

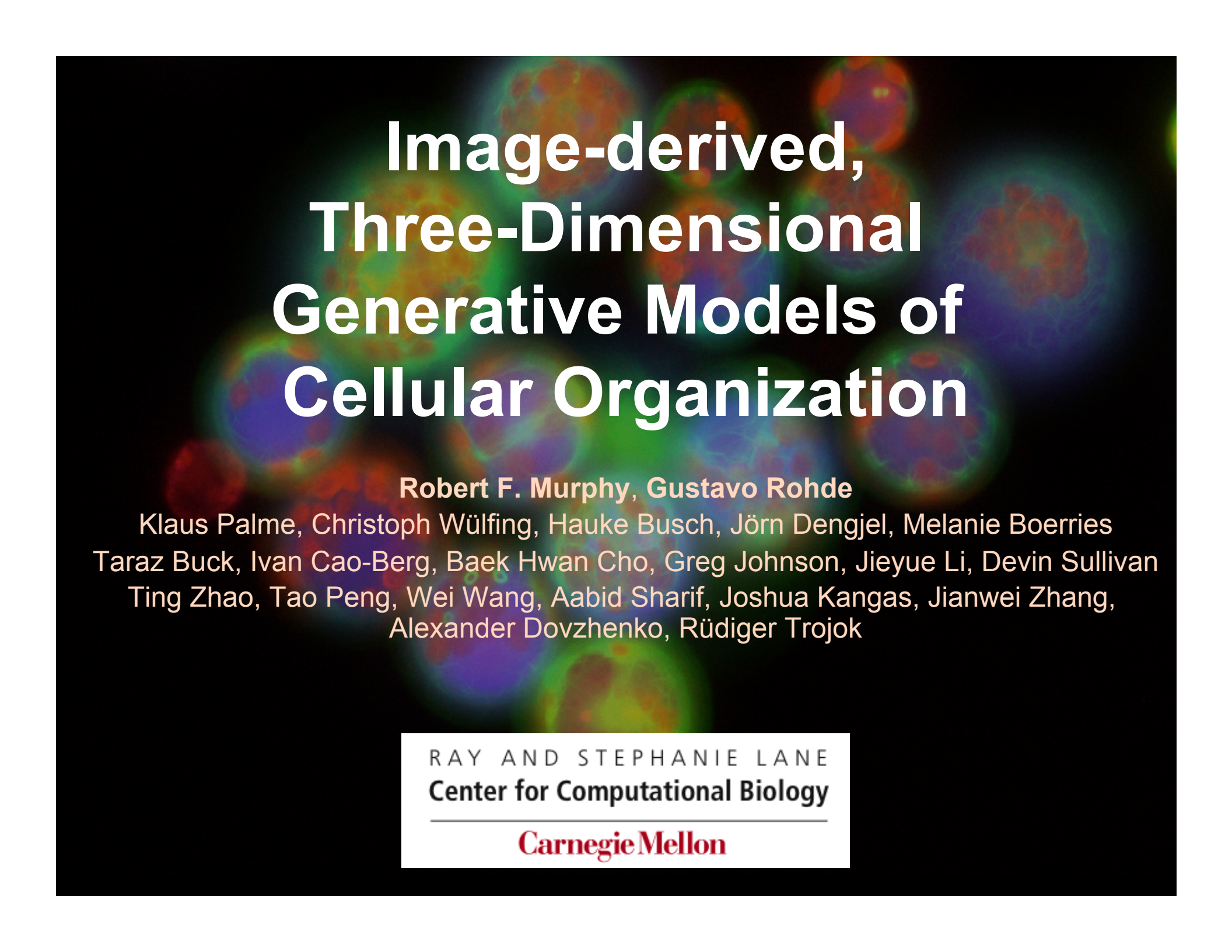


Image-derived, Three-Dimensional Generative Models of Cellular Organization

Robert F. Murphy, Gustavo Rohde

Klaus Palme, Christoph Wülfing, Hauke Busch, Jörn Dengjel, Melanie Boerries
Taraz Buck, Ivan Cao-Berg, Baek Hwan Cho, Greg Johnson, Jieyue Li, Devin Sullivan
Ting Zhao, Tao Peng, Wei Wang, Aabid Sharif, Joshua Kangas, Jianwei Zhang,
Alexander Dovzhenko, Rüdiger Trojok

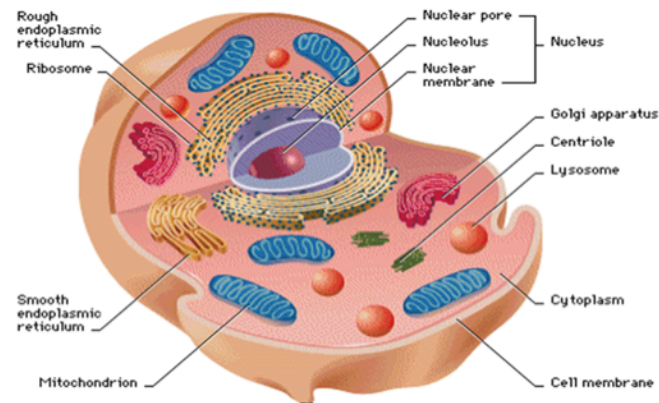
RAY AND STEPHANIE LANE
Center for Computational Biology

Carnegie Mellon



How do we learn and represent

- the number, sizes, shapes, positions of subcellular structures
- the distribution of proteins across those structures





High throughput image analysis

- Many groups imaging subcellular distributions by various tagging methods and microscopy methods
- Dominant approach to analysis uses classification or regression (with image features)
- However...



Assigning words not sufficient!

- Doesn't capture
 - new phenotypes
 - fractional distributions
 - suborganelle patterns
 - spatiotemporal distribution
 - cell type variation
 - conditional variation

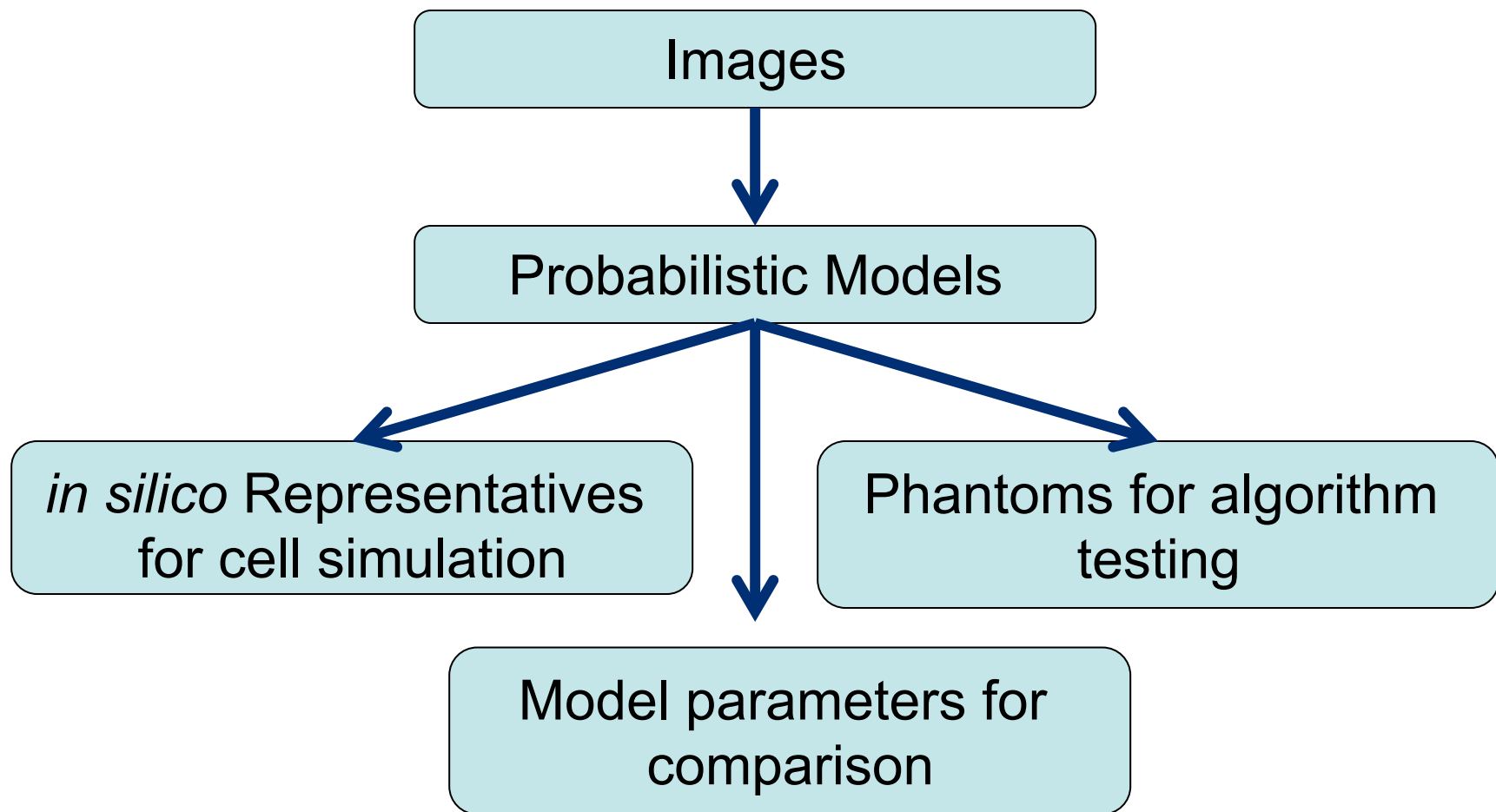


Want to Use Diverse Data

- From different:
 - Imaging systems
 - Cell lines
 - Protocols
- Feature values not “global”

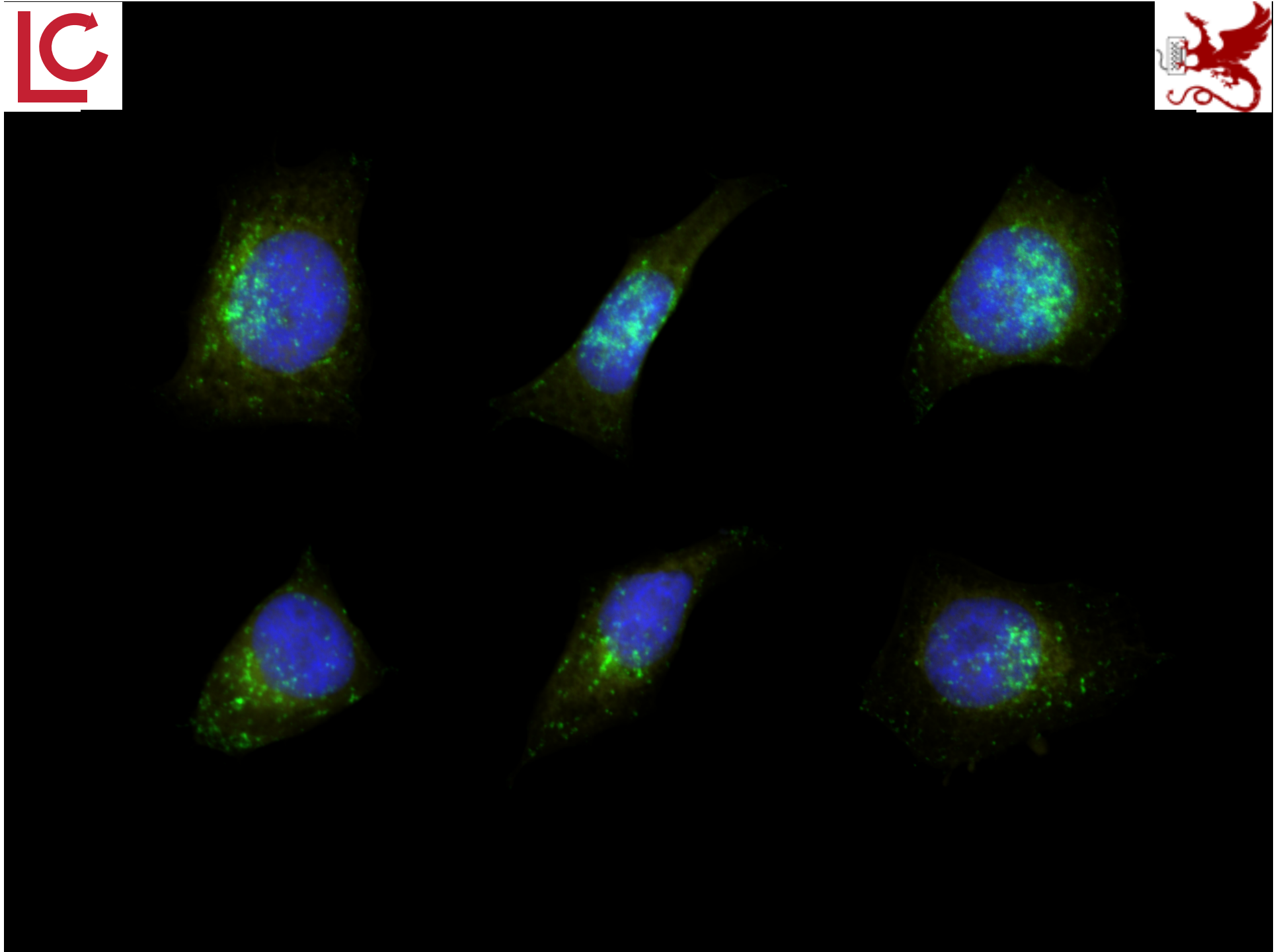


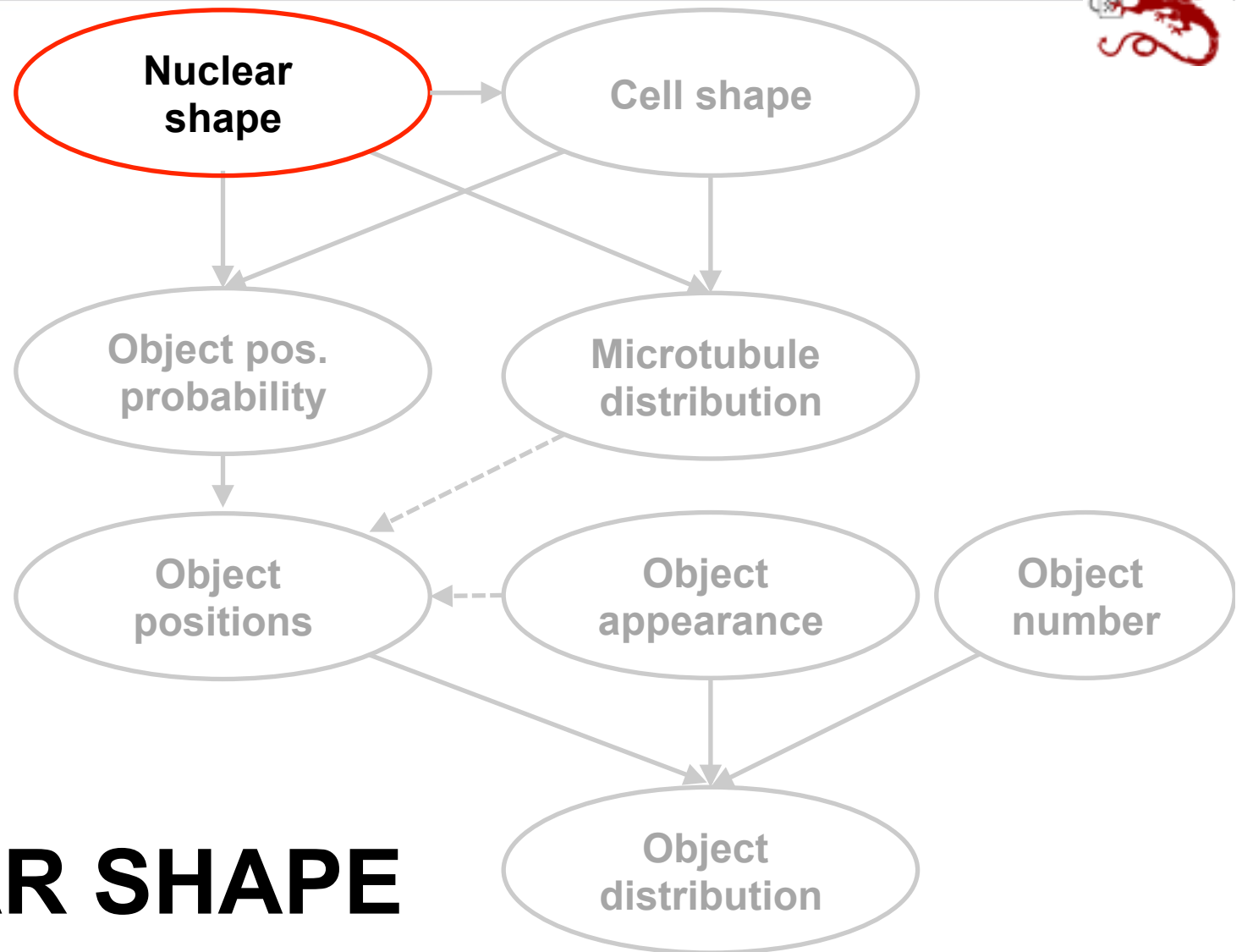
Image-derived generative models of subcellular organization





**INPUTS:
IMAGES**

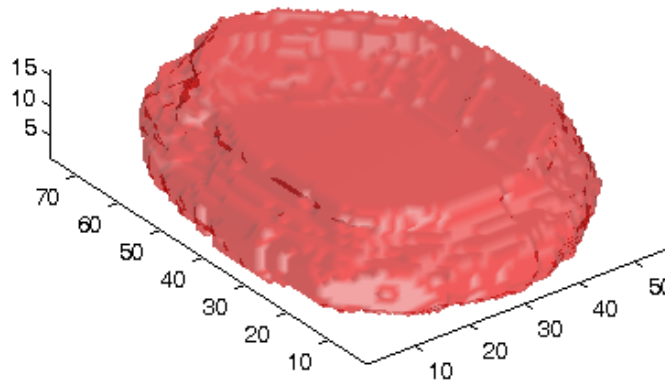




**MODEL:
NUCLEAR SHAPE**

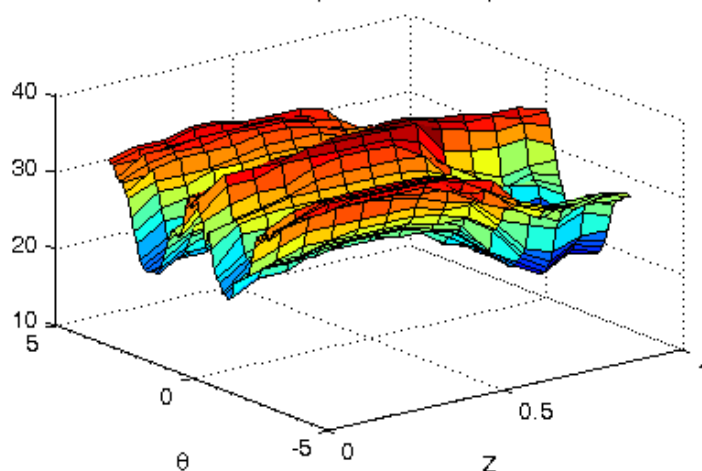


3D nuclear model: cylindrical spline surface

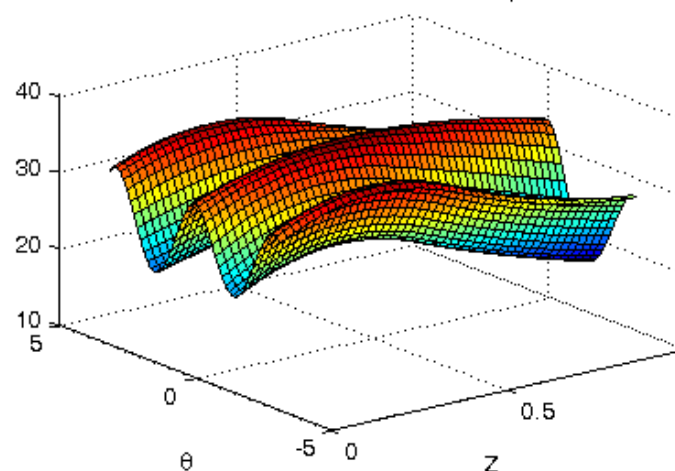


Tao
Peng

Resampled surface map

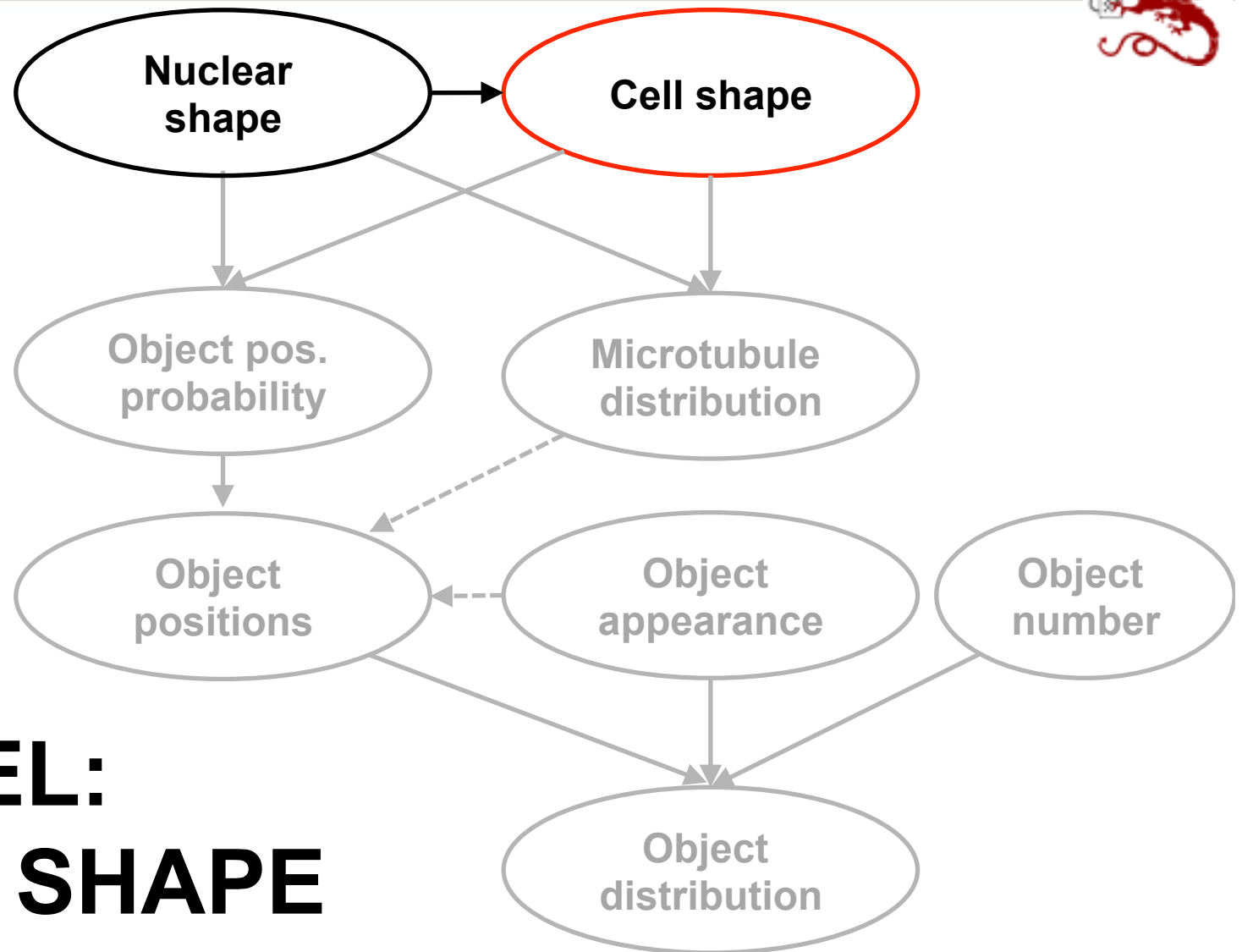


Reconstructed surface map



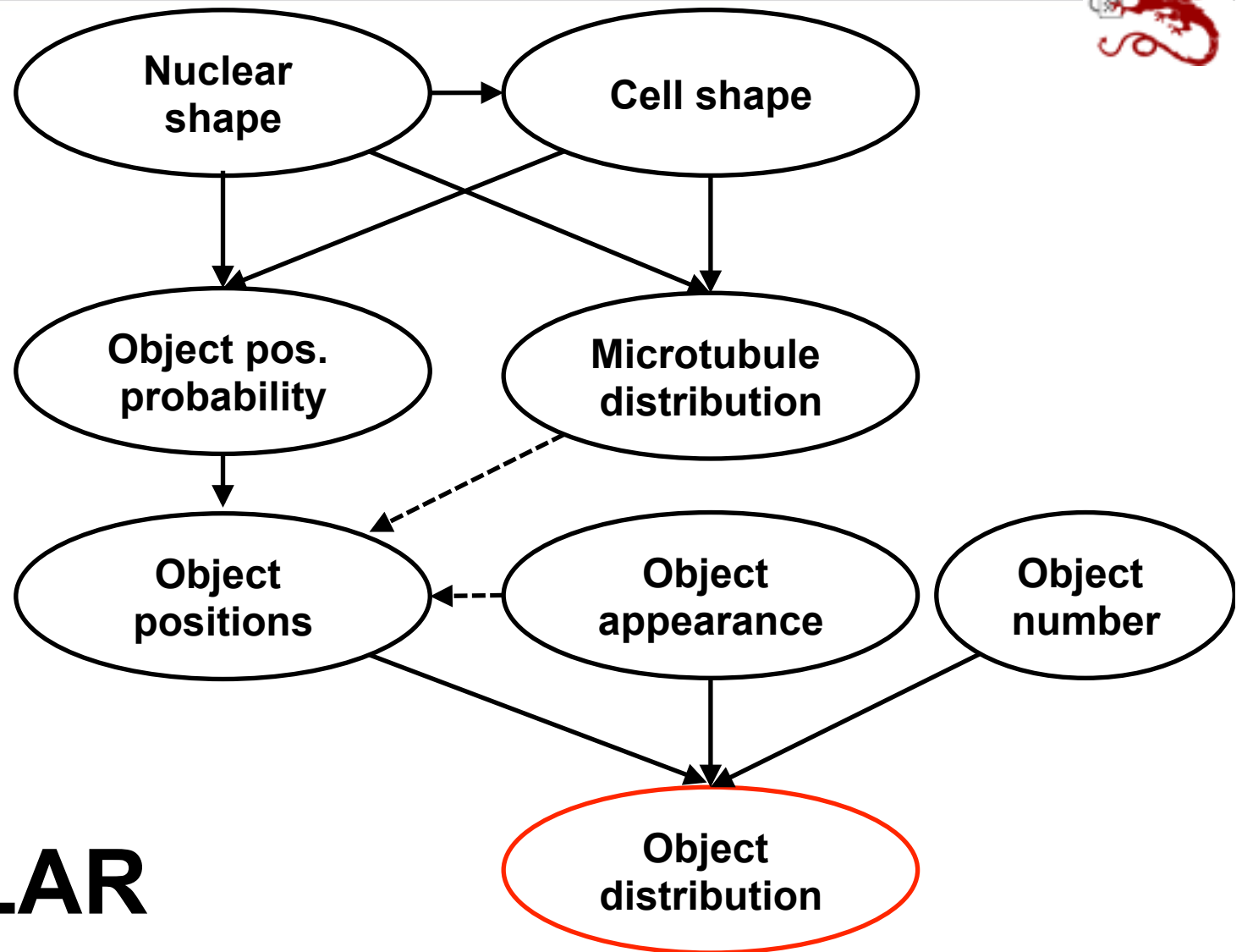
32
parameters
for spline
coefficients,
1 for height





**MODEL:
CELL SHAPE**





**MODEL:
VESICULAR
ORGANELLES**



Protein Objects Model: Position

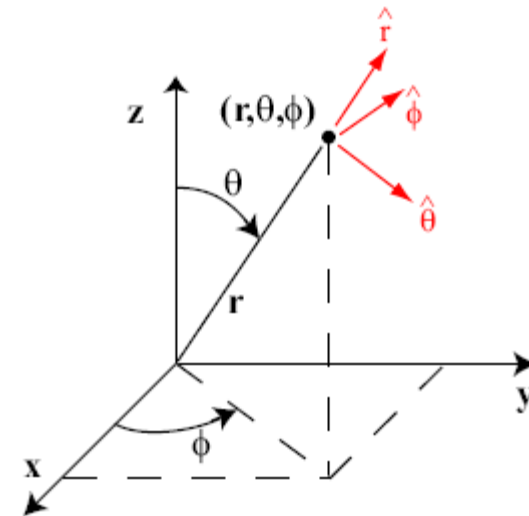
3D

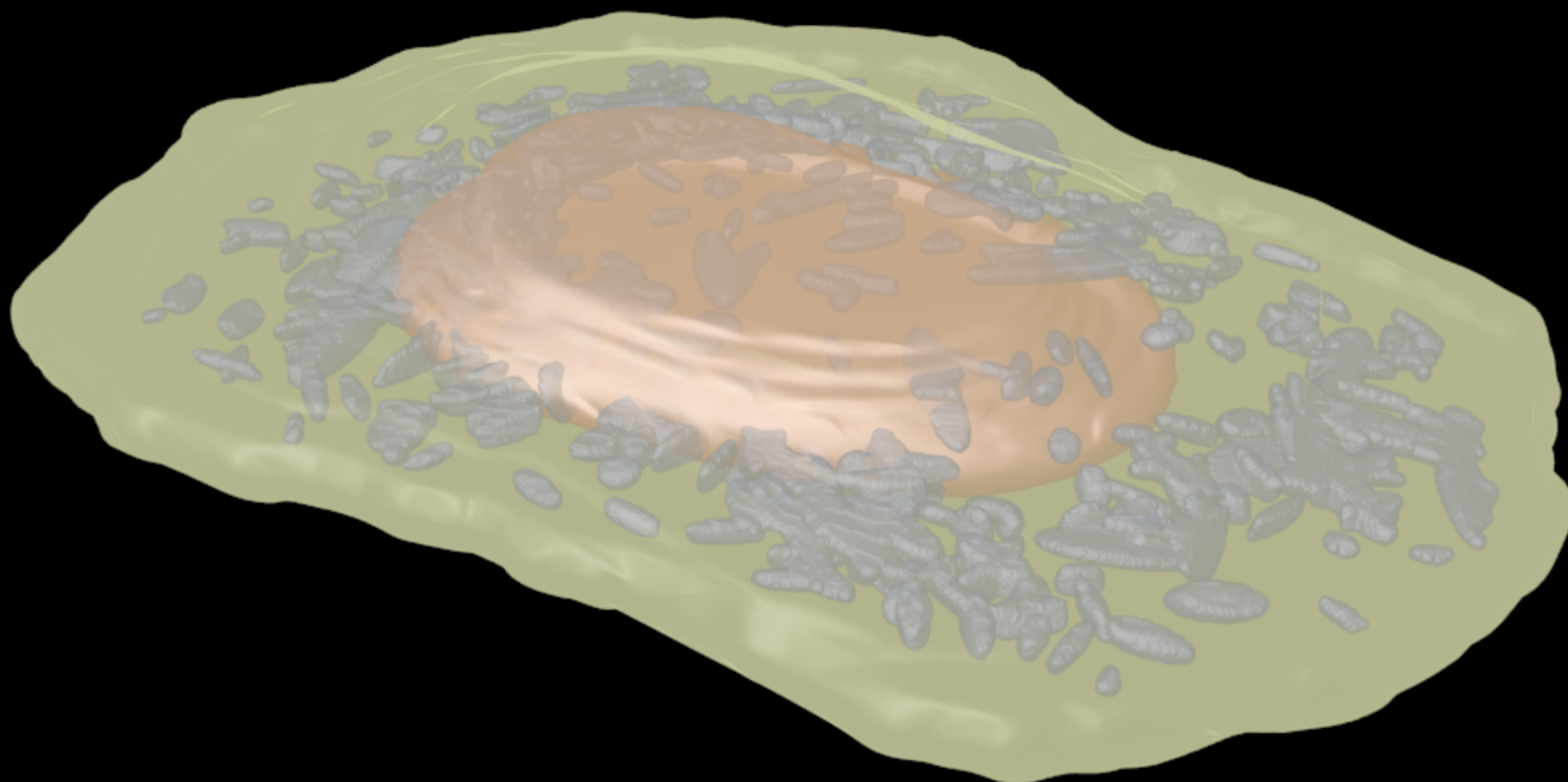
$$P(r, a) = \frac{e^{\tau(r, \theta, \varphi)}}{1 + e^{\tau(r, \theta, \varphi)}}$$

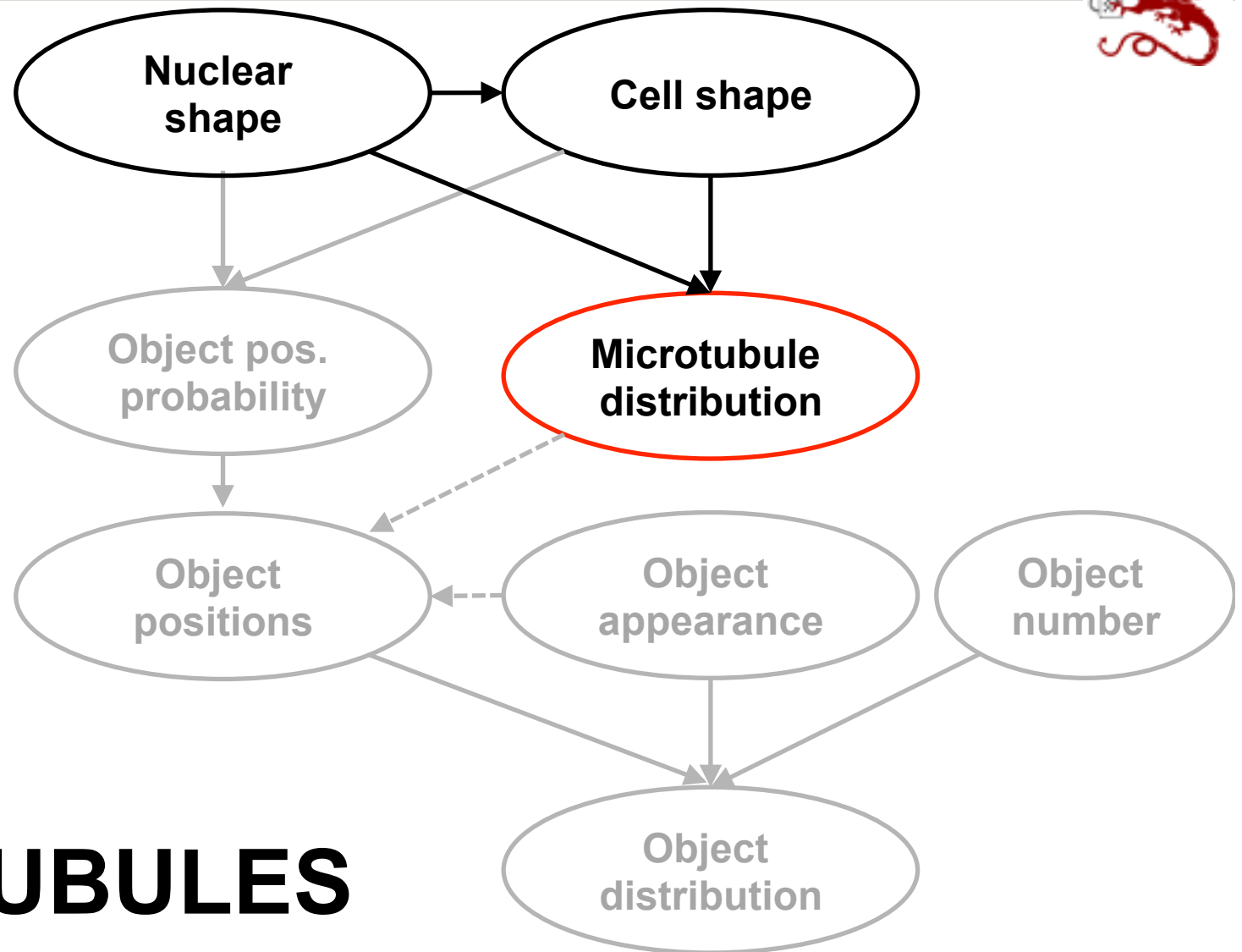
$$\tau(r, \theta, \varphi) = \beta_0 + \beta_1 r + \beta_2 r^2 + \beta_3 \sin \theta \cos \varphi + \beta_4 \sin \theta \sin \varphi + \beta_5 \cos \theta$$

Radial
preference

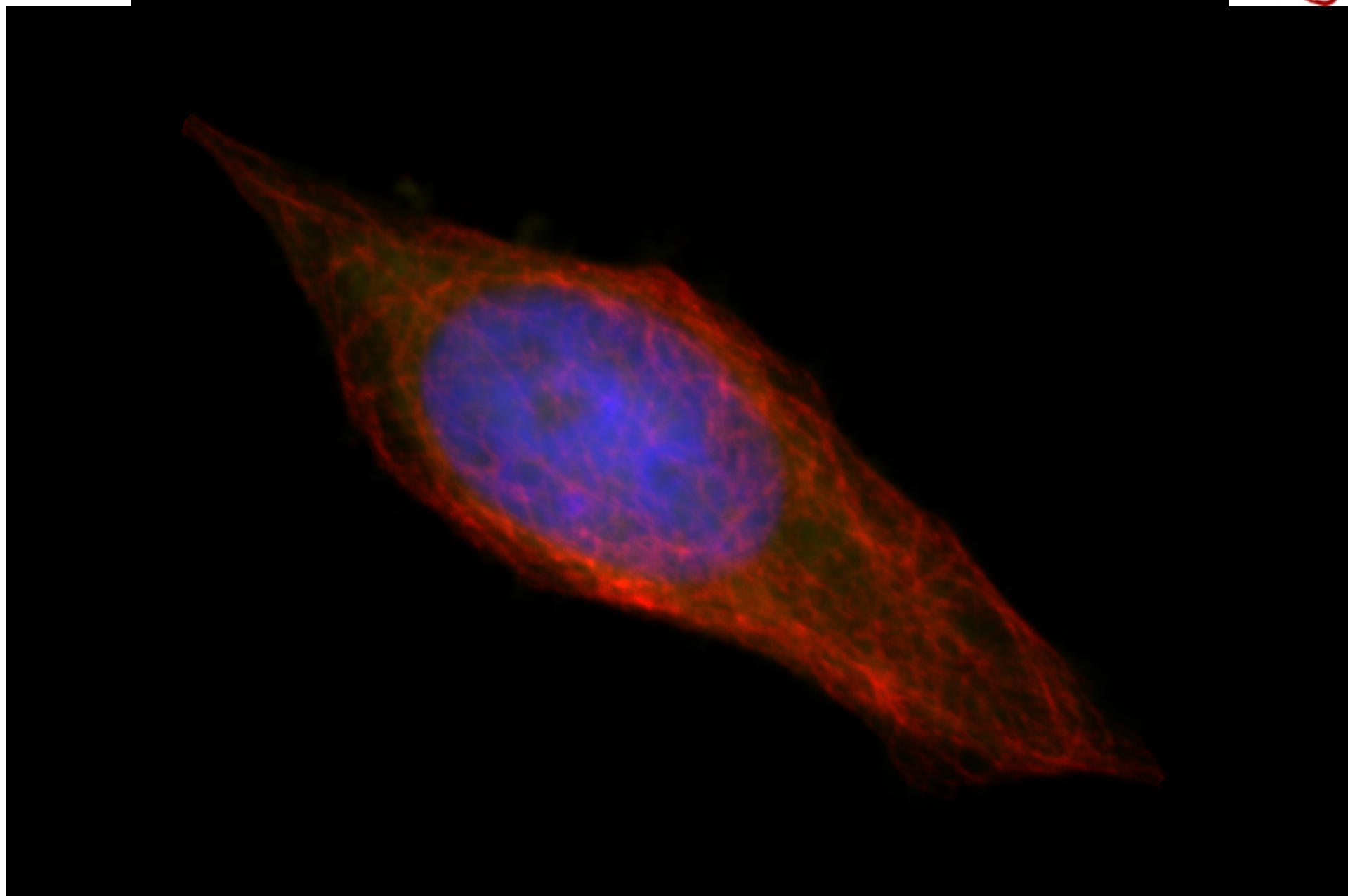
Angular
preference

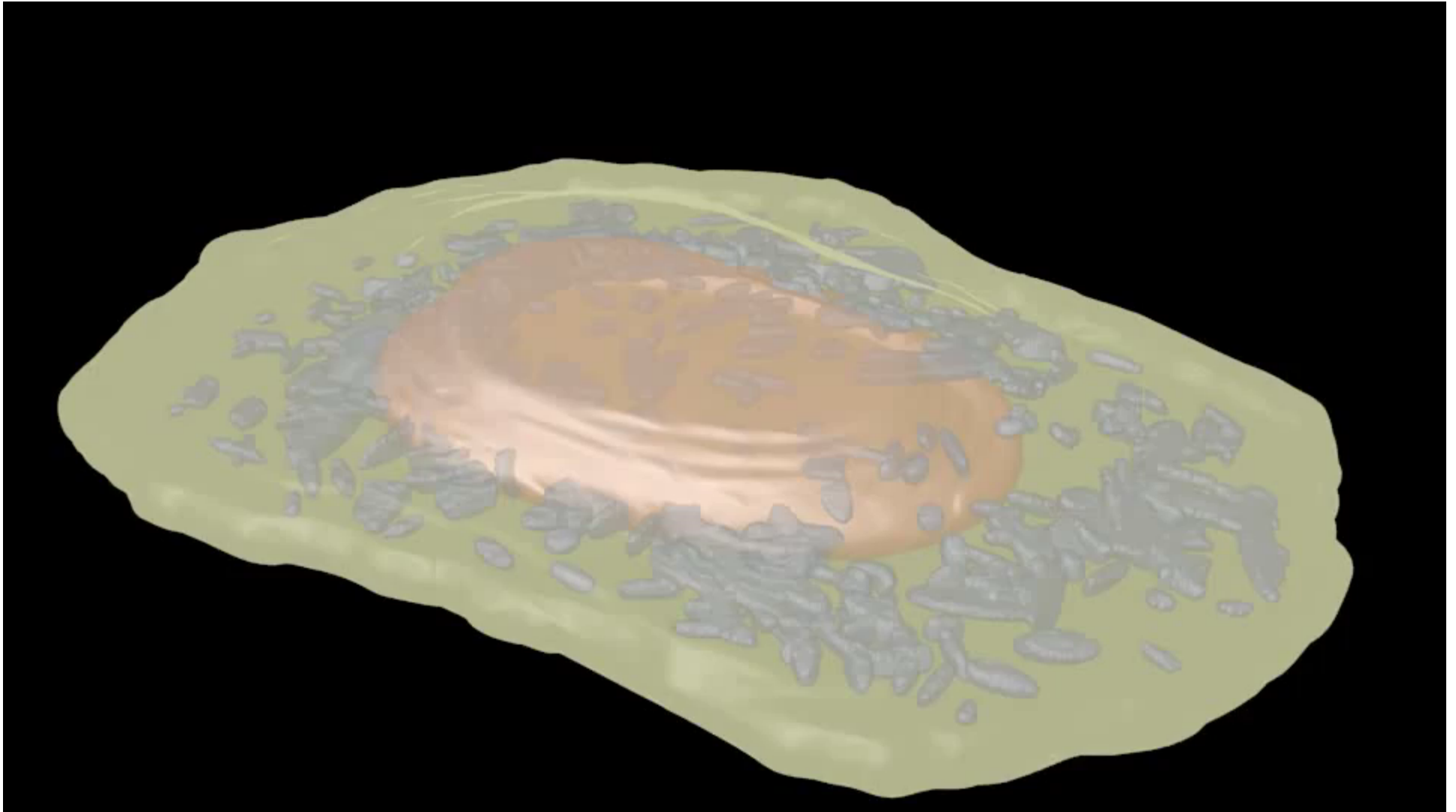






**MODEL:
MICROTUBULES**





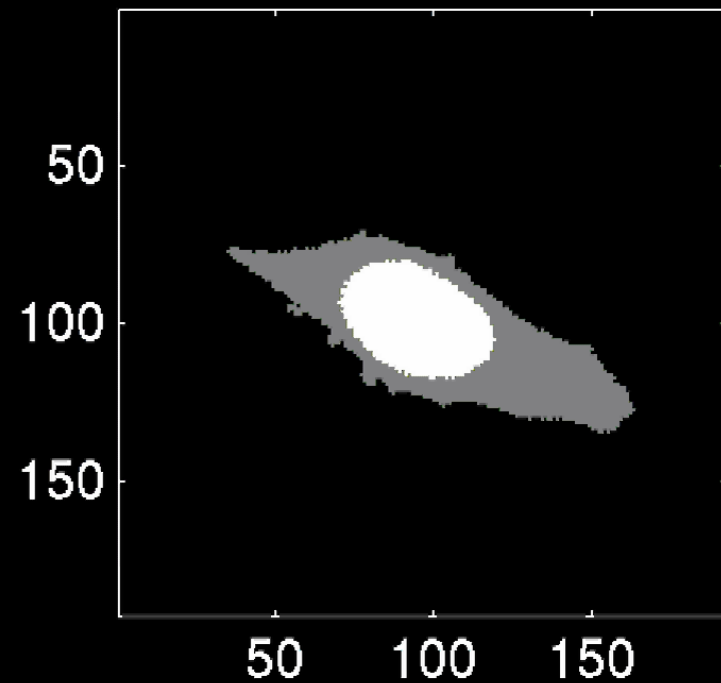
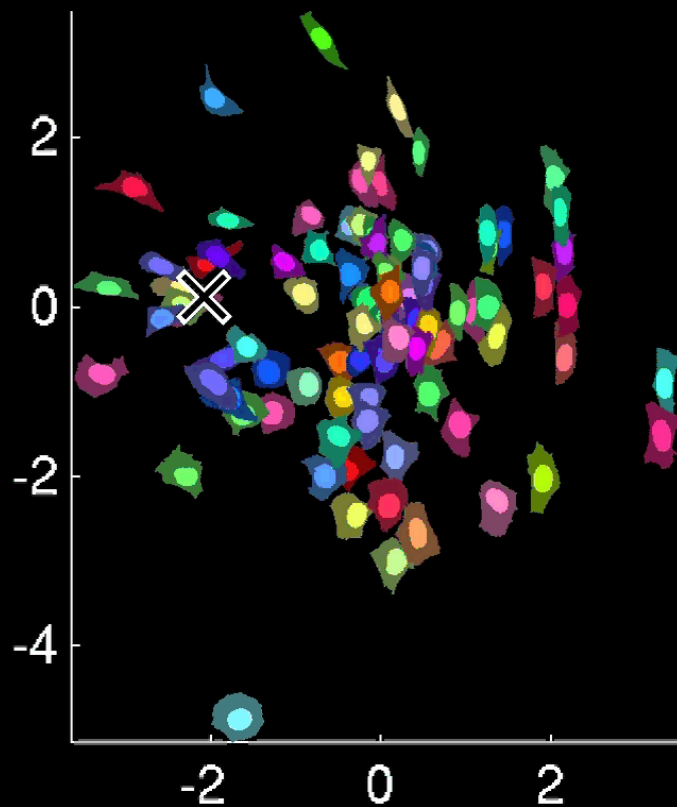


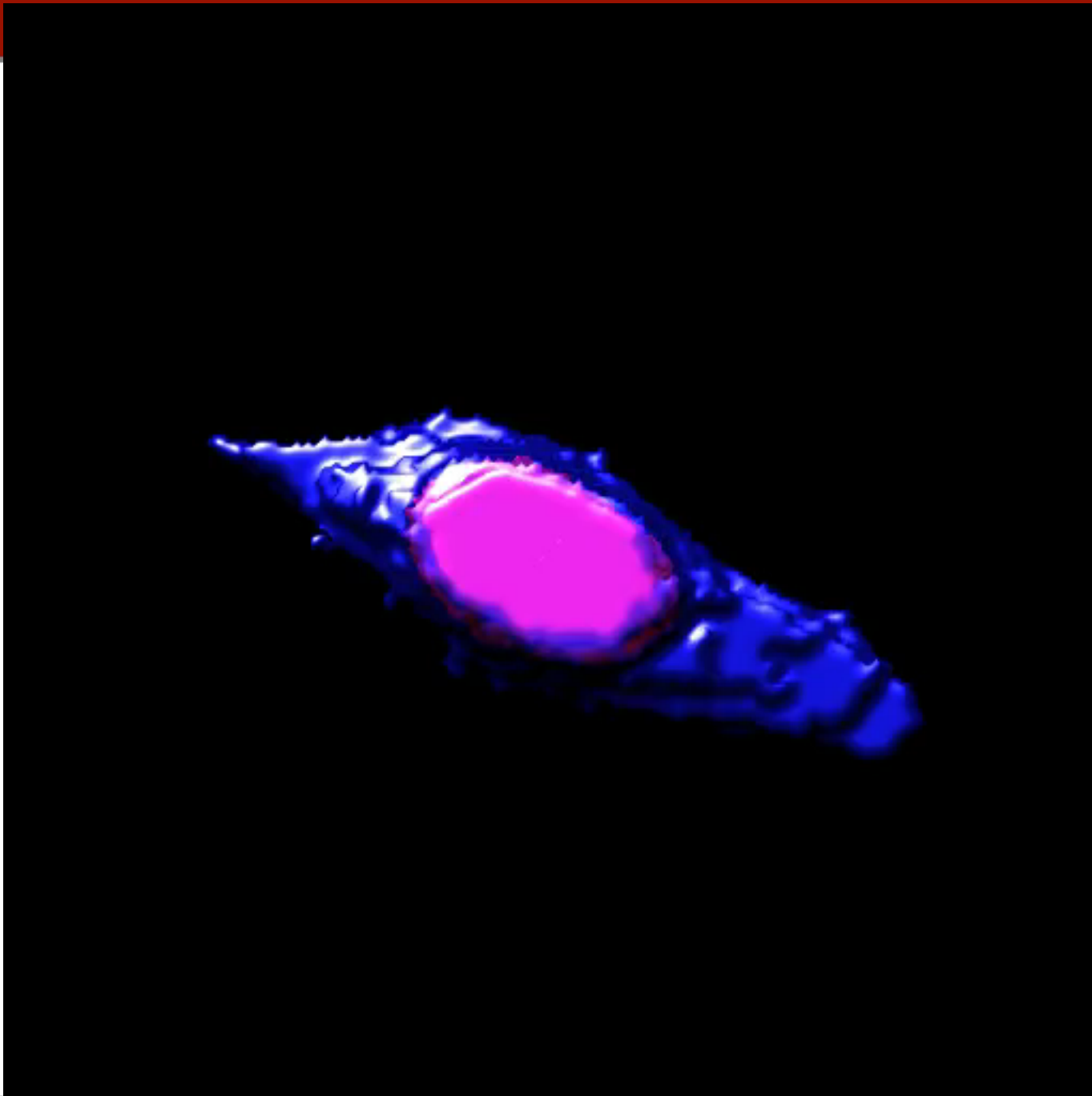
Shape space

- Can measure distance between all pairs of shapes to construct a “shape space”
- Captures essential aspects of how shapes vary
- Can be applied in 2D, 3D, 4D and to more than one component at a time



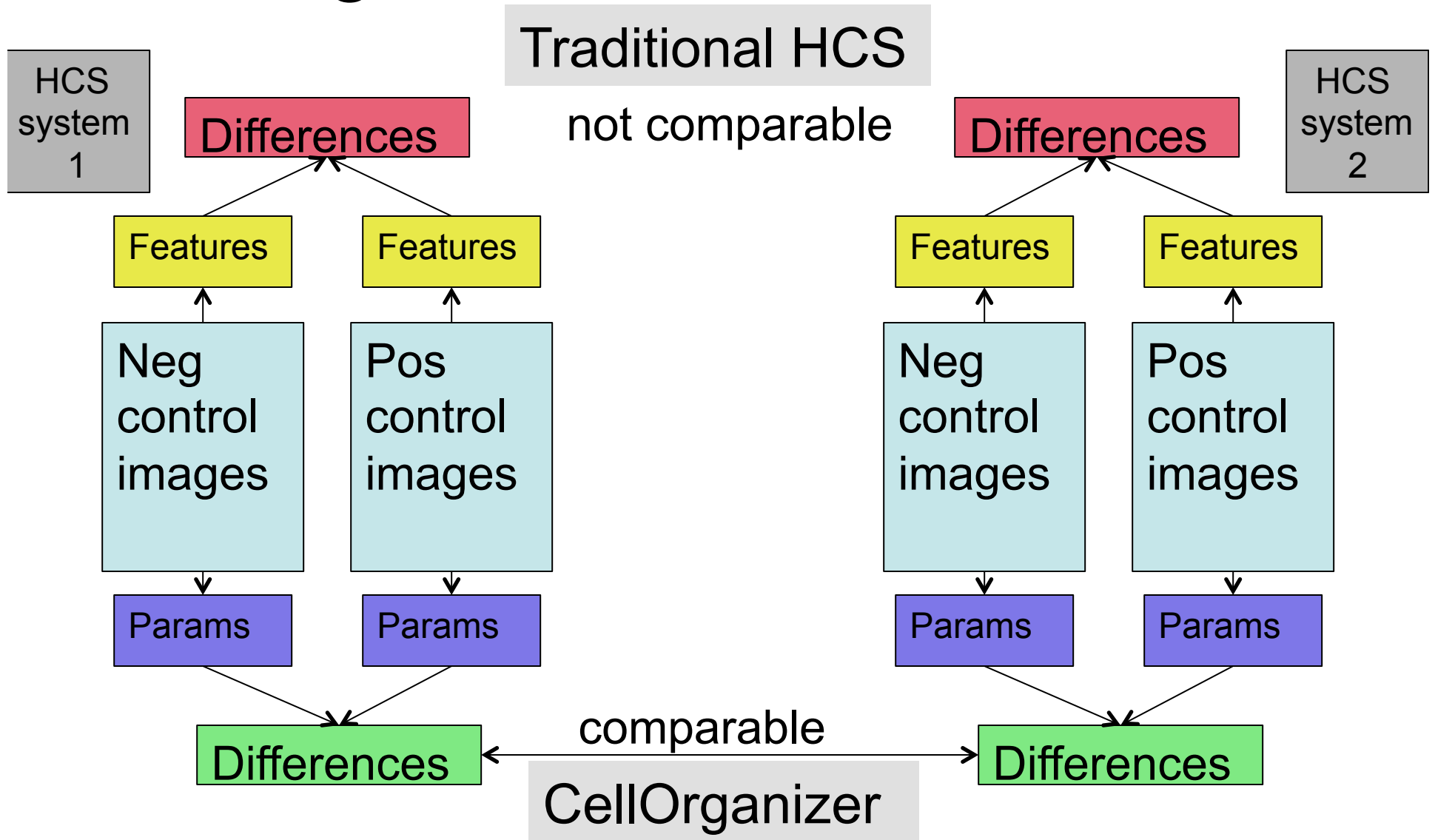
Random walk in cell/nuclear shape space







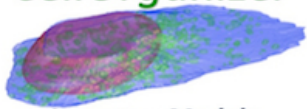
CellOrganizer vs. traditional HCS





CellOrganizer.org

CellOrganizer



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People

RAY AND STEPHANIE LANE
Center for Computational Biology



Project leaders



[Robert F. Murphy](#)



[Gustavo Rohde](#)

Major collaborators



[Klaus Palme](#)



[Christoph Wülfing](#)



[Hauke Busch](#)



[Jörn Dengjel](#)



[Melanie Boerries](#)

Current team members



Taraz Buck



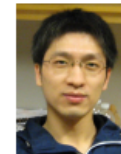
Ivan Cao-Berg



Baek Hwan Cho



Greg Johnson



Jieyue Li



Devin Sullivan

Past contributors

Ting Zhao

Alexander Dovzhenko

Tao Peng

Rüdiger Trojok

Wei Wang

Aabid Sharif

Joshua Kangas

Jianwei Zhang



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