# Continuous Limit of a Chemotaxis Model

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#### **1** Introduction

Modeling multicellular behavior: Continuous and discrete models The Cellular Potts Model

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The chemotaxis model Results

#### **4 Numerical Comparison**

Methods

Results

#### INTRODUCTION: Modeling multicellular behavior

Example 1: Life cycle of slime mold Dictyostelium discoideum



http://biology.kenyon.edu/Microbial\_Biorealm/eukaryotes/dictyosteliida/dictyosteliida.html

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#### Composite photograph of *Dictyostelium discoideum* life cycle



Photo by Mark Grimson and Larry Blanton, Texas Tech University

### Example 2: Cell Sorting

Randomly mixed differentiated cells can sort out



Simulation by James Glazier and F. Graner

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# Example 3: Organogenesis in early development: Precartilage condensation



Stuart A. Newman, NYMC

# Basic "Ingredients" for pattern formation in multicellular systems

1. cell movement

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- 2. cell differentiation

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- 3. cell proliferation and death

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- 4. cellular secretion and absorption of extracellular scaffolding

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- to predict previously unidentified phenomena
- to guide experiments

# Why Modeling?

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- simplify overwhelming complexity by forcing a hierarchy of importance
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- failure of models can identify missing components

#### Model modules





• discrete models:



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#### • continuous models:

represent cells via cell density  $\rho(x, t)$  (continuous variable of space x and time t)

 $\rho(x,t)$  =density of cells at location x, time t

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•  $J_{diffusion} = -D\nabla \rho$  Brownian motion (Fickian diffusion)

•  $J_{\text{chemotaxis}} = \chi \nabla \mathbf{c}(\mathbf{x}, \mathbf{t})$  chemotaxis up the gradients of a chemical c(x, t)

• Cellular Automata Models



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Lattice-gas Cellular Automata
 every occupied lattice site has a (discretized) velocity

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#### (Incomplete) List of Applications:

- Glazier/Graner(early 90s): testing Steinberg's differential adhesion hypothesis
- Marée et al. (late 1990s+): fruiting body formation of Dictyostelium discoideum
- COMPUCELL group (2000s): modeling chondrogenesis in vertebrate embryos
- Turner/Sherratt (1990s): tumor growth
- ETC



#### Cellular Potts Model: Set-up



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Hamiltonian (energy)= interaction energy + volume constraint energy + surface constraint energy+chemical energy

$$E = \sum_{\text{sites } i,j} J_{\tau(\sigma_i),\tau(\sigma_j)} + c_V \sum_{\text{cells } \sigma_i} (V_i - V_{target})^2 + c_S \sum_{\text{cells } \sigma_i} (S_i - S_{target})^2 + \sum_{\text{cells } \sigma_i} \mu_{\sigma_i} C_i$$

Introduction

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- 1. Choose a random site *i*
- 2. Choose a random cell index  $\sigma'$
- 3. Decide if the index  $\sigma$  of the site *i* should be "flipped" to  $\sigma'$ :

$$\operatorname{Prob}(\sigma \to \sigma') = \begin{cases} 1 & \Delta E < 0 \\ \exp(-\beta \Delta E) & \Delta E \ge 0 \end{cases}.$$

(Here  $\Delta E = E_{after} - E_{before}$  and  $\beta \dots 1$ /temperature.)



Picture of Chondrogenesis Simulation with CPM (COMPUCELL group)

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Simulation by James Glazier and F. Graner

# THE GENERAL PROBLEM OF THE CONTINUOUS LIMIT OF A DISCRETE MODEL

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**Turner, Sherratt, Painter, Savill (2004)** Derivation of diffusion equation for 1-D Potts without chemical energy

#### Why is the continuous limit intersting?

• more analytical, more and faster computational tools are available for **PDEs** 

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- often matching parameter values of discrete models to measurements is hard. (Example: Cell-cell interaction strength in CPM.) Parameters in PDEs are often easier to determine.
- Theoretical interest: Consistency of different models













 $P(x,t+\varepsilon^2\Delta t) =$ 





$$P(x, t + \varepsilon^2 \Delta t) = (1 - T^-(x, t) - T^+(x, t))P(x, t)$$



. . .



**Basic Technique** 

 $x-2\varepsilon\Delta x$   $x-\varepsilon\Delta x$  x  $x+\varepsilon\Delta x$   $x+2\varepsilon\Delta x$ 

$$P(x,t+\varepsilon^{2}\Delta t) = (1 - T^{-}(x,t) - T^{+}(x,t))P(x,t)$$
  
+T^{+}(x - \varepsilon \Delta x,t)P(x - \varepsilon \Delta x,t)





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Taylor expansion in  $\varepsilon$ , throw away terms  $\mathcal{O}(\varepsilon^3)$ 

Example

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$$\varepsilon^{2} \frac{\partial P}{\partial t} = \varepsilon^{2} \frac{T \Delta x^{2}}{\Delta t} \frac{\partial^{2} P}{\partial x^{2}} + \mathcal{O}(\varepsilon^{3})$$
Diffusion equation,  $D = T \Delta x^{2} / \Delta t$
#### CONTINUOUS LIMIT FOR A CPM CHEMOTAXIS MODEL



#### Chemotaxis 1 D Cellular Potts Model



## Chemotaxis 1 D Cellular Potts Model

 $E = E(x_{CM}, L) = J_{cm}(2L + 2\Delta x) + \lambda(L - L_T)^2 + \mu c(x_{CM})L$ 

 $c(x) \cdots$  external chemical field  $L \cdots$  cell length  $x_{CM} \cdots$  center of mass



## Chemotaxis 1 D Cellular Potts Model

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 $c(x) \cdots$  external chemical field

 $L \cdots$  cell length

 $x_{CM} \cdots$  center of mass

Potts parameters:

 $L_T \cdots$  target length,  $\lambda \cdots$  cell length constraint parameter,  $\mu \cdots$  chemical energy parameter,  $J_{cm} \cdots$  cell-medium interaction energy parameter

# Result 1: "Full" PDE

Let p(x, L, t) be the probability distribution for the cell location and cell length.

Up to  $\mathcal{O}(\varepsilon)$ , one gets the following PDE:

 $\partial_t P(x,L,t) = D(\partial_x^2 + 4\partial_L^2)P + 8D\beta\lambda\partial_L(\tilde{L}P) + D\beta L\mu\partial_x \left[Pc'(x)\right]$ 

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where:

$$D = \frac{(\Delta x)^2}{8\Delta t} + \mathcal{O}(\varepsilon),$$
  

$$\tilde{L} = L - L_m(x), \qquad L_m(x) = \frac{2J_{cm} + \mu c(x)}{2\lambda}$$

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$$\cdot \qquad \frac{1}{Z_0}\int_0^\infty \exp\left(-\beta\lambda\left(L - [L_T - L_m(x)]\right)^2\right)L\,dL + \mathcal{O}(\varepsilon)$$

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with  $L_m(x) = \frac{2J_{cm} + \mu c(x)}{2\lambda}$ For "reasonable" parameter ranges  $(\sqrt{\beta\lambda}[L_T - L_m(x)] >> 0)$ , approximation:

 $\chi(x) = \frac{(\Delta x)^2}{8\Delta t} \beta \mu \left( L_T - L_m(x) \right) + \mathcal{O}(\varepsilon)$ 

## **Derivation of Keller-Segel model**

If the cells also secrete the chemical, we get the Keller-Segel model

$$\frac{\partial c}{\partial t} = D_c \cdot \partial_x^2 c + k_c p - k_d p$$
$$\frac{\partial p}{\partial t} = D \cdot \partial_x^2 p + \partial_x (\chi(x) \cdot p \, \partial_x c)$$

#### NUMERICAL VALIDATION

Set up



Potts Monte Carlo typically 200,000 single cell runs





Potts Monte Carlo typically 200,000 single cell runs Numerical solution of chemotaxis PDE





Potts Monte Carlo typically 200,000 single cell runs Numerical solution of chemotaxis PDE

 $100/\varepsilon$  lattice sites;  $200/\varepsilon^2$  time steps (For plots renormed to 100 Potts lattice sites; Time  $t = 0 \cdots 200$ ;  $\Delta x = \Delta t = 1$ .)

#### Test 1



**Numerical Tests** 

## Test 1: Comparisons for time t = 200



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## Test 1: Comparisons for time t = 200 cont'd



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Test 3



Test 4

