

Week 8: Modeling of Cell Clusters - Structure, Dynamics, and Emergent Mechanics

November 8

ME 480 – Mechanobiology: how mechanics regulate life

Sangwoo Kim

- Introduction
- Discrete vs Continuum
- Mathematical Modeling
- Physical/Mechanical Modeling

What is the Scientific Modeling?

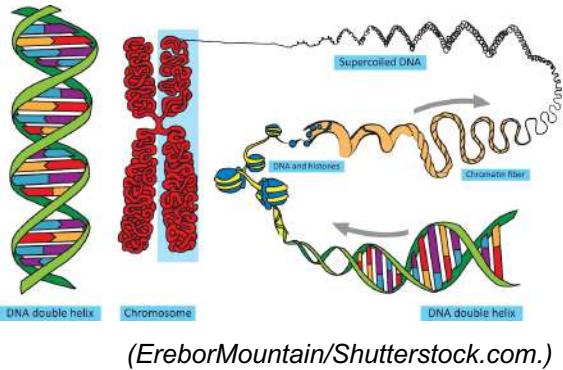


(Wikipedia)

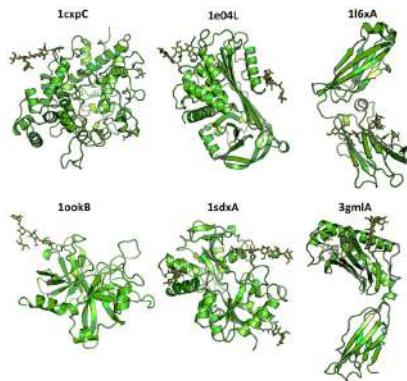
*The sciences do not try to explain, they hardly even try to interpret, they mainly make models. By a model is meant a **mathematical construct** which, with the addition of certain verbal interpretations, describes **observed phenomena**. The justification of such a mathematical construct is solely and precisely that it is expected to work.*

John von Neumann

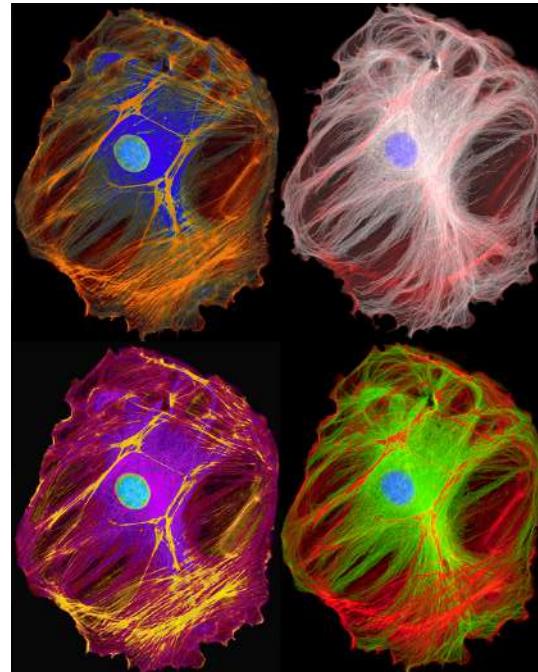
DNA packaging



Protein structure



(Lee et al. *Sci Rep* 2015)

Cytoskeleton
Single cell migration

(<https://sitn.hms.harvard.edu/art/2015/actin-four-ways/>)

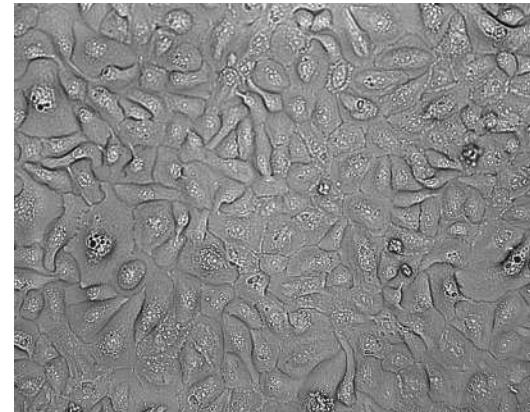
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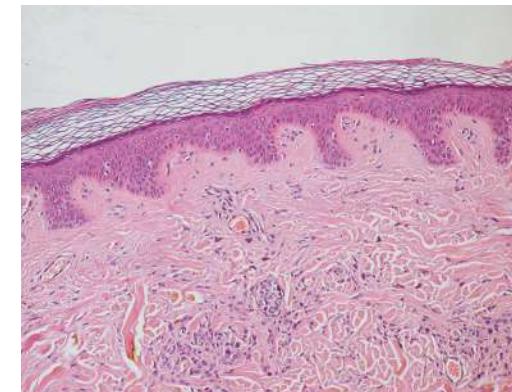
mm

Length scale

Animal tissues

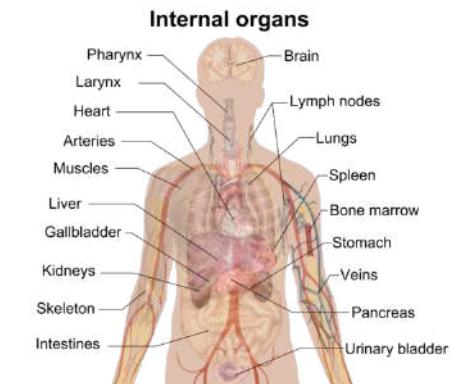


(Thomas et al. *Journal of Allergy and Clinical Immunology*, 2017)



(Wikipedia: loose connective tissue)

Organs

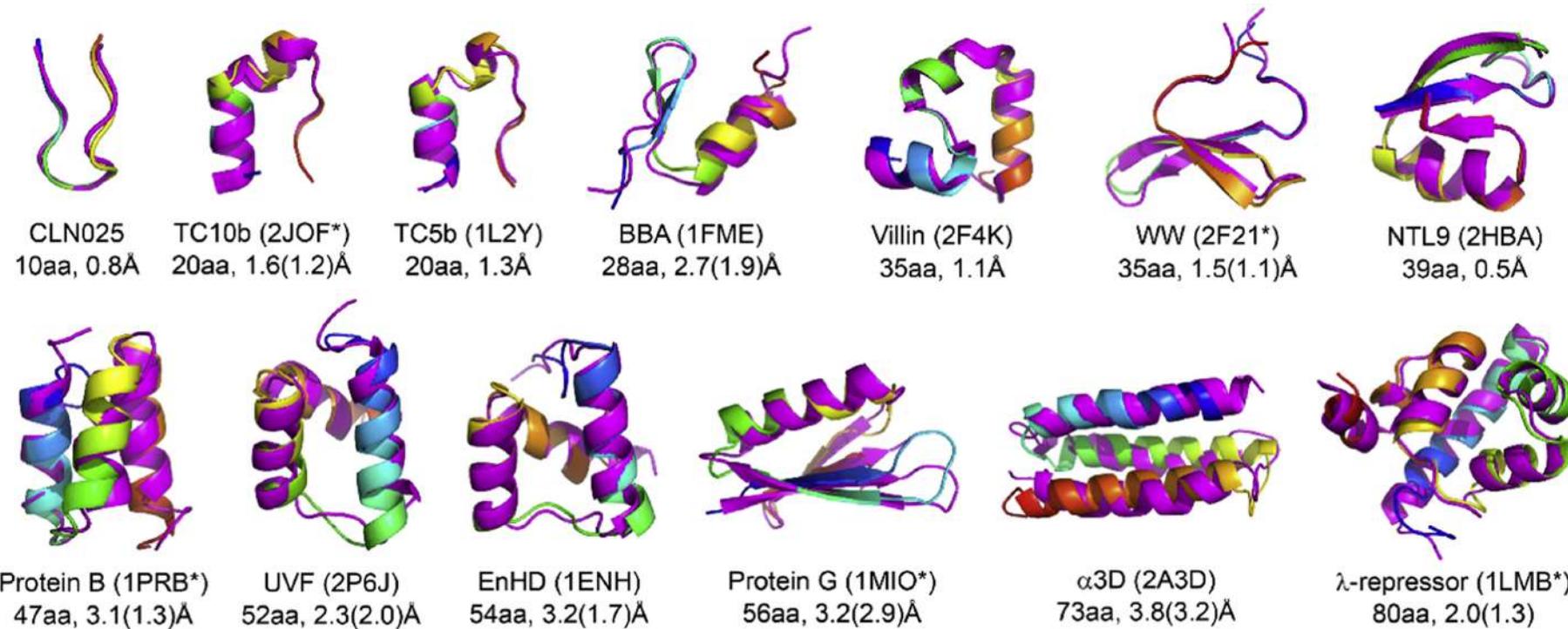


(Wikipedia: Organ)

Bone

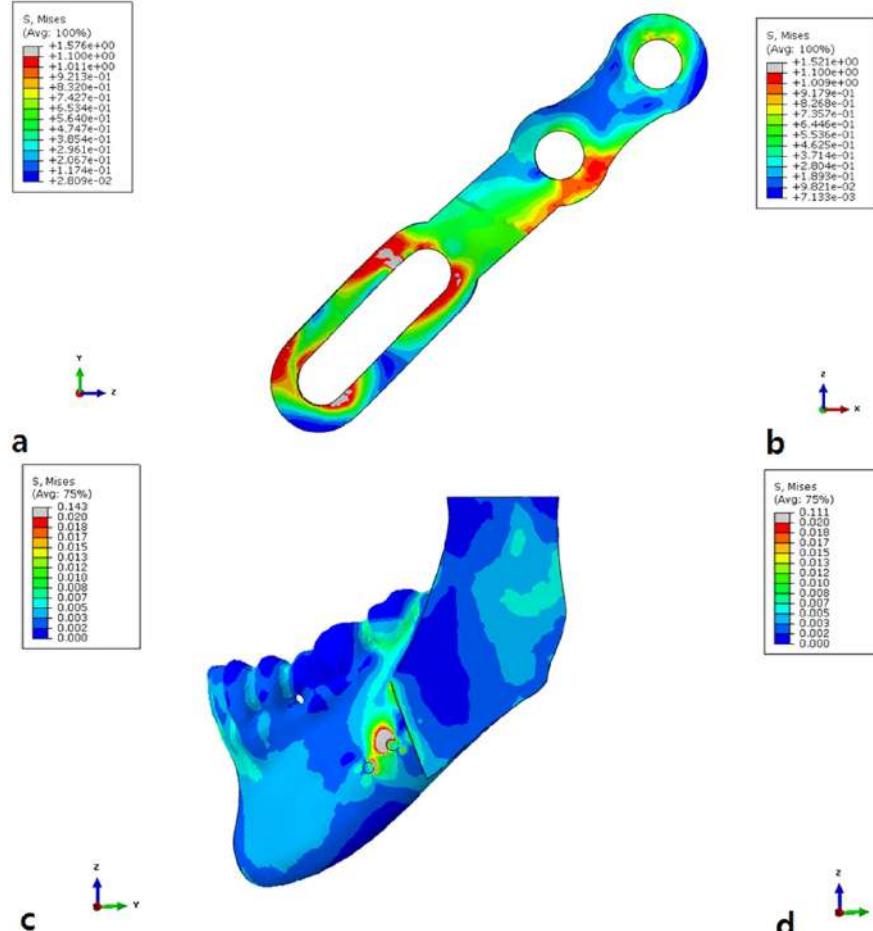


(Wikipedia: bone)



(Geng et al. Computational and Structural Biotechnology Journal, 2019)

- Discrete modeling approach
- Degrees of freedom as positions /orientations of atoms
- Compute forces/moment acting on each atom of protein
- Forces/moment are computed from a molecular mechanics force field
- Apply Newton's laws of motion to predict the spatial position/orientation
- Large-scale Atomic /Molecular Massively Parallel Simulator (LAMMPS)



(Kim et al. Sci Rep, 2018)

- Continuum mechanics modeling (FEM)
- Based on fundamental mechanical principles
 - mass conservation
 - linear momentum conservation
 - angular momentum conservation
 - energy conservation
- Constitutive equations
 - Elastic vs Plastic
 - Newtonian vs Non-Newtonian
 - Viscoelastic
 - Viscoplastic
 - Hyperelastic
- Abaqus, Comsol Multiphysics

Keyword: Continuum mechanics for biological tissues

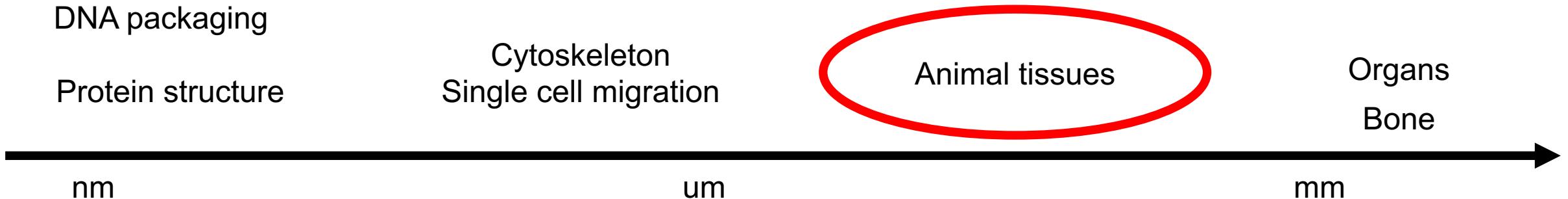
Discrete Modeling

- Resolution at cellular scale (or even subcellular scale)
- How to represent individual cells?
- What is dominant interaction between cells?
- Computationally challenging to study tissues with a large number of cells

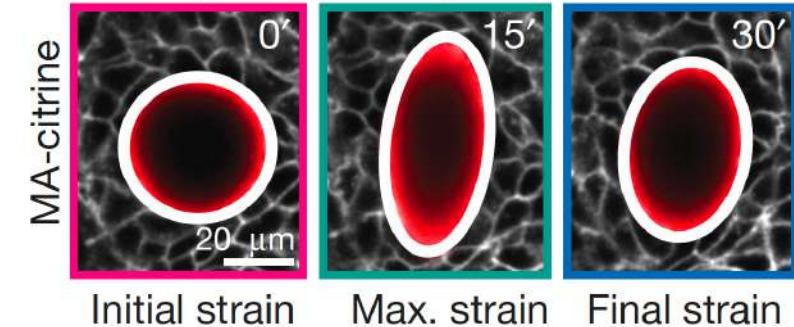
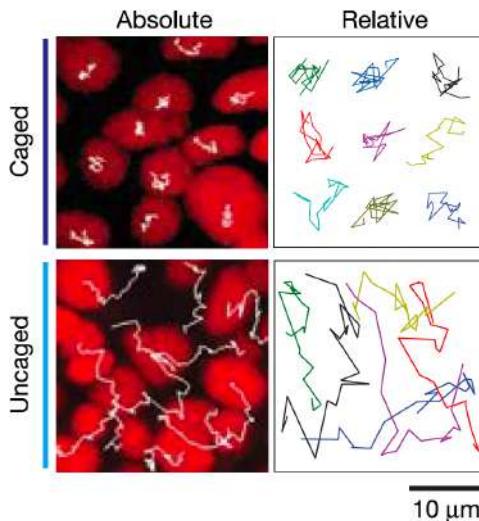
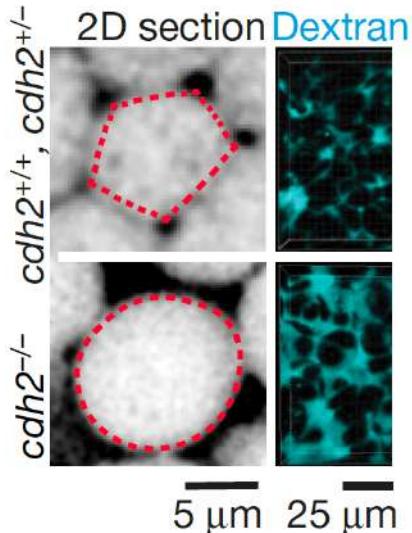
Continuum Modeling

- Computationally efficient to study large system
- Study of a large system for a long time
- Local events cannot be predicted
- How to derive constitutive equations?

Discrete vs Continuum??



We will mainly discuss about discrete modeling approaches today



(Mongera18)

Structure

- Measures from shapes of cells and subcellular elements
 - Cell size
 - Cell shape
 - Cell orientation
- Image analysis for a fixed time point

Dynamics

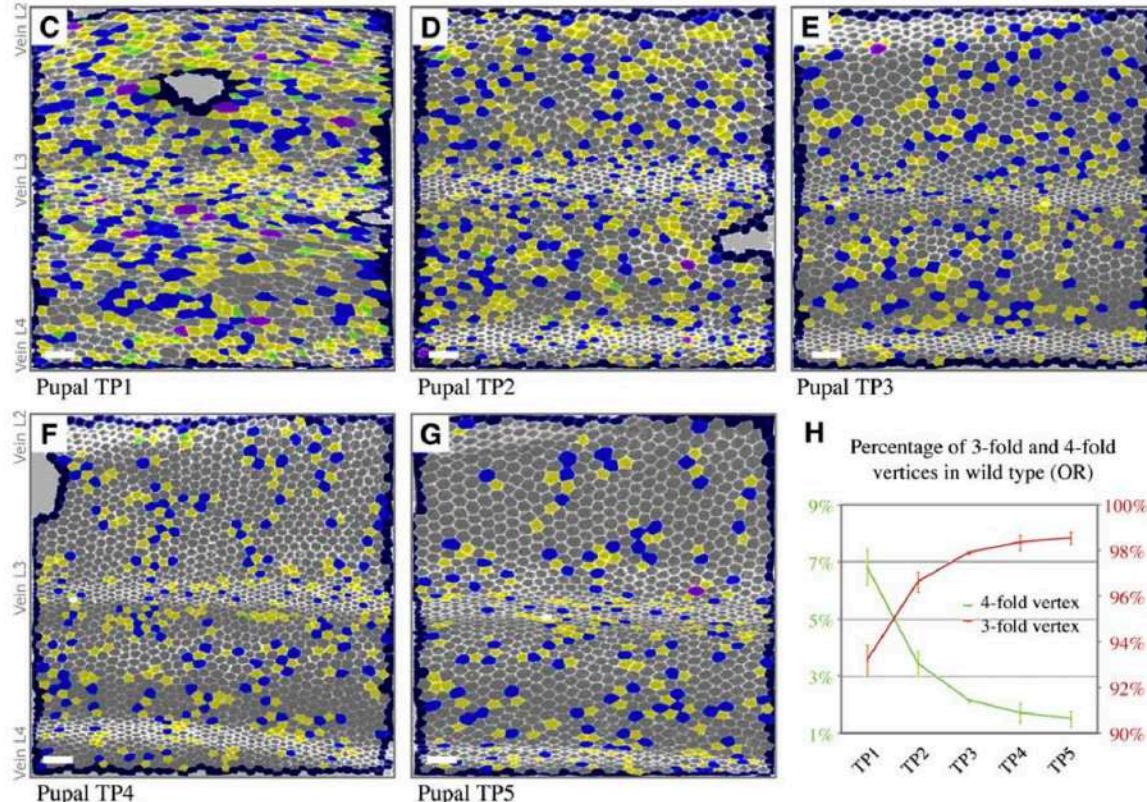
- Time-lapse movies of experimental data
- Image analysis over a period of time
- MSD, neighbor exchange event, etc

Mechanical properties

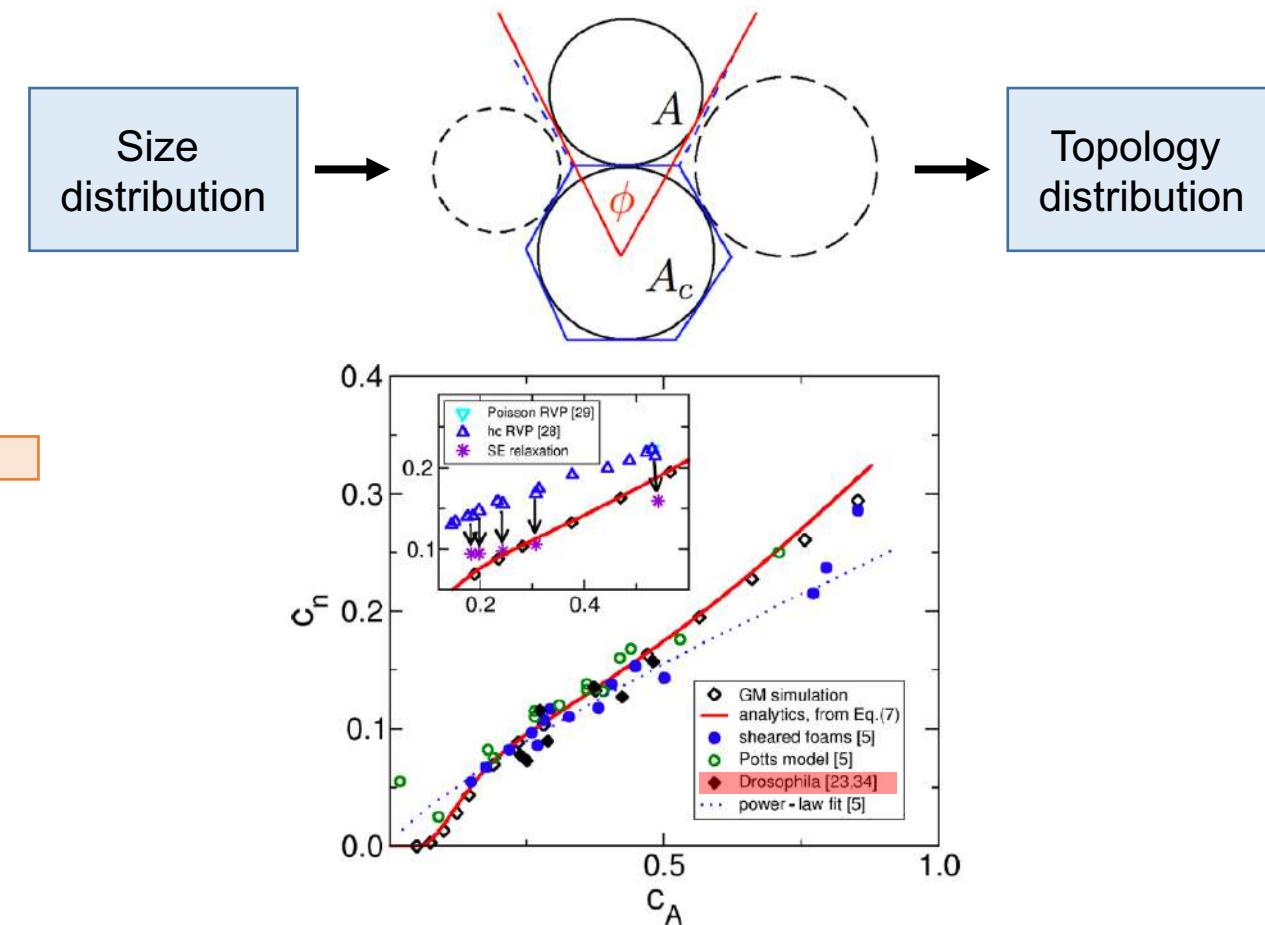
- Mechanical testing is required
- Macroscopic properties vs cellular/subcellular properties
- AFM, optical tweezer, micropipette, microbeads, droplets, etc
- Rheological test

How can we explain these observed measures in cell clusters based on models?

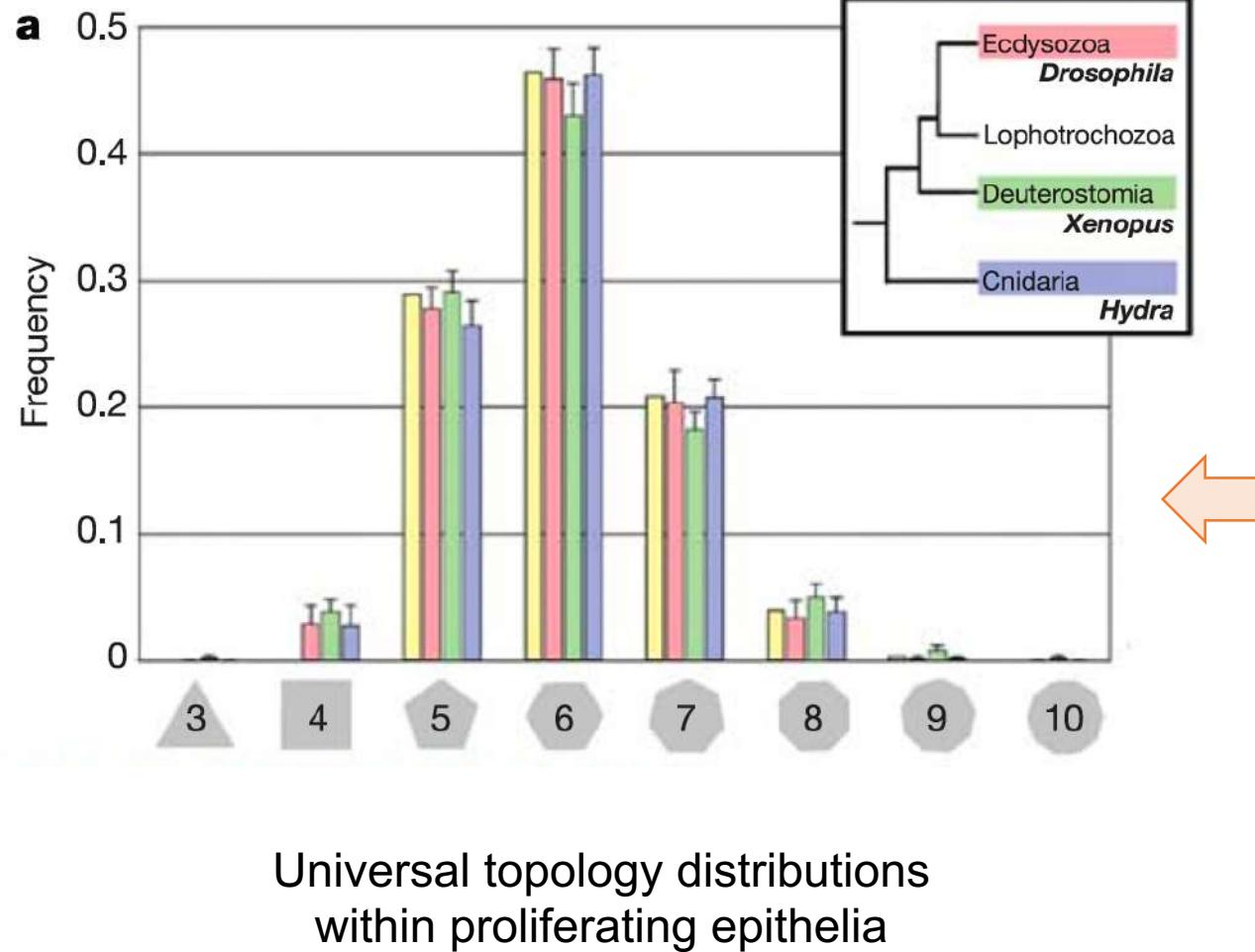
Can mathematical modeling explains observed phenomena in cell clusters?



Structural ordering of wing epithelium of *Drosophila* embryo

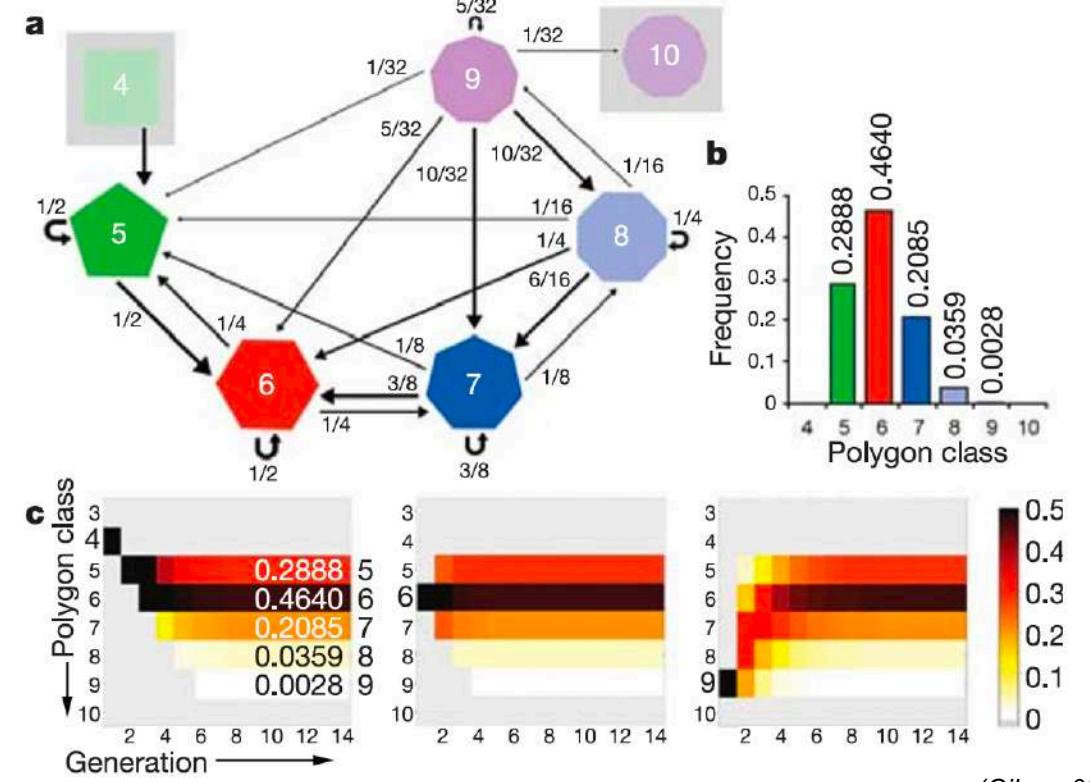


Universal relation between size and topology

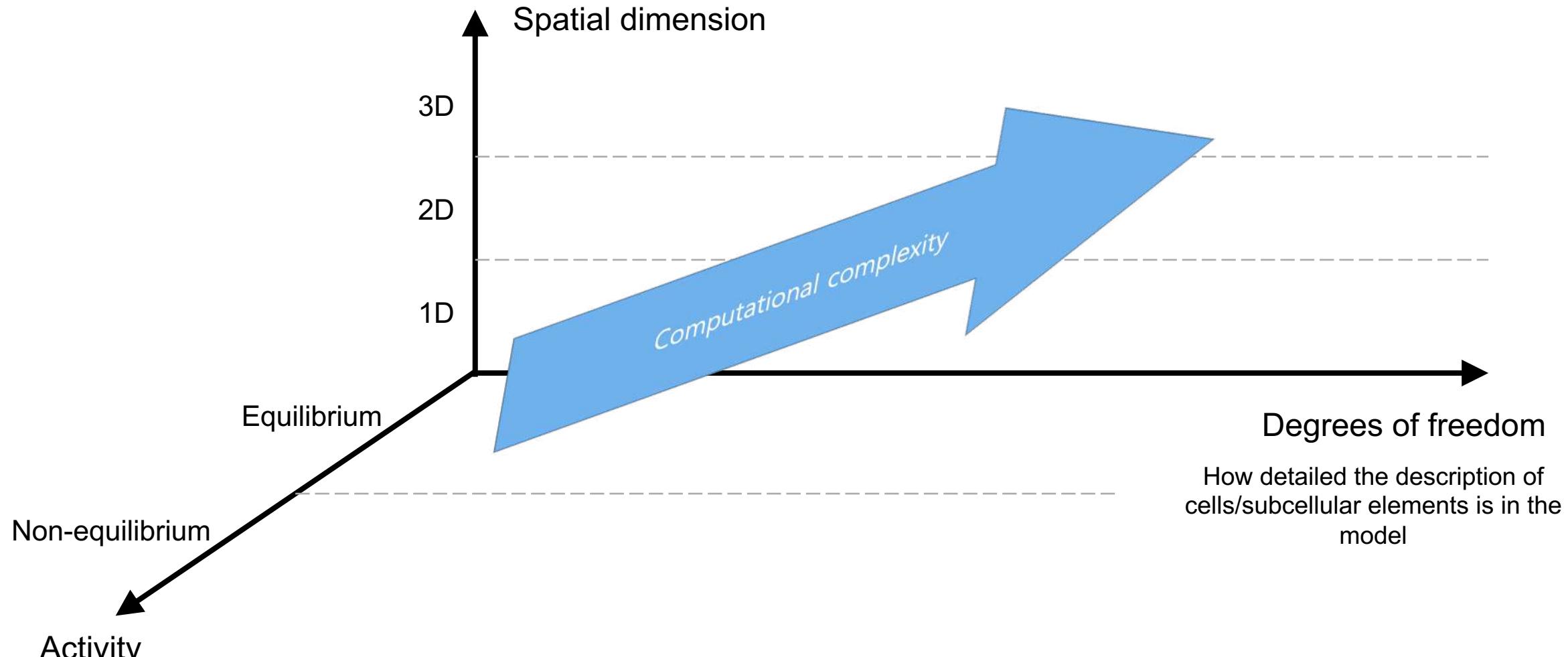


Markov chain: stochastic model describing a sequence of possible events in which the probability of each event depends only on the state attained in the previous event

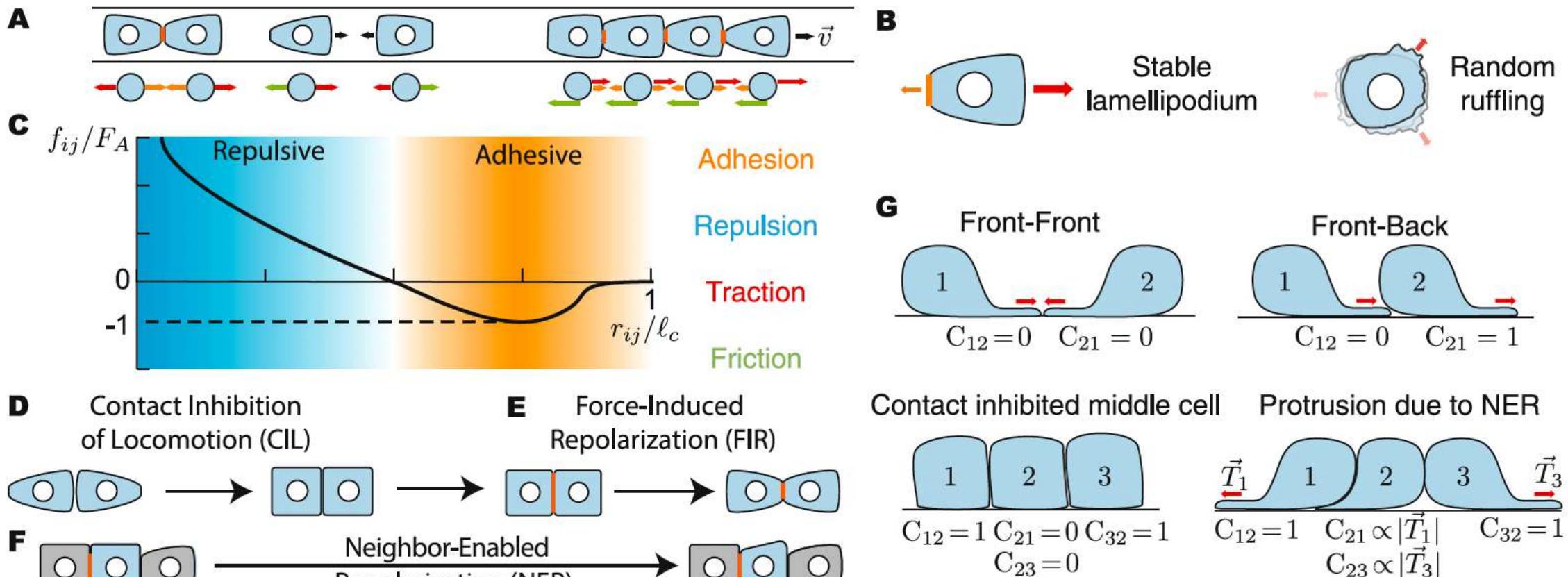
Random division plane + neighbor addition by adjacent dividing cells



A robust equilibrium topology distribution can be derived from a Markov chain model



Combination of soft matter physics, statistical mechanics, continuum mechanics and computational geometry



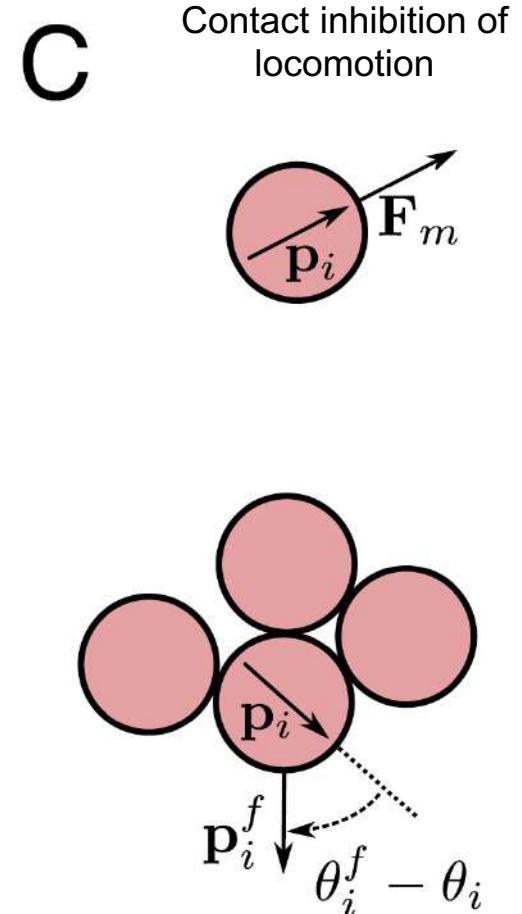
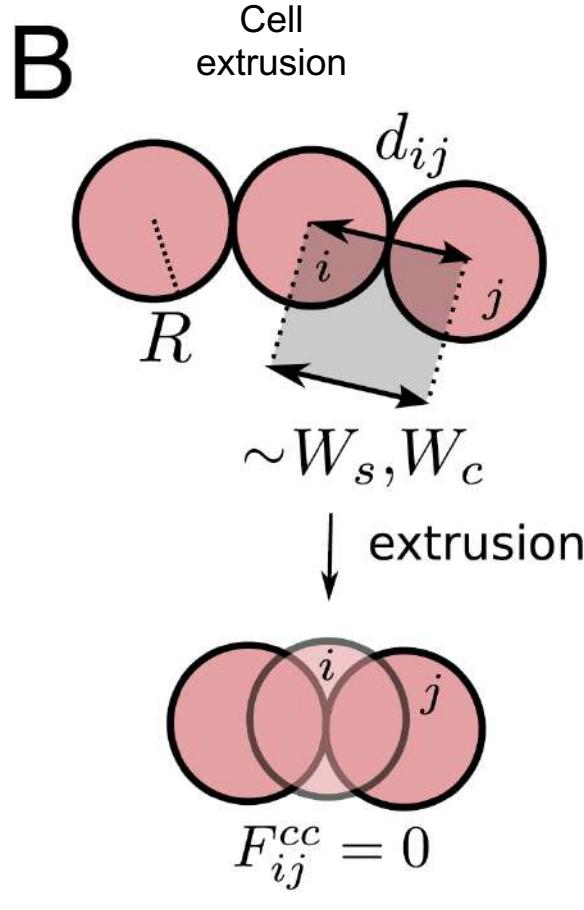
(George17)

Single cell: $\xi \vec{v} = \vec{T} + \vec{F}_{ext}$

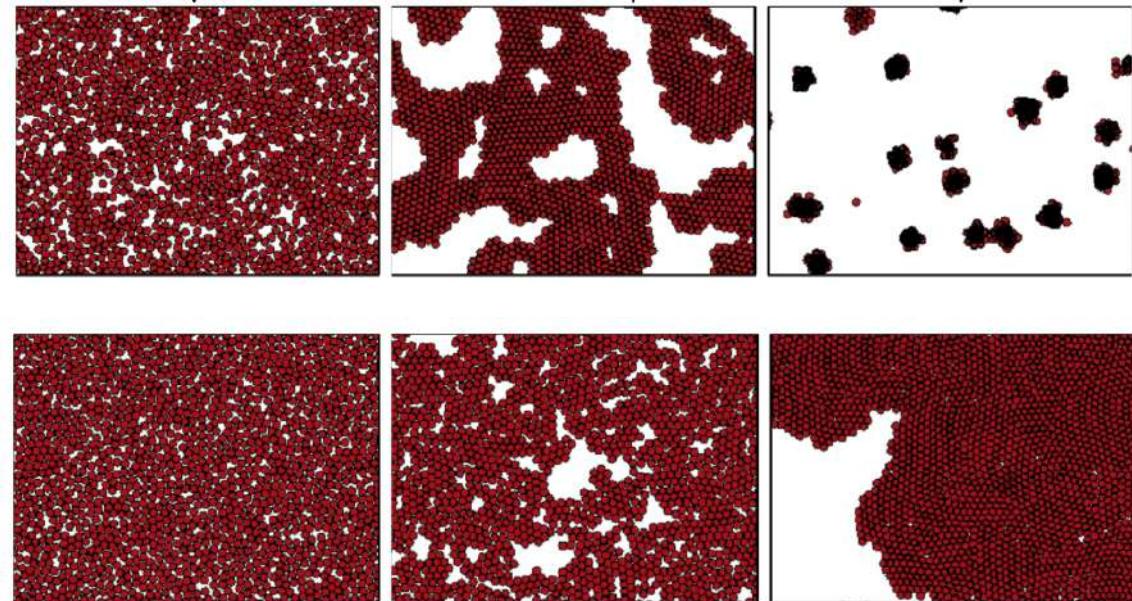
Viscous friction Traction force External force

Multiple cells: $\xi \vec{v}_i = \vec{T}_i + \sum_{j \neq i} \vec{F}_{ji}$

Viscous friction Traction force Interaction force



Different tissue structure



(Smeets16)

$$F_m \vec{p}_i = \gamma_s \dot{\vec{x}}_i + \sum_j^{nn} [F_{ij}^{cc} \hat{n}_{ij} + \gamma (\dot{\vec{x}}_i - \dot{\vec{x}}_j)]$$

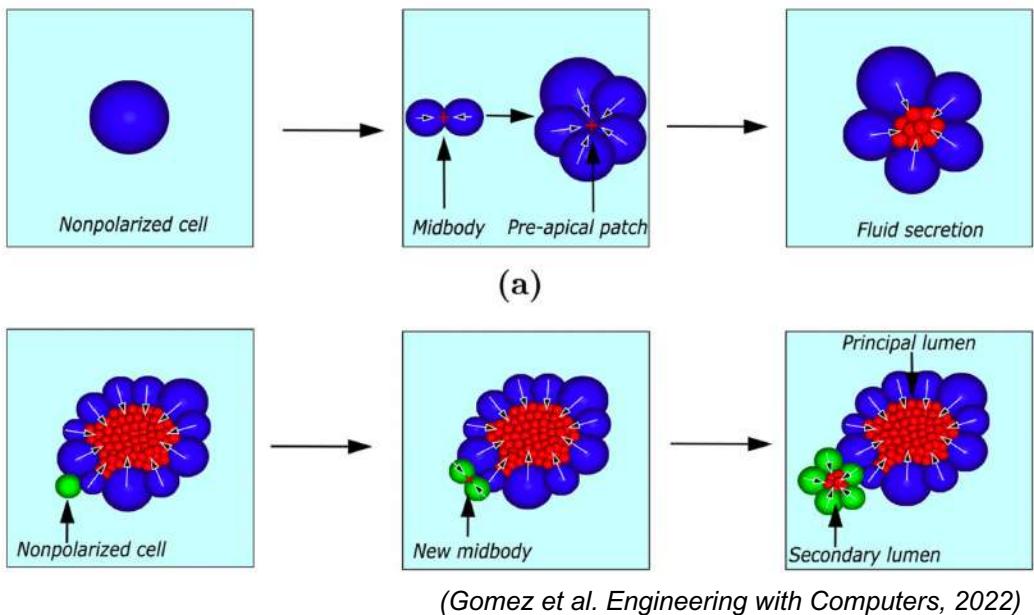
Self propulsion

Cell-substrate friction

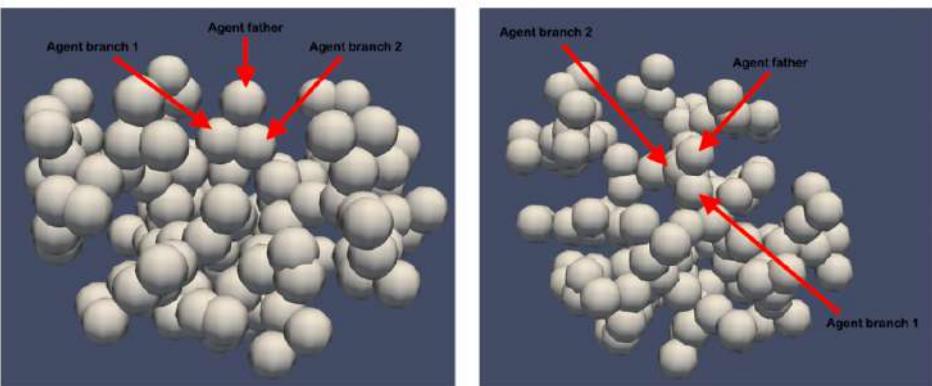
Cell-cell interaction

Cell-cell friction

Lumen morphogenesis

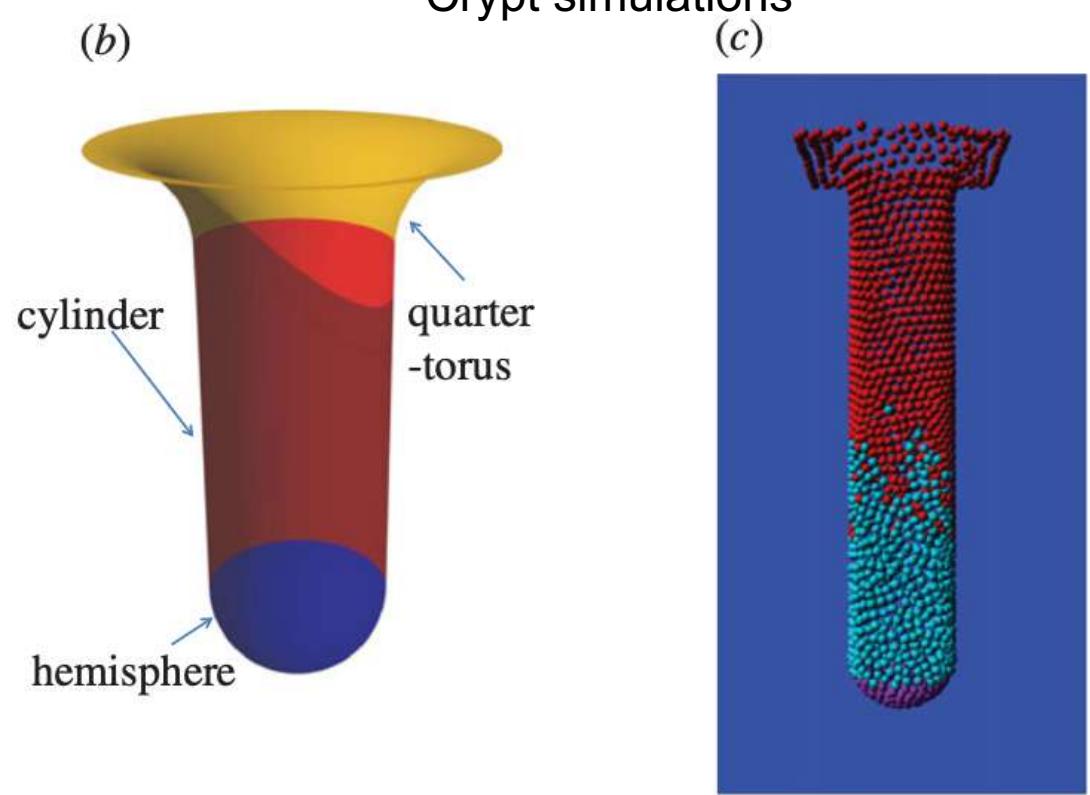


Lung fibrosis



(Cogno et al. *Symmetry*, 2022)

Crypt simulations



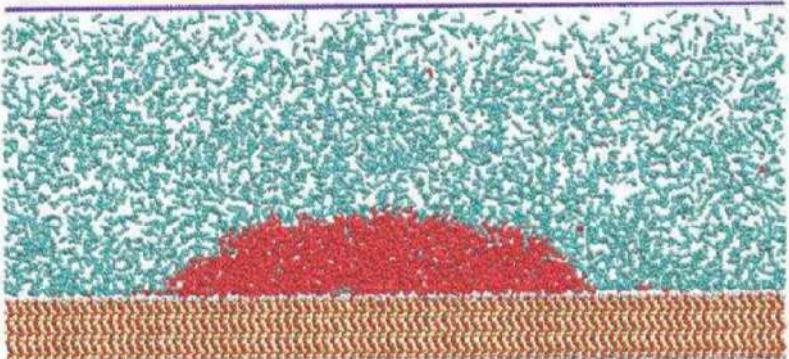
(Dempster et al. *R Soc Open Sci*, 2017)

MD simulation: isotropic atoms
Agent-based model
Soft particle model
Self-propelled particle model
Active Brownian particle model



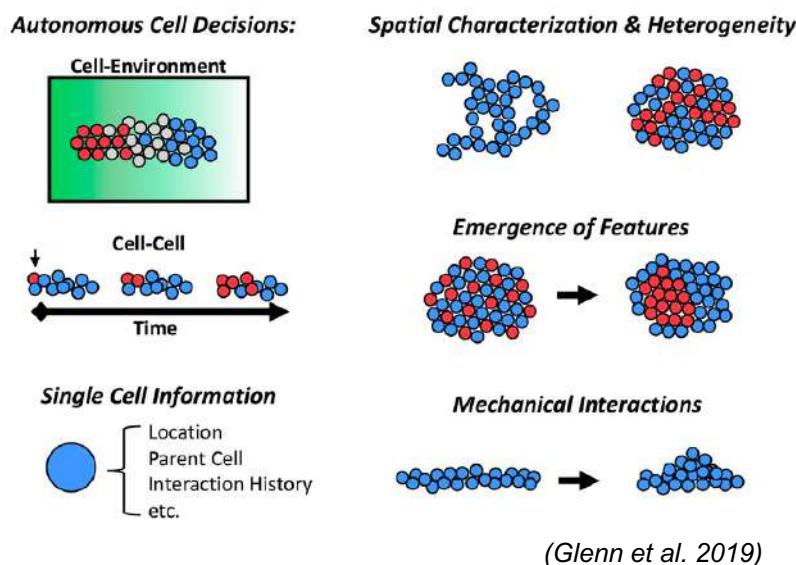
Tissue morphogenesis based on
cell-cell interaction or cell-
substrate interaction

MD simulation

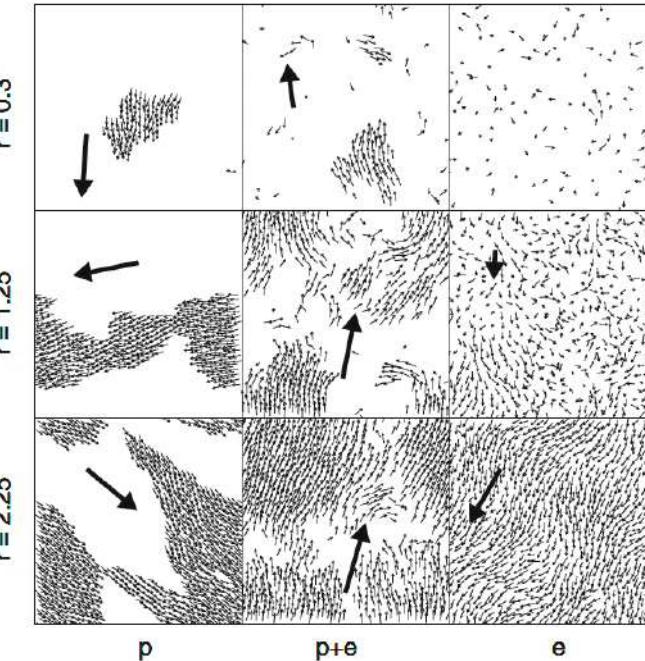


(Sethi et al. 2021)

Agent-based model

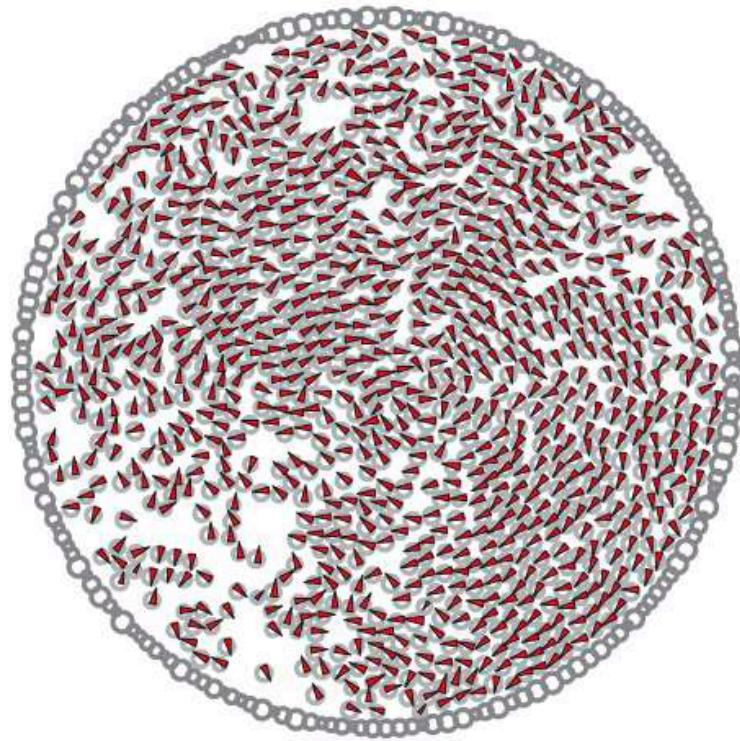
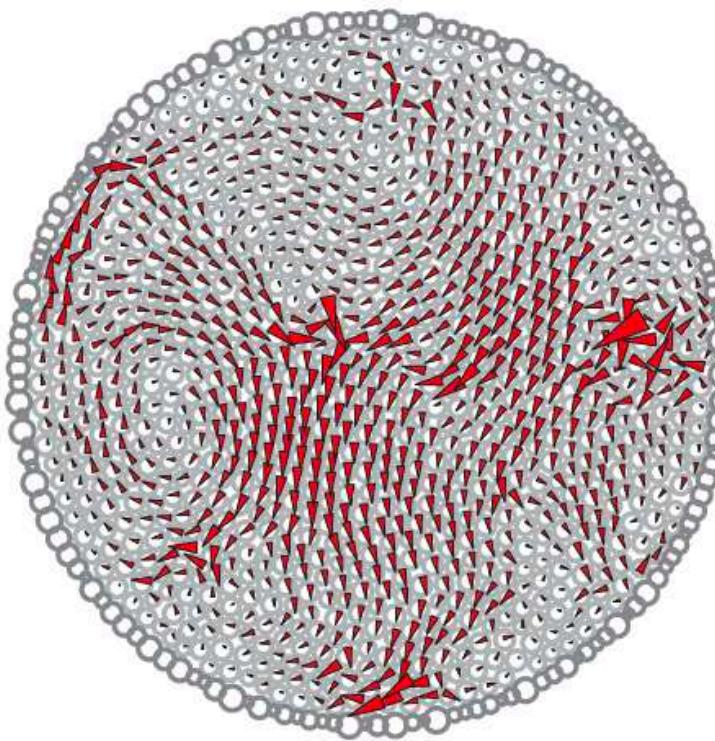
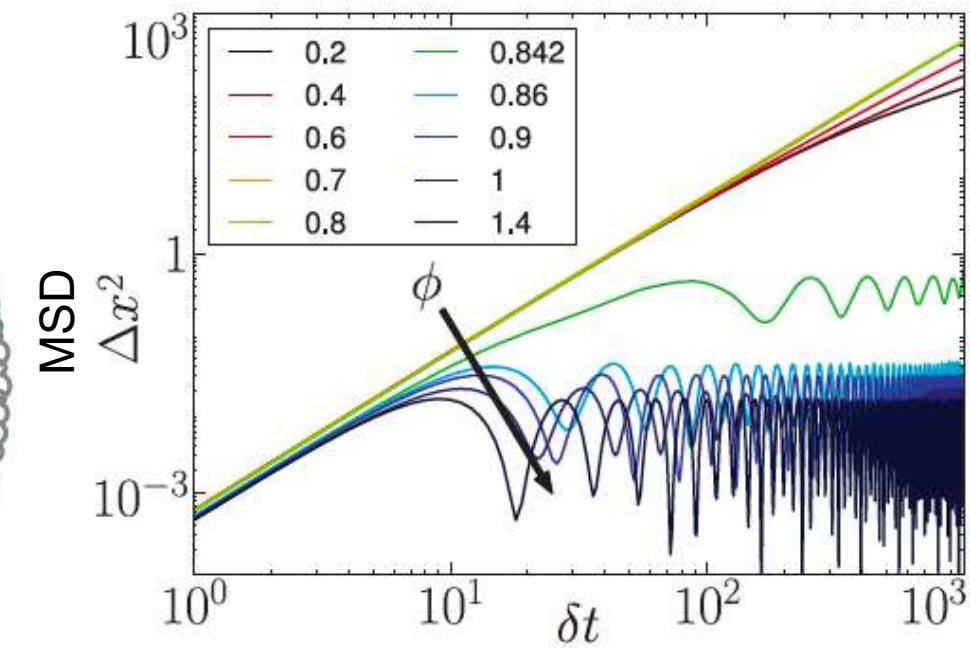


Active Brownian particle model



(Romanczuk et al. 2012)

- Flexibility to implement different types of interactions
- Computational efficient
- Unable to study role of shape changes in biological tissues

 $\phi = 0.6$  $\phi = 0.95$ *(Henkes11)*

$$\dot{\vec{r}}_i = v_0 \hat{n}_i + \mu \sum_{j=1}^{z_i} \vec{F}_{ij}$$

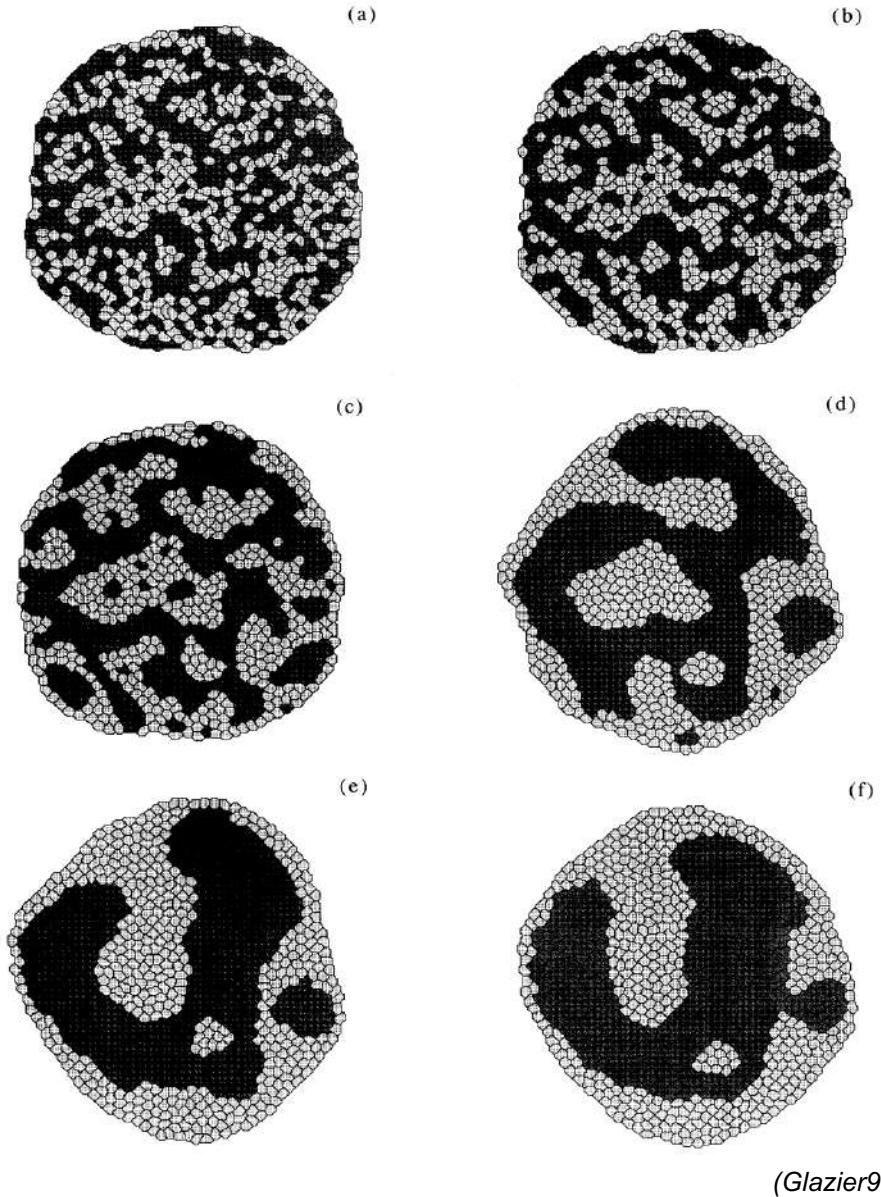
Cell velocity Self propulsion Cell-cell interaction

Typical 2D rectangular CPM lattice

1	1	1	2	2	5	5	5	5
1	1	2	2	2	5	5	5	5
1	1	2	2	2	5	5	5	4
1	2	2	2	2	7	7	4	4
7	7	7	7	7	7	7	4	4
6	6	6	3	3	3	7	4	4
6	6	6	3	3	3	7	4	4
6	6	3	3	3	3	7	4	4

(Scianna12)

- Lattice based model
- Each cell is a subset of connected lattice sites that shares the same cell ID
- Lattice sites that are not occupied by cells are extracellular spaces
- The dynamics are governed by an energy functional, Hamiltonian (H)
- Update of sites using Monte-Carlo simulation algorithm with Metropolis criterion
 - Randomly choose site i
 - Switch the cell ID of site i to the cell ID of site j that is randomly chosen site among neighboring sites of site i
 - Compare energy before and after the change
 - If an energy is lower, accept a new configuration. If not, accept a new configuration with a probability of $e^{-\Delta H/T}$



$$\begin{aligned} H_{Potts} &= \sum_{\substack{(i,j)(k,l) \\ \text{neighbors}}} J(\tau(\sigma(i,j)), \tau(\sigma(k,l)))(1 - \delta_{\sigma(i,j)\sigma(k,l)}) \\ &+ \lambda \sum_{\sigma} (a(\sigma) - A_{\tau(\sigma)})^2 \end{aligned}$$

Energy = surface energy + area elasticity

τ : type of cells

σ : cell ID

J : surface tension

- Cell sorting behavior depending on relations of distinct surface tensions
- Differential adhesion hypothesis (differential interfacial tension hypothesis)

Cellular Potts model is a special version of Potts model in statistical physics, that is a generalization of **Ising model**

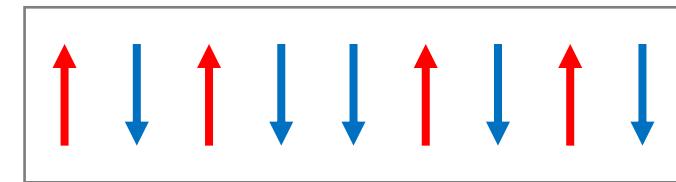
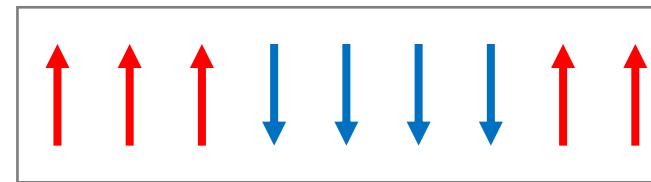
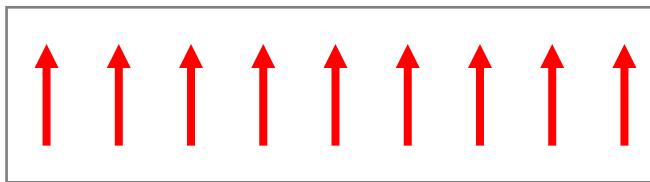
What is Ising model?

A: a mathematical model of ferromagnetism (a collection of atomic spins aligns in the same direction, yielding a net magnetic moment in macroscopic scale)

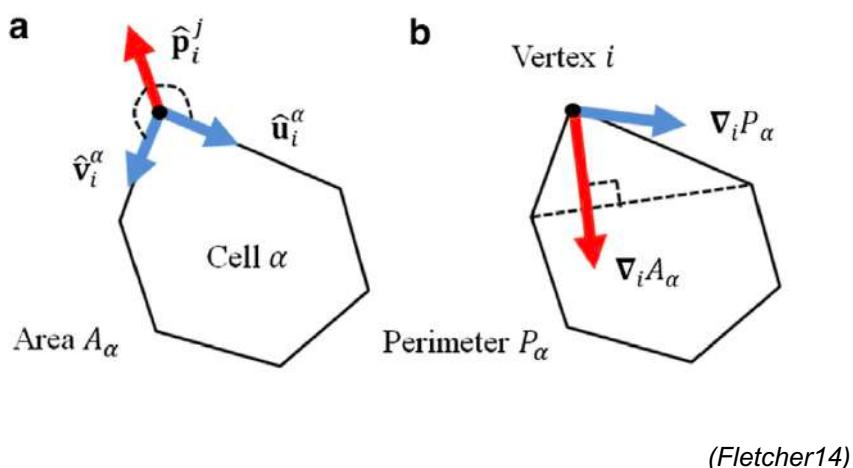
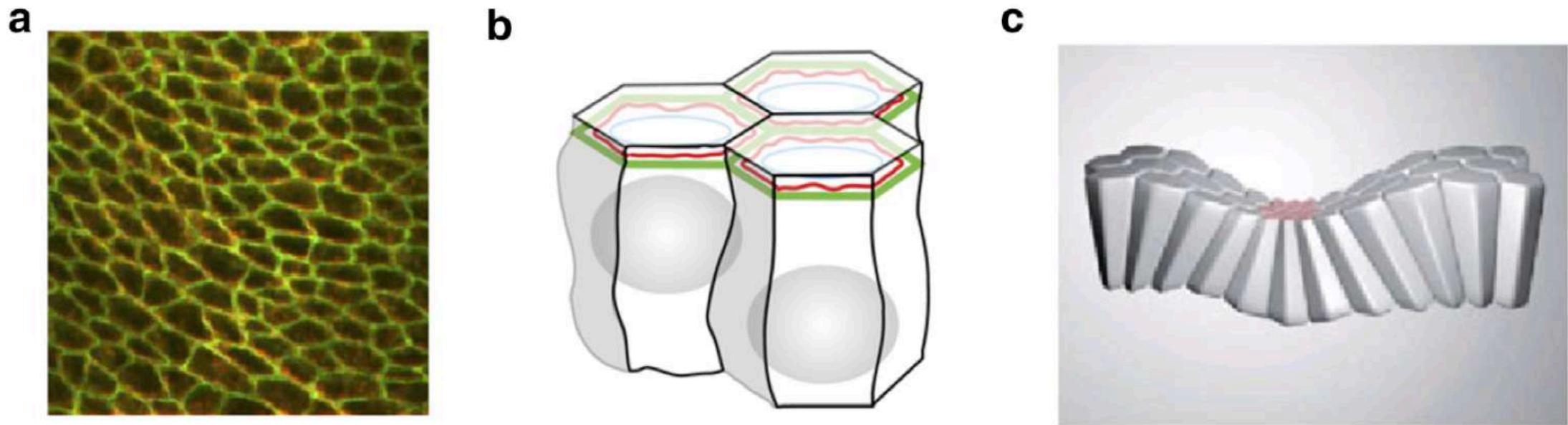
$$H_{Ising} = -J \sum_{\langle ij \rangle} \sigma_i \sigma_j - h \sum_i \sigma_i$$

Interaction between neighboring sites

Energy contribution from external field



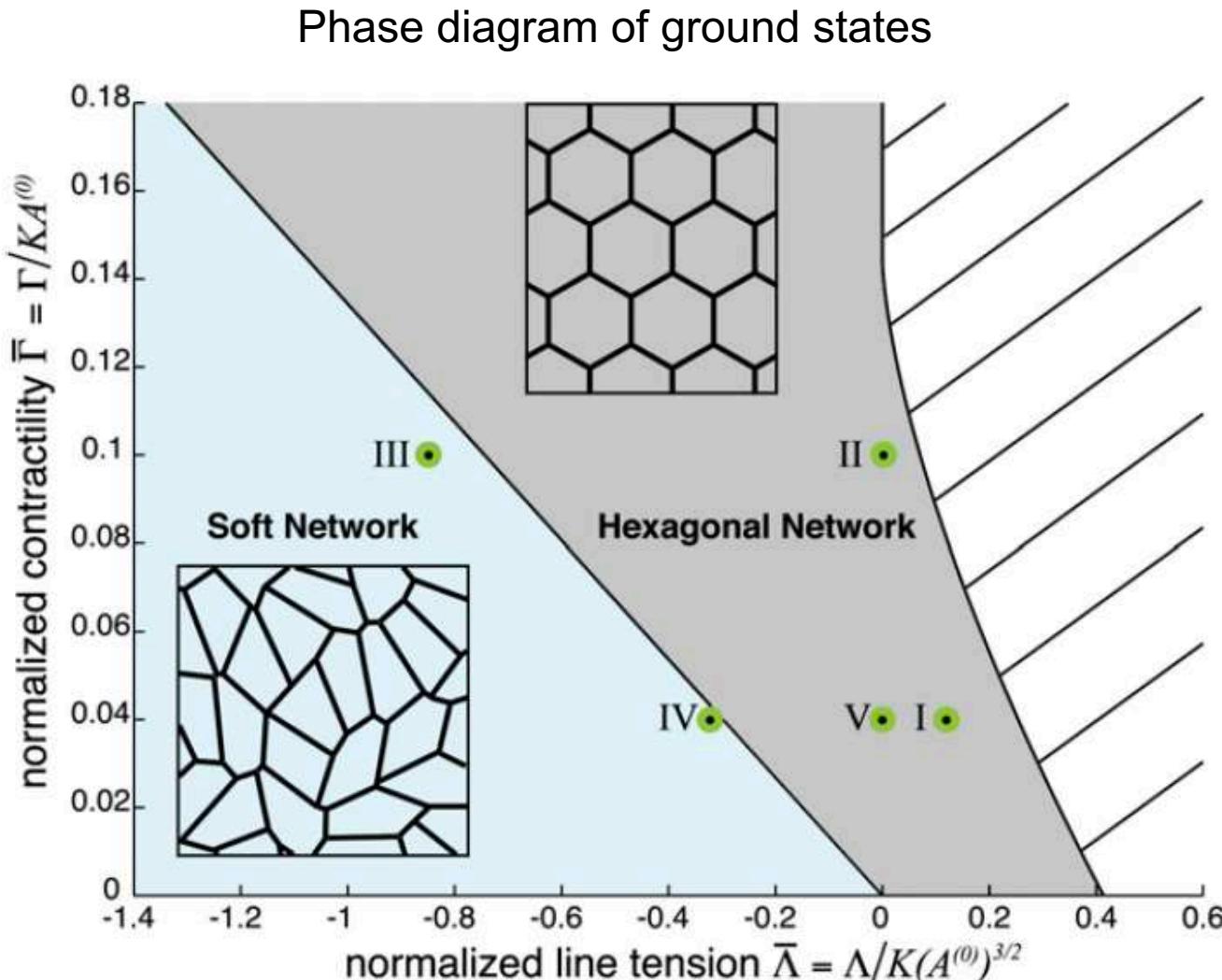
Temperature



- Confluent epithelial layer can be simplified as 2D polygonal packings
- Cell shape is described by positions of vertices at the tricellular junctions
- The dynamics is governed by an energy functional

$$E = \sum_i K_A (A_i - A_{i,0})^2 + K_P (P_i - P_{i,0})^2$$

Area elasticity	Perimeter elasticity
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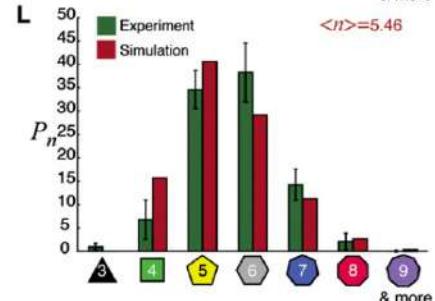
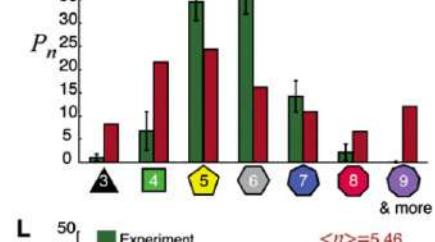
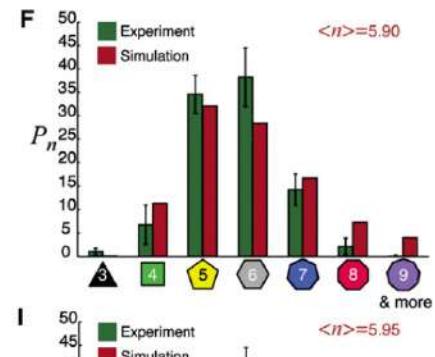
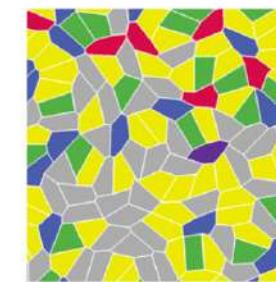
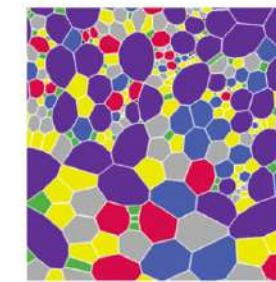
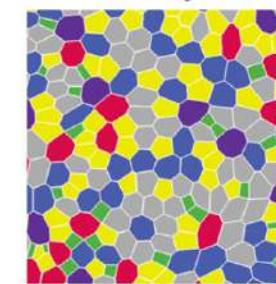
$$E = \sum_i \frac{K_A}{2} (A_i - A_{i,0})^2 + \frac{\Gamma_\alpha}{2} P_i^2 + \sum_{\langle ij \rangle} \Lambda L_{ij}$$

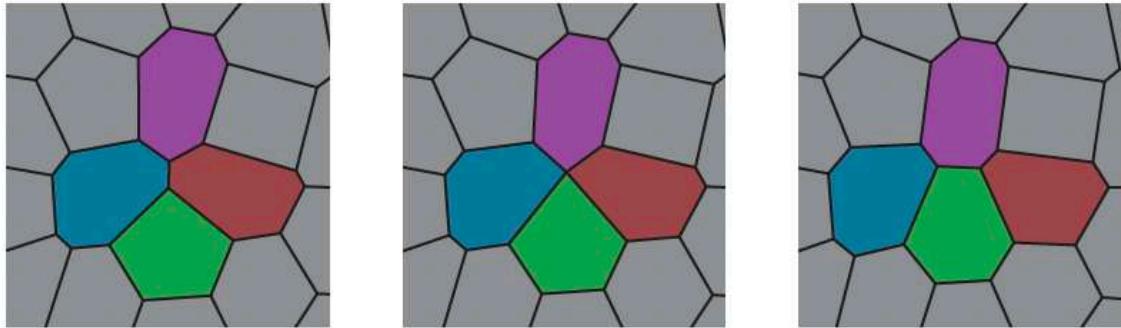
Area elasticity

Perimeter contractility

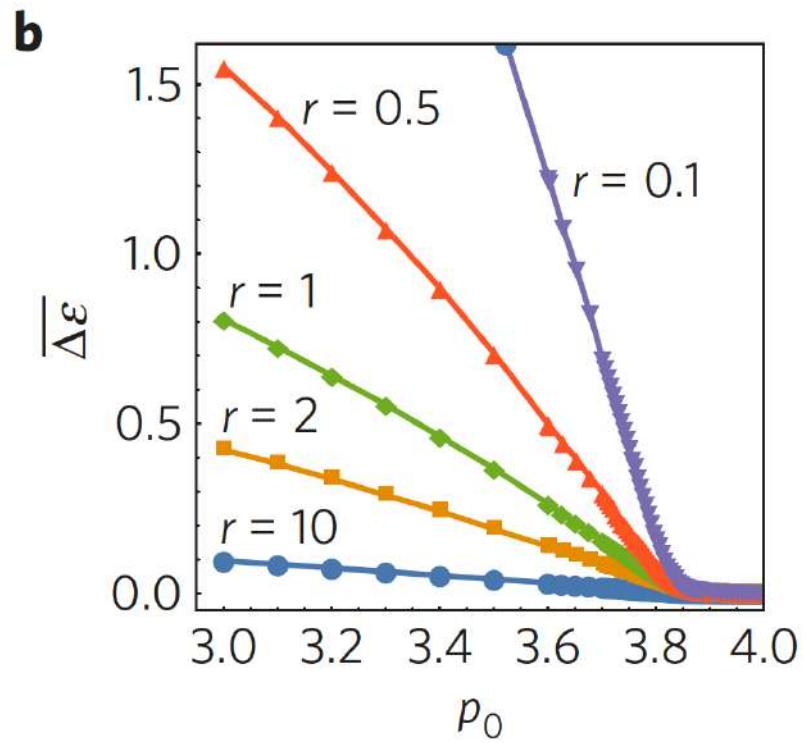
Line tension

Different tissue structures can be realized depending on cellular parameters





Energy barrier for cell rearrangement vanishes



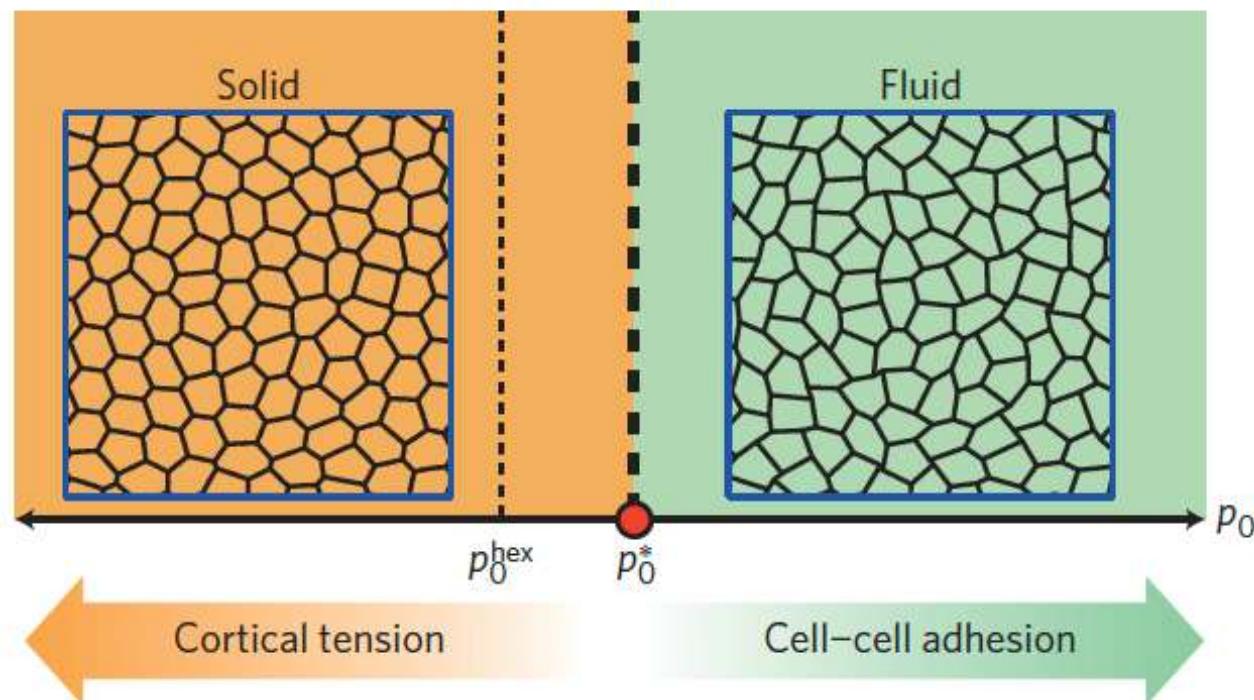
(Bi15)

$$\varepsilon = \sum_i (a_i - 1)^2 + \frac{(p_i - p_0)^2}{r}$$

Area elasticity Perimeter elasticity

Isotropic cell shape
Finite tension

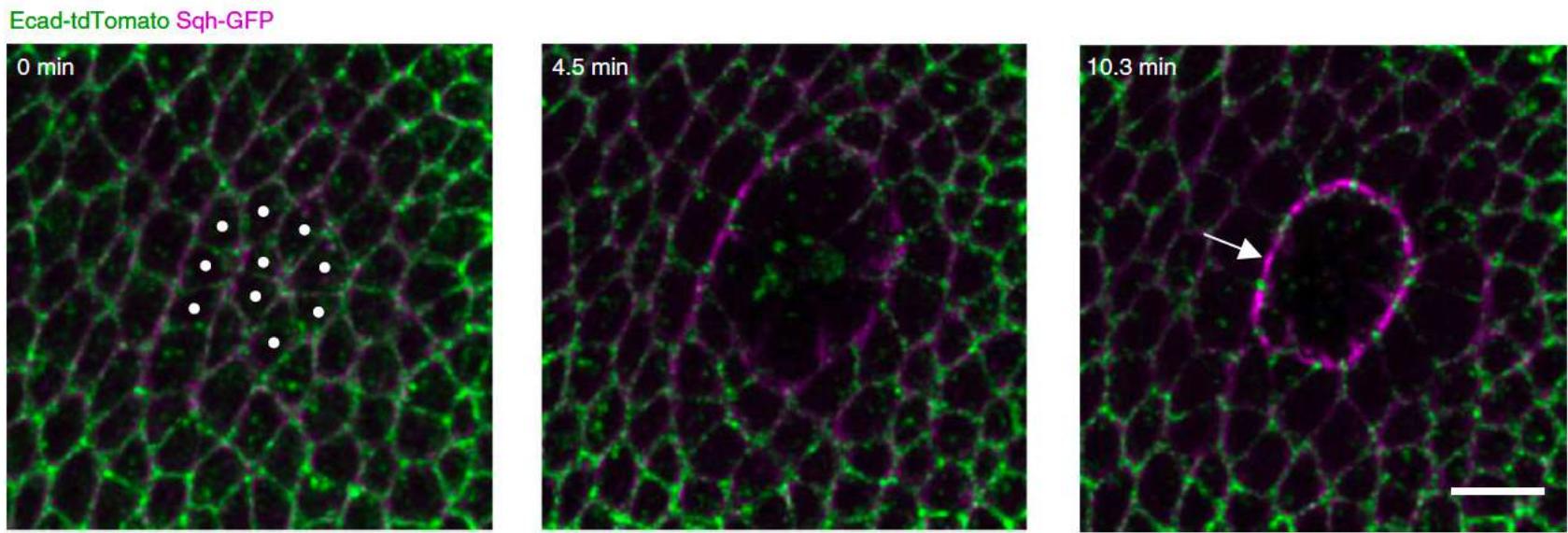
Anisotropic cell shape
Zero tension



Effective tension: $\Gamma_{ij} = \frac{2}{r} [(p_i - p_0) + (p_j - p_0)]$

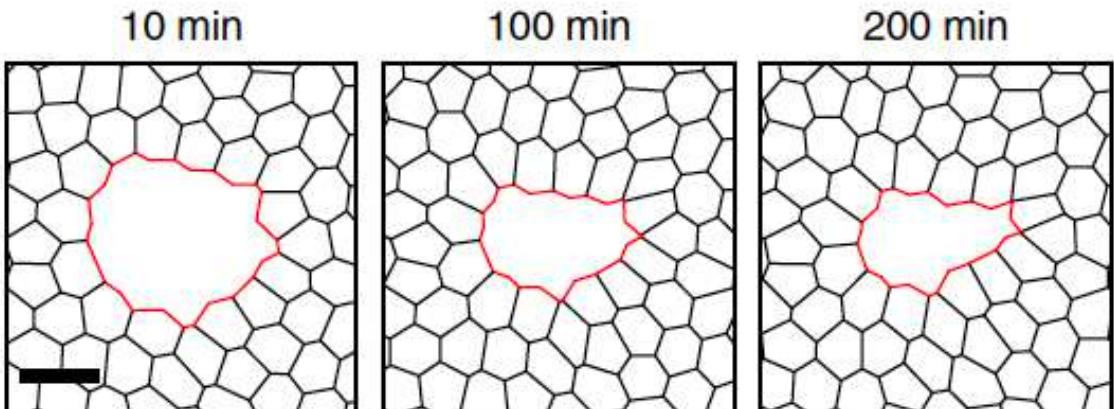
Laser ablation of epithelial layer in *Drosophila* wing imaginal disc

Accumulation of myosin to form pulse ring at the wound boundary

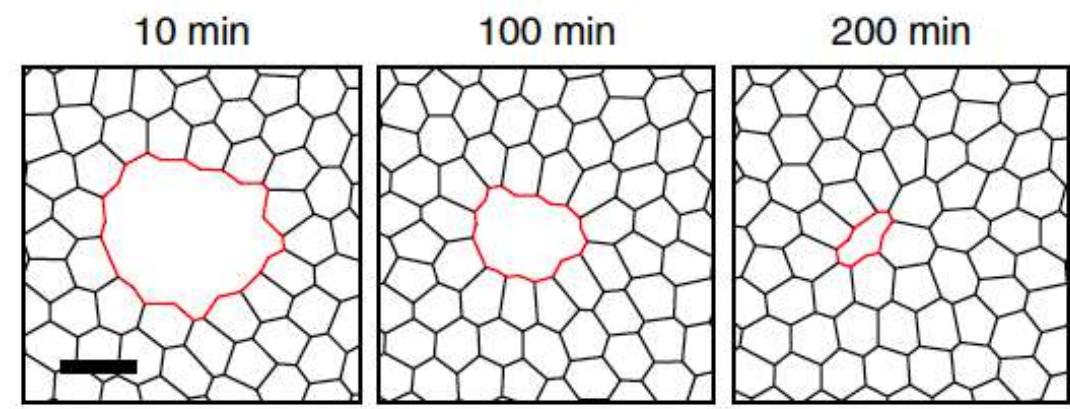


(Tetley19)

Without intercalation



With intercalation

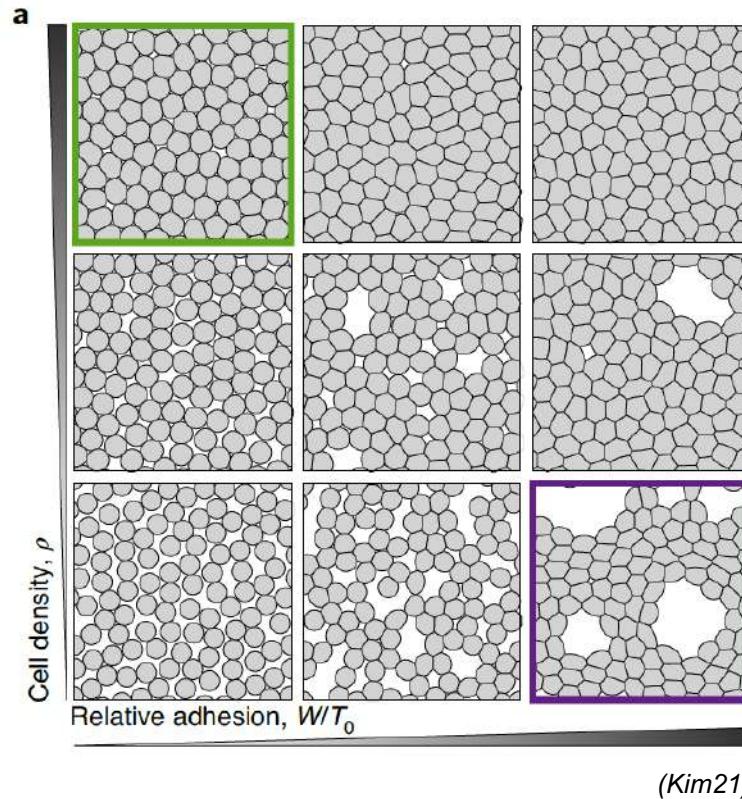


Vertex dynamics: $\eta_R \frac{d\vec{R}_\alpha}{dt} = \sum_{i,j \in F(\alpha)} \vec{T}_{ij} H(T_{ij}) + \vec{N}_{ij}$

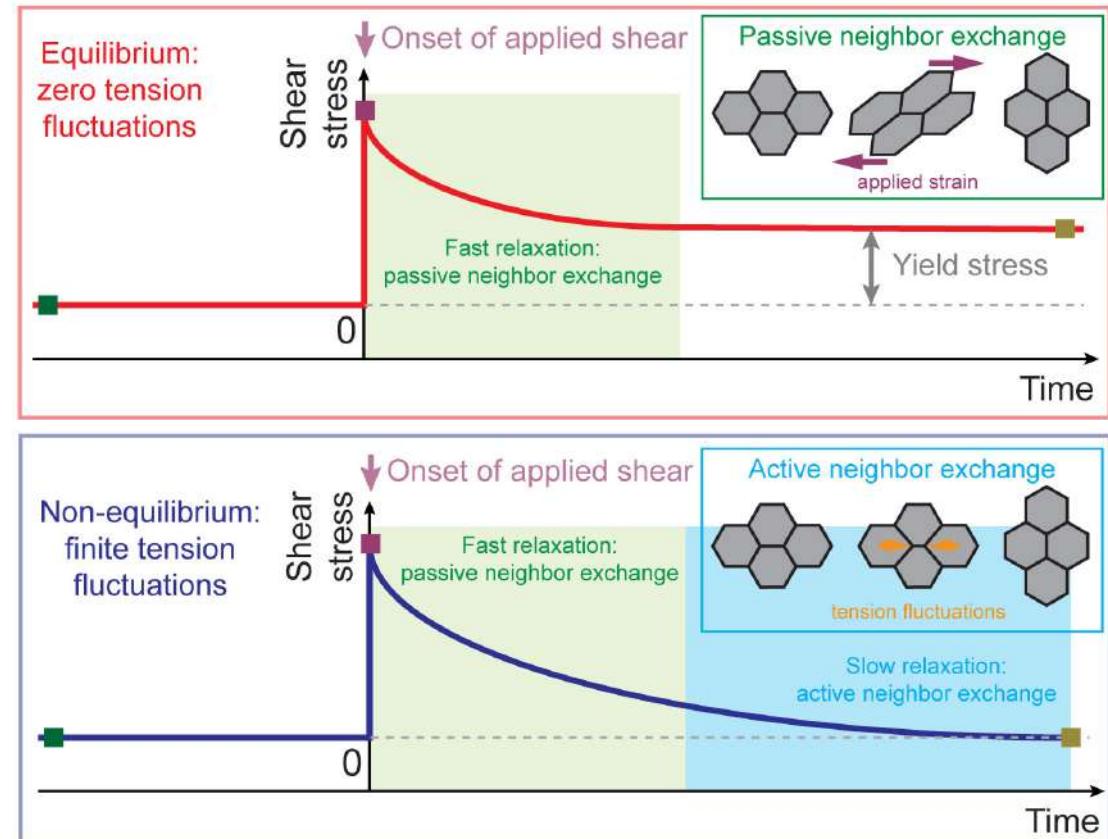
Viscous friction Tangential force Normal force

The model includes spaces between cells, complex cell shape and junctional tension dynamics

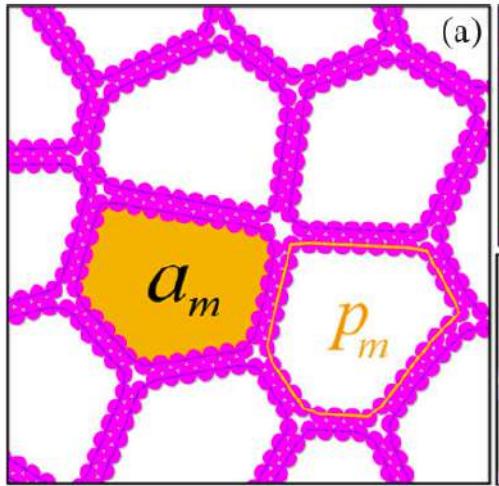
Structural transition from non-confluent state to confluent states



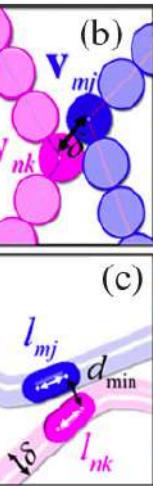
Active fluctuation governs longtime stress relaxation and tissue fluidization



Rough surface method



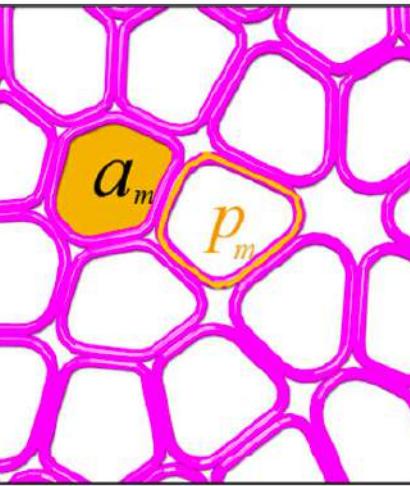
(a)



(b)



(c)

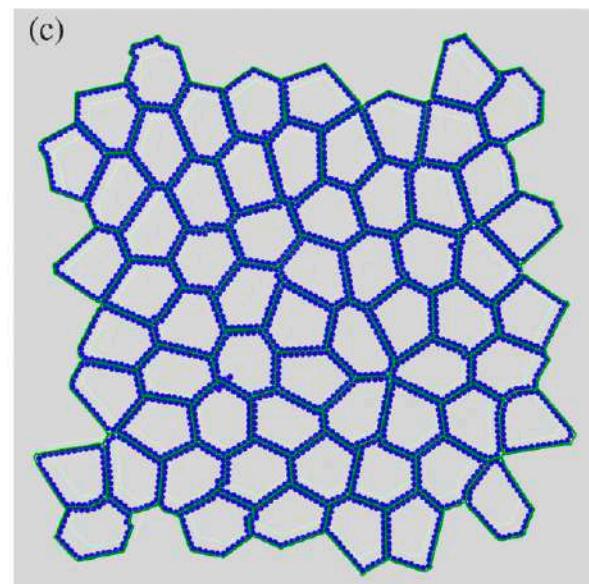
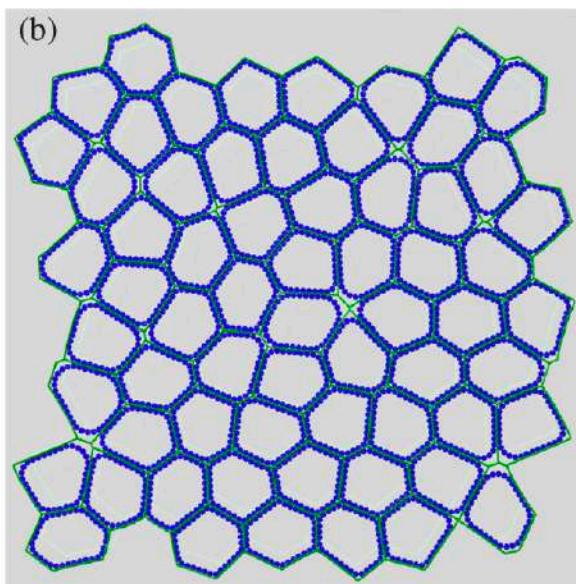
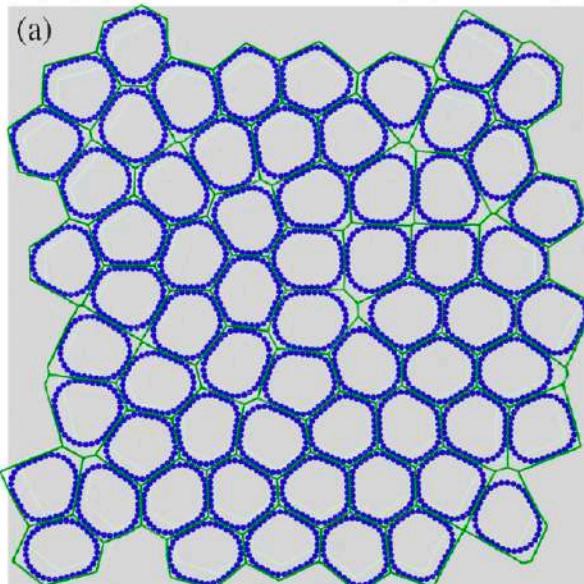


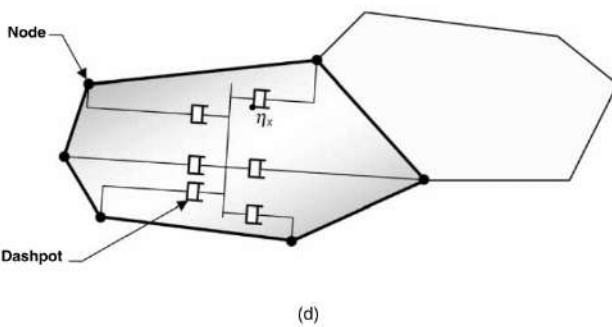
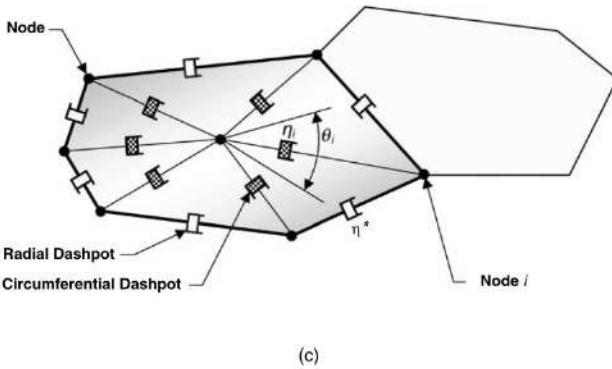
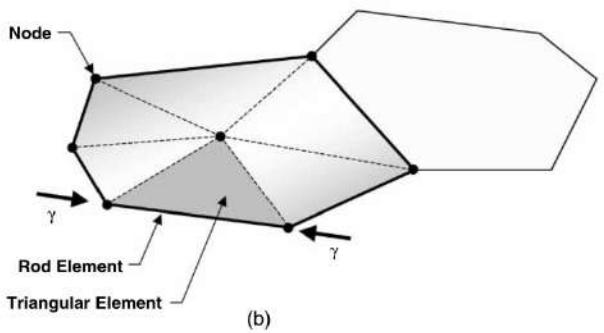
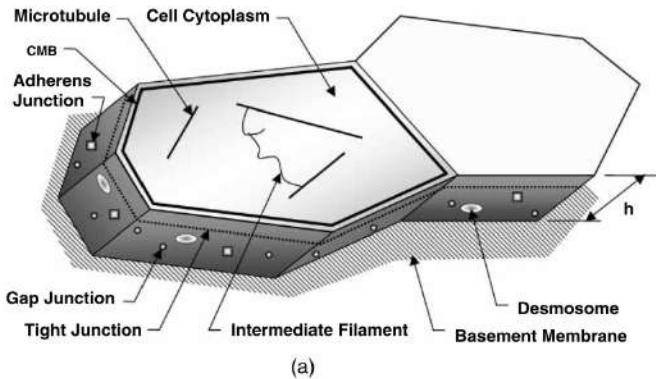
(d)



(Boromand18)

- Energy = junction contractility + area elasticity + line tension + junction bending + repulsive interaction
- Two different methods to deal with cell boundary
- More detailed description of cell shape compared to vertex model
- Double interface for cell-cell junction, (a single interface for the conventional vertex model)
- Able to simulate non-confluent systems





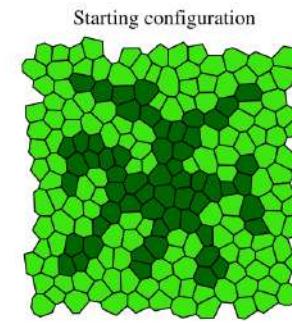
(Brodland07)

Vertex model
geometric
description

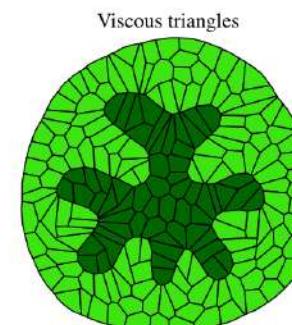
+

Constant-force rod
elements for cell-cell
contact & viscous
triangular elements for
cytoplasm

Cell sorting behavior

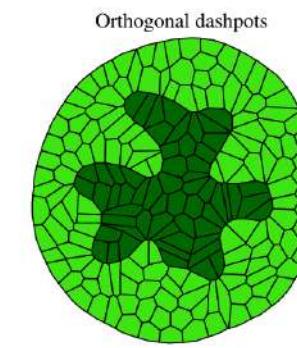


$\tau=0$

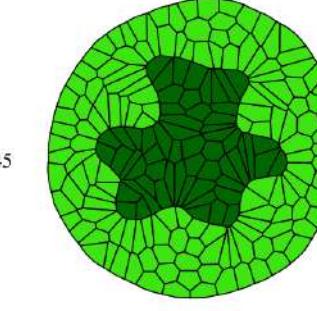


$\tau=9$

NNC = 56

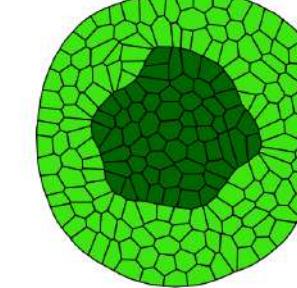


NNC = 153



$\tau=45$

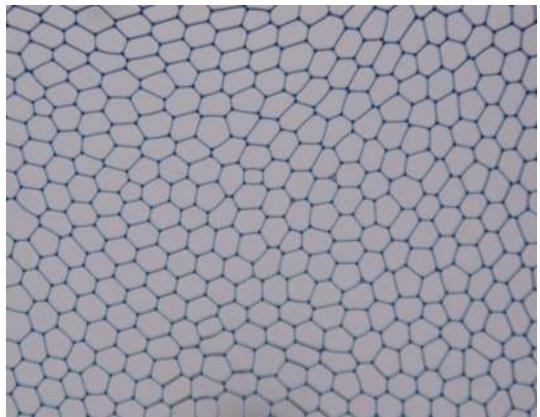
NNC = 189



NNC = 313

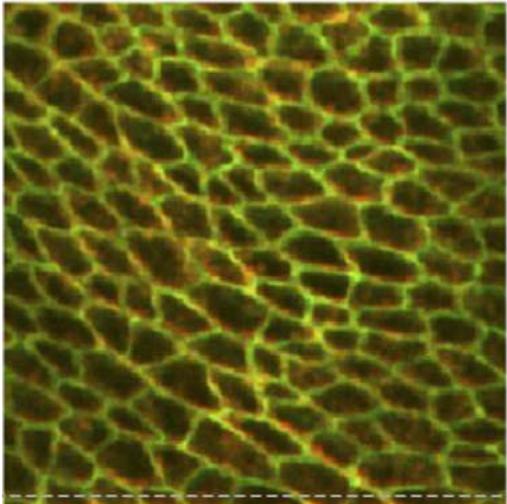
EPFL From Where: Vertex Model

Liquid foam



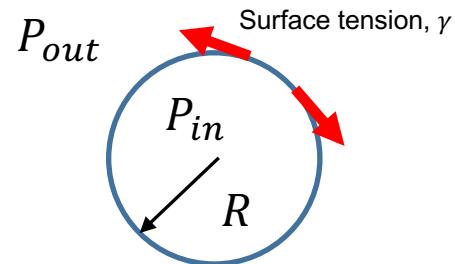
(Hilgenfeldt group)

Epithelial layer



(Fletcher et al. 2014)

Governing mechanics:

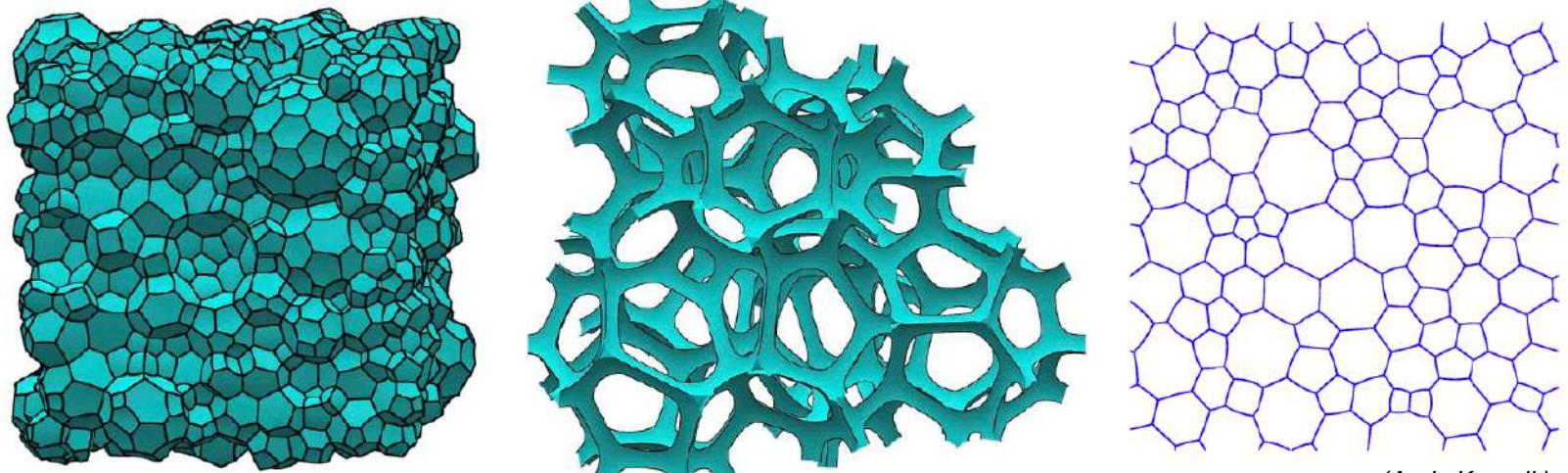


$$P_{in} - P_{out} = \frac{\gamma}{R}$$

- Short timescale: minimizing interfacial area (length in 2D)
- Long timescale: coarsening

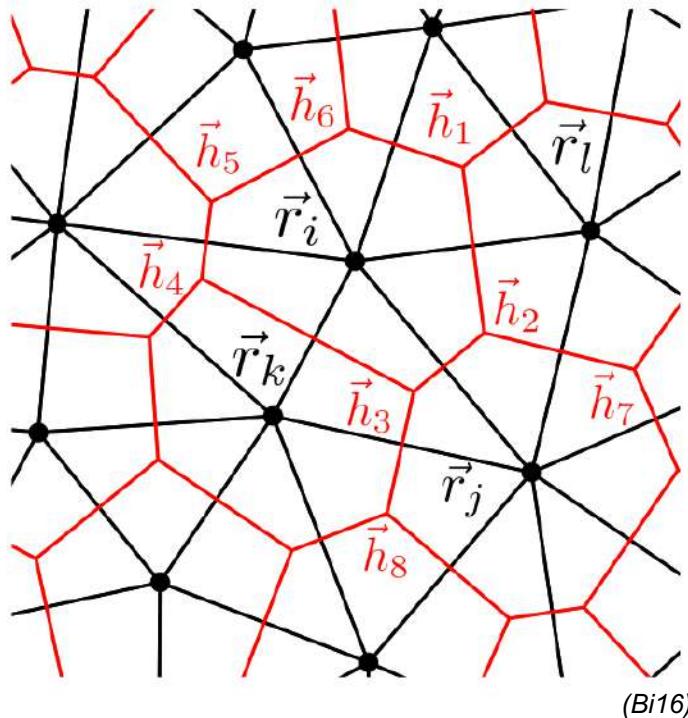
$$E = \gamma \sum L_{ij}$$

Dry foam simulations



Simulation software: Surface Evolver

Voronoi model: hybrid between the particle model and the vertex model

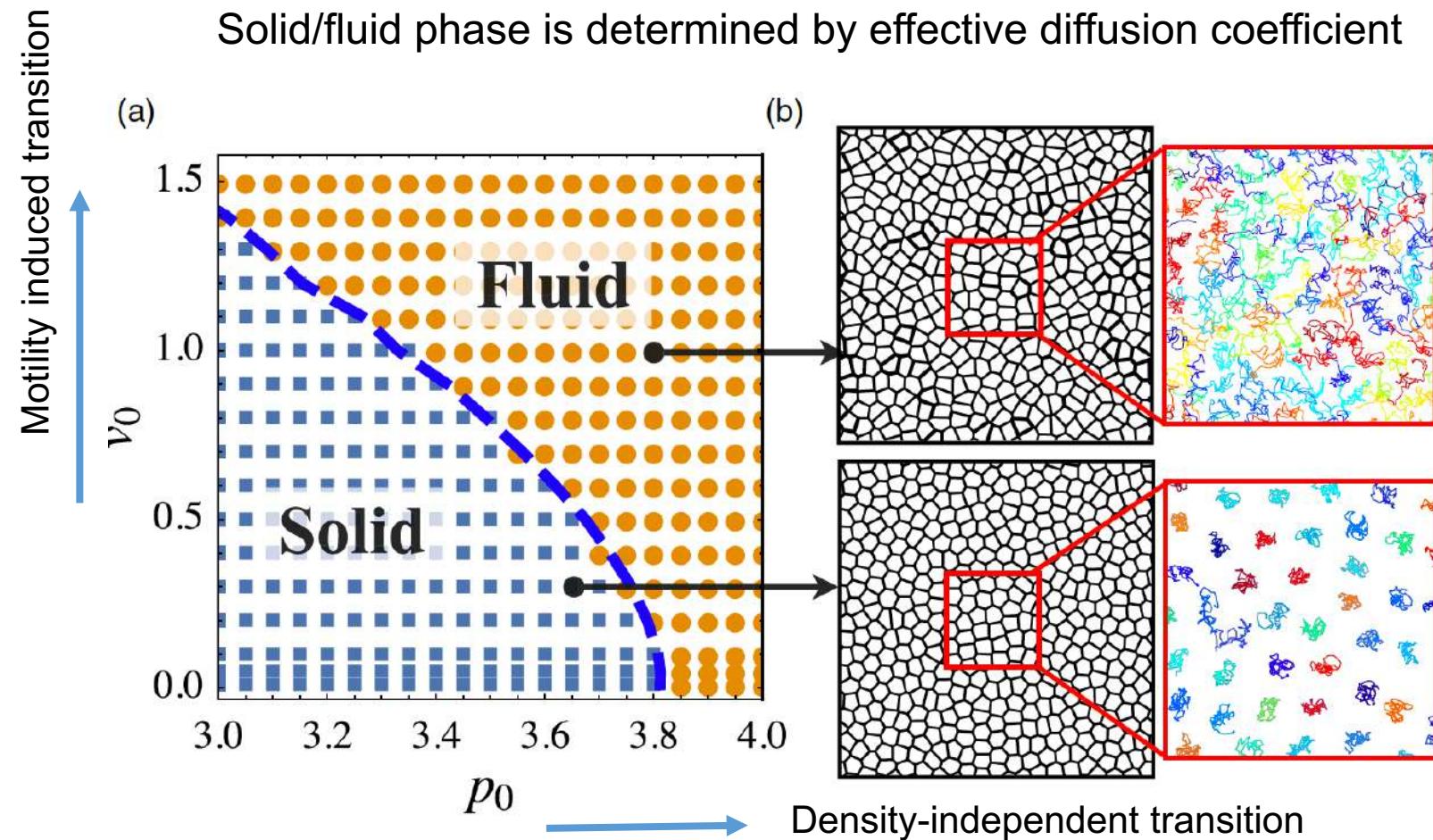


Degrees of freedom: particle position
 Energy functional: depending on Voronoi tessellation properties

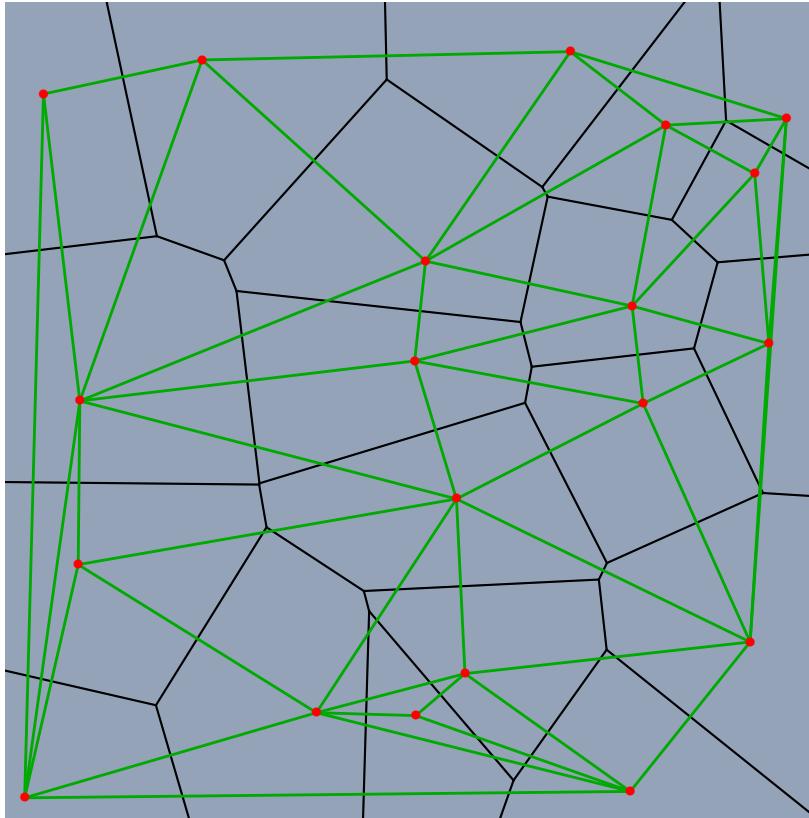
$$E = \sum_i K_A (A_i - A_{i,0})^2 + K_P (P_i - P_{i,0})^2$$

Cell dynamics: $\frac{d\vec{r}_i}{dt} = \mu \vec{F}_i + \nu_0 \hat{n}_i$

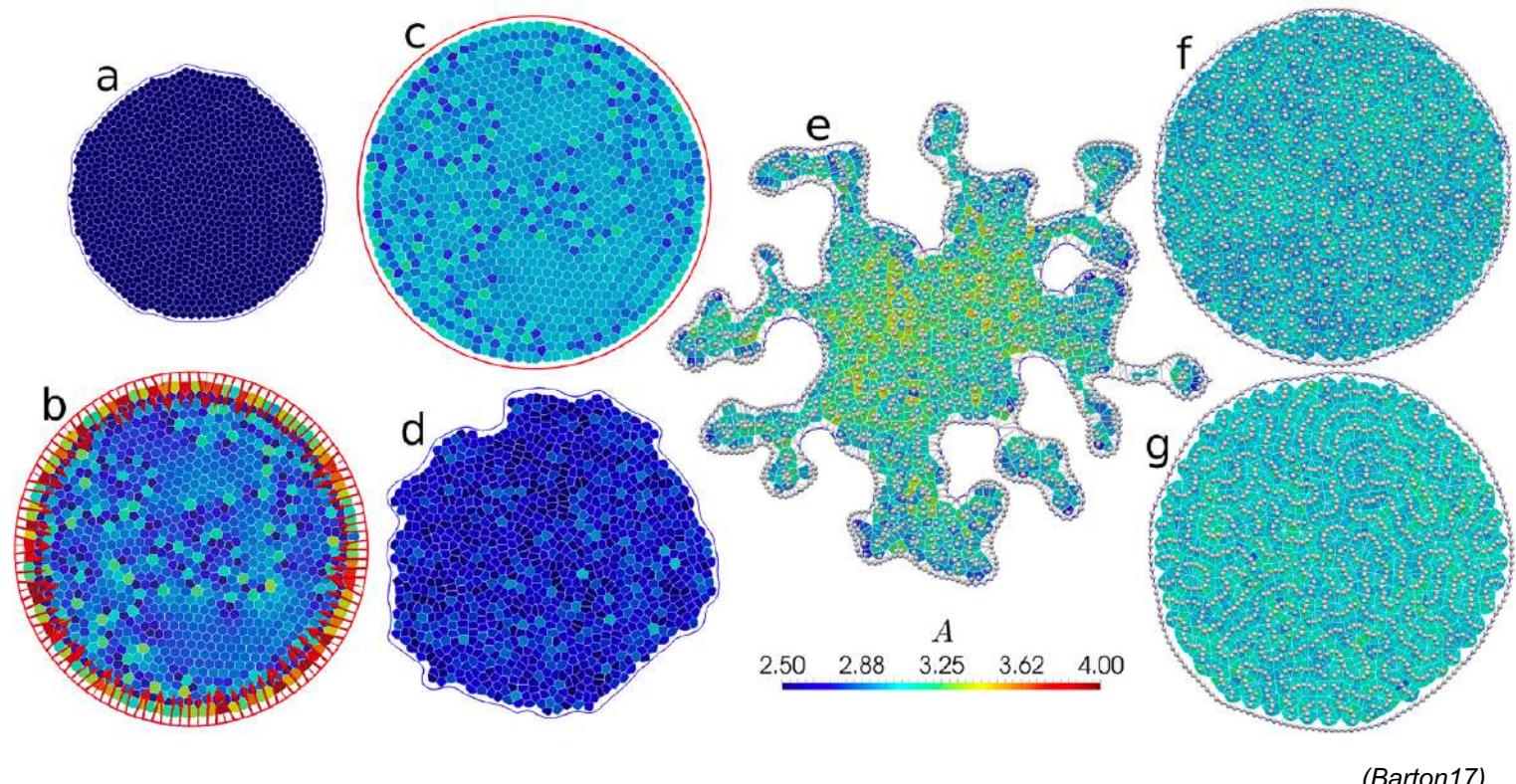
Solid/fluid phase is determined by effective diffusion coefficient



- Generalized version of Voronoi model: Use Delaunay triangulation for computational efficiency
- Voronoi tessellation and Delaunay triangulation is dual graph

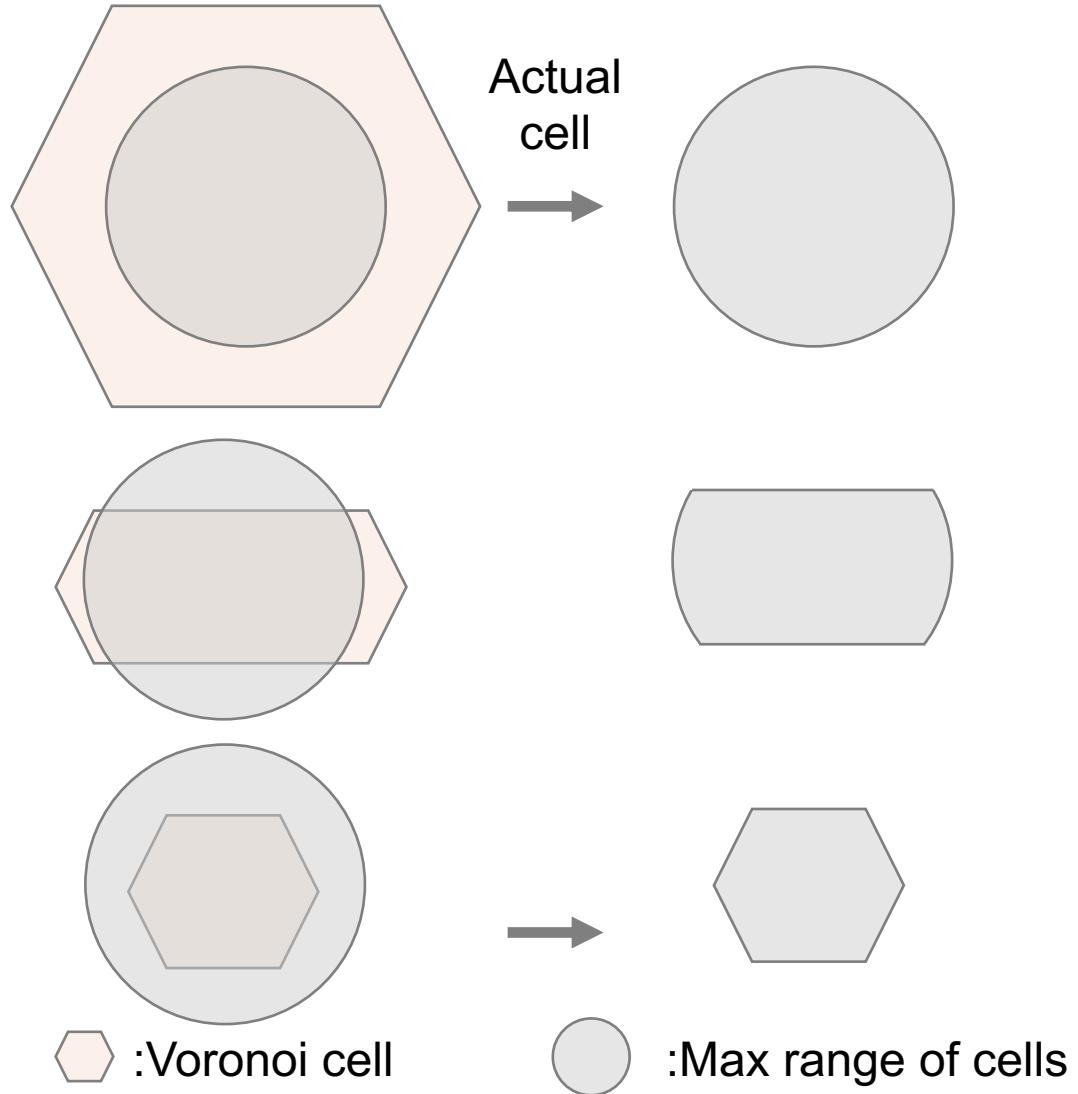


Examples of Voronoi tessellation
and Delaunay triangulation

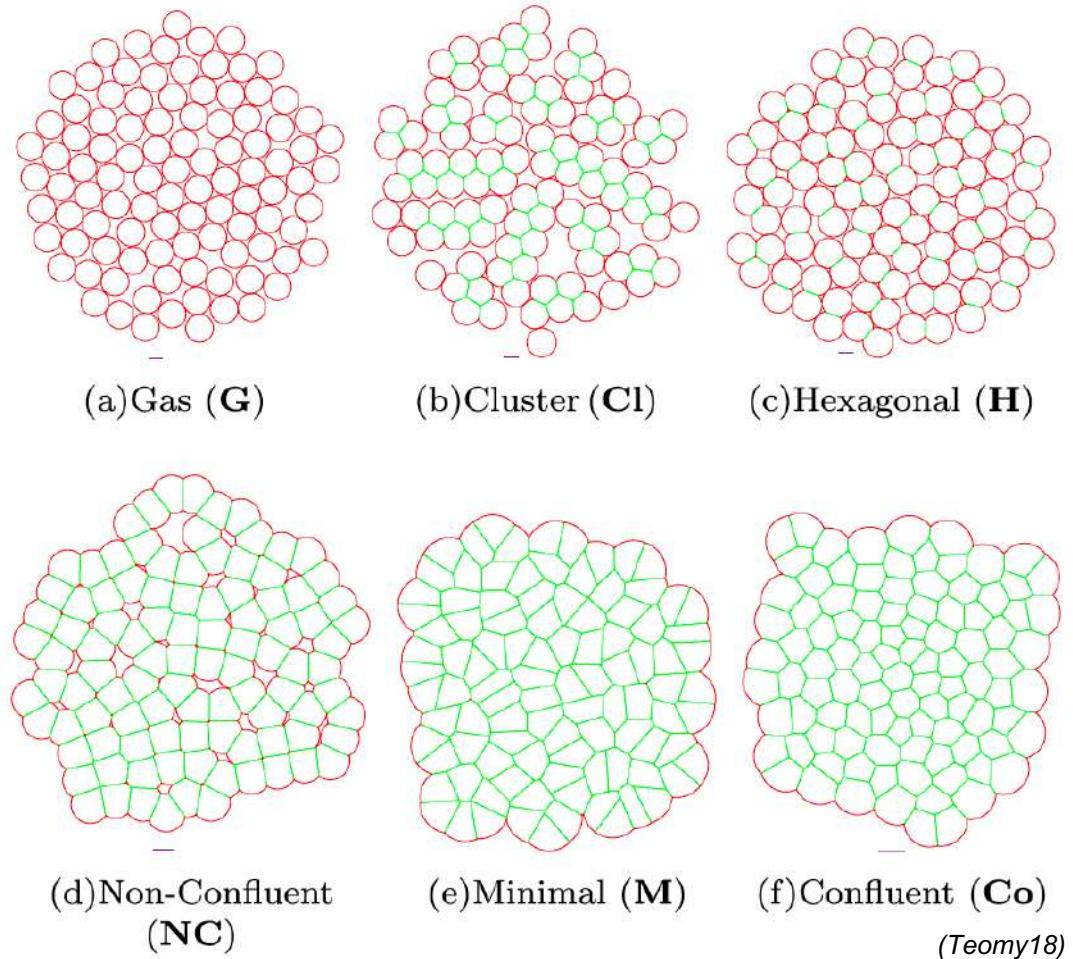


- Add cell division, cell alignment, etc.

Modified Voronoi model with a maximum cell radius → Can simulate non-confluent systems



Distinct classes of tissue structures



Single cell phase field
 1: cell interior
 0: outside of cell
 Rapid decrease from 1 to 0

Monolayer is constructed based on multiple fields

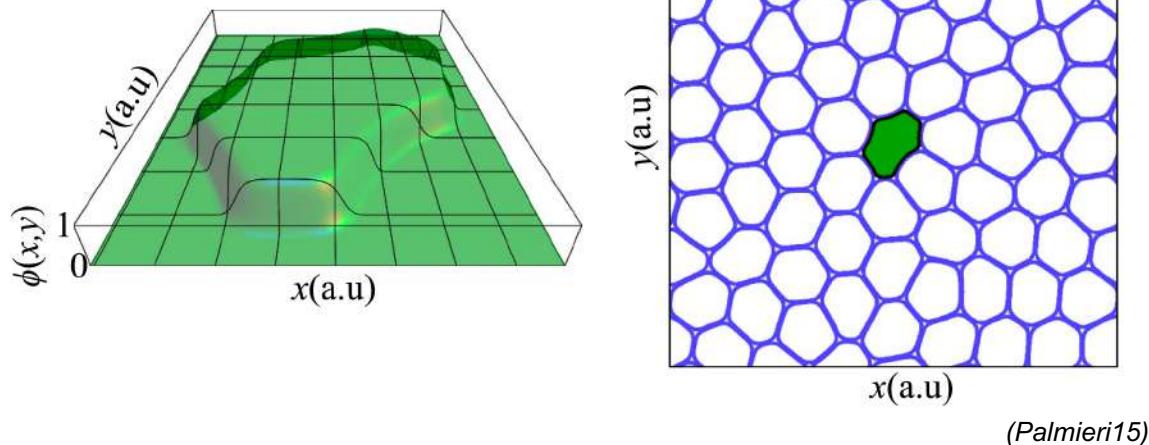
Governing equation :

$$\frac{\partial \phi_n}{\partial t} + \vec{v}_n \cdot \nabla \phi_n = -\frac{1}{2} \frac{\delta F}{\delta \phi_n}$$

Time derivative of each field

Cell
translational
velocity

Functional derivative of free energy



Free energy: $F = F_0 + F_{int}$

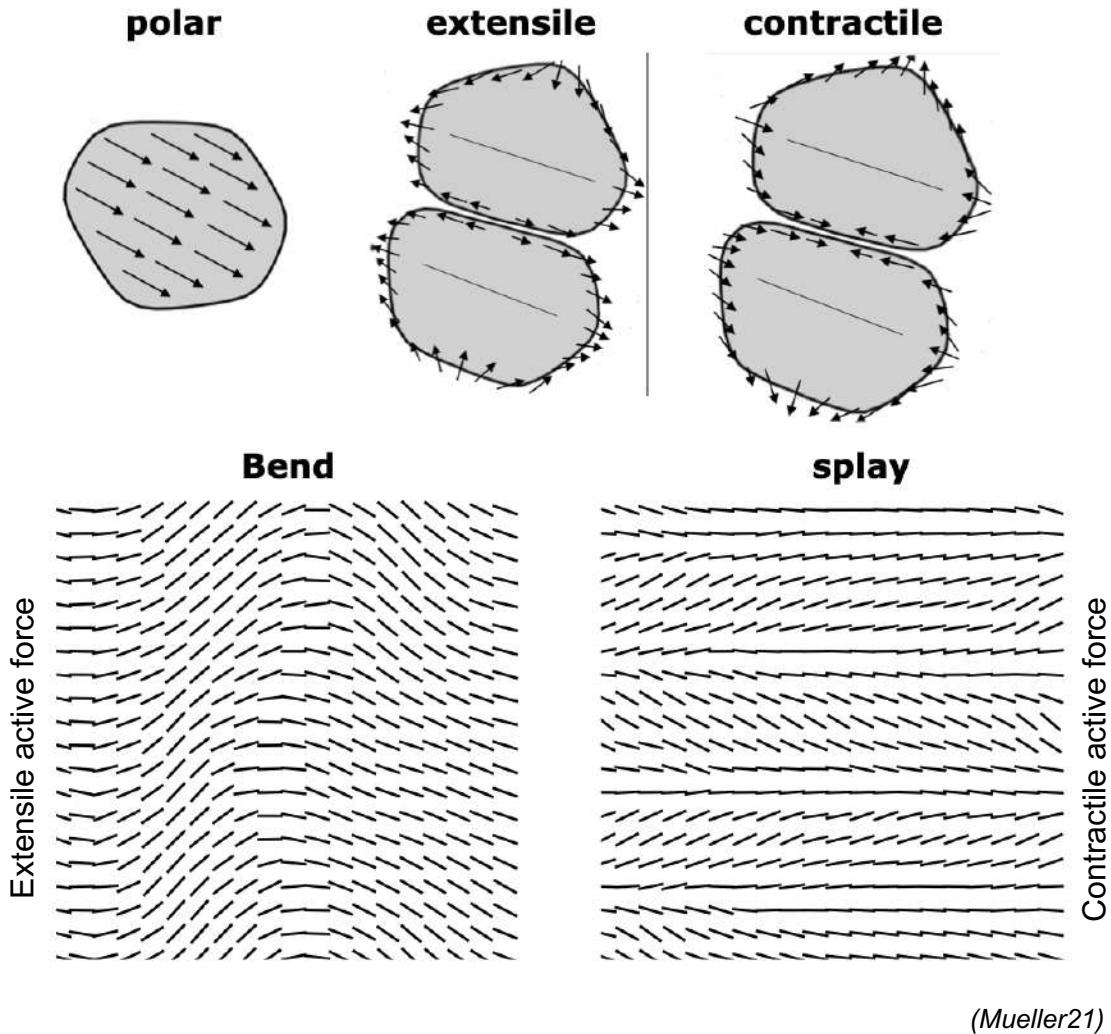
Free energy of a single cell Free energy from interactions

$$F_0 = \sum_n \left[\gamma_n \int dx \int dy \left((\nabla \phi_n)^2 + \frac{30}{\lambda^2} \phi_n^2 (1 - \phi_n)^2 \right) + \frac{\mu_n}{\pi R^2} \left(\pi R^2 - \int dx \int dy \phi_n^2 \right)^2 \right]$$

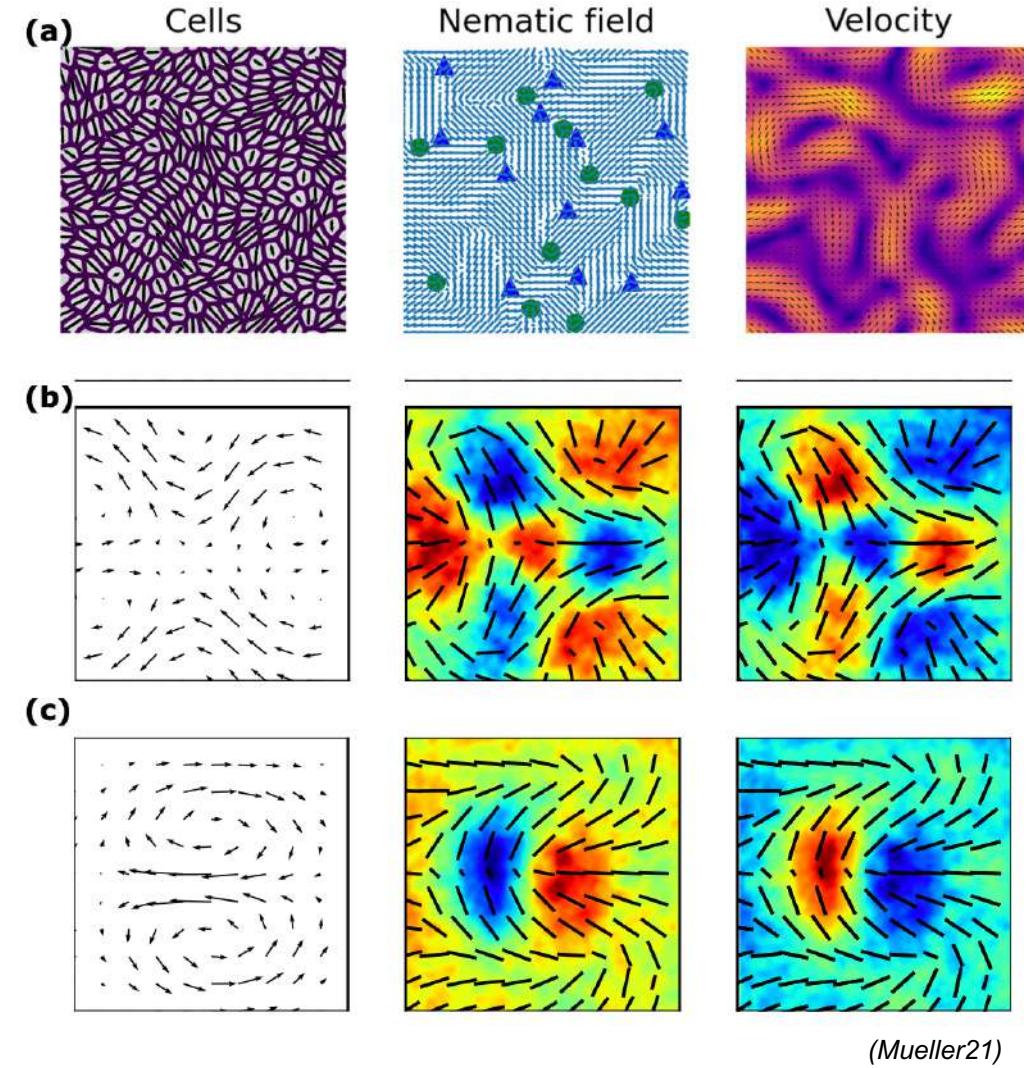
$$F_{int} = \frac{30\kappa}{\lambda^2} \int dx \int dy \sum_{n,m \neq n} \phi_n^2 \phi_m^2 \quad \text{Steric repulsion between cells}$$

- N scalar fields, $\{\phi_i\}$, describe cell shape
- Continuum limit of Cellular Potts model
- Extreme deformation is possible
- No need to deal with topological transition

Active force and instabilities in cell monolayer

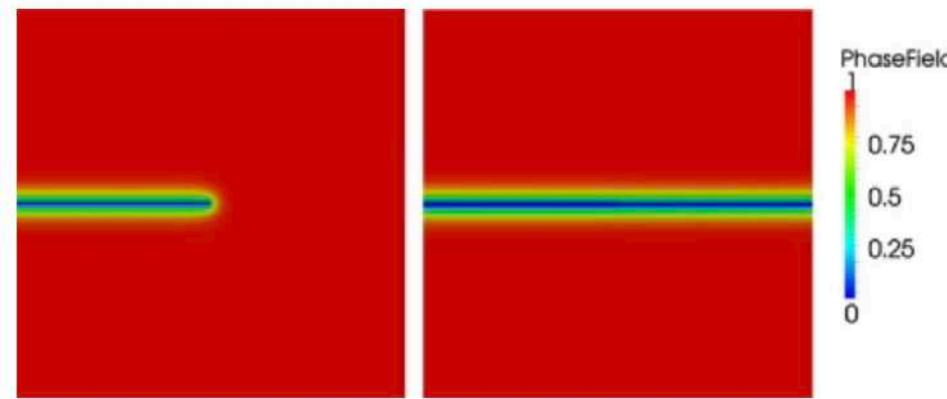


Emergence of active turbulence and nematic field

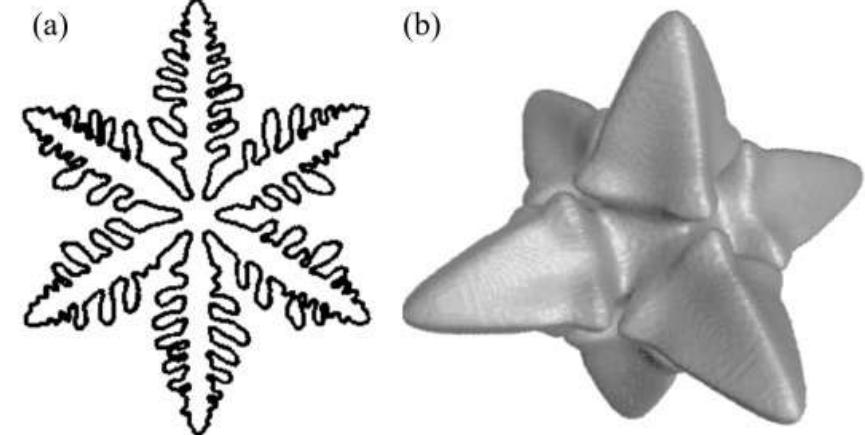


An efficient method for problems on materials modeling

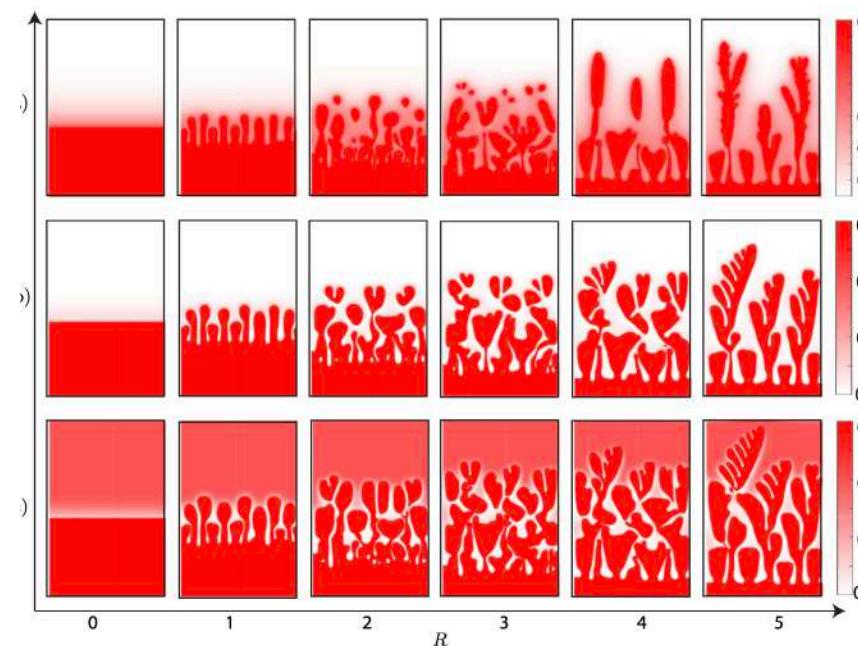
fracture



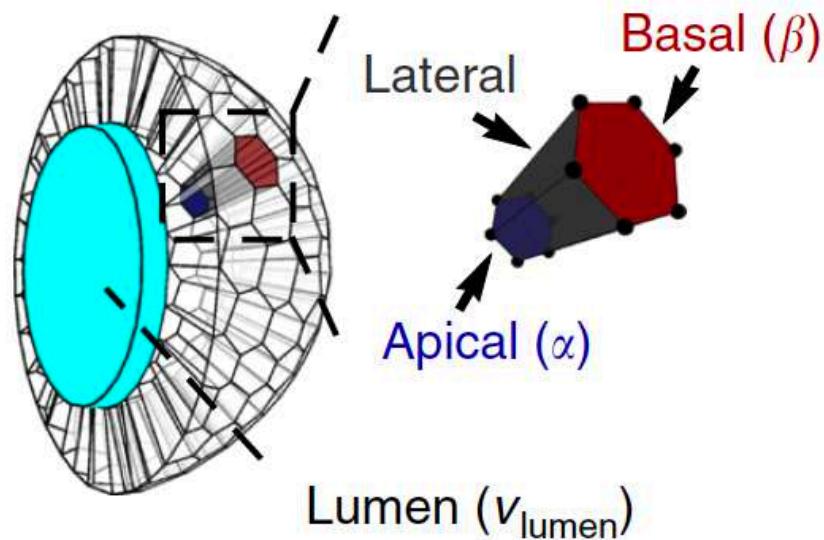
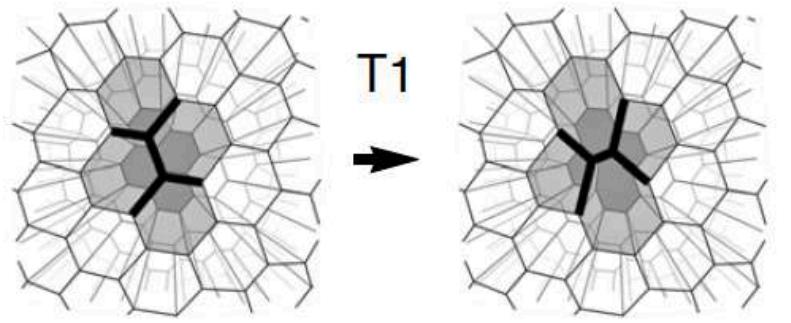
Solidification: dendritic growth



Viscous fingering



3D model for epithelial monolayer:
apical and basal polarity

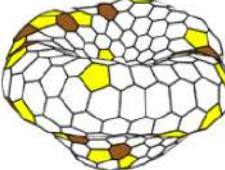
a**b**

$$w = \sum_i \left[\alpha a_a^{(i)} + \beta a_b^{(i)} + \frac{1}{2} a_l^{(i)} \right]$$

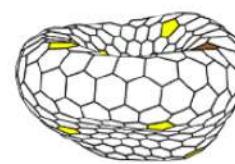
Apical tension Basal tension Lateral tension

i

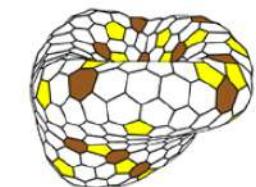
Low rate
($k_{T1}^{(0)} = 50$)



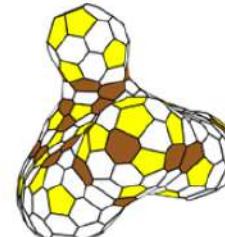
Moderate fluctuations
($\sigma^{(0)} = 0.15$)



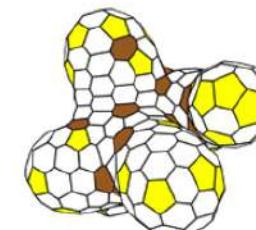
Moderate fluctuations
($\sigma^{(0)} = 0.15$)

**j**

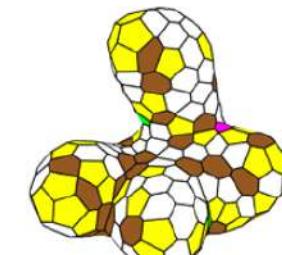
High rate
($k_{T1}^{(0)} = 200$)



Strong fluctuations
($\sigma^{(0)} = 0.35$)

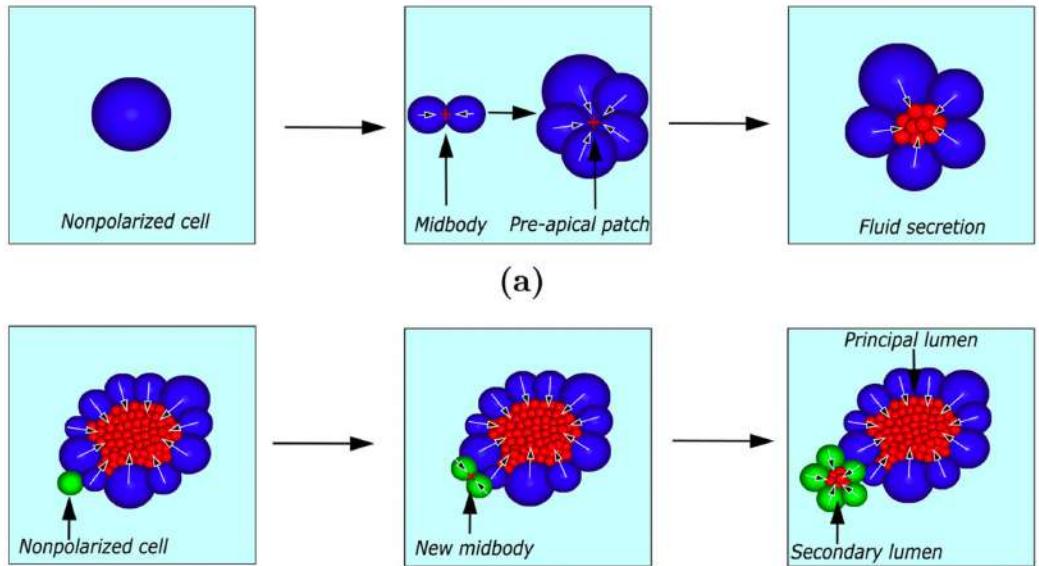
**m**

Strong fluctuations
($\sigma^{(0)} = 0.25$)

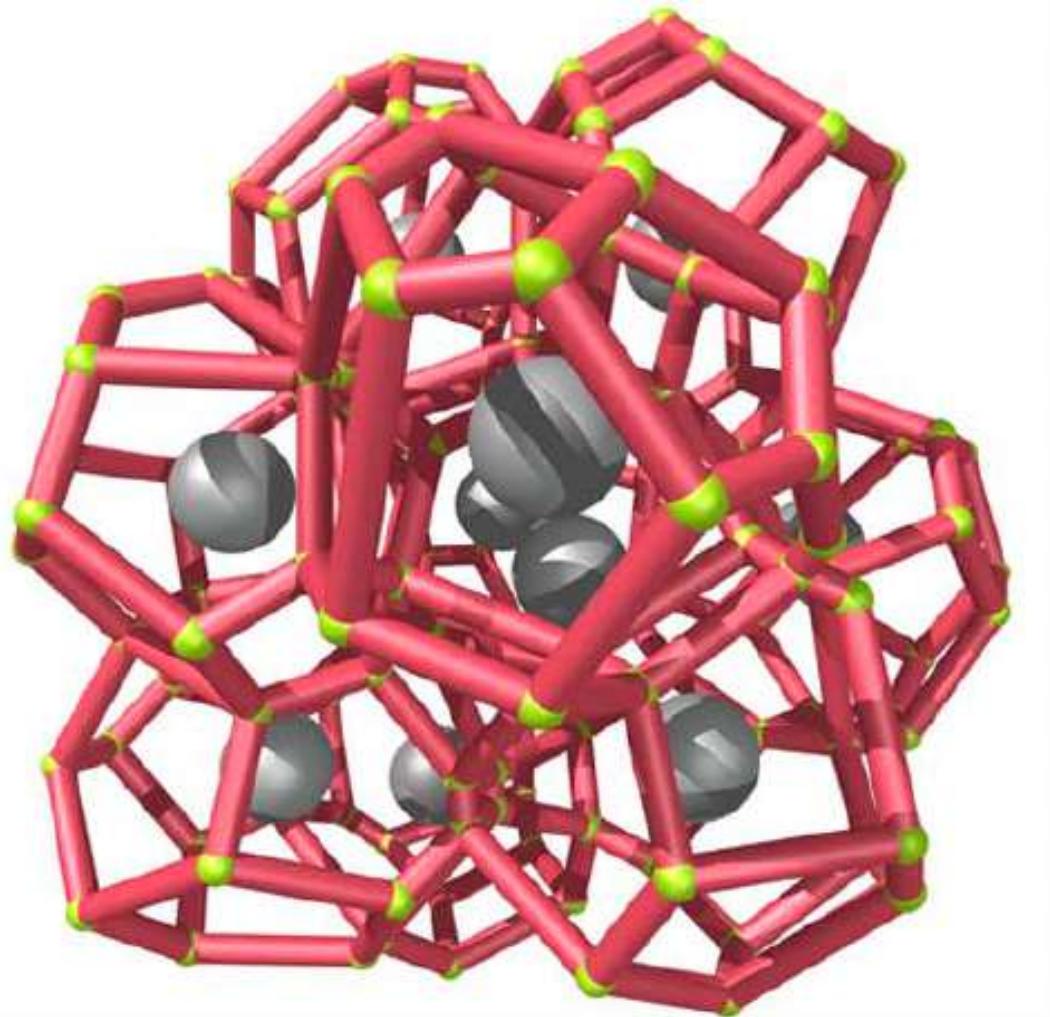


Different cellular properties lead to distinct budding morphology

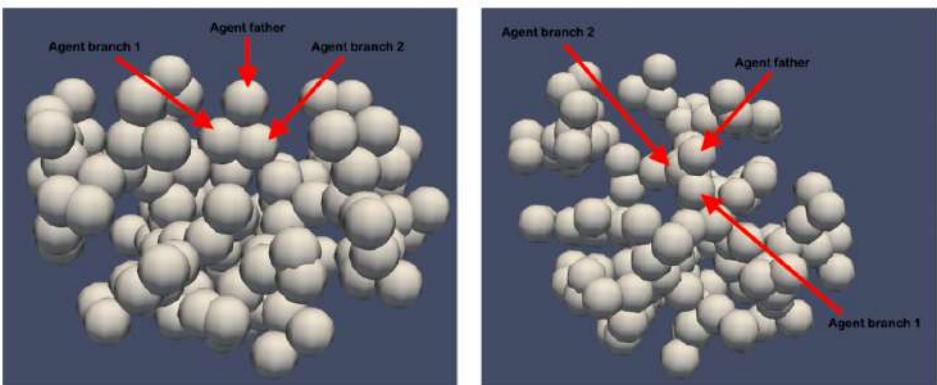
Lumen morphogenesis



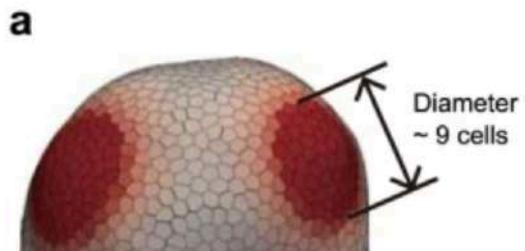
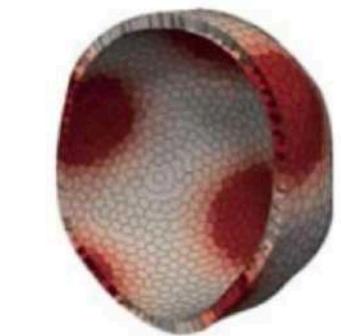
Self Propelled Voronoi Model



Lung fibrosis



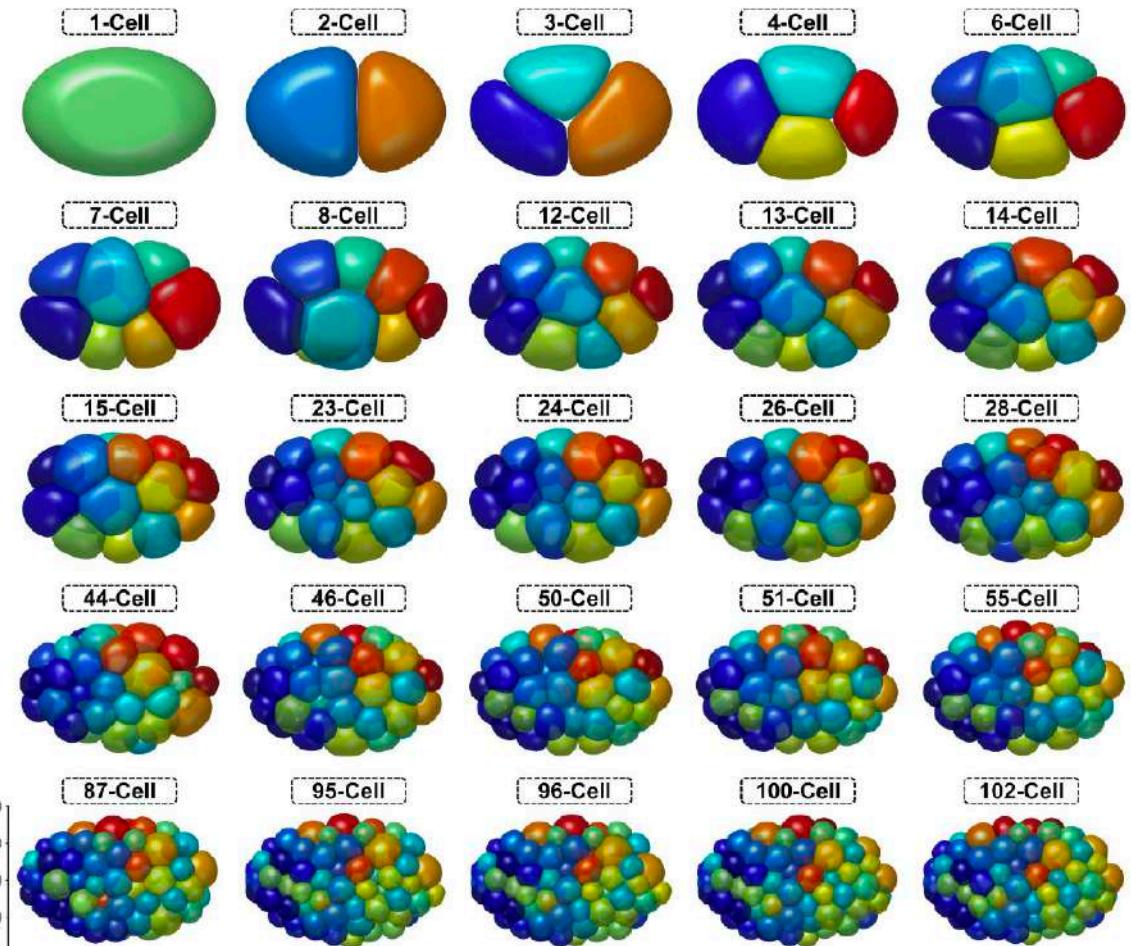
Vertex model

Activator concentration
0 1**b**

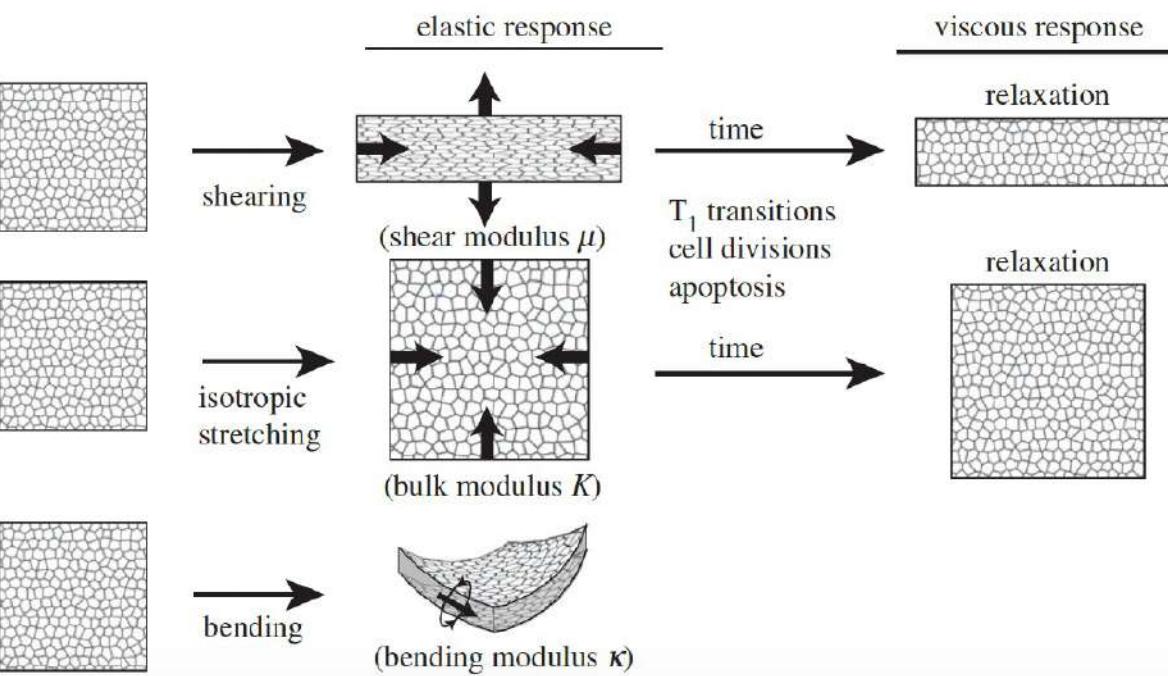
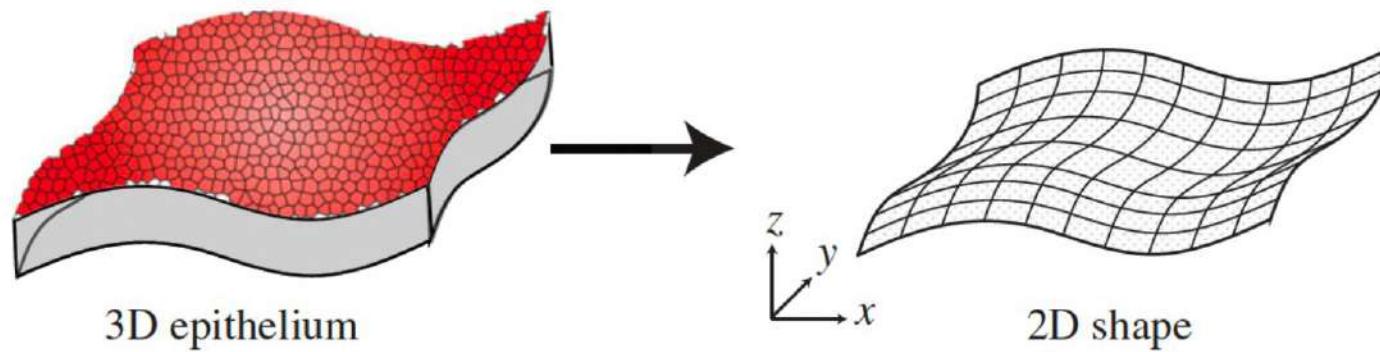
3D compacted aggregate

(Okuda18)

Phase field model



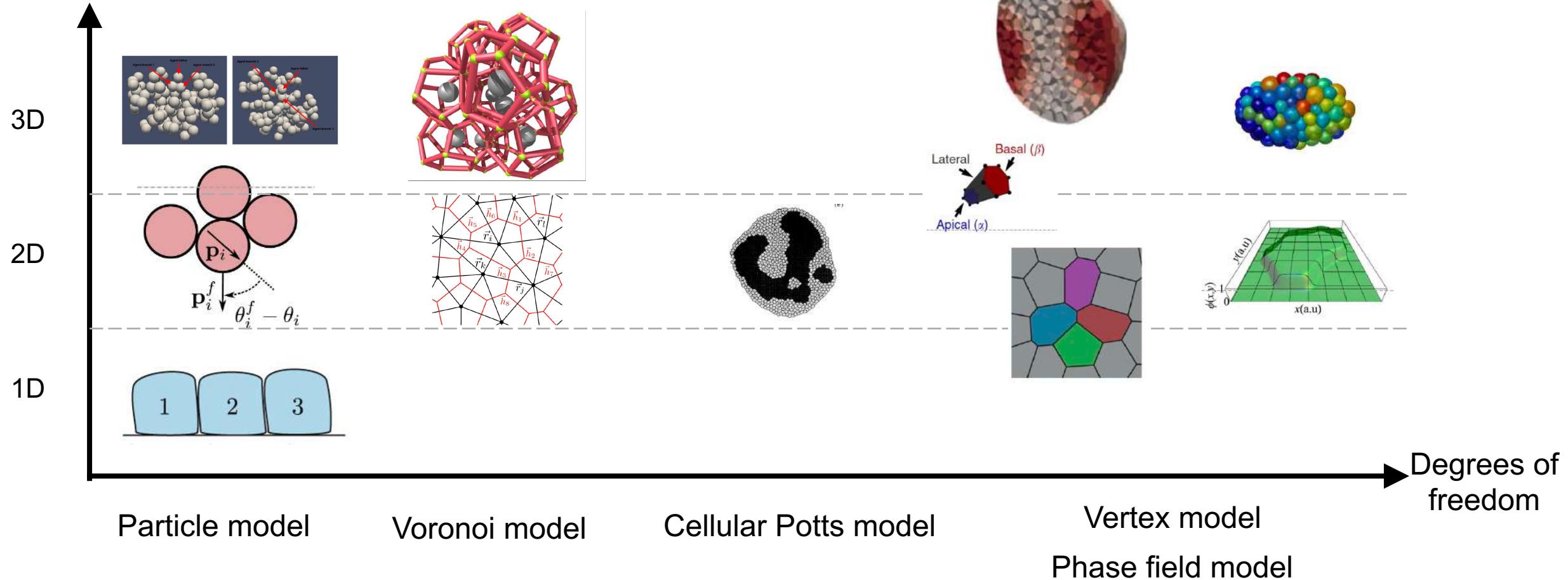
(Kuang22)



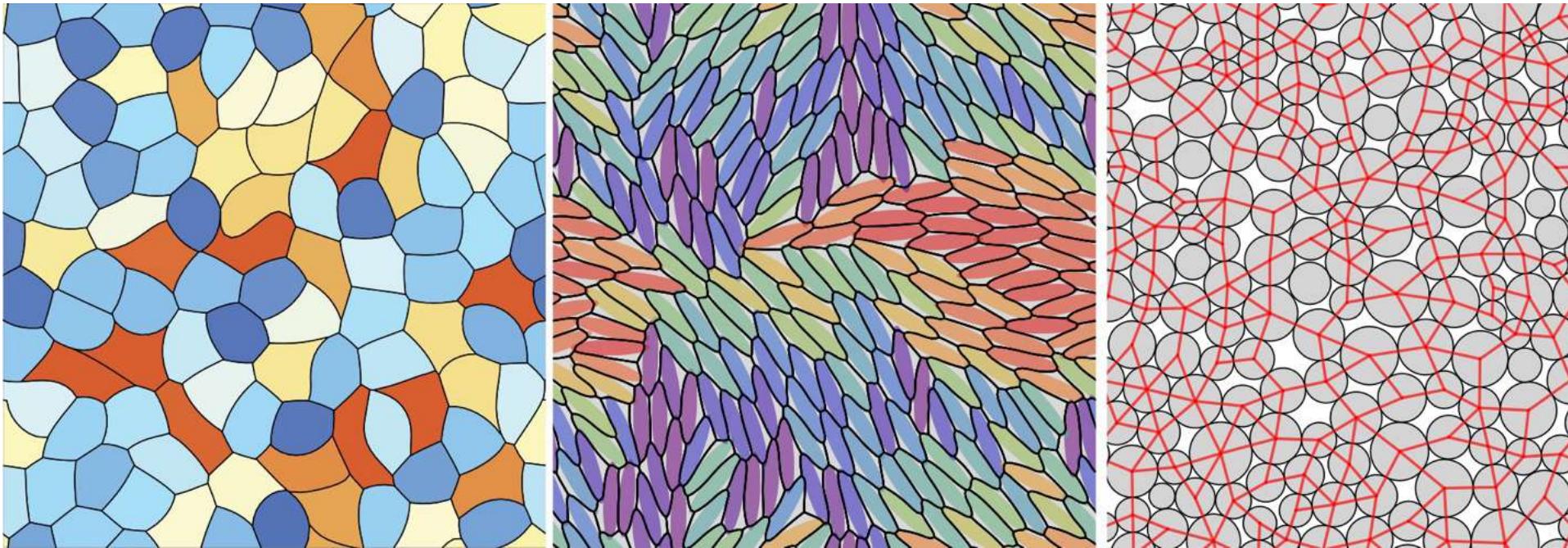
How one can derive constitutive equation from discrete simulations?

Viscoelastic?
Viscoplastic?
Hyperelastic?

Spatial dimension



- Mongera18: A fluid-to-solid jamming transition underlies vertebrate body axis elongation
- Classen05: Hexagonal Packing of Drosophila Wing Epithelial Cells by the Planar Cell Polarity Pathway
- Miklius12: Analytical Results for Size-Topology Correlations in 2D Disk and Cellular Packings
- Gibson06: The emergence of geometric order in proliferating metazoan epithelia
- George17: Connecting individual to collective cell migration
- Smeets16: Emergent structures and dynamics of cell colonies by contact inhibition of locomotion
- Henkes11: Active jamming: Self-propelled soft particles at high density
- Scianna12: Multiscale developments of the Cellular Potts Model
- Glazier93: Simulation of the differential adhesion driven rearrangement of biological cells
- Fletcher14: Vertex Models of Epithelial Morphogenesis
- Farhadifar07: The Influence of Cell Mechanics, Cell-Cell Interactions, and Proliferation on Epithelial Packing
- Bi15: A density-independent rigidity transition in biological tissues
- Tetley19: Tissue fluidity promotes epithelial wound healing
- Kim21: Embryonic tissues as active foams
- Boromand18: Jamming of Deformable Polygons
- Brodland07: A new cell-based FE model for the mechanics of embryonic epithelia
- Bi16: Motility-Driven Glass and Jamming Transitions in Biological Tissues
- Barton17: Active Vertex Model for cell-resolution description of epithelial tissue mechanics
- Teomy18: Confluent and nonconfluent phases in a model of cell tissue
- Palmieri15: Multiple scale model for cell migration in monolayers: Elastic mismatch between cells enhances motility
- Mueller21: Phase field models of active matter
- Rozman20: Collective cell mechanics of epithelial shells with organoid-like morphologies
- Merkel17: A geometrically controlled rigidity transition in a model for confluent 3D tissues
- Okuda18: Combining Turing and 3D vertex models reproduces autonomous multicellular morphogenesis with undulation, tubulation, and branching
- Kuang22: MorphoSim: An efficient and scalable phase-field framework for accurately simulating multicellular morphologies



Anyone interested in modeling of biological/living systems and soft/active matter?
Contact me for potential research opportunities!!

sangwoo.kim@epfl.ch