Animal pigmentation patterns from CA and PDE

References to:

Wolfram, *NKS*, pages 422-429

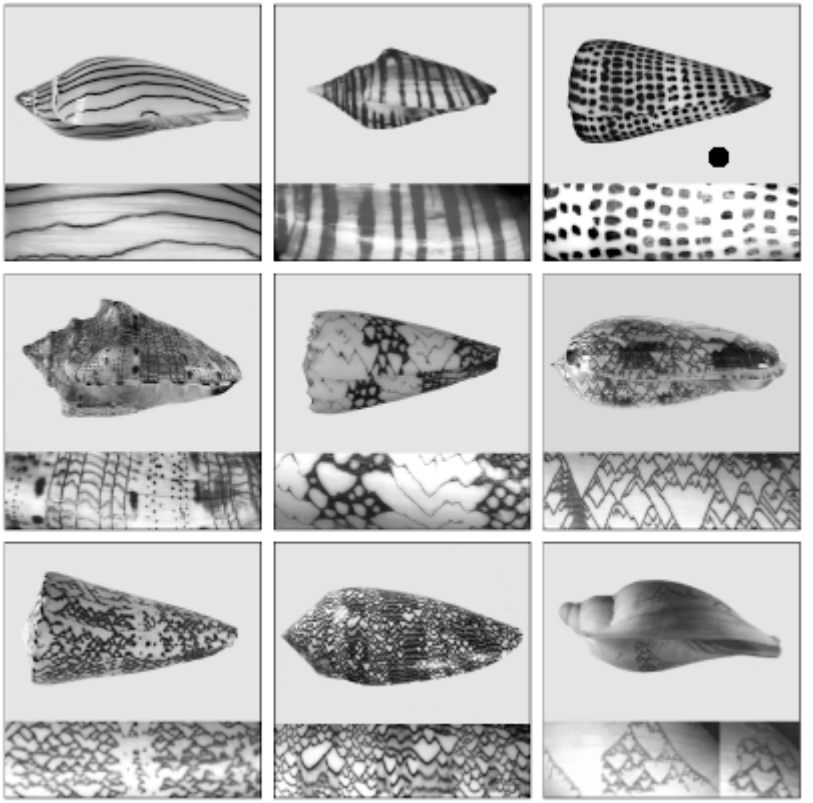
Bar-Yam, *Dynamics of Complex Systems*, Ch. 7

Young, *A Local Activator-Inhibitor Model of Vertebrate Skin Patterns*

Presented by Rich Drewes, Feb 1 2005

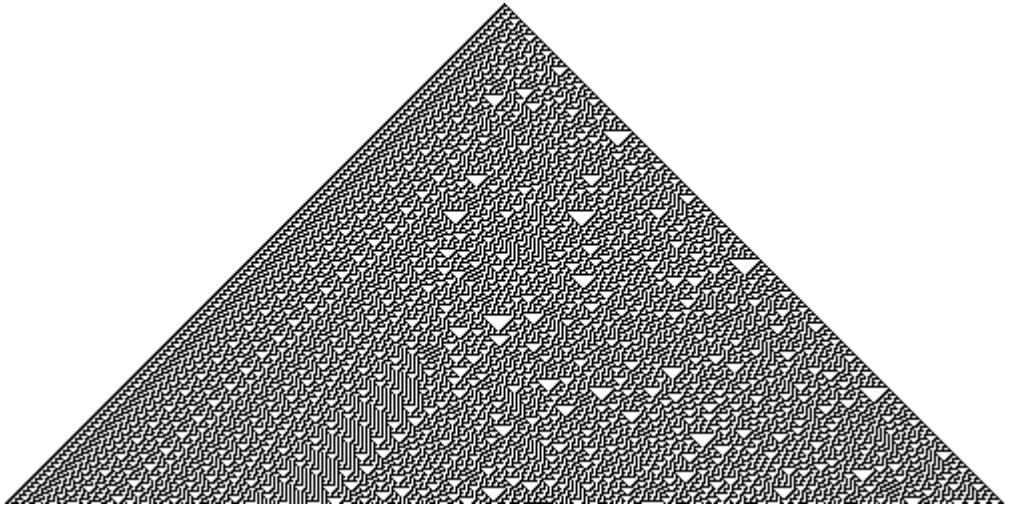
CS 790R

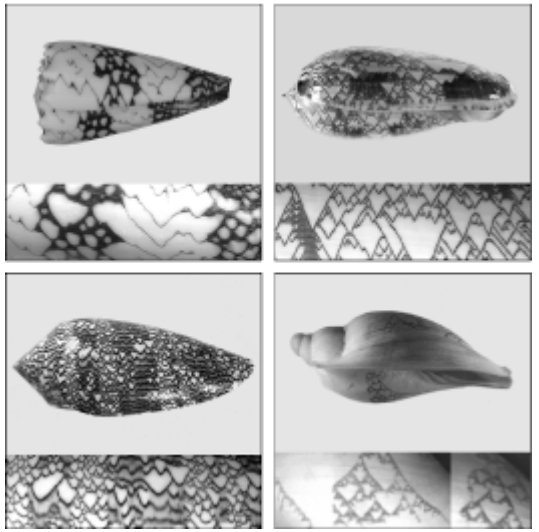
Biological pigment patterns are complex. This implies some complex underlying generation mechanism, right?

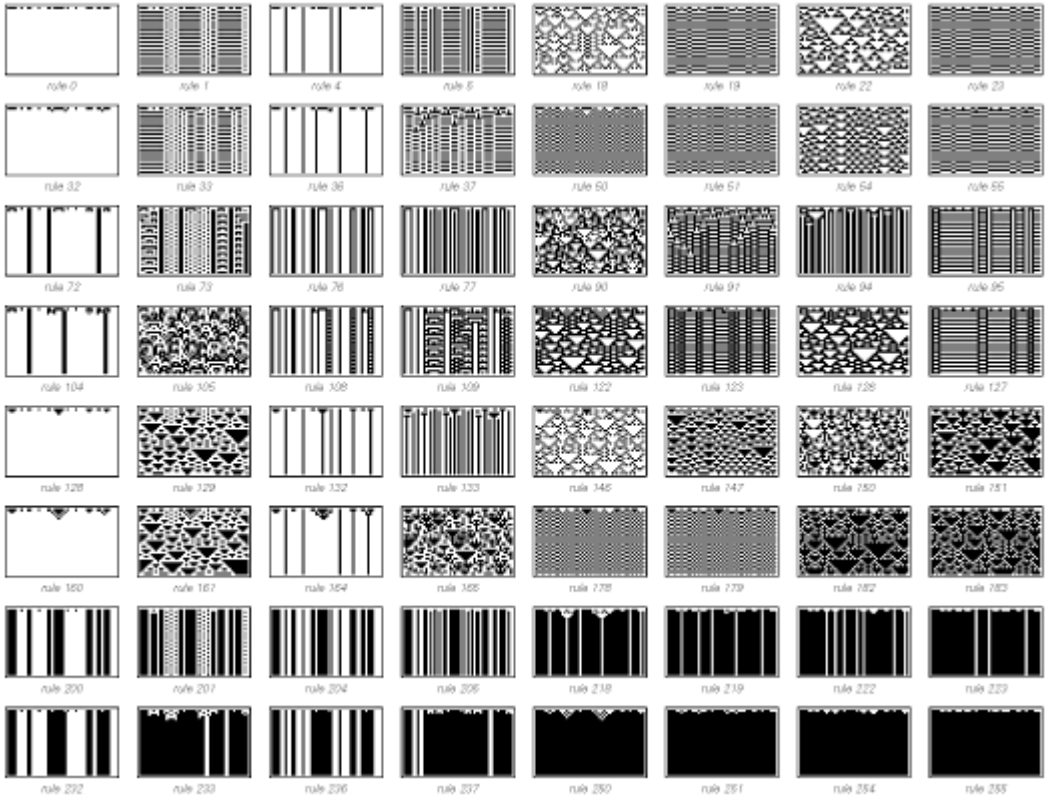


Wolfram, NKS p. 423

“. . . one notices the remarkable fact that the range of patterns that occur in the two cases is extremely similar.”



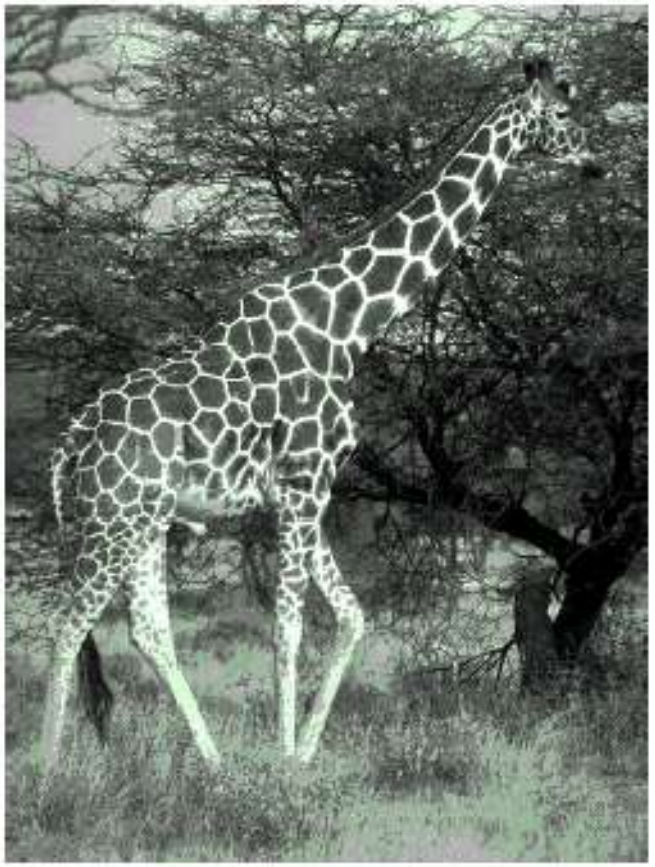




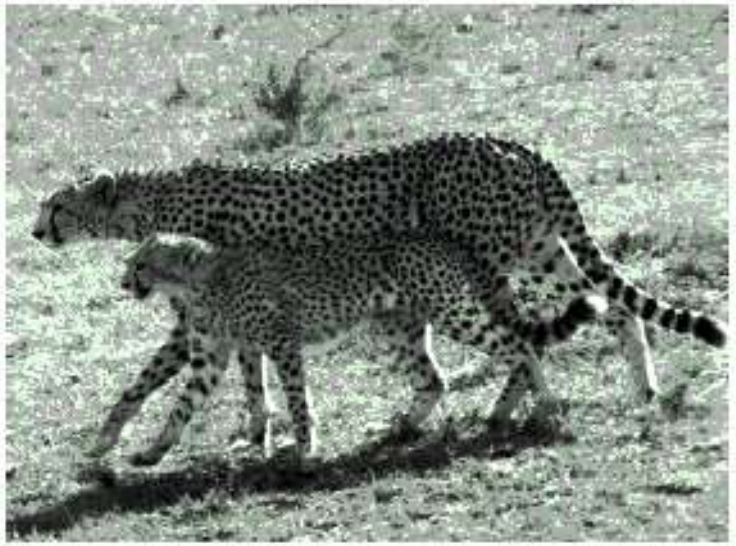
Wolfram, NKS

Those are 1-D CA examples;
most animal patterns are 2-D

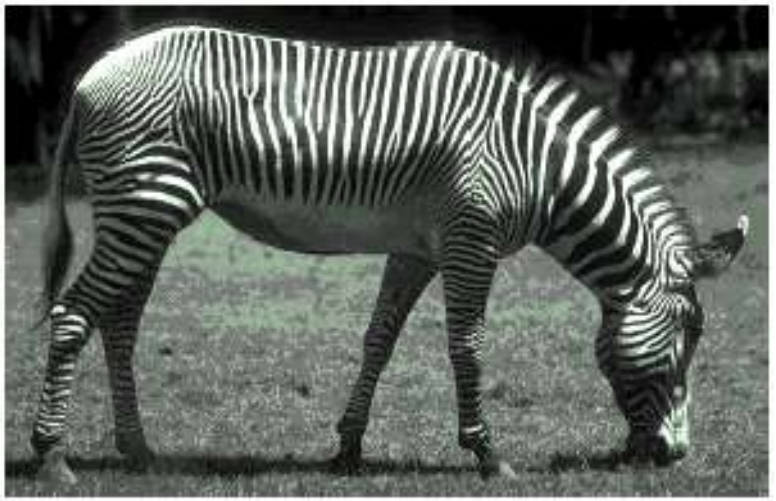
Clusters of cells develop, where cells tend to be same as average of nearby elements and opposite to average color of elements further away:
local activation, long range inhibition



It would be nice if our models for pigmentation pattern formation accounted for a variety of patterns (stripes, spots, solid colors) with one mechanism



Bar-Yam, p. 628



This problem of pigmentation is a subset of a more general and fundamental biological problem: differentiation

Differentiation:
a fundamental problem of biology

Requires formation of cells with different properties out of initially homogeneous, undifferentiated cells (and later, creation of specific structures that support interconnection of these regions of different purpose)

For animal pigments, this problem reduces to “just” creation of a spatial pattern in a 2D surface; more generally, it could be a spatio-temporal pattern in some other substrate

Is pigmentation a model for general physiology?

Bar-Yam begins by considering abstractly what tools are available to biology that might be used in pattern formation

Cell + environment -> phenotype

DNA is not a blueprint
More like a program, with environment as data

"DNA is not itself a complex organism" only the embodiment is, the complex set of *temporal* protein construction machines in the environment

Generally, we human engineers find that creating dynamic processes that lead to consistent results is very hard (unless the processes are deterministic).

“Seeds” of pattern formation

Antiferromagnet on square lattice sort of similar--
but that has no characteristic length scale, as do biological pigment patterns

How get a length scale? Some long range effect is needed

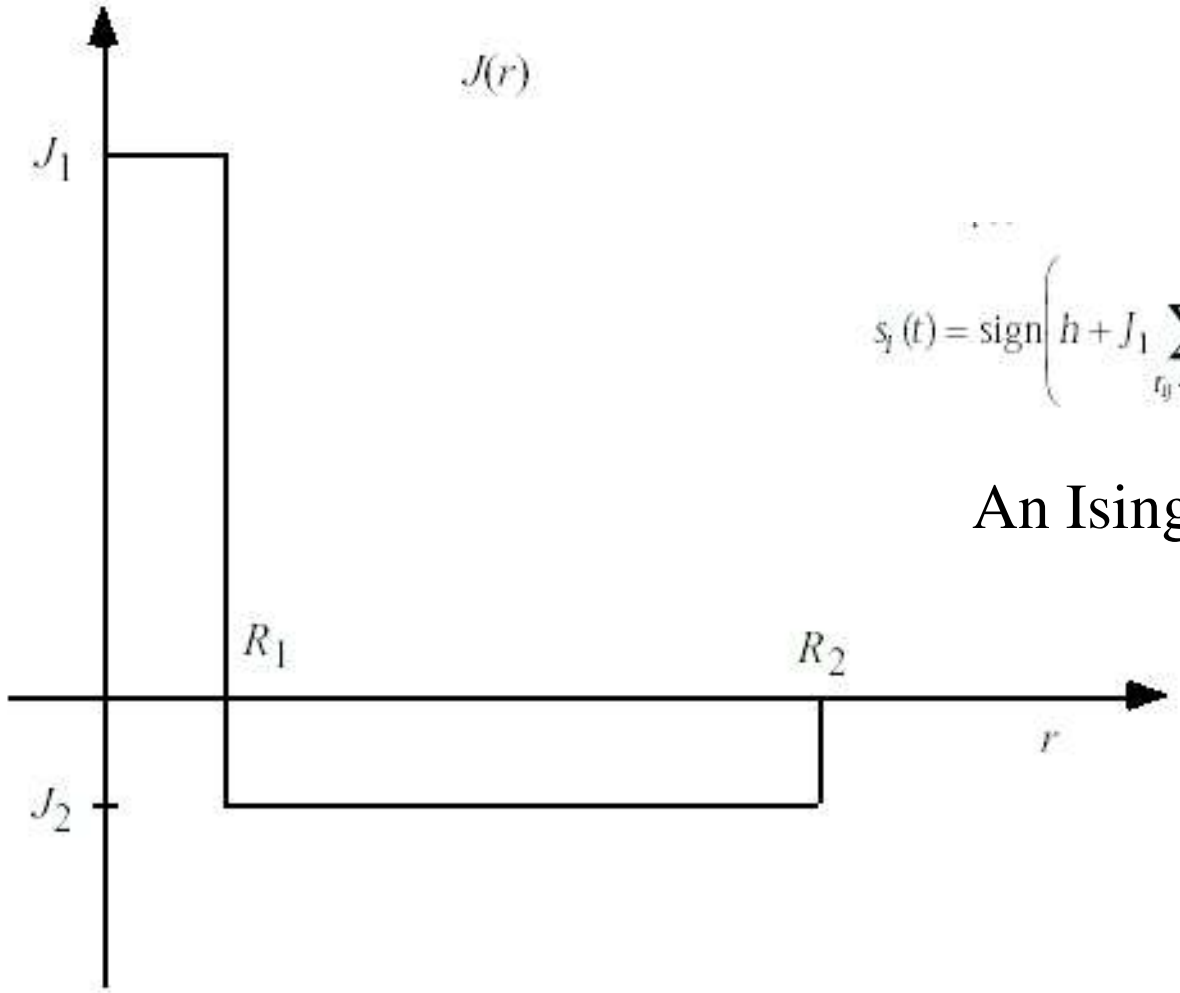
Chemical emission into extracellular space is a natural candidate: chemicals diffuse over distance

Ising model: interacting binary variables, “simplest CA”

Magnetic domain formation analogy

Pigmentation patterning is somewhat similar to real magnetic materials which form “domains” with some length-scale:
local activating quantum effect is activating
longer distance alignment effect is antiferromagnetic (inhibiting)

Local activation, long range inhibition

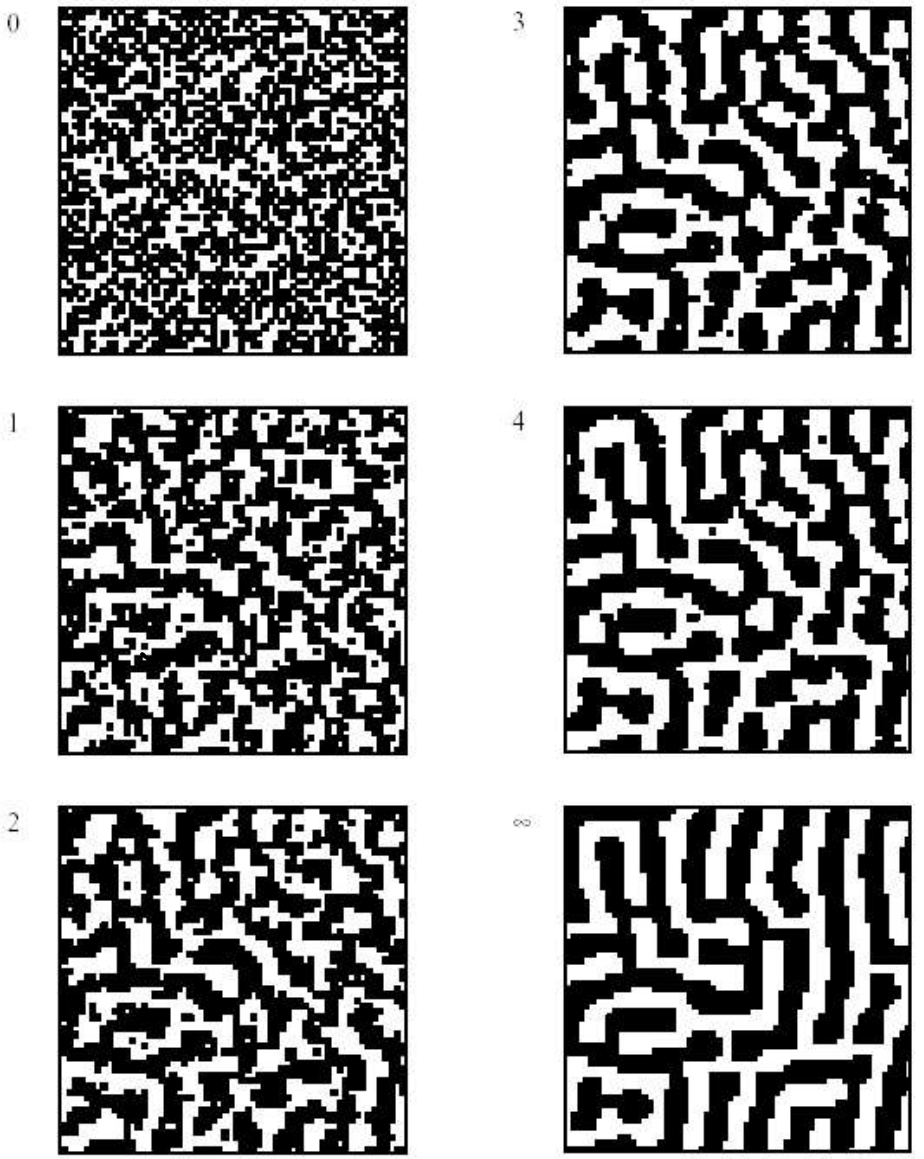


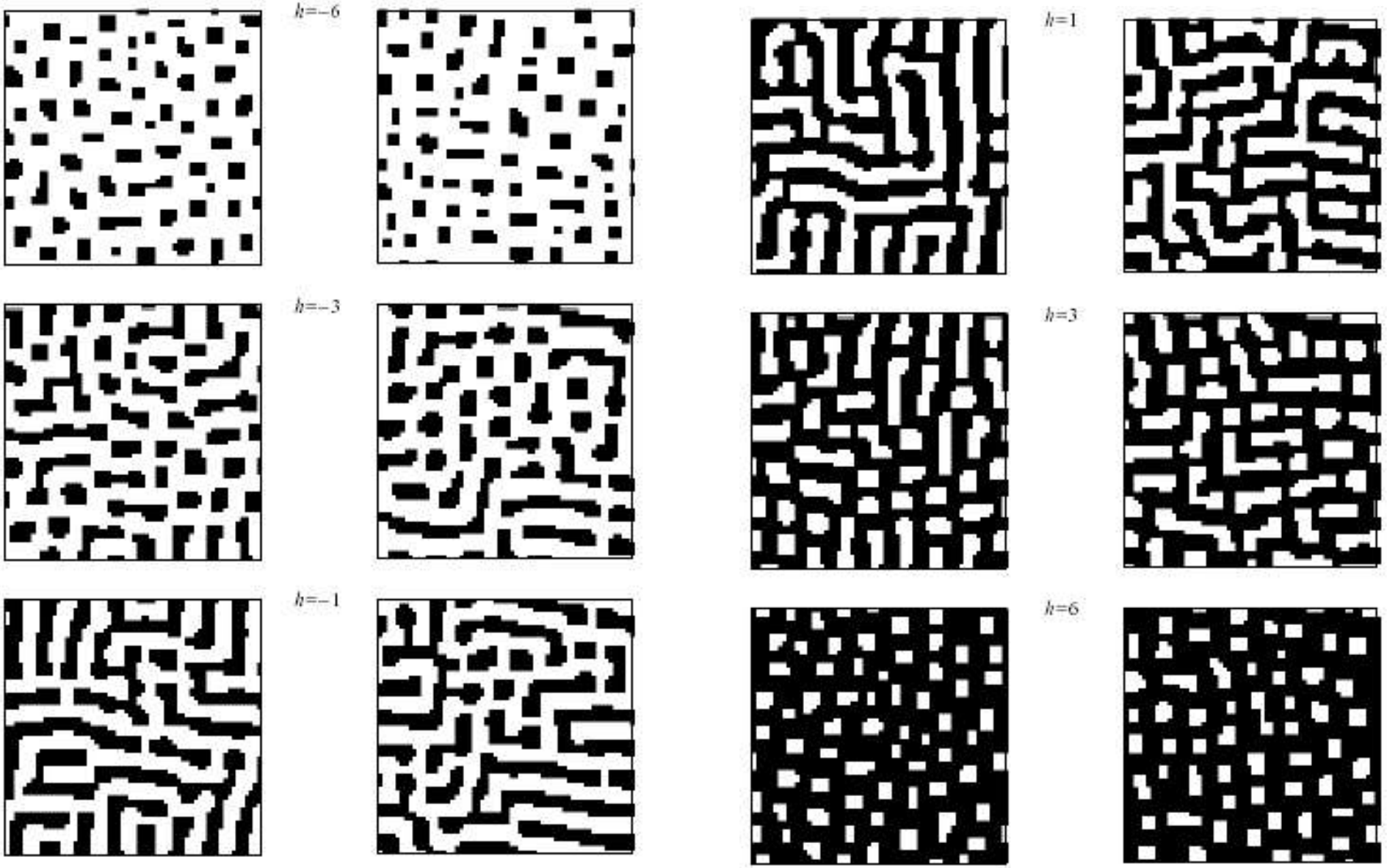
$$s_i(t) = \text{sign}\left(h + J_1 \sum_{r_{ij} < R_1} s_j(t-1) + J_2 \sum_{R_1 < r_{ij} < R_2} s_j(t-1) \right)$$

An Ising-type model

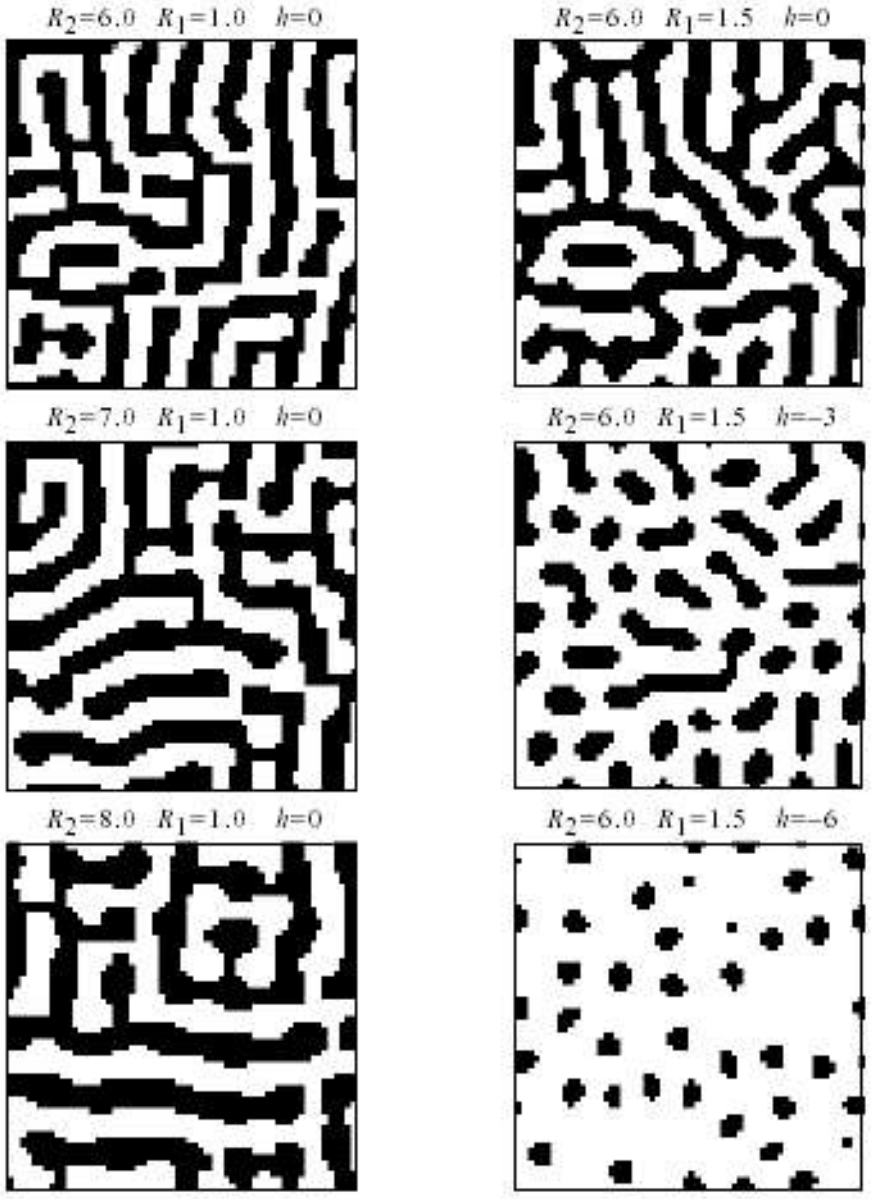
Bar-Yam p. 631

The parameters are $R_1 = 1$, $R_2 = 6$, $J_1 = 1$, $J_2 = -0.1$, and $h = 0$.





Bar-Yam 7.2.4


R_2=6.0 R_1=1.0 h=0
R_2=6.0 R_1=1.5 h=0
R_2=7.0 R_1=1.0 h=0
R_2=6.0 R_1=1.5 h=–3
R_2=8.0 R_1=1.0 h=0
R_2=6.0 R_1=1.5 h=–6

Bar-Yam 7.2.5

Stability

These are *equilibrium* patterns.

Changing the initial fraction of on/off cells doesn't change final result very much qualitatively, since the end result is an equilibrium with similar gross patterns, but the precise final state is quite sensitive to the specific initial arrangement.

This is the goal of a stable (end result) dynamic process!

Ergodic theorem

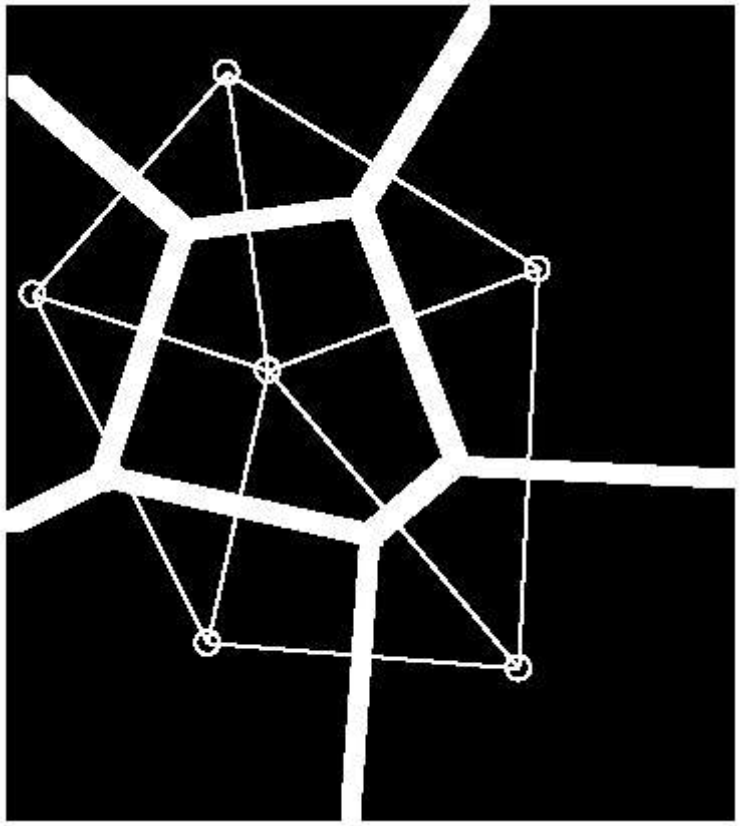
and patterns in equilibrium (question 7.2.1)

Ergodic theorem: "Closely related to the discussion of fast coordinates is the ergodic theorem. The ergodic theorem states that a measurement performed on a system by averaging a property over a long time is the same as taking the average over the ensemble of the fast coordinates. This theorem is used to relate experimental measurements that are assumed to occur over long times to theoretically obtained averages over ensembles. The ergodic theorem is not a theorem in the sense that it has been proven in general, but rather a statement of a property that applies to some macroscopic systems and is known not to apply to others. The objective is to identify when it applies." (p. 90)

Patterns in equilibrium?

Bar-Yam points out that the presence of patterns in equilibrium may appear to contradict an earlier result. In fact, it does not for several reasons (lack of thermal fluctuations, inapplicability of ergodic theorem, presence of correlation length large relative to system size).

But . . . activation-inhibition alone doesn't capture much of the variation seen in real animals



Perhaps a CA model that *grows* out from a set of starting points might work better?

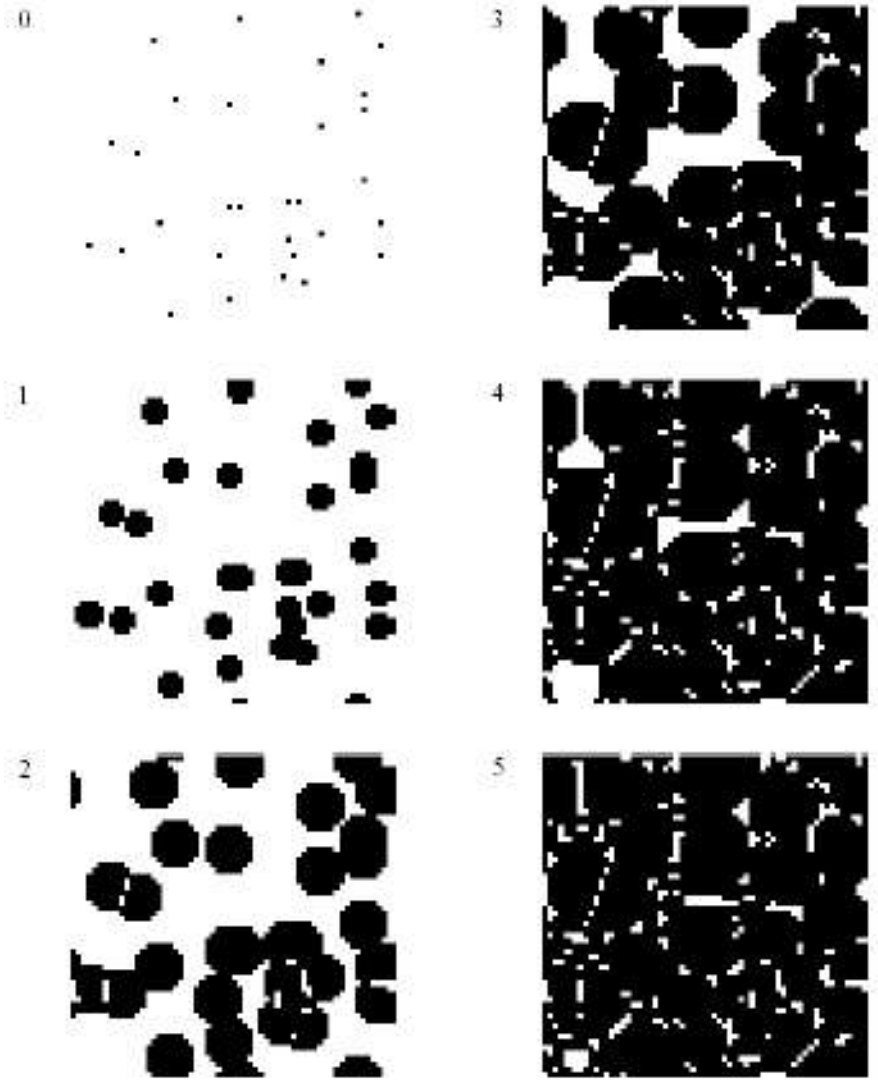
First attempt

Grow outward from a set of initial points

Turn cell on if there are some, but not too many on neighbors

Never turn off once on

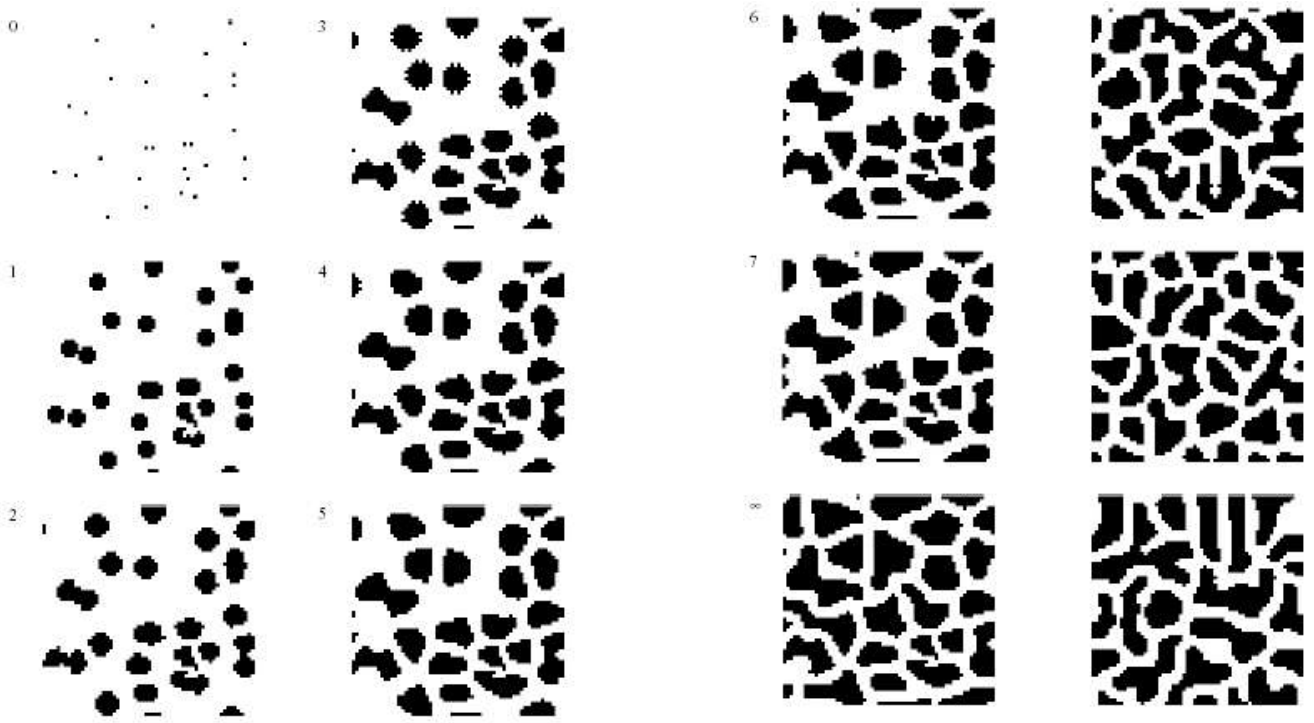
Results . . . not good yet



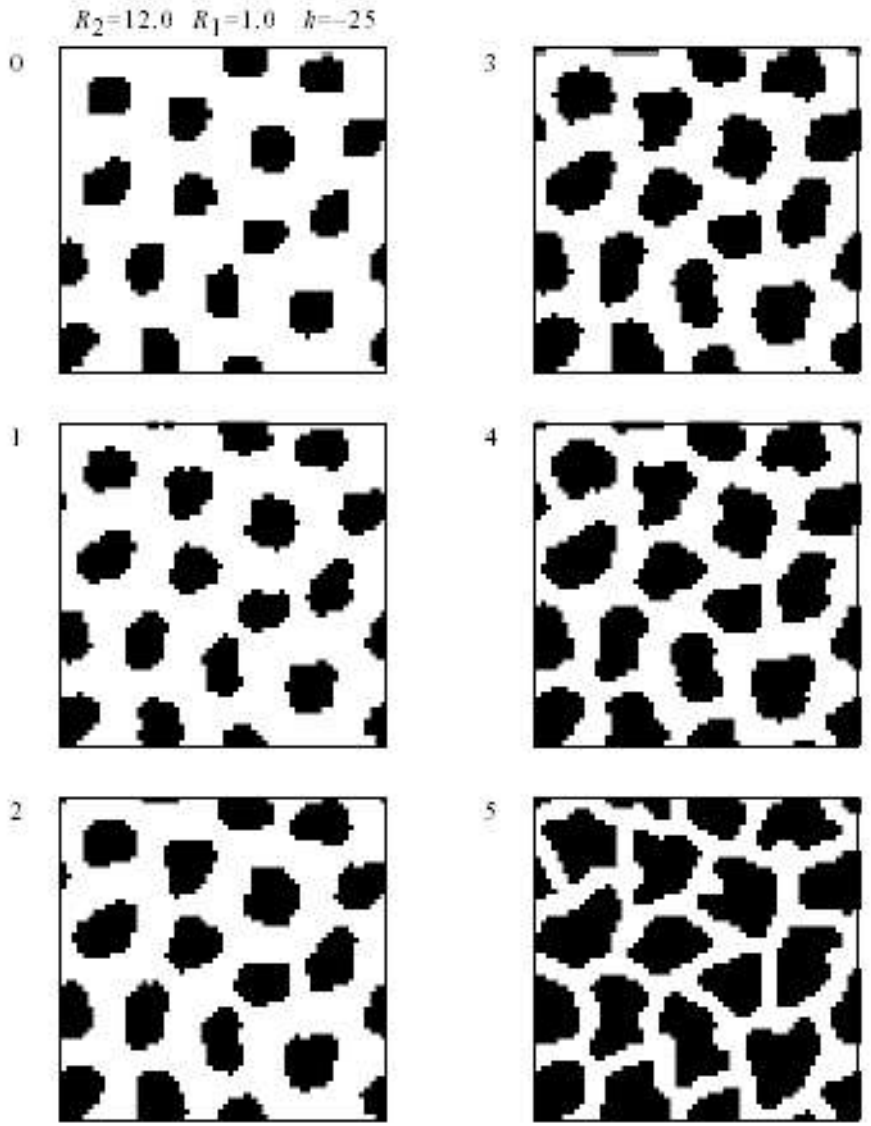
Bar-Yam Figure 7.2.9

Next attempt

Extend the inhibitory region to larger area than just neighbors.
Looks better, but shapes are still not quite like those of giraffe—they are too irregular.



Bar-Yam Figure 7.2.10



Bar-Yam Figure 7.2.11

Starting with a more regularly spaced initial grid of points (perhaps created from activation-inhibition) results in even more giraffe-like results

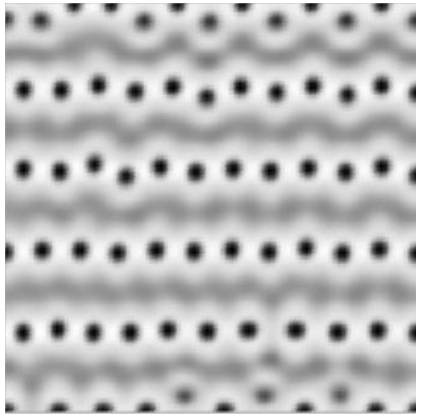
Chemical diffusion models

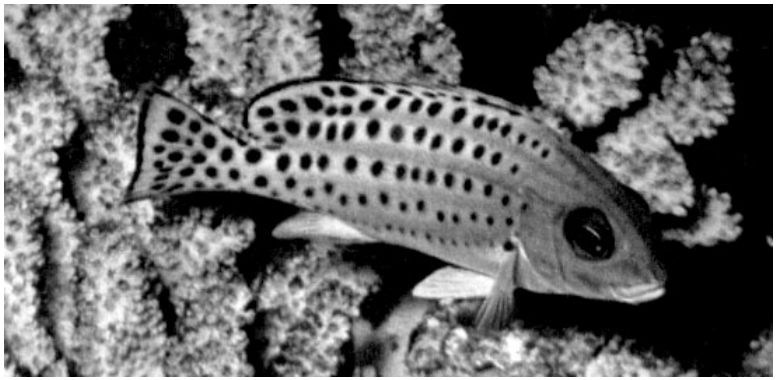
(Bar-Yam 7.2.3)

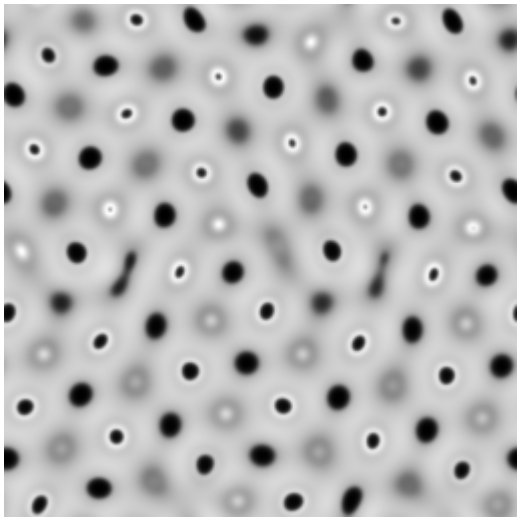
Random walk distance from origin of thermally jostling molecule is proportional to sqrt(Dt). This suggests exploring patterns generated by evolution of molecular density.

$$\frac{dn(\mathbf{x};t)}{dt} = D\nabla^2 n(\mathbf{x};t)$$ The diffusion equation

Turing investigated some of this, and resulting patterns are called "Turing Patterns"







http://hopf.chem.brandeis.edu/yanglingfa/pattern/t2/

Diffusion leads to movement of molecules toward smoothing of densities. So how can this result in patterns?

Answer: through several kinds of *interacting* molecules.
Interactions affect local densities.

Particularly important are situations where a reacting molecule is also a catalyst that speeds a reaction (autocatalysis).

Chemical reactions

(Bar-Yam 7.2.4)

$$\frac{dn_i(x;t)}{dt} = D\nabla^2 n_i(x;t) + R_i(\{n_j(x;t)\})$$

The *R* term represents changes in concentration due to chemical reactions.

R in turn depends on concentrations (why?)

Chemical reactions

"reaction is proportional to probabilities of encounters between reagents" e.g.

$$\sim n_A n_B$$

"thus reactions give rise to differential equations coupling the densities of the different molecules"

Chemical reactions

Stoichiometric considerations for a proposed reaction give something like:

$$A \rightarrow 0$$
$$B \rightarrow 0$$
$$2A + D \rightarrow 2A + B$$
$$2A + C \rightarrow 3A + C$$
$$C + B \leftrightarrow E$$

activator-inhibitor system

$$A \rightarrow 0$$
$$0 \rightarrow B$$
$$2A + B \rightarrow 3A$$

activator-substrate system

Chemical reactions

$$\frac{dn_A}{dt} = -k_1 n_A + k_3 n_A^2 n_C = -k_1 n_A + k_3' n_A^2 / n_B$$

$$\frac{dn_B}{dt} = -k_4 n_B n_C + k_5 n_E + (k_3 n_A^2 n_D - k_2 n_B)$$

$$\frac{dn_C}{dt} = -k_4 n_B n_C + k_5 n_E$$

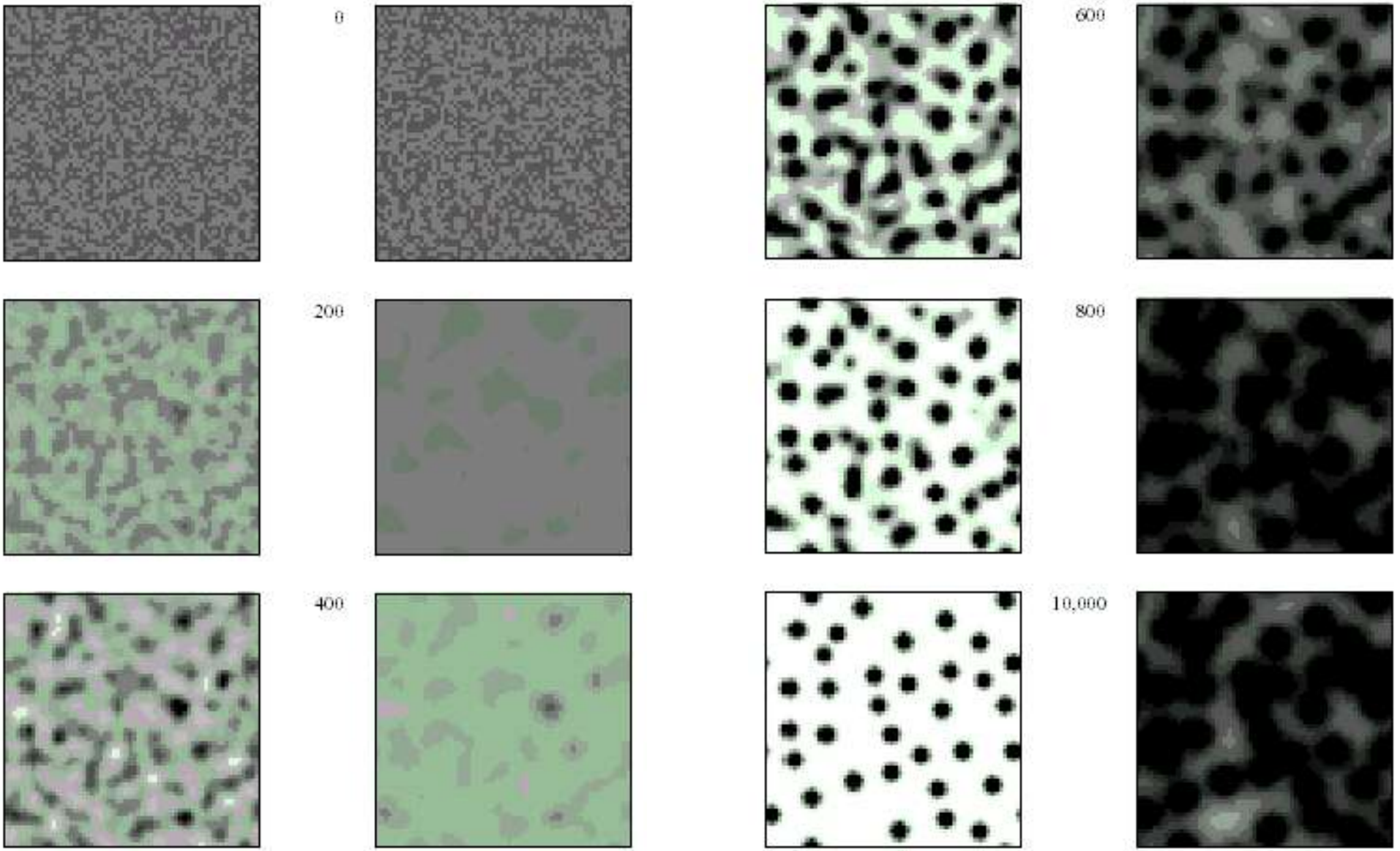
Patterns arising from reaction-diffusion

Ultimately, the source of patterns may be same as with CA: short range activation, long range inhibition.

The differential equation version has the advantage of obscurity.

The long range inhibition is actually accomplished via diffusion; the PDE form shows this directly.

Substituting the reaction terms into the basic diffusion equation and simulating gives us:

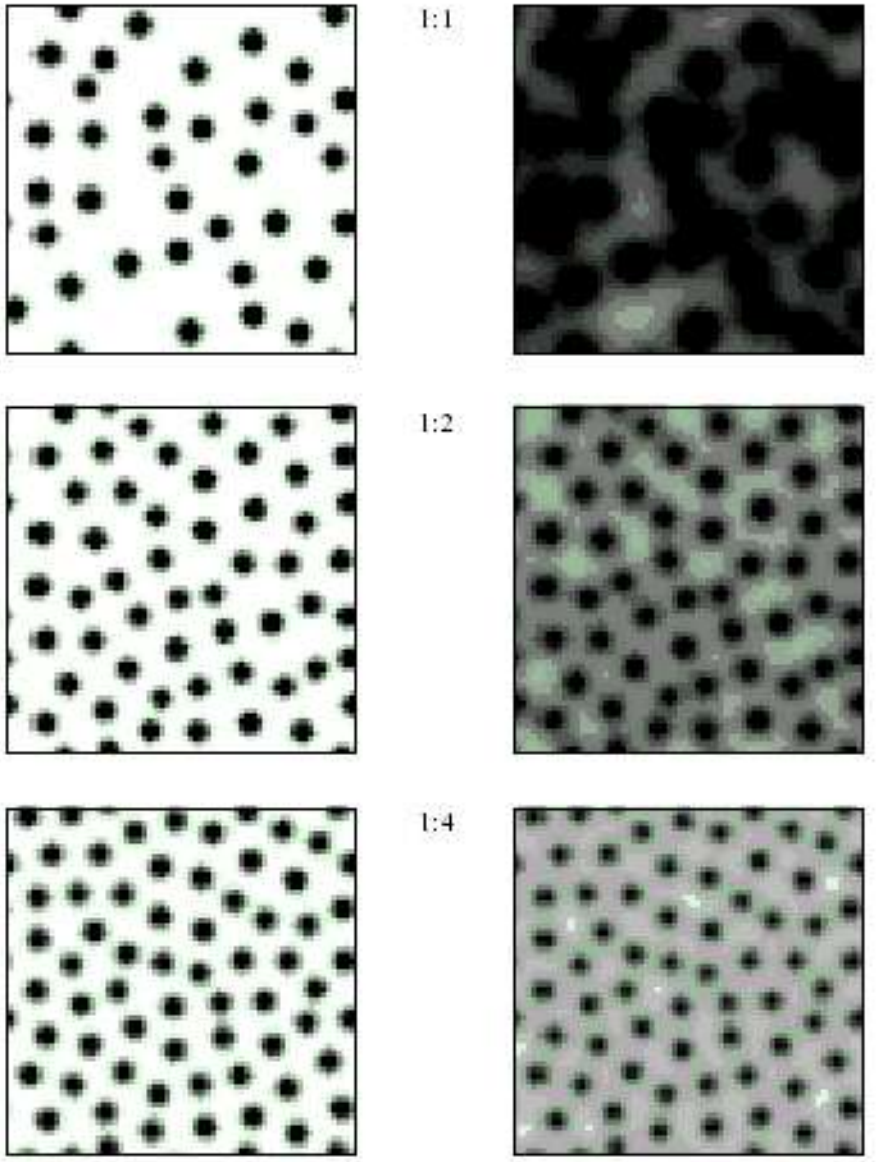


Simulating? How?

Basically, by conversion from differential equations to discrete-time difference equations.

More results, with different reaction constants

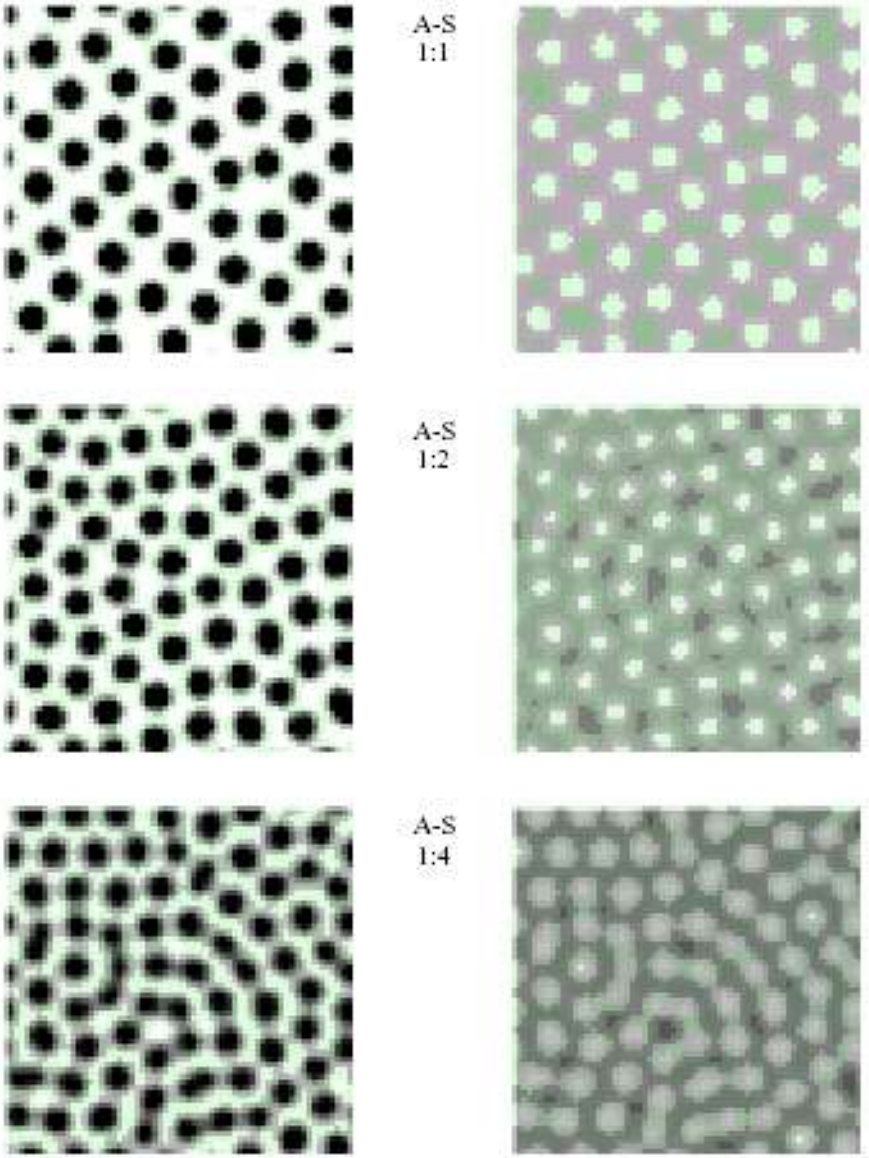
activator, A



inhibitor, B

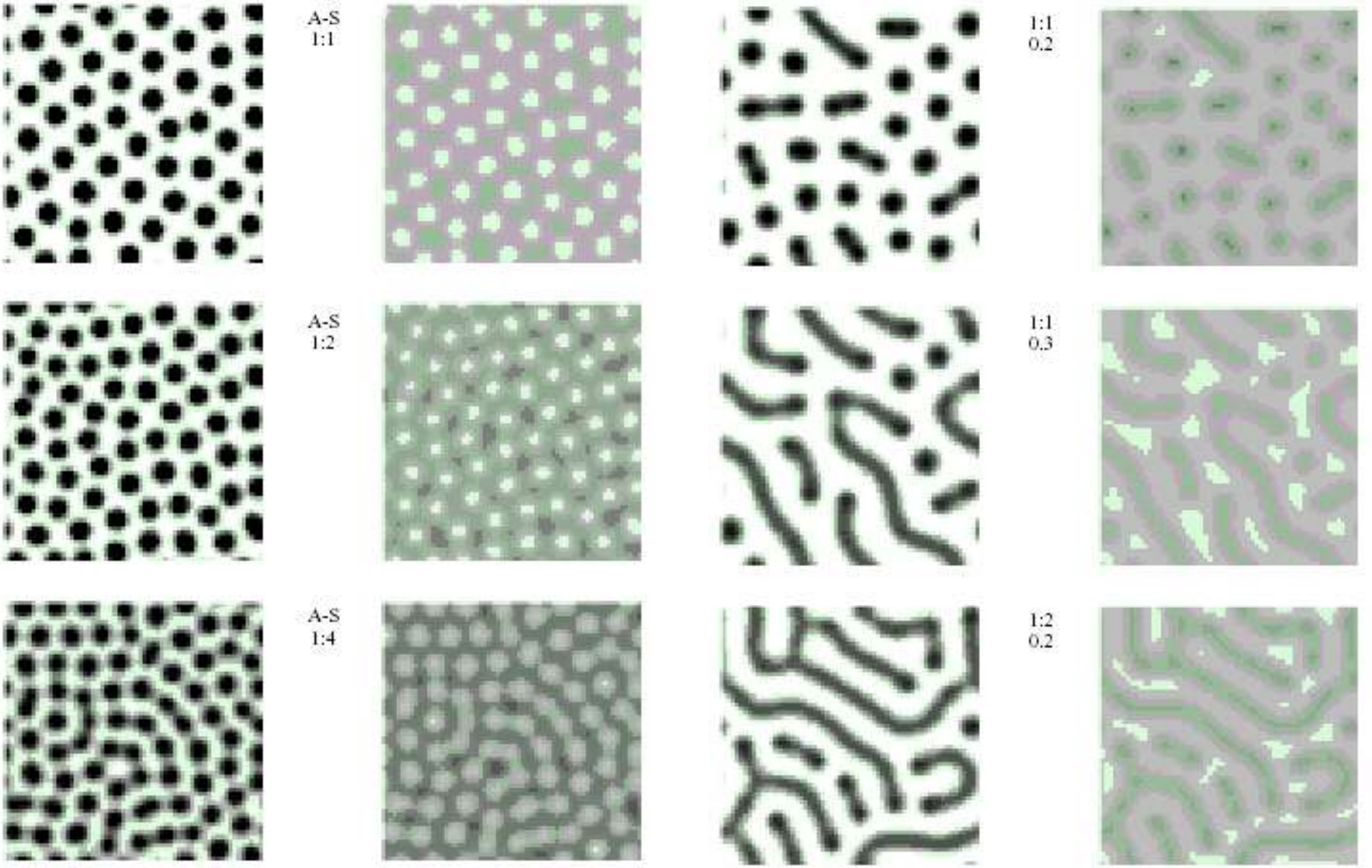
Bar-Yam 7.2.14

activator



substrate

A model variant that produces stripes



In summary,

“. . . we see that the conditions under which patterns can be generated include cases where there are two types of molecules, one diffusing rapidly and the other slowly. The slow diffuser A autocatalyzes a reaction that increases its own density. The fast diffuser B reacts with the slow diffuser and decreases the density of A in the vicinity of a high-density region of A. This results in patterns like that of the activation-inhibition CA model in the previous section. The primary difference between the two sets of differential equations is that the fast diffuser B acts to inhibit in two distinct ways, in the activator-inhibitor system through its presence, and in the activator-substrate system through its absence (depletion).” (Bar-Yam p. 669)

Final thoughts

Finite difference form of PDE *is* a CA. In the basic, original CA actions were longer-range and cells were binary. In the difference equation form actions are nearest-neighbor only and cell sites encode multiple real numbers representing concentrations. (Bar-Yam p. 667)

"Diffusion in the absence of reactions causes the density to become uniform and patterns are not possible." (Bar-Yam p. 668)

"a uniform solution of the equations continues to exist even when patterns are formed. However, this uniform solution is unstable." (Bar-Yam p. 668)

A nice feature of the diffeq form, as compared to CA, is that the diffeq form has no hard-coded length scale. It arises from the diffusion constants.