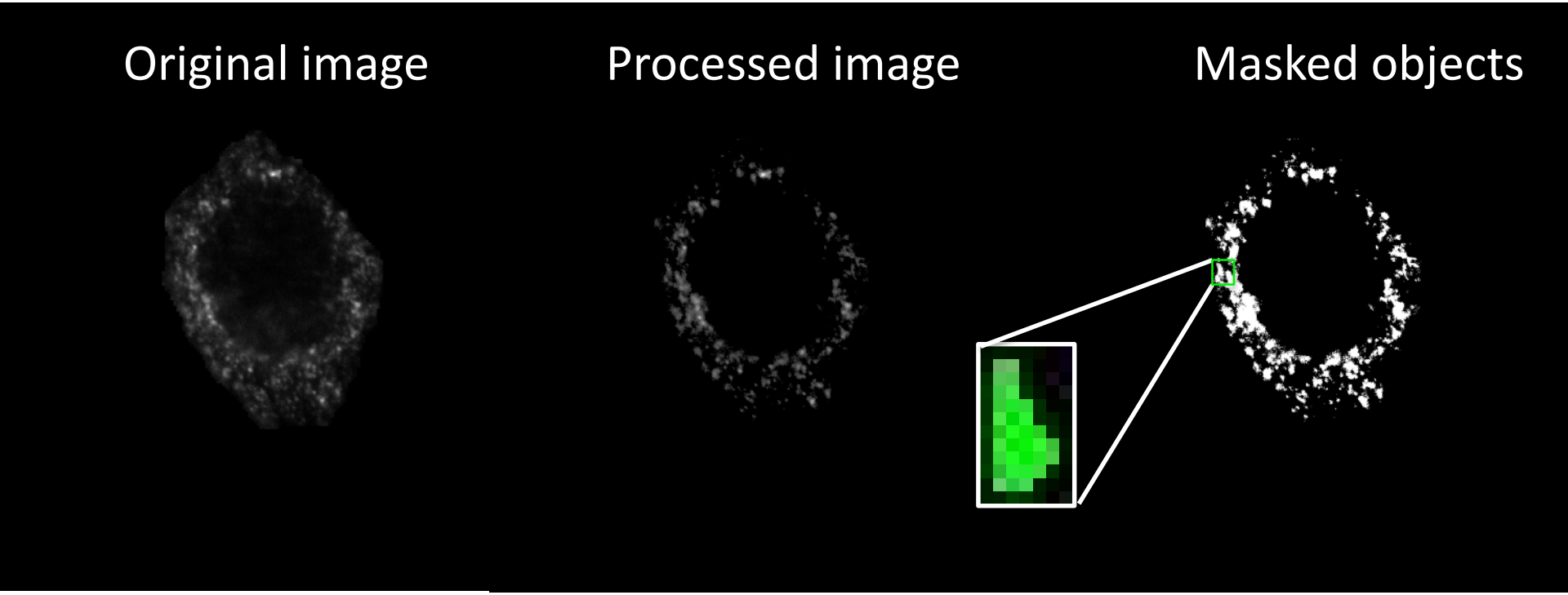


Processed image



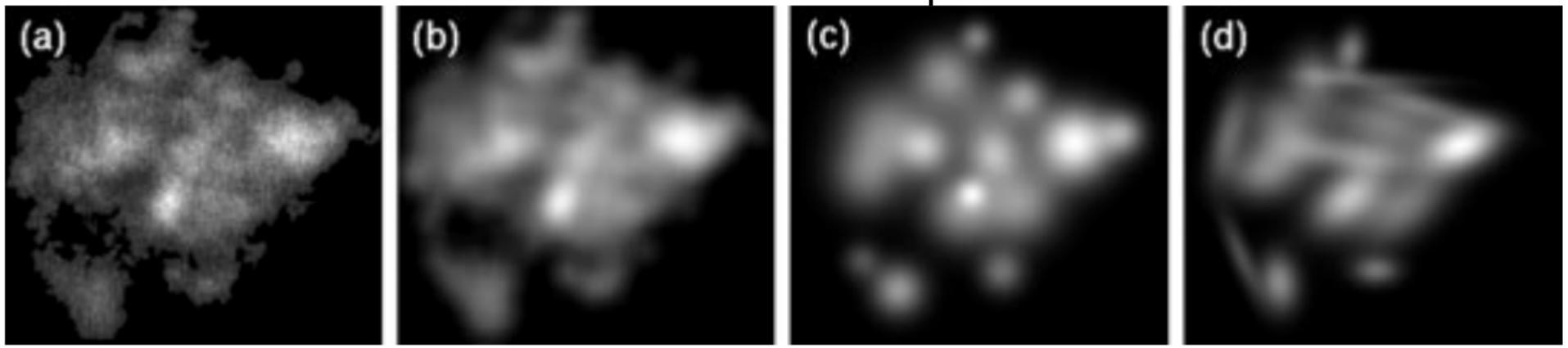
Masked objects

Protein image processing

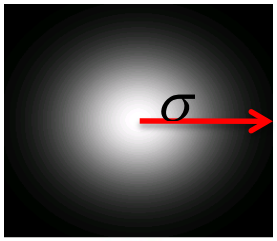


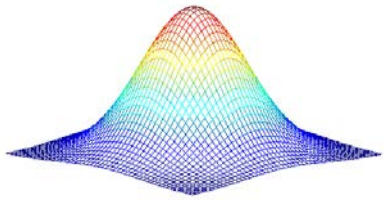
Fitting Vesicular Organelles

Original | Filtered | Fitted Gaussians: Spherical | Fitted Gaussians: Full covariance



Example object



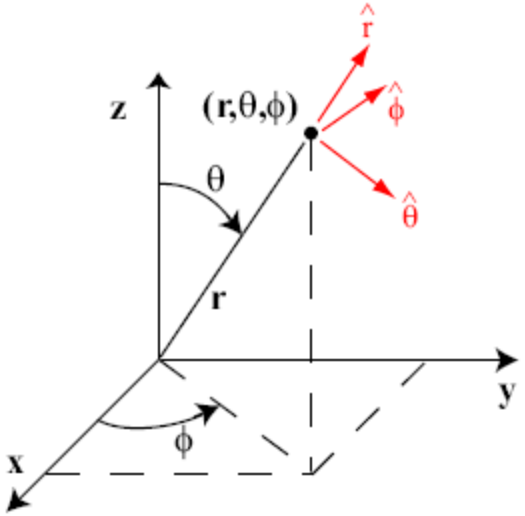


Gaussian object model parameters

Number of objects in a cell N
Object size σ_x, σ_y, σ_z
Single object fluorescence F

Protein Objects Model: Position

3D

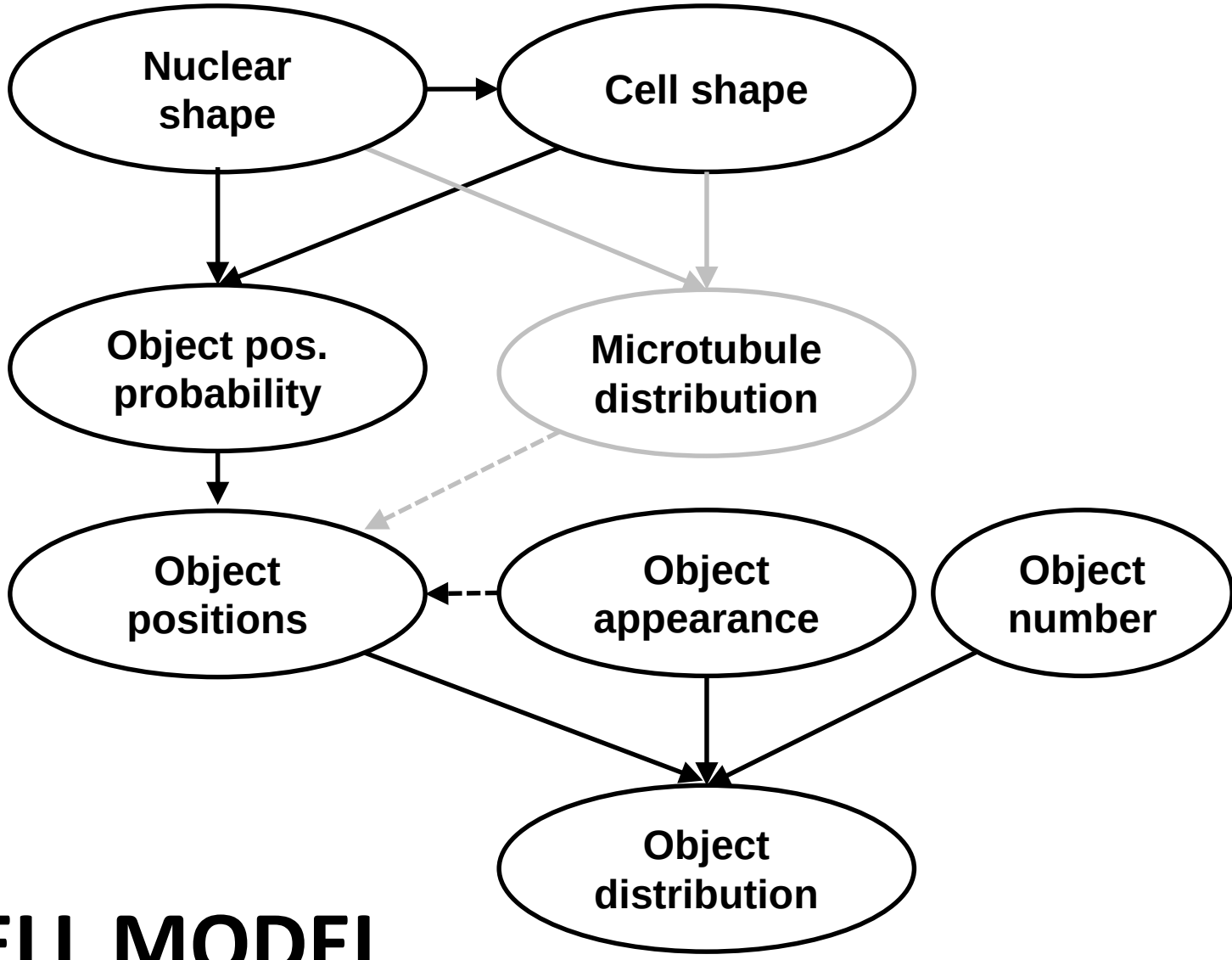


$$P(r,a) = \frac{e^{\tau(r,\theta,\varphi)}}{1+e^{\tau(r,\theta,\varphi)}}$$

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

Radial preference

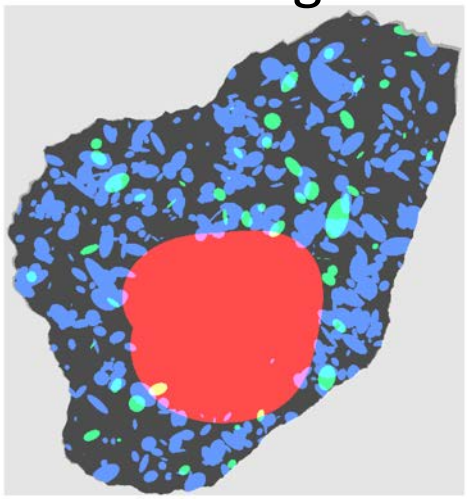
Angular preference



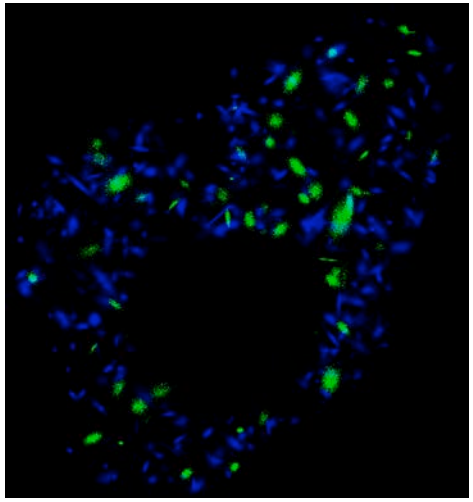
WHOLE CELL MODEL

Synthetic cells

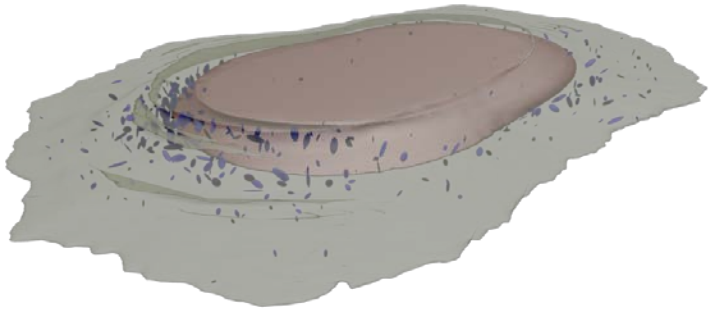
Tiff images



"Sampled" images



Idealized organelle meshes



CellOrganizer

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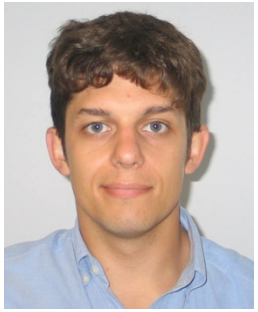

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Questions?