

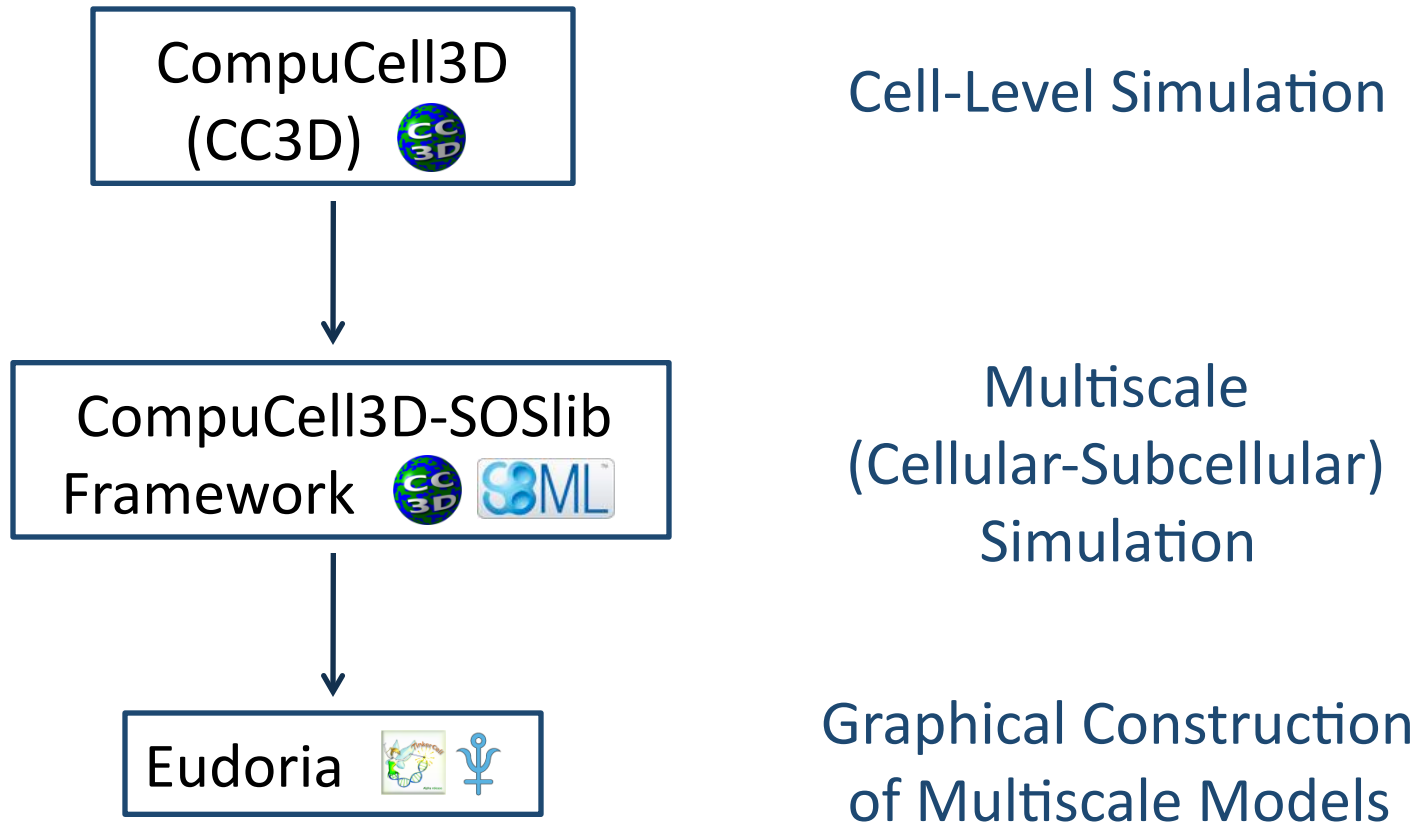
# Multiscale Simulation Using CompuCell3D and the SBML ODE Solver Library

Ryan Roper  
University of Washington  
Dept of Bioengineering

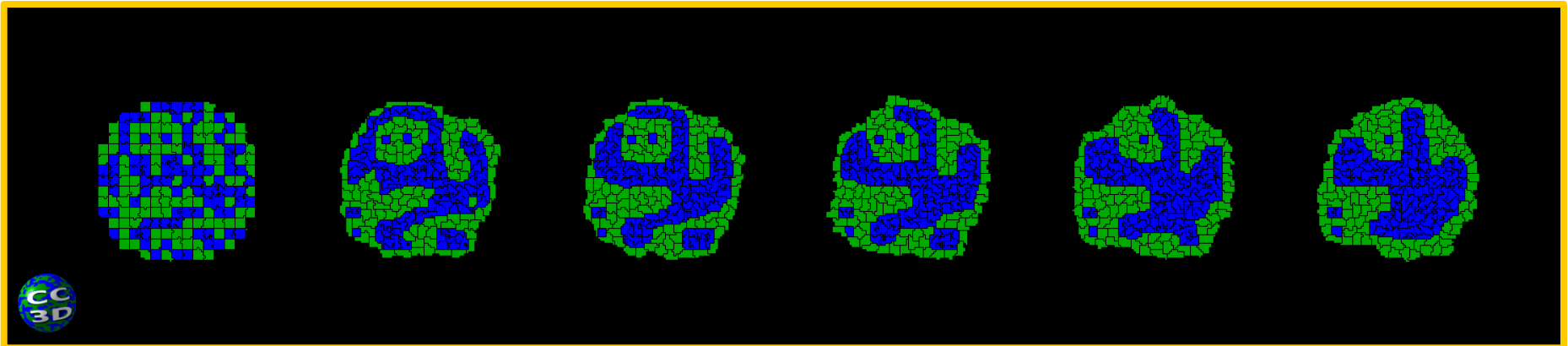
**Sauro Lab**  
University of Washington  
Dept of Bioengineering  
Seattle, WA, USA

**Glazier Lab**  
Biocomplexity Institute  
Indiana University  
Bloomington, IN, USA

# Overview



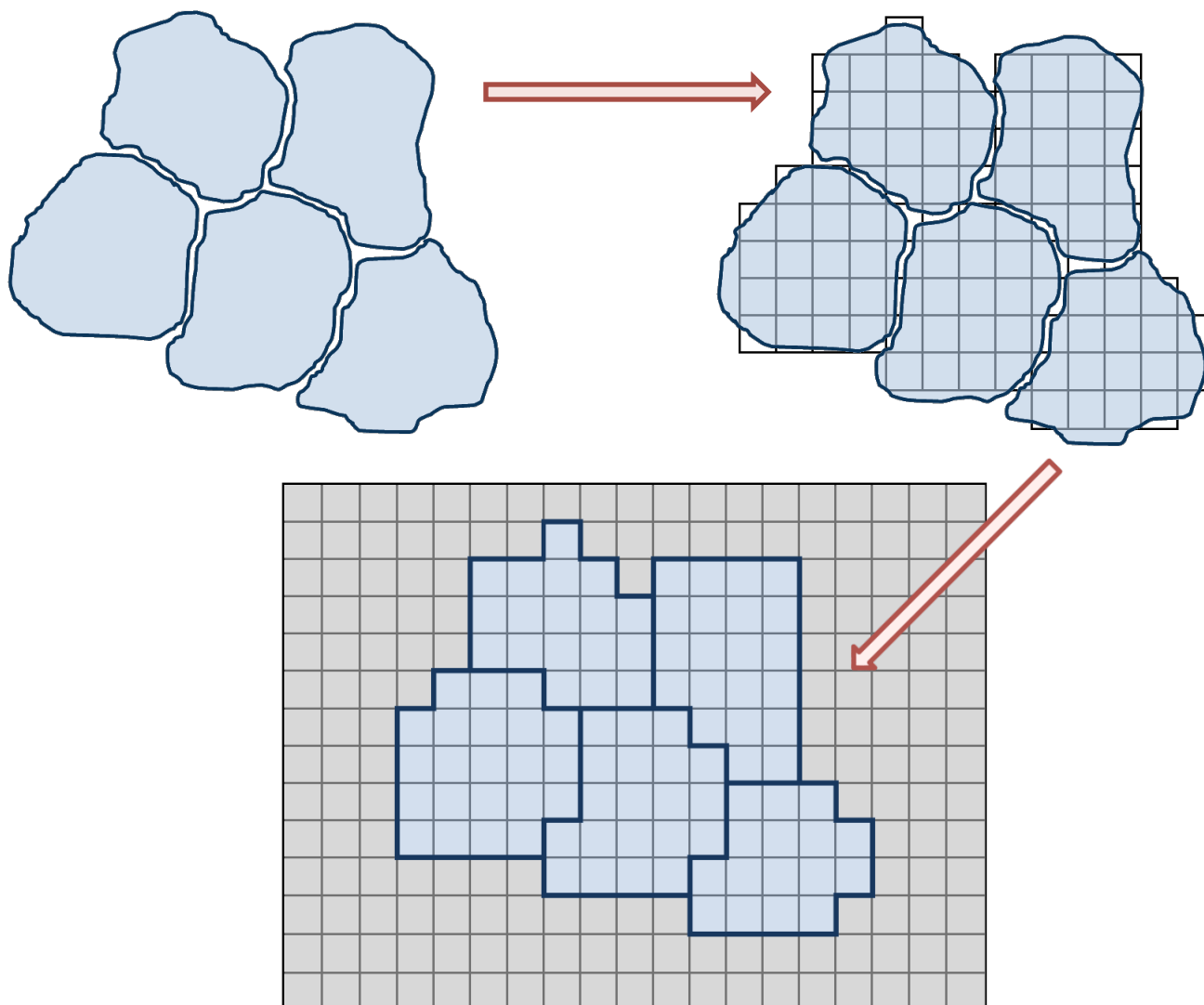
# Cell Sorting Simulation using CC3D



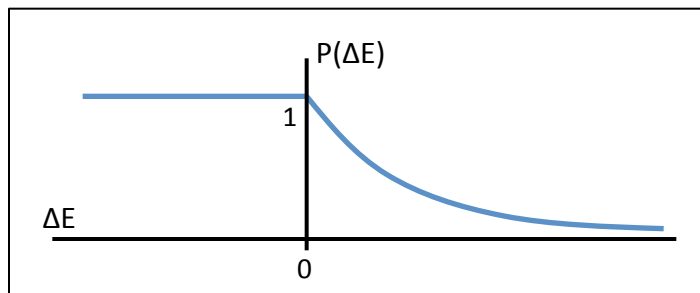
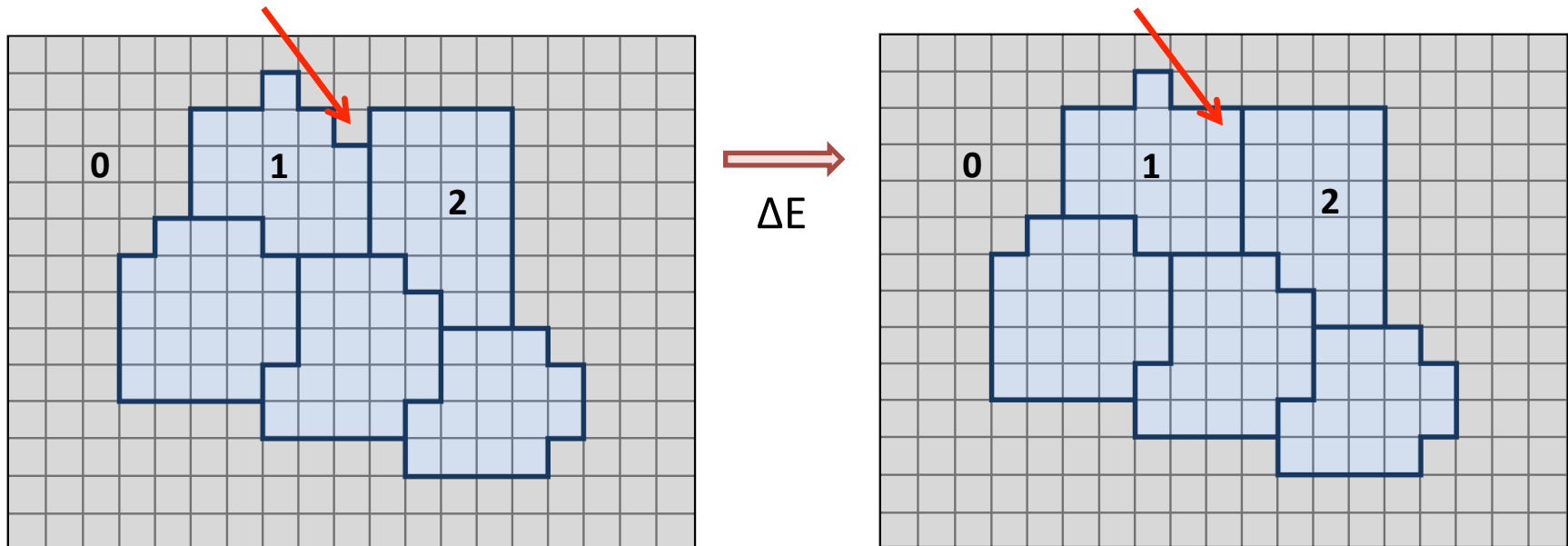
CompuCell3D (CC3D) 

- Implements Cellular Potts Model (CPM)
- Evolves lattice by Monte Carlo Simulation

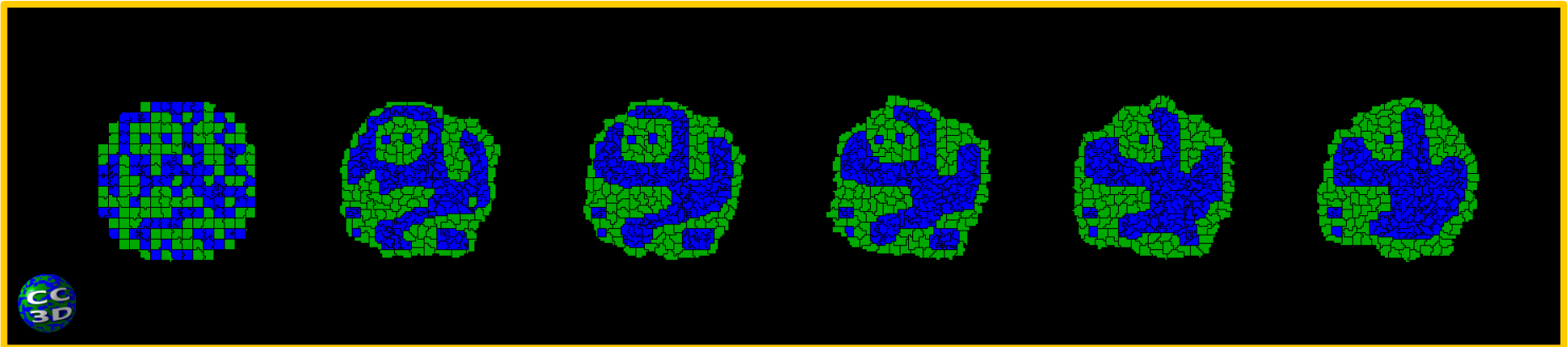
# Lattice-Based Representation of Cells



# Energy Minimization

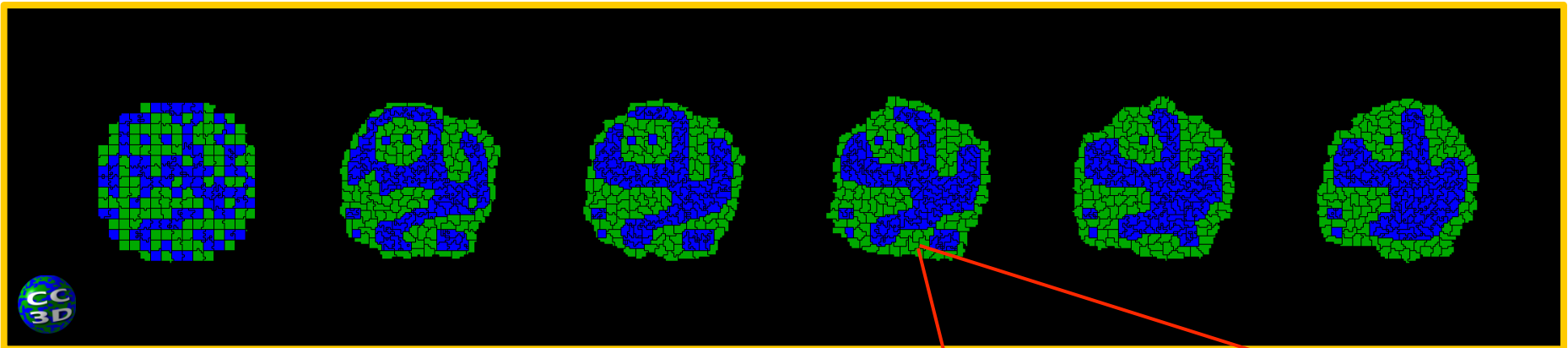


# What is Modeled in Cell Sorting Simulation?

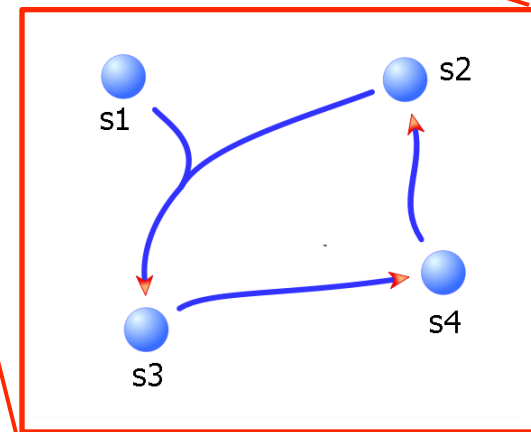


Cells are modeled with static physical properties that are independent of intracellular state

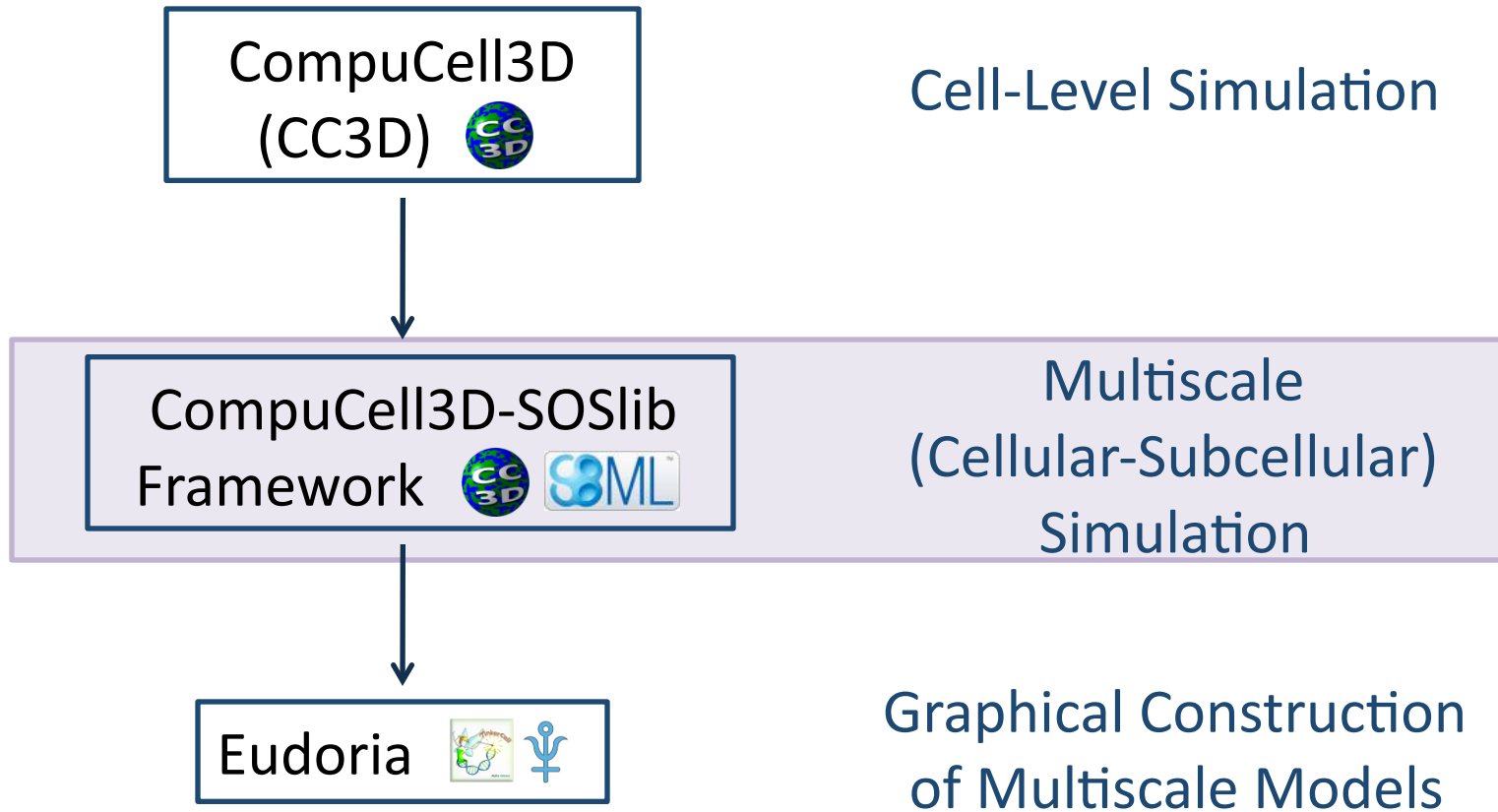
# Incorporation of Intracellular States



How do we incorporate the intracellular time-evolution of chemical species concentrations?



# Overview






# CC3D-SOSlib Framework for Multiscale Simulation

CompuCell3D (CC3D) 

- Implements Cellular Potts Model (CPM)
- Evolves lattice by Monte Carlo Simulation

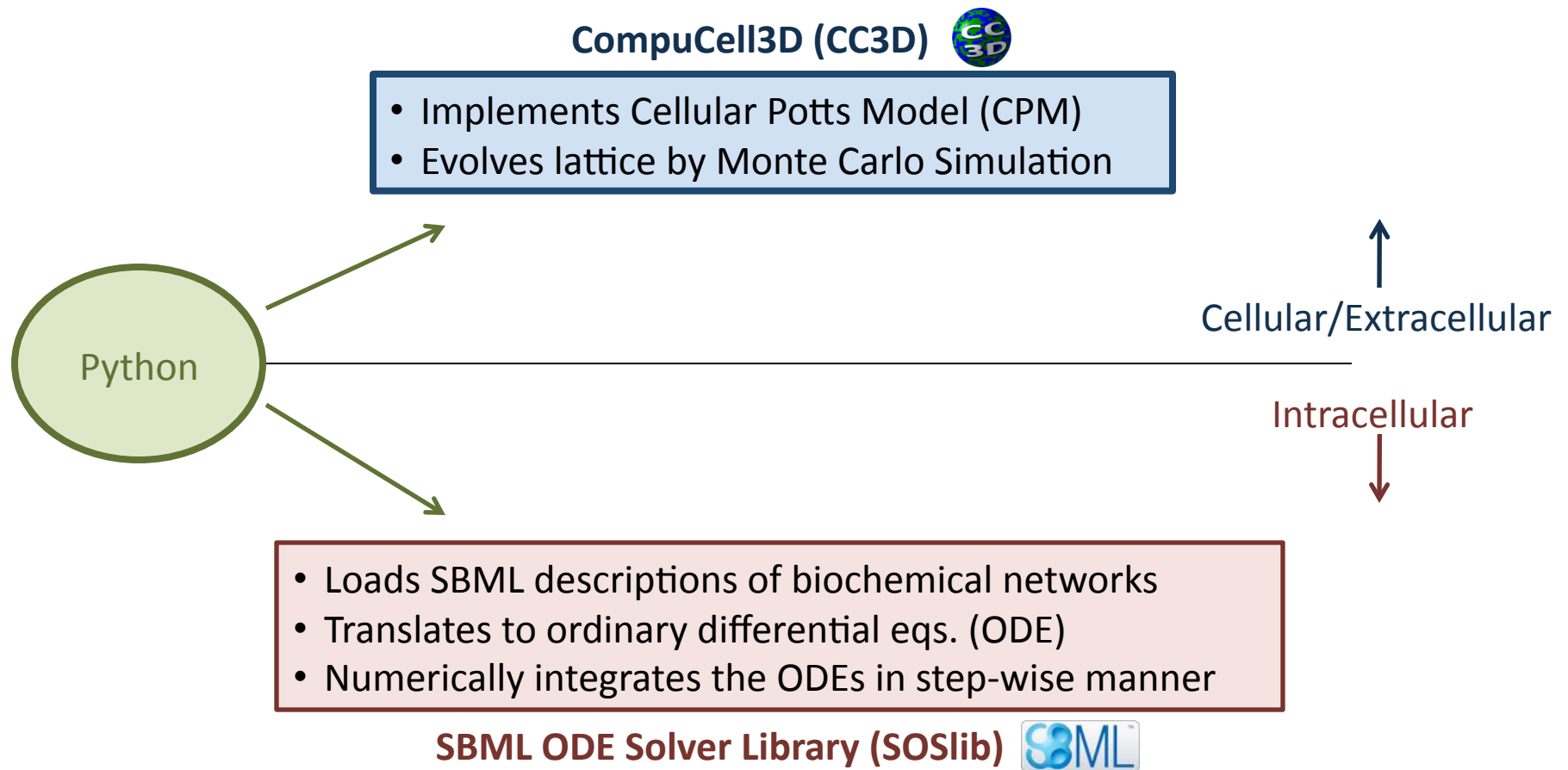
Cellular/Extracellular 

Intracellular 

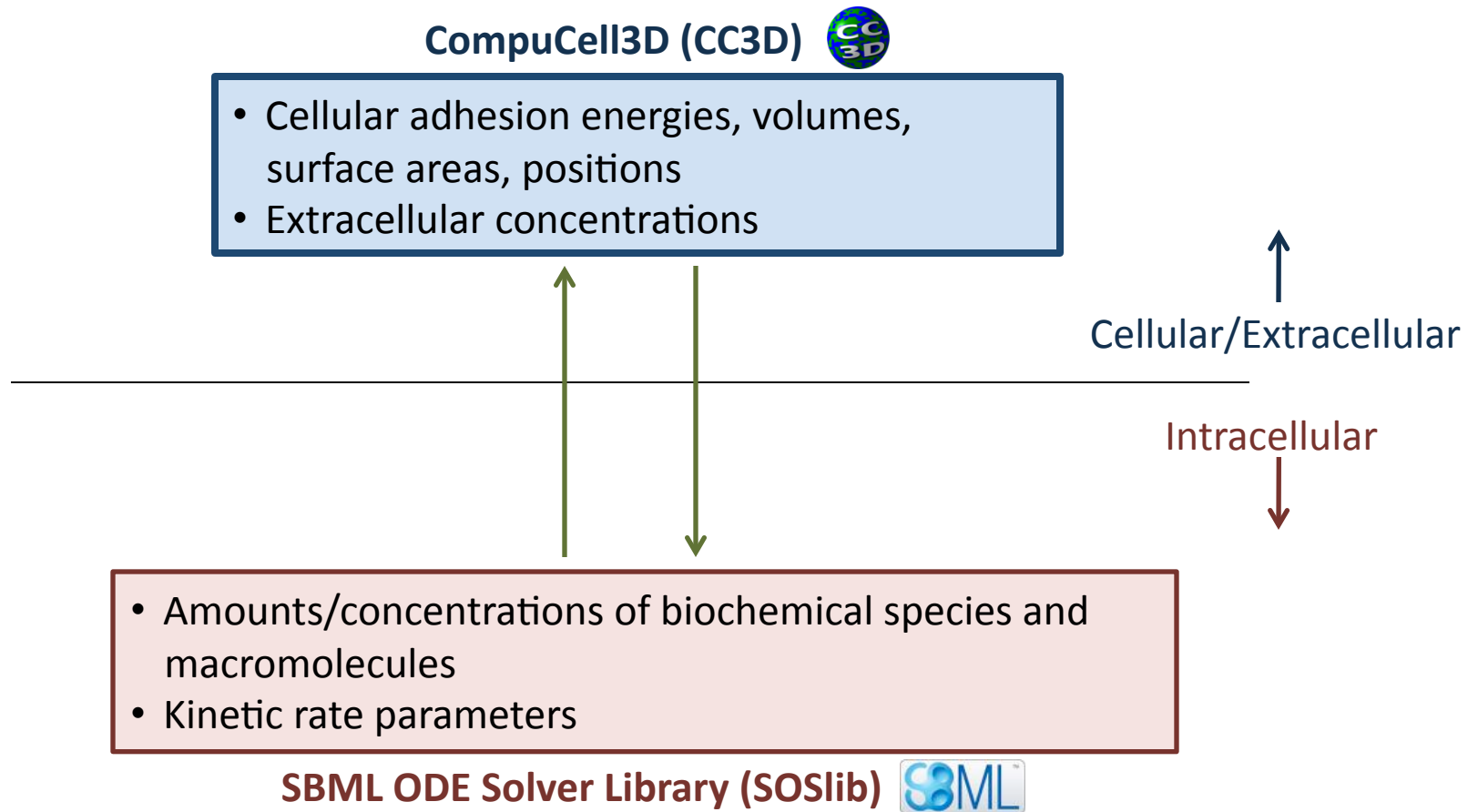
- Loads SBML descriptions of biochemical networks
- Translates to ordinary differential eqs. (ODE)
- Numerically integrates the ODEs in step-wise manner

SBML ODE Solver Library (SOSlib) 

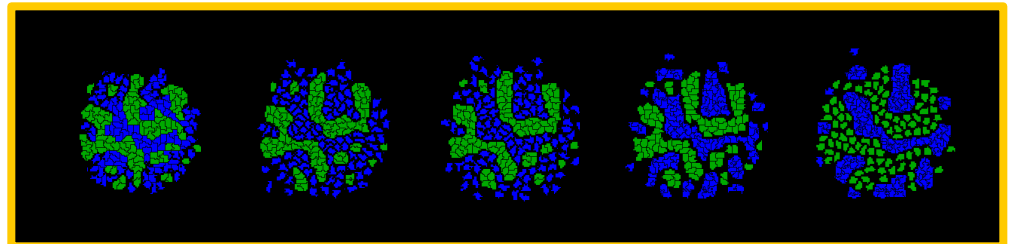
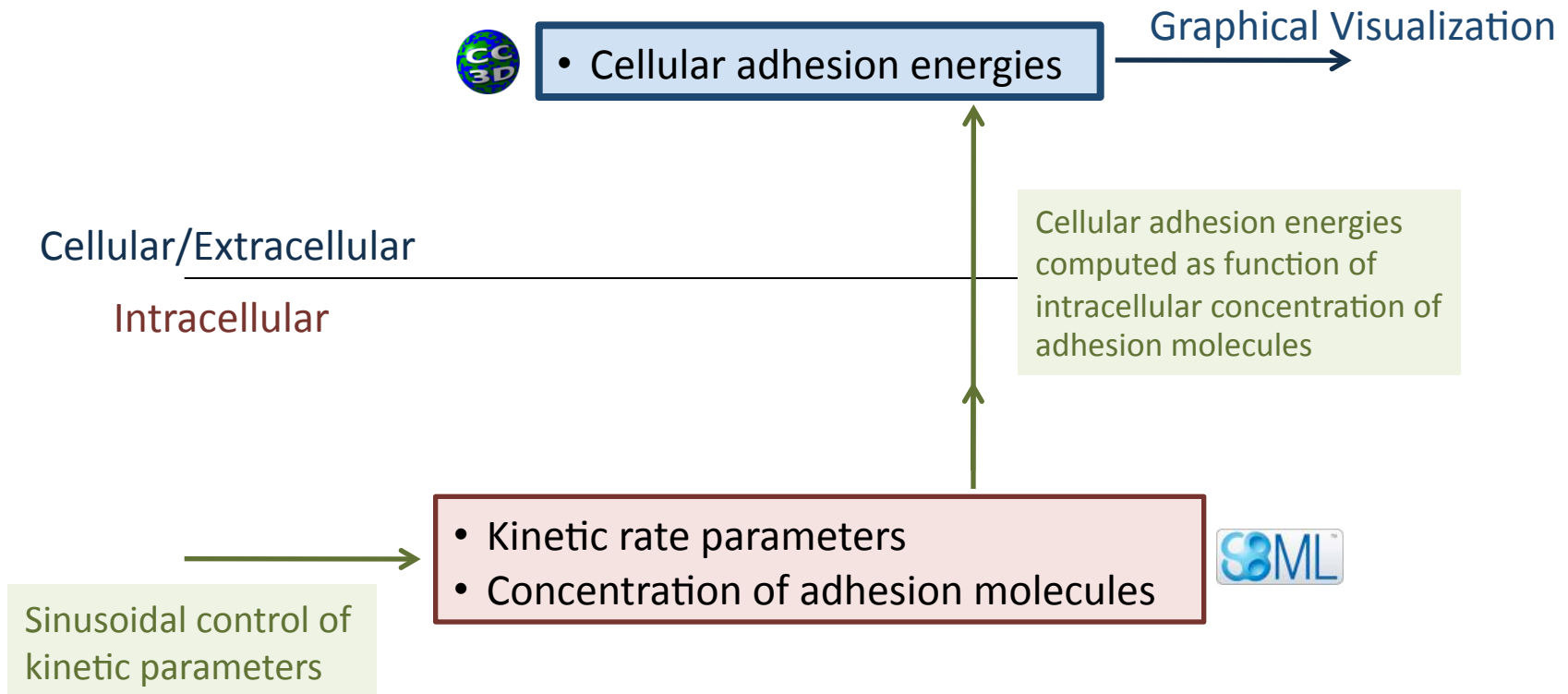
# CC3D-SOSlib Framework for Multiscale Simulation



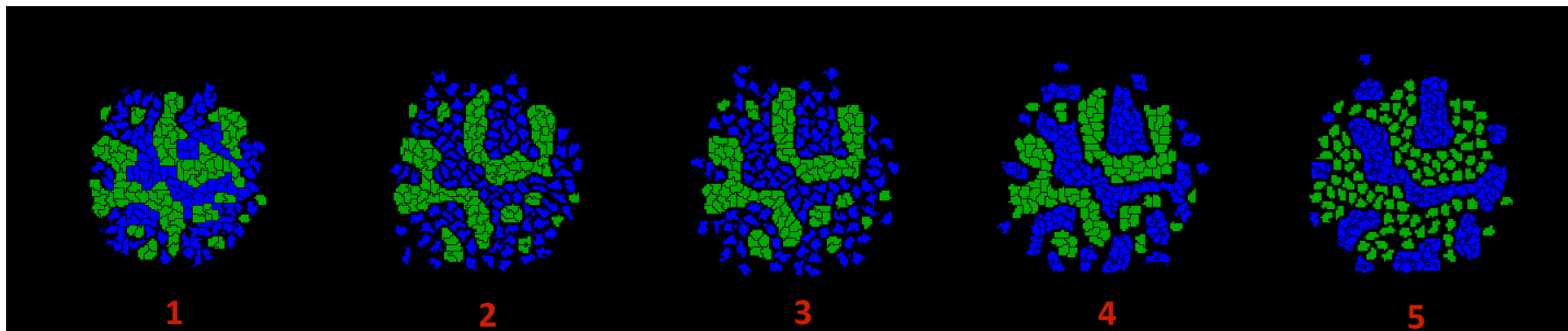
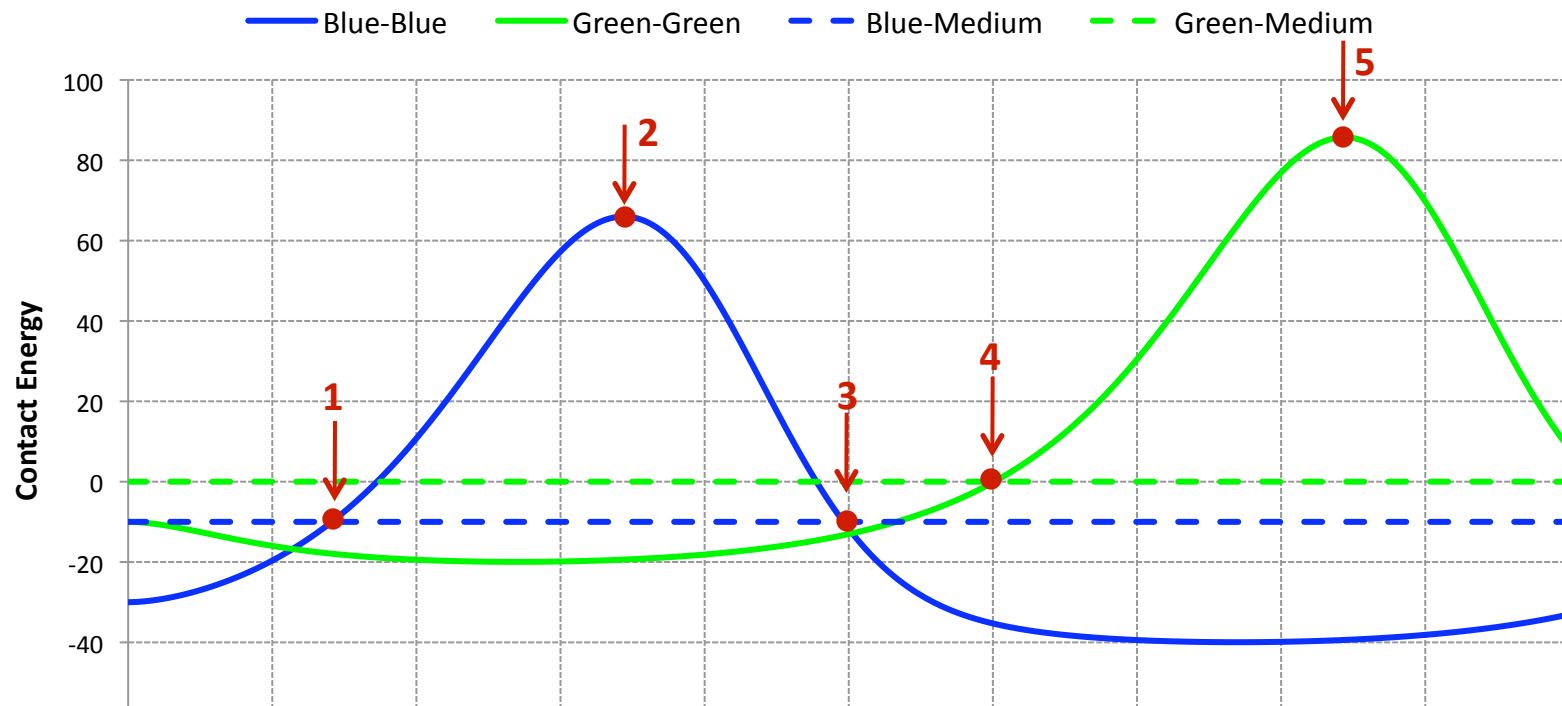
# Exchange of Biological Information within the CC3D-SOSlib Framework



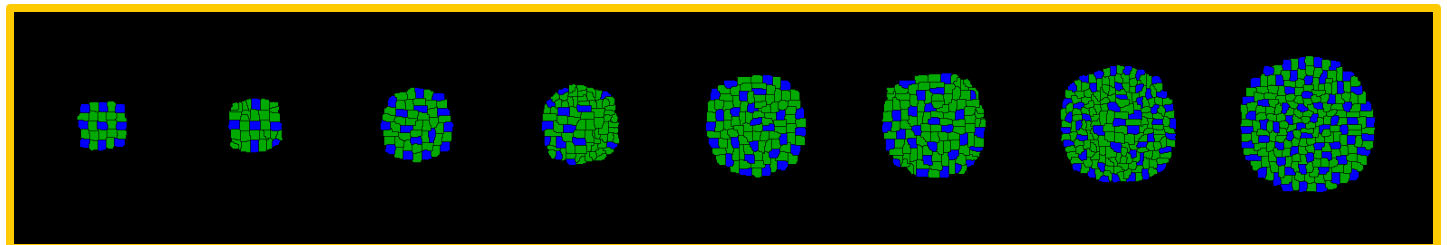
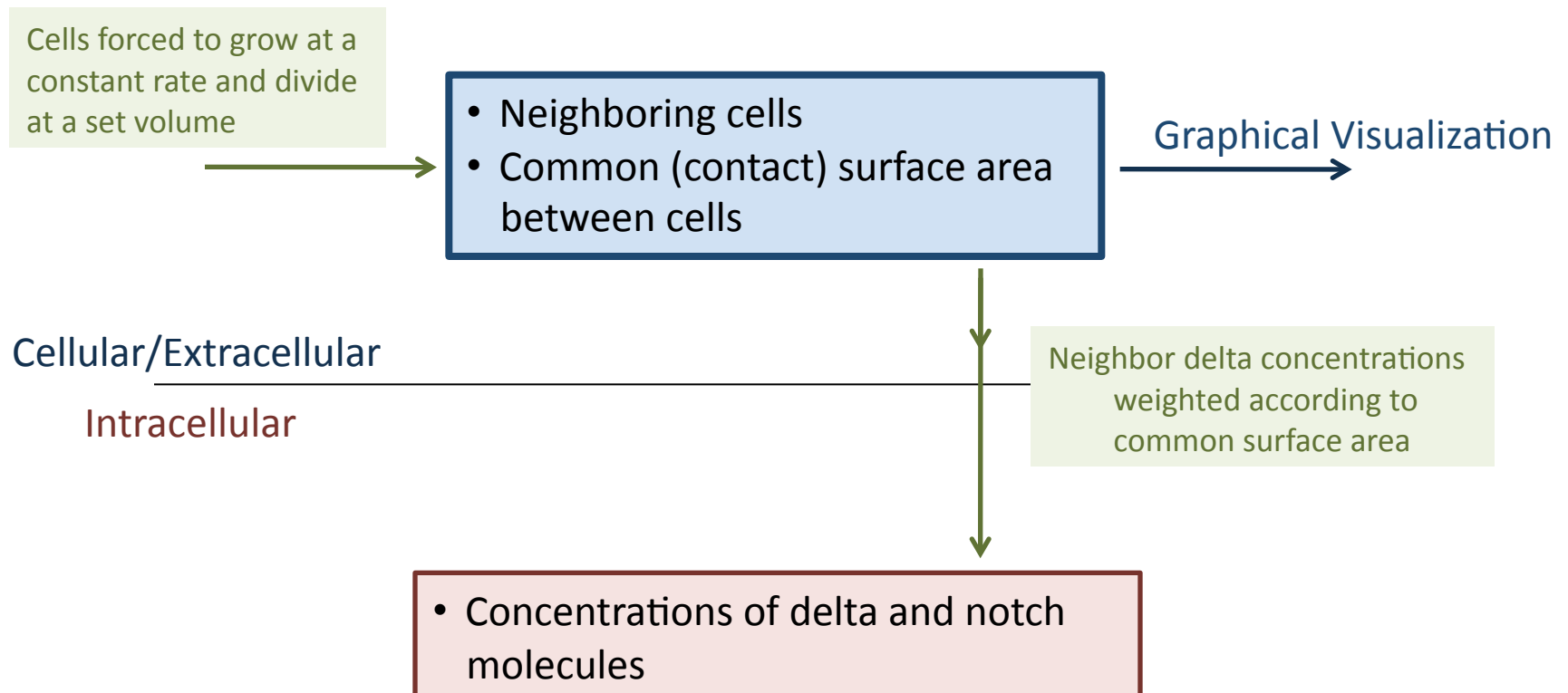
# Changing Adhesion Energy Simulation



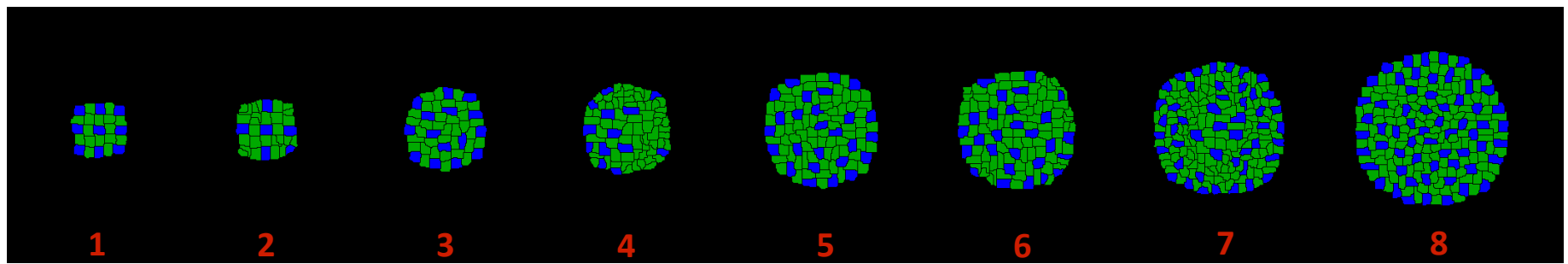
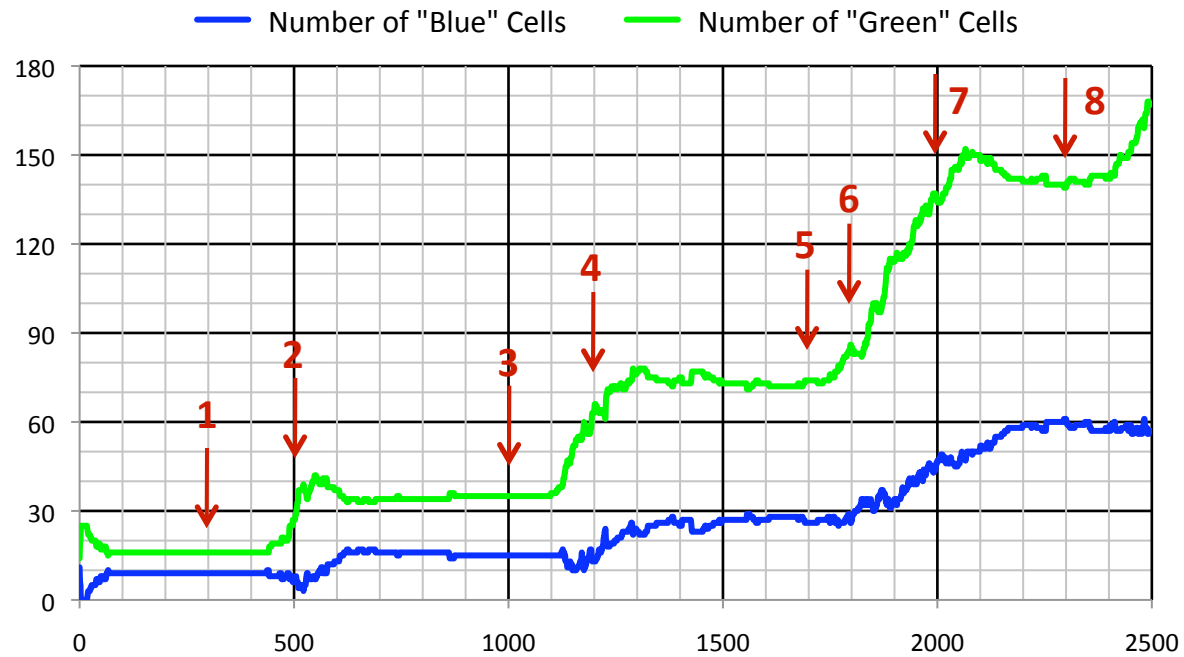
# Changing Adhesion Energy Simulation



# Delta-Notch Simulation with Cell Growth



# Delta-Notch Simulation with Cell Growth



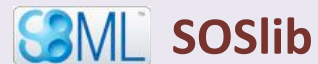
# Files for Multiscale Simulation



- CC3D XML Input File
- PIF file for cell positions and shapes

Python  
Scripts

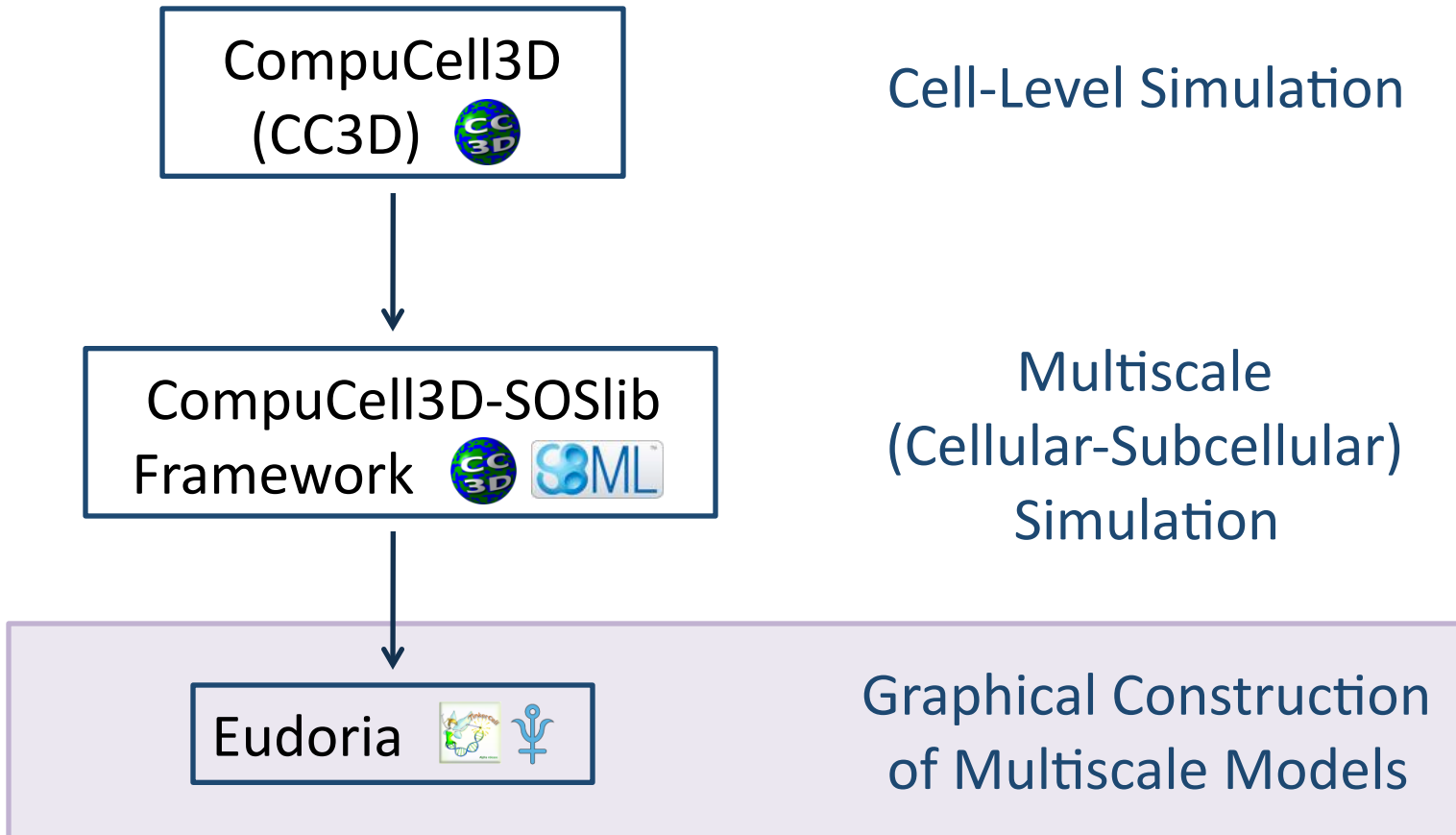
SBML specification of  
intracellular models



SOSlib



# Overview



# Tinkercell for Biochemical Network Design



Graphical construction  
of biochemical networks

The screenshot displays the Tinkercell software interface for biochemical network design. The central workspace shows a network diagram with three species (s1, s2, s3) and two reactions (J0, J1). The interface includes several panels:

- Parts Tree:** A sidebar on the left showing a library of biochemical components.
- Connections Tree:** A sidebar on the left showing the hierarchical structure of the network.
- History:** A panel on the right showing a list of recent actions, such as "items moved by ...".
- Attributes View:** A table on the right showing the parameters and values for the network components.
- Output Window:** A panel at the bottom left showing the results of a simulation, including error messages.
- Functions:** A panel at the bottom right showing a list of available functions for network analysis.

Name	Parameter	Value
J0	k0	1
J1	k0	1
s1	concentration	1
s2	concentration	1
s3	concentration	1

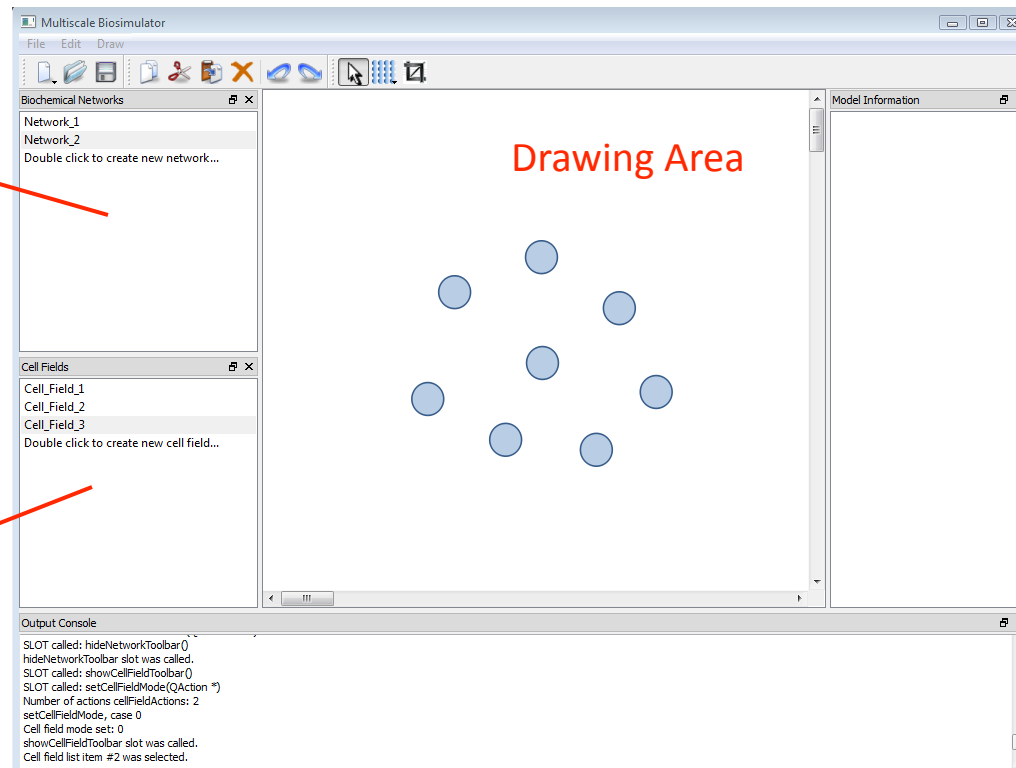
```
>>> Python initializing (init.py) ... DO NOT EXIT AT THIS TIME
Error: about.txt not found
>>>
Error: No module named init
>>>
```

Tools for Biochemical  
Network Analysis

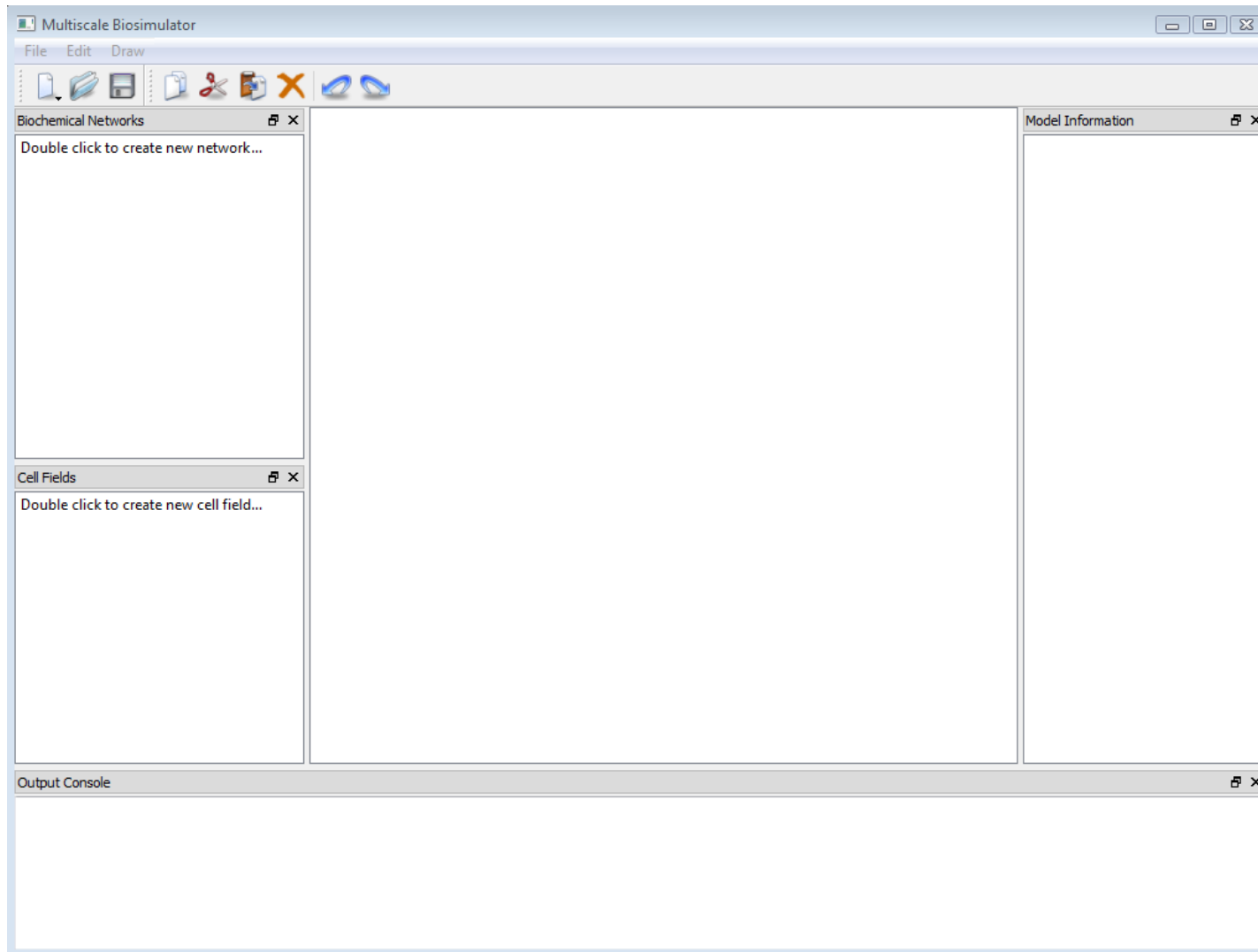
# Eudoria for Multiscale Cellular Systems Design

Biochemical  
Networks

Cell Fields



# Eudoria with CompuCell3D



# Eudoria in the Short Term

- **PIF file generation:**  
Specify cell types, sizes and locations
- **CC3D XML generation:**  
Specify Potts parameters, contact energies, volume and surface area plugins, etc.
- **Python script template generation:**  
Extend basic capabilities of CC3D and allow customization by modelers
- **SBML generation**

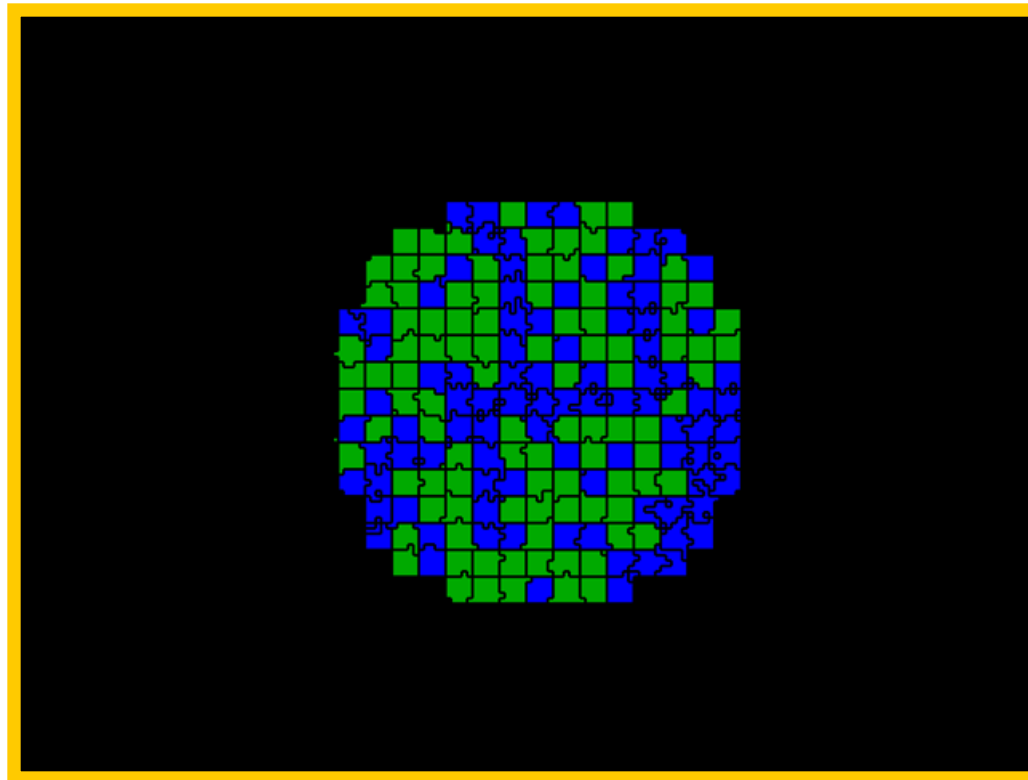
# Eudoria in the Long Term

- Move from only model-building and CC3D file-generation to multi-methodology simulation
  - Lattice-based simulation (CPM)
  - Lattice-free simulation
  - Hybrid simulation
- Conform, internally, to methodology-independent model specifications (CBO and SBO)
- Generate model specification files in relevant markup languages (e.g. Cell Behavior Markup Language, when it exists)

# Acknowledgments

- Sauro, Glazier Labs (Ryan Roper, NIH, GM076692)
- Deepak Chandran (Tinkercell) - NSF (FIBR 0527023), Microsoft
- Lucian Smith (Antimony) – NIH (GM081070)

# Changing Adhesion Energy Simulation





# Delta-Notch Simulation with Cell Growth

