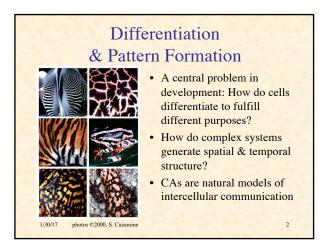
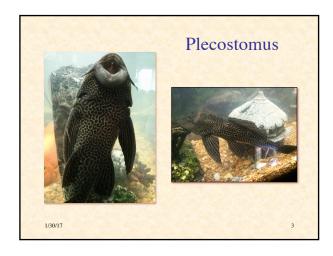
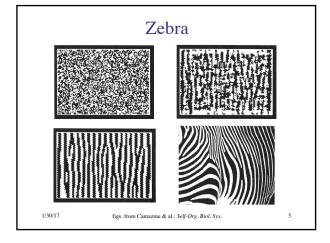
B. Pattern Formation





Vermiculated Rabbit Fish 1007 1007 1007 1008

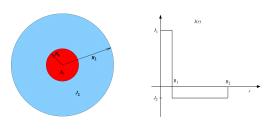


Activation & Inhibition in Pattern Formation

- Color patterns typically have a characteristic length scale
- Independent of cell size and animal size
- Achieved by:
 - short-range activation ⇒ local uniformity
 - long-range inhibition ⇒ separation

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Interaction Parameters



- R_1 and R_2 are the interaction ranges
- J_1 and J_2 are the interaction strengths

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CA Activation/Inhibition Model

- Let states $s_i \in \{-1, +1\}$
- and h be a bias parameter
- and r_{ij} be the distance between cells i and j
- Then the state update rule is:

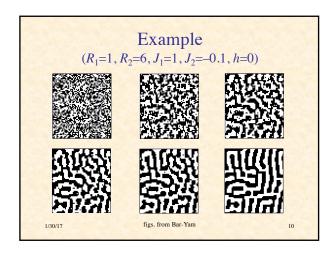
$$s_{i}(t+1) = \operatorname{sign}\left[h + J_{1} \sum_{r_{ij} < R_{1}} s_{j}(t) + J_{2} \sum_{R_{1} \le r_{ij} < R_{2}} s_{j}(t)\right]$$

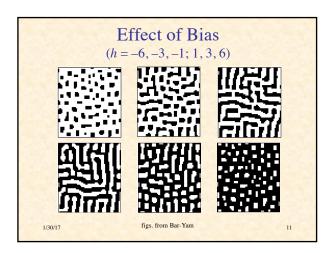
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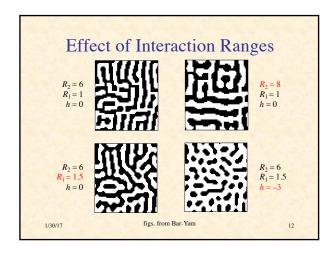
Demonstration of NetLogo Program for Activation/Inhibition Pattern Formation

RunAICA.nlogo

1/30/1







Differential Interaction Ranges

- How can a system using strictly local interactions discriminate between states at long and short range?
- E.g. cells in developing organism
- Can use two different *morphogens* diffusing at two different rates
 - activator diffuses slowly (short range)
 - inhibitor diffuses rapidly (long range)

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Digression on Diffusion

• Simple 2-D diffusion equation:

$$\dot{A}(x,y) = D\nabla^2 A(x,y)$$

• Recall the 2-D Laplacian:

$$\nabla^2 A(x,y) = \frac{\partial^2 A(x,y)}{\partial x^2} + \frac{\partial^2 A(x,y)}{\partial y^2}$$

- The Laplacian (like 2nd derivative) is:
 - positive in a local minimum

- negative in a local maximum

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Reaction-Diffusion System

$$\frac{\partial A}{\partial t} = D_{A} \nabla^{2} A + f_{A} (A, I)$$

$$\frac{\partial I}{\partial I} = D_{I} \nabla^{2} I + f_{I} (A, I)$$

reaction

$$\frac{\partial}{\partial t} \begin{pmatrix} A \\ I \end{pmatrix} = \begin{pmatrix} D_A & 0 \\ 0 & D_I \end{pmatrix} \begin{pmatrix} \nabla^2 A \\ \nabla^2 I \end{pmatrix} + \begin{pmatrix} f_A(A,I) \\ f_I(A,I) \end{pmatrix}$$

$$\dot{\mathbf{c}} = \mathbf{D}\nabla^2 \mathbf{c} + \mathbf{f}(\mathbf{c}), \text{ where } \mathbf{c} = \begin{pmatrix} A \\ I \end{pmatrix}$$

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General Reaction-Diffusion System

$$\frac{\partial c_i}{\partial t} = \sum_{\alpha} k_{\alpha} \mathbf{v}_{i\alpha} \left(\prod_{k=1}^{n} c_k^{m_{k\alpha}} \right) - \nabla \cdot \mathbf{j}_i$$

where $\mathbf{j}_i = \vec{\mu}_i c_i - \mathbf{div} \ \mathbf{D}_i c_i$ (flux)

where k_{α} = rate constant for reaction α

and $v_{i\alpha}$ = stoichiometric coefficient

and $m_{k\alpha}$ = a non-negative integer

and $\vec{\mu}_i$ = drift vector

and \mathbf{D}_i = diffusivity matrix

where **div** $\mathbf{D}c = \sum_{k} \mathbf{e}_{j} \sum_{k} D_{jk} \frac{\partial c}{\partial x_{k}}$

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Framework for Complexity

- change = source terms + transport terms
- source terms = local coupling
- = interactions local to a small region
- transport terms = spatial coupling
- = interactions with contiguous regions
- = advection + diffusion
- advection: non-dissipative, time-reversible
- diffusion: dissipative, irreversible

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NetLogo Simulation of Reaction-Diffusion System

- 1. Diffuse activator in X and Y directions
- 2. Diffuse inhibitor in X and Y directions
- 3. Each patch performs:

stimulation = bias + activator – inhibitor + noise if stimulation > 0 then

set activator and inhibitor to 100

set activator and inhibitor to 0

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Demonstration of NetLogo Program for Activator/Inhibitor Pattern Formation

Run Pattern.nlogo

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Continuous-time Activator-Inhibitor System

- Activator *A* and inhibitor *I* may diffuse at different rates in *x* and *y* directions
- Cell becomes more active if activator + bias exceeds inhibitor
- Otherwise, less active
- A and I are limited to [0, 100] (depletion/saturation)

$$\frac{\partial A}{\partial t} = d_{Ax} \frac{\partial^2 A}{\partial x^2} + d_{Ay} \frac{\partial^2 A}{\partial y^2} + k_A (A + B - I)$$

$$\frac{\partial I}{\partial t} = d_{\rm ix} \frac{\partial^2 I}{\partial x^2} + d_{\rm iy} \frac{\partial^2 I}{\partial y^2} + k_{\rm I} (A + B - I)$$

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Demonstration of NetLogo Program for Activator/Inhibitor Pattern Formation with Continuous State Change

Run Activator-Inhibitor.nlogo

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Turing Patterns

- Alan Turing studied the mathematics of reaction-diffusion systems
- Turing, A. (1952). The chemical basis of morphogenesis. *Philosophical Transactions of the Royal Society* **B 237**: 37–72.
- The resulting patterns are known as *Turing* patterns

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Observations

- With local activation and lateral inhibition
- And with a random initial state
- You can expect to get Turing patterns
- These are stationary states (dynamic equilibria)
- Macroscopically, Class I behavior
 - Microscopically, may be class III

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A Key Element of Self-Organization

- Activation vs. Inhibition
- Cooperation vs. Competition
- Amplification vs. Stabilization
- Growth vs. Limit
- Positive Feedback vs. Negative Feedback
 - Positive feedback creates
 - Negative feedback shapes

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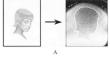
Reaction-Diffusion Computing

- Has been used for image processing
 - diffusion ⇒ noise filtering
 - reaction ⇒ contrast enhancement
- Depending on parameters, RD computing
 - restore broken contours
 - detect edges
 - improve contrast

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Image Processing in BZ Medium







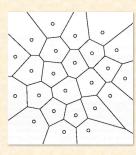


• (A) boundary detection, (B) contour enhancement, (C) shape enhancement, (D) feature enhancement

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 $Image < Adamatzky, Comp.\ in\ Nonlinear\ Media\ \&\ Autom.\ Coll.$

Voronoi Diagrams



- Given a set of generating points:
- Construct a polygon around each generating point of set, so all points in a polygon are closer to its generating point than to any other generating points.

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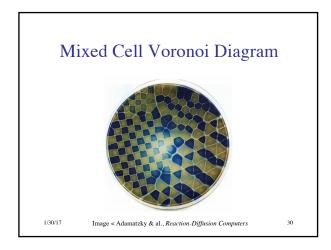
Image < Adamatzky & al., Reaction-Diffusion Computers

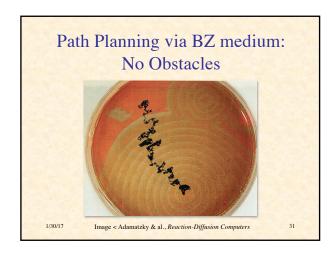
Some Uses of Voronoi Diagrams

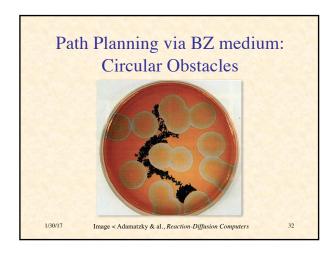
- Collision-free path planning
- Determination of service areas for power substations
- Nearest-neighbor pattern classification
- Determination of largest empty figure

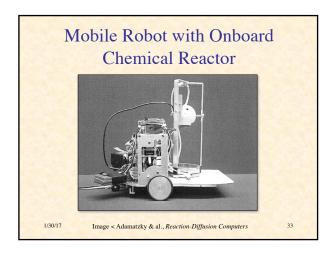
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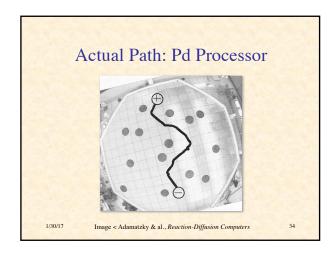
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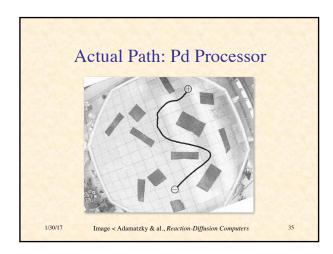


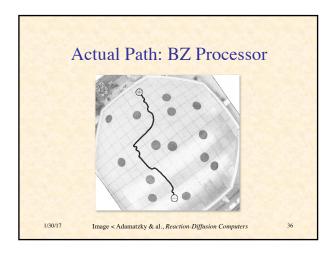












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- 2. Adamatzky, Adam, De Lacy Costello, Ben, & Asai, Tetsuya. *Reaction Diffusion Computers*. Amsterdam: Elsevier, 2005.

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