

Design Patterns of Pattern Formation and Morphogenesis in a Declarative Programming Language

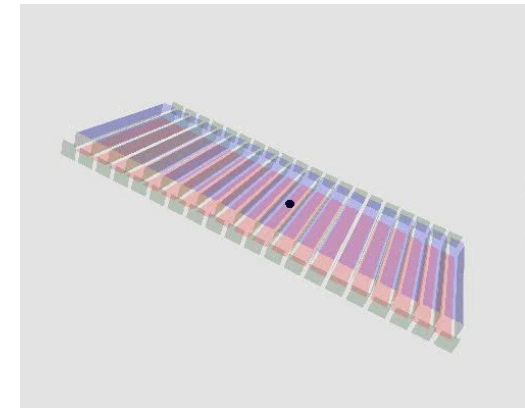
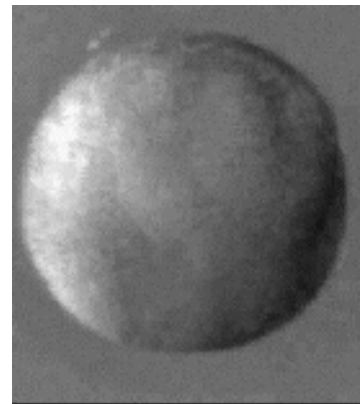
Jean-Louis Giavitto

CNRS

IBISC, Université d'Evry

LIS team, MGS project

<http://mgs.spatial-computing.org>



Modelling morphogenesis: the approach of A. Turing

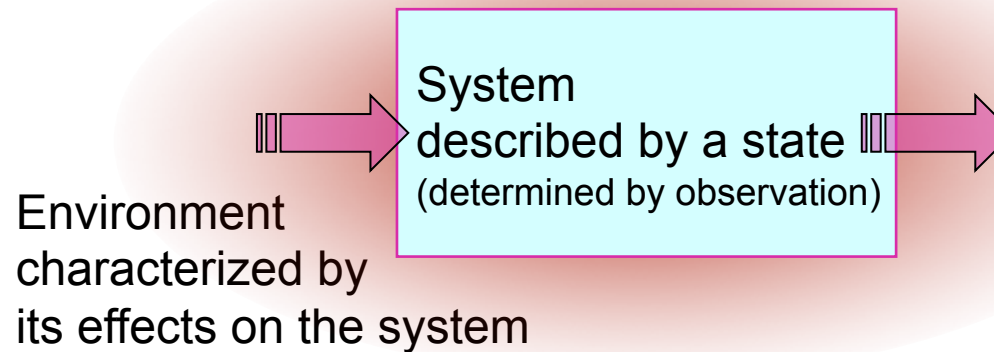


THE CHEMICAL BASIS OF MORPHOGENESIS

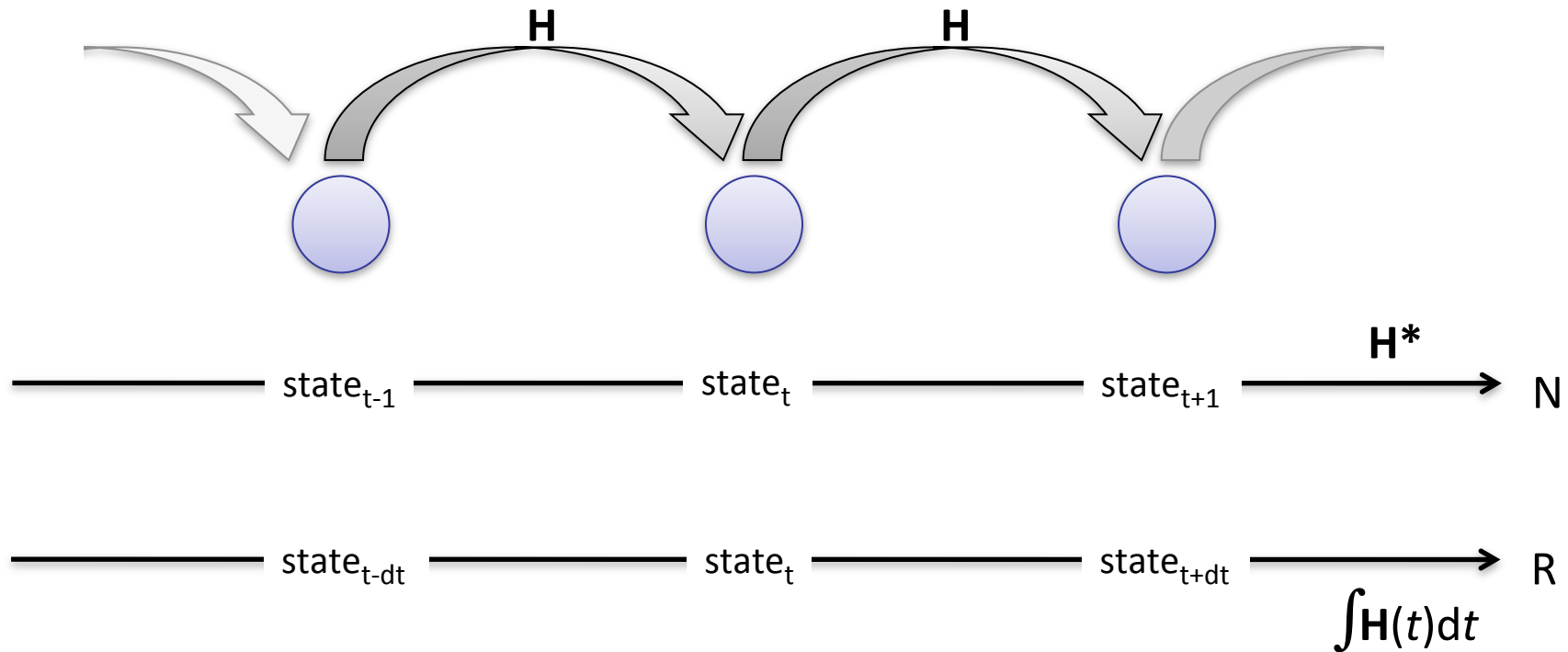
BY A. M. TURING, F.R.S. *University of Manchester*

(Received 9 November 1951—Revised 15 March 1952)

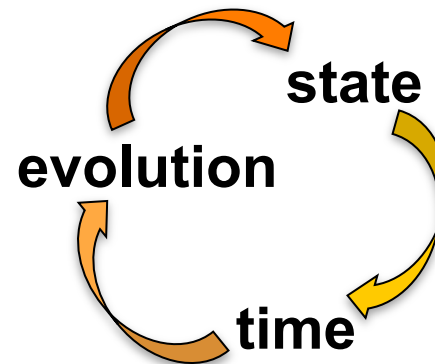
With either of the models one proceeds as with a physical theory and defines an entity called 'the state of the system'. One then describes how that state is to be determined from the state at a moment very shortly before. With either model the description of the state consists of two parts, the mechanical and the chemical.



Specifying a dynamical system (for simulation)



- Specification of**
- **structure of state**
 - **structure of time**
 - **evolution function**



Morphogenesis as a Dynamical System

Modelling a dynamical system

- state, including space (e.g. fields)
- time
- evolution function

| C : continuous, D : discrete | PDE | Coupled ODE | Iteration of functions | Cellular automata | ... |
|---|------------|------------------------|-----------------------------------|------------------------------|------------|
| <i>state</i> | C | C | C | D | ... |
| <i>time</i> | C | C | D | D | ... |
| <i>space</i> | C | D | D | D | ... |



Modelling morphogenesis: the approach of A. Turing

The model takes two slightly different forms. In one of them the cell theory is recognized but the cells are idealized into geometrical points. In the other the matter of the organism is imagined as continuously distributed. The cells are not, however, completely ignored, for various physical and physico-chemical characteristics of the matter as a whole are assumed to have values appropriate to the cellular matter.

- **Uniform matter, continuous-oriented system description**

One choice is to ignore cells completely, e.g., Physiome models tissues as continua with bulk mechanical properties and detailed molecular reaction networks, which is computationally efficient for describing dense tissues and non-cellular materials like bone, extracellular matrix, fluids, and diffusing chemicals, *but not for situations where cells reorganize or migrate*.

versus

- **Cell-oriented discrete system description**

Multi-cell simulations are useful to interpolate between single-cell and continuum-tissue extremes because cells provide a natural level of abstraction for simulation of tissues, organs and organisms.

Treating cells phenomenologically reduces the millions of interactions of gene products to several behaviors: most cells can move, divide, die, differentiate, change shape, exert forces, secrete and absorb chemicals and electrical charges, and change their distribution of surface properties.

(CompuCell3D manual)

Aggregate- vs. Entity-based models

Modelling morphogenesis: the predefined medium

The interdependence of the chemical and mechanical data adds enormously to the difficulty, and attention will therefore be confined, so far as is possible, to cases where these can be separated.

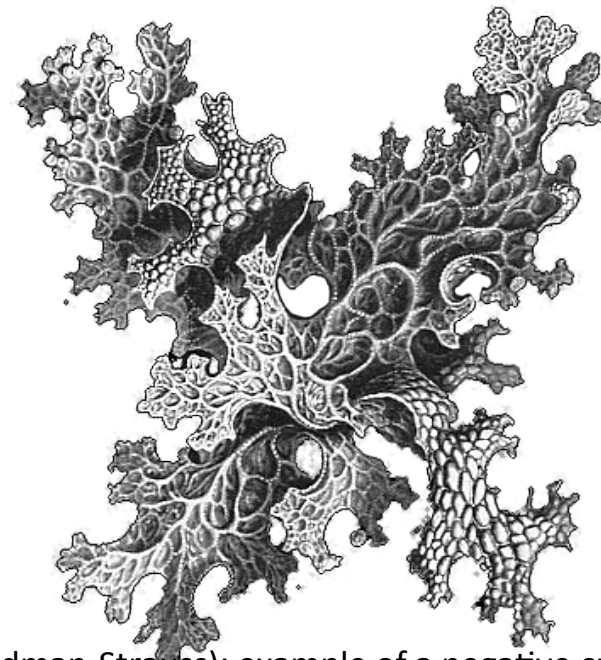
Suppose, for instance, that a ‘leg-evocator’ morphogen were being produced in a certain region of an embryo, or perhaps diffusing into it, and that an attempt was being made to explain the mechanism by which the leg was formed in the presence of the evocator. It would then be reasonable to take the distribution of the evocator in space and time as given in advance and to consider the chemical reactions set in train by it.

Compatible with

- the notion of morphogenetic field
- cell fate

But

- there is evidence for **feedback loops between the shape and the process inhabiting the shape**



from E. Haenkel (cited by C. Goodman-Strauss): example of a negative curvature surface. Curvature can be controlled while the surface is growing along a ‘front’

The medium/process problem

In determining the changes of state one should take into account

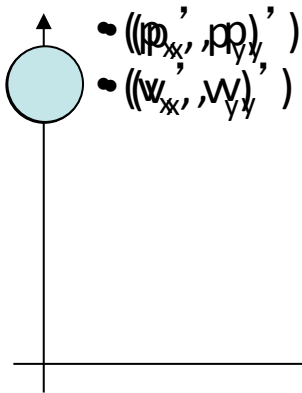
- (i) The changes of position and velocity as given by Newton's laws of motion.
- (ii) The stresses as given by the elasticities and motions, also taking into account the osmotic pressures as given from the chemical data.
- (iii) The chemical reactions.
- (iv) The diffusion of the chemical substances. The region in which this diffusion is possible is given from the mechanical data.

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a falling ball



at any time a state is a position and a speed

A dynamical system (DS)

The medium/process problem

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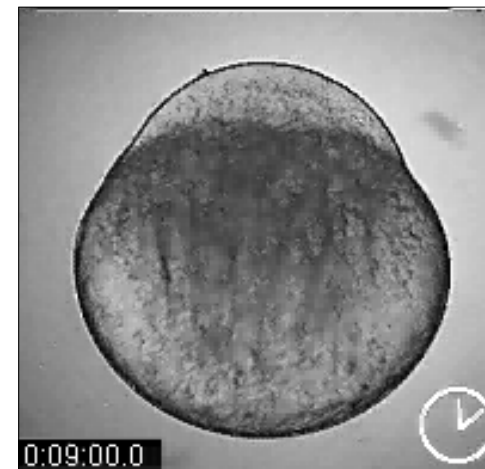
a falling ball



at any time a state is a position and a speed

A dynamical system (DS)

a developing embryo

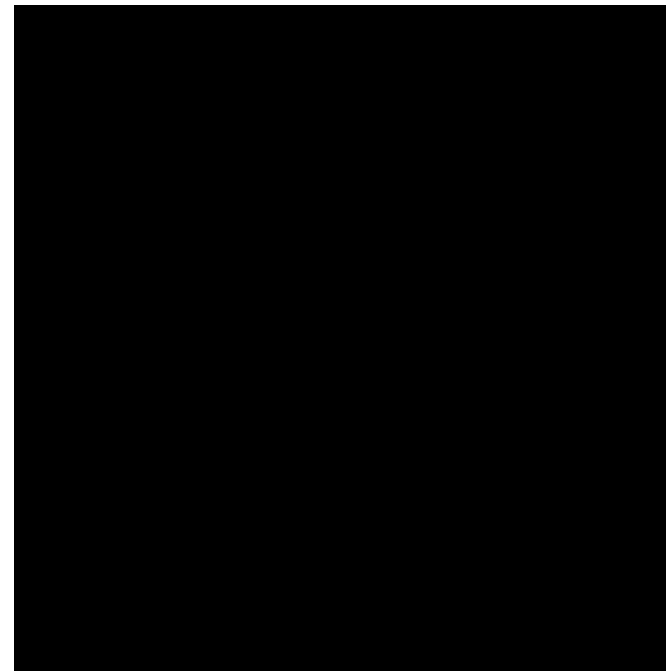


*the structure of the state
(chemical and mechanical state of each cell)
is changing in time*

**A dynamical system with a dynamical structure
(DS)²**

What has changed since Turing' s time

It might be possible, however, to treat a few particular cases in detail with the aid of a digital computer. This method has the advantage that it is not so necessary to make simplifying assumptions as it is when doing a more theoretical type of analysis. It might even be possible to take the mechanical aspects of the problem into account as well as the chemical, when applying this type of method. The essential disadvantage of the method is that one only gets results for particular cases. But this disadvantage is probably of comparatively little importance.



P. Prusinkiewicz, c.2003

Diffusion and reaction in a deformable surface (E. Coen' s *expanding canvas* metaphor). Spring-mass system. No topological change.

Software as Science ?



M.-P. Cani & F. Bertails

- **Intelligibility**

The entire process should be accessible for analysis into a finite, not very large number of stages, each stage being represented as a monotonic function of some definite initial conditions and a single variable such as time, or distance, etc. (Gurwitsch, 1944)

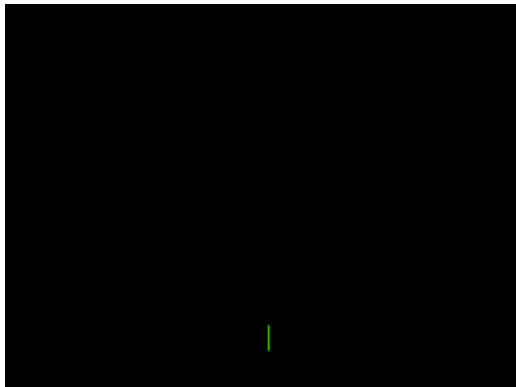
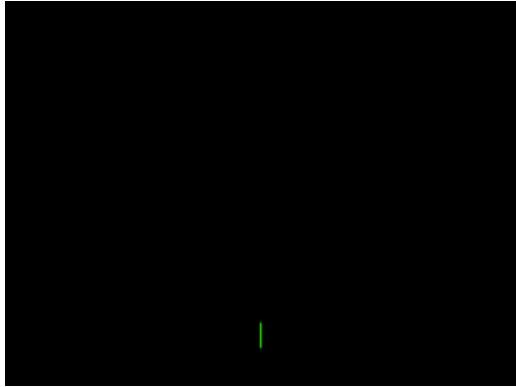
→ compress behavior or shape in few rules

- Simulation is only a first step: models must enable **reasoning**

→ stay close to mathematical formalism

A program is a formal object (and some form of reasoning on it is possible) but a 10^6 lines of codes is not an explanation !

A good example of **declarative** formalism: Lindenmayer systems



P. Prusinkiewicz

- The structure of a tree can be coded by a string of parenthesised symbols
- A symbol is an elementary part of the plant
- The symbol between [and] represents a sub-tree
- Additional conventions are used to represent main axis, orientation, depth, etc.
- A rule
$$s_0 \rightarrow s_1 s_2 s_3 \dots$$
represents the evolution of s_0

Diffusion and reaction in a linear *growing medium*

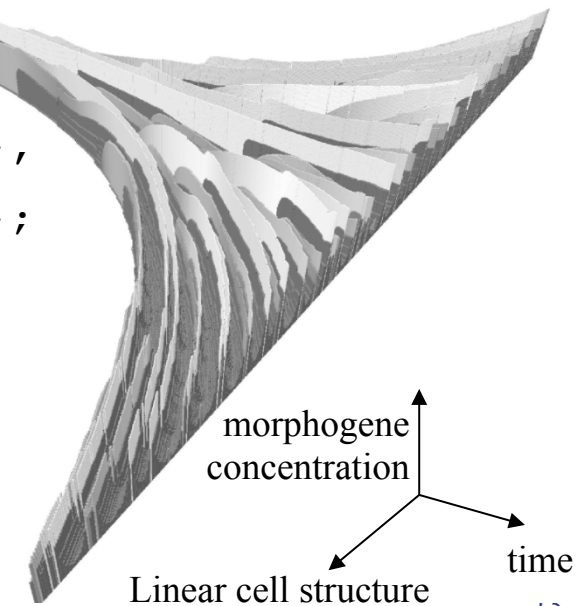
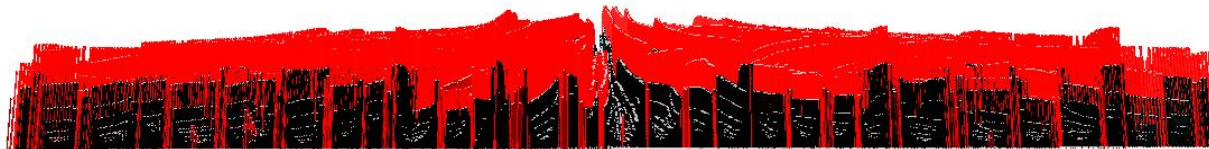
M. Hammel and P. Prusinkiewicz (1996)

The following rules state that a differentiated cell (heterocyst) returns to a vegetative state if the concentration of the activator is too low. In addition, if the cell is large enough, it continues to grow.

```
e / (D(e) & (e.a < thr) | (e.x >= shorter*gr))
=> {type="C", a=e.a/gr, h=e.h/gr, x=e.x*gr, p=e.p};
```

The following rule specifies when a cell with a left polarity divides. Only vegetative cells can divide (hence the predicate C in the rule guard) and it must be large enough. The volume of the two daughter cells remains the same, so there is no variation in the concentration.

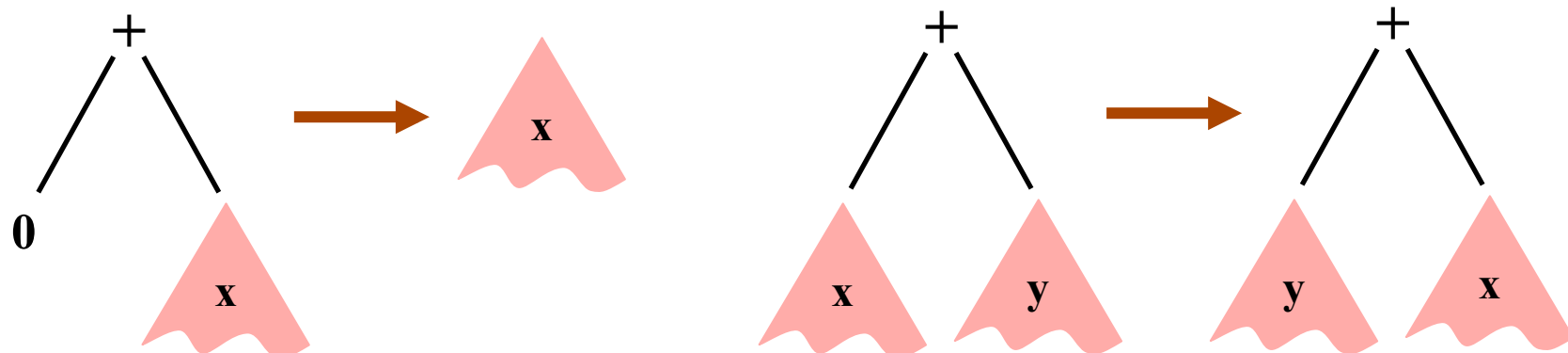
```
e / (C(e) & (e.x >= lm) & (e.p == L))
=> {type="C", a=e.a, h=e.h, x=e.x*shorter, p=L},
    {type="C", a=e.a, h=e.h, x=e.x*longer, p=R};
```



Rewriting systems (and abstract transition systems)

- Rewriting system
 - Used to formalize equational reasoning
 - A generative device (grammar)
 - Replace a sub-part of an entity by an other
 - Set of rewriting rules $\alpha \rightarrow \beta$
 - α : pattern specifying a sub-part
 - β : expression evaluating a new sub-part

- Example: arithmetic expressions simplification



A non-standard interpretation



e_1 can be a cell and e_2 a signal

e_1 and e_2 can be interacting cell

$+$ is the possibility of *interaction* between entities (or some other relationships)

\rightarrow is the passing of time, a local evolution, a transition, the concretization of the interaction

Examples: if e is a cell and i a biochemical signal

$e + i \rightarrow e'$ growth (evolution of e on signal

i)

$e + i \rightarrow e+i'$ quorum sensing

$e + i \rightarrow e' + e''$ division

$e + i \rightarrow .$ apoptose

Complex systems \leftrightarrow Rewriting techniques

Modelling

State (space)

hierarchical and tree organizations

arbitrary complex organizations

Evolution function

interactions \rightarrow evolution

local evolution laws

Simulation

Trajectories

Time management

discrete, event-based,
synchronous vs. asynchronous

Specification

Data structure

formal trees (or terms)

?

Set of rules

α : pattern \rightarrow β : expression

rewriting rules

Application

Derivations

Rule application strategy

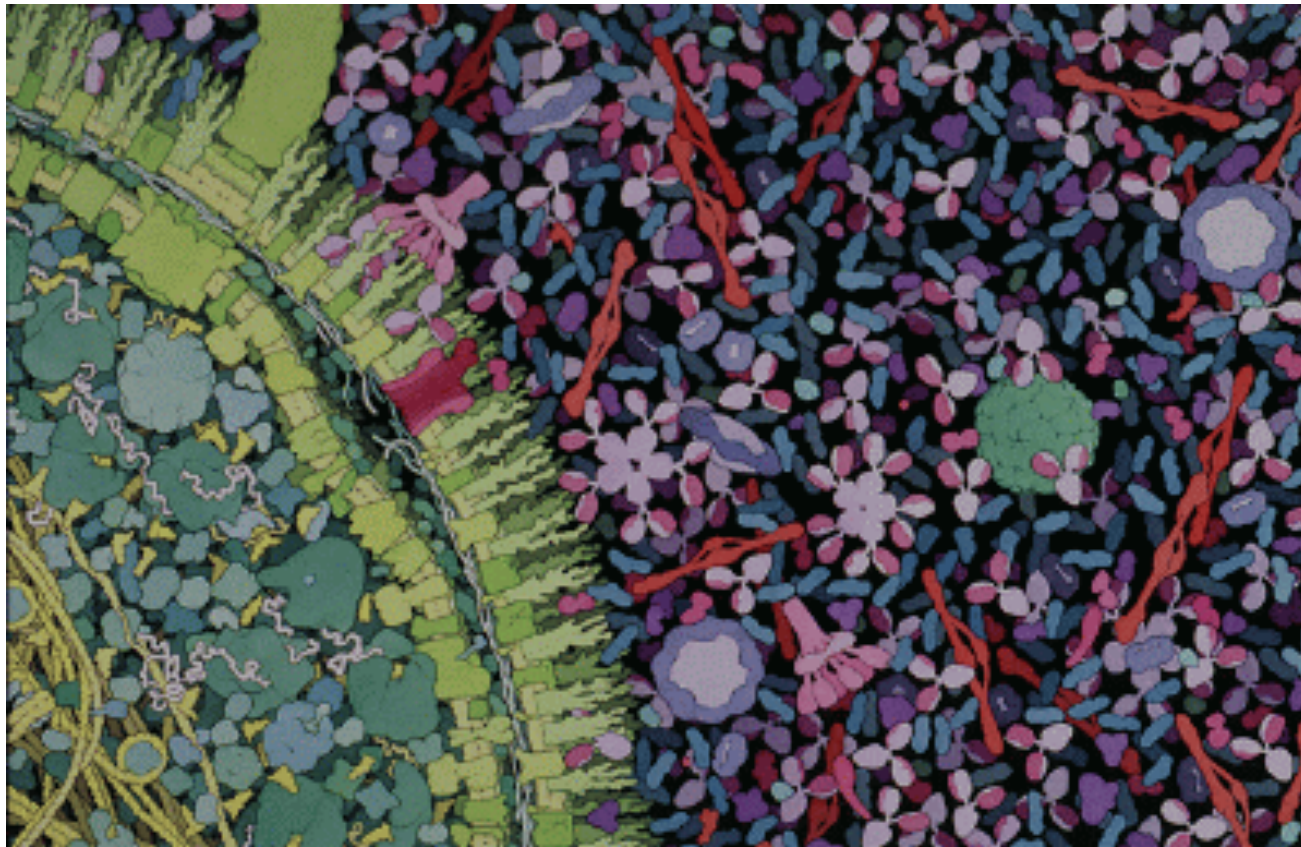
maximal parallel, sequential,
deterministic, stochastic

Properties

- *local evolution rules*
mandatory when you cannot express a global function/relation because the domain of the function/relation is changing in time
- *interaction based approach*
the l.h.s. of a rule specifies a set of elements in *interaction*, the r.h.s. the result of the interaction
- *the phase space is well defined but not well known*
a generative process enumerates the elements but membership-test can be very hard
- *various kind of time evolution* (for the same set of rules)
- *demonstration by induction*
on the rules or on the derivation (e.g. growth function in L system)

How to extend to arbitrary spatial structure?

- Anabaena was « easy » because of the linear uniform structure
- How to handle the complex spatial structure of a cell?



David S. Goodsell

The MGS project

- Language dedicated to the simulation of $(DS)^2$
- Declarative (declarative simulation vs procedural)
- Abstract rewriting of complex spatial structures:
 - Data structure = topological collections
sequence, generalized array, (multi-)set, arbitrary graph, Delaunay triangulation, g-map, ..., cell complexes
 - Control structure = transformation
 - two powerful languages to specify sub-collections (elements in interaction)
 - Various rule application strategies: maximal parallel, asynchronous, stochastic, Gillespie-like, ...

Topological collection: representing the underlying space

Representation of space and structure

– Structure:

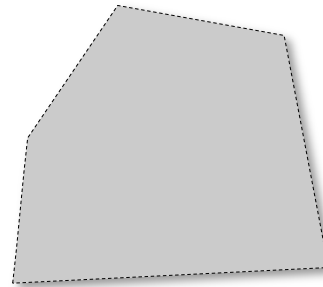
- Collection of *topological cells*



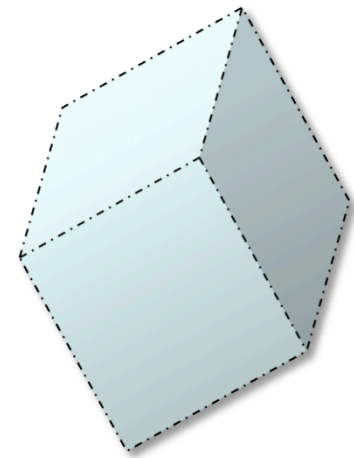
0-cell



1-cell



2-cell



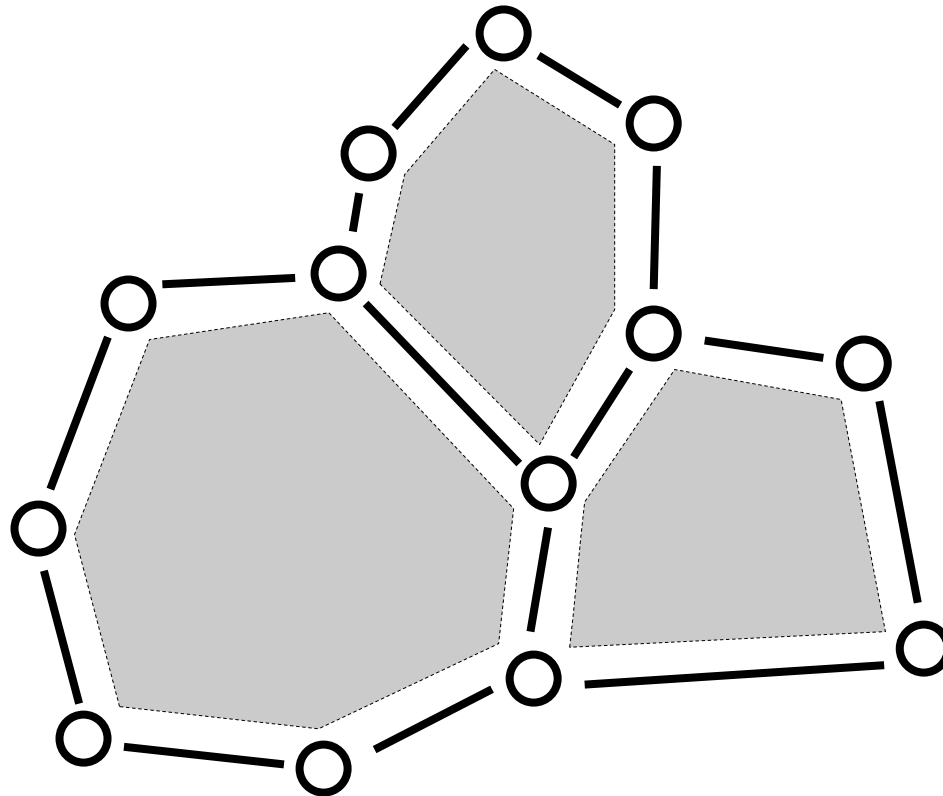
3-cell

Topological collection: representing the underlying space

Representation of space and structure

– Structure:

- Collection of topological cells
- *Incidence relationships*



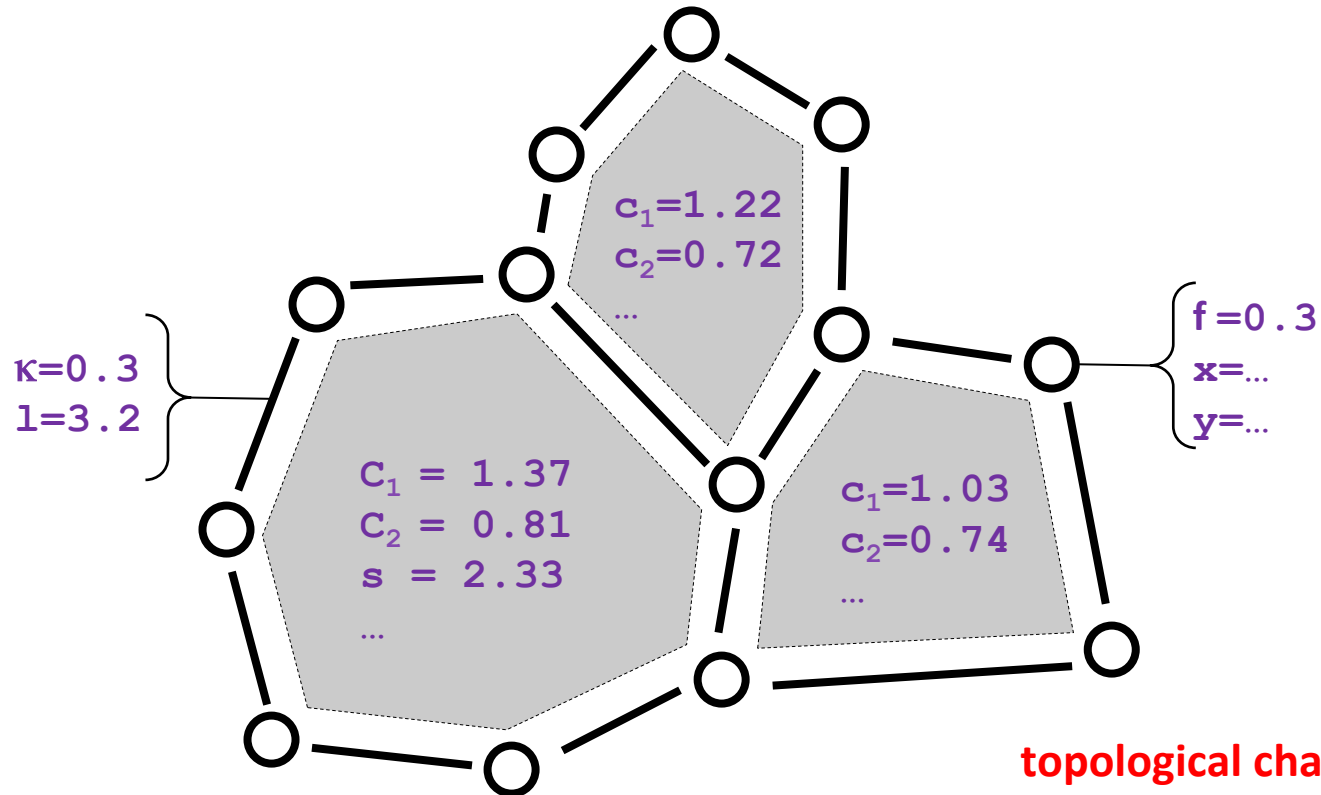
Topological collection: a data-field over topological cells

Representation of space and structure

– Structure:

- Collection of topological cells
- Incidence relationship

– Data : *associating values with topological cells* \approx field in physics



Higher dimensional objects for complex simulations

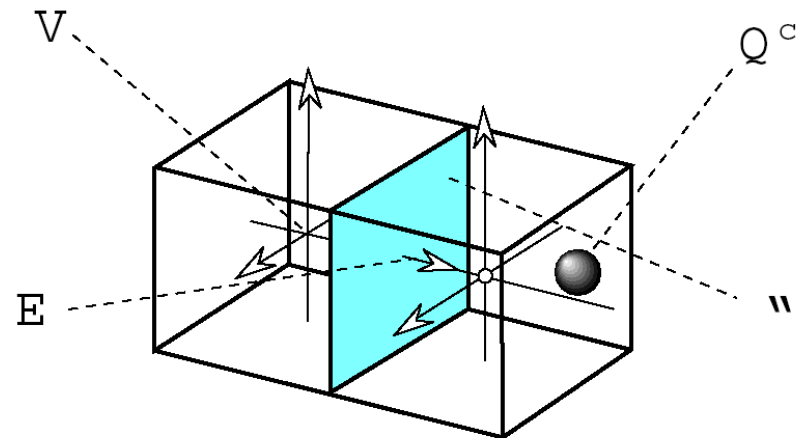
Example of electrostatic Gauss law [Tonti 74]

- Electric charge content ρ : dimension 3
- Electric flux Φ : dimension 2
- Law available on a arbitrary complex domain

$$\phi = \iint w \cdot dS = \frac{Q^c}{\epsilon_0} = \iiint_{(V)} \frac{\rho}{\epsilon_0} d\tau$$

electric field in space:

- V: electric potential (dim 0)
- E: voltage (dim 1)
- w: electric flux (dim 2)
- Qc: electric charge (dim 3)



Topological rewriting = transformation

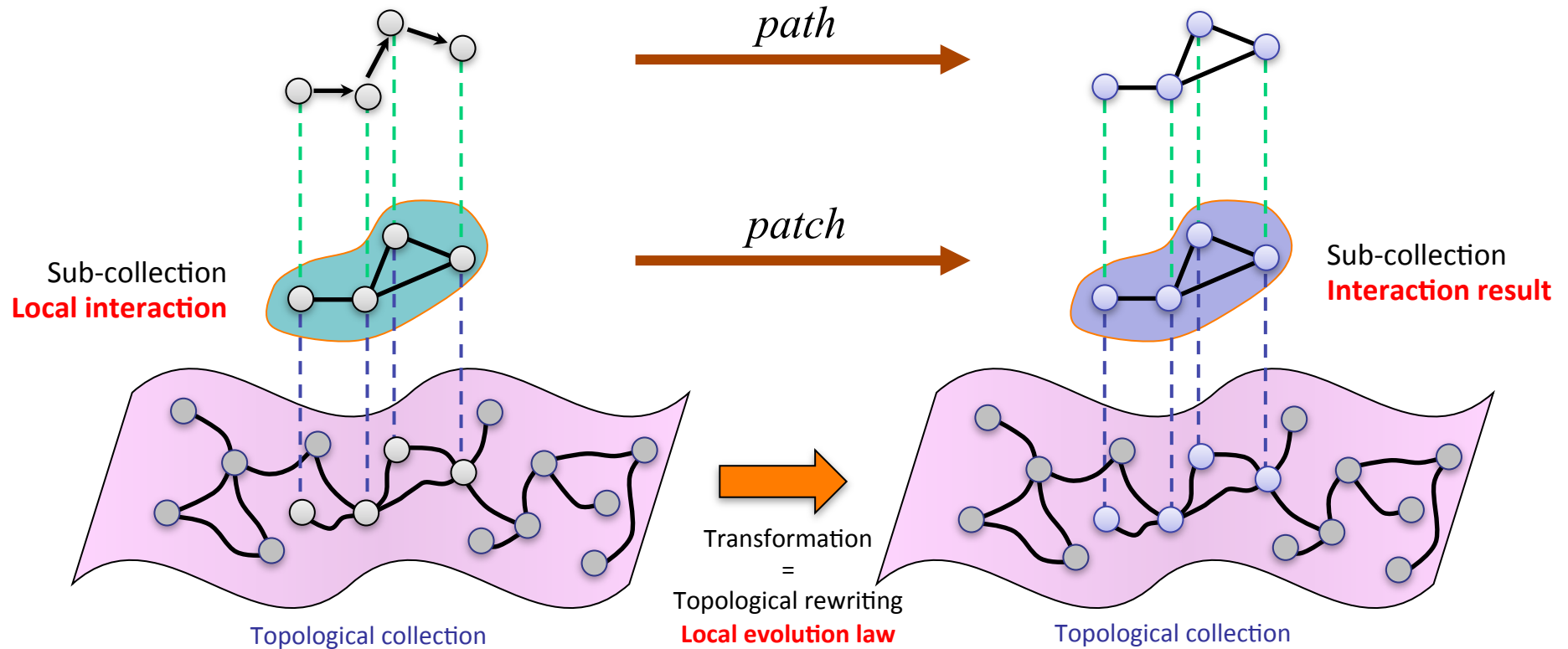
$1 + 2 \rightarrow \dots$ (arithmetic) term rewriting
↙
arithmetic operation

$a . b \rightarrow \dots$ string rewriting (~ L systems)
↙
string concatenation

$2H + O \rightarrow H_2O$ multiset rewriting (~ chemistry)
↙
multiset concatenation (= the chemical soup)

$V_1 \cdot \sigma_1 + V_2 \cdot \sigma_2 \rightarrow \dots$ **topological rewriting (MGS)**
↙
gluing cell in a cell complex

Transformation




Pattern matching : specifying a sub-collection of elements in interaction

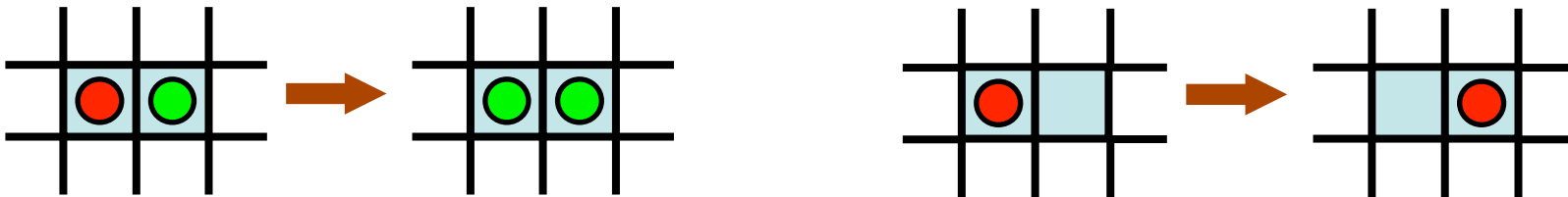
- *Path transformation* (path = sequence of neighbor elements)
 - Concise but limited expressiveness
- *Patch transformation* (arbitrary shape)
 - Longer but higher expressiveness

Example: Diffusion Limited Aggregation (DLA)

- Diffusion: some particles are randomly diffusing; others are **fixed**
- Aggregation: if a **mobile** particle meets a **fixed** one, it stays fixed

```
trans dla = {  
  `mobile , `fixed => `fixed, `fixed ;  
  `mobile , <undef> => <undef>, `mobile  
}
```

 *NEIGHBOR OF*

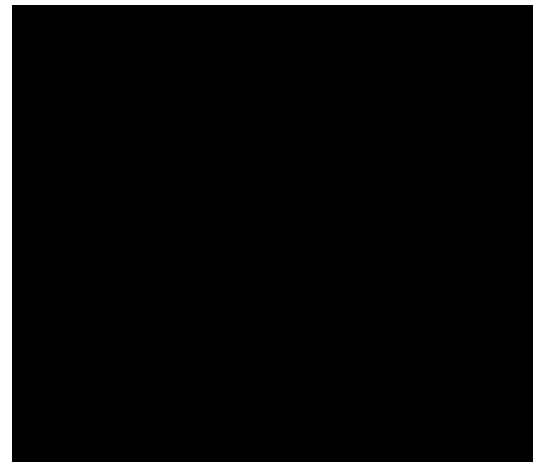
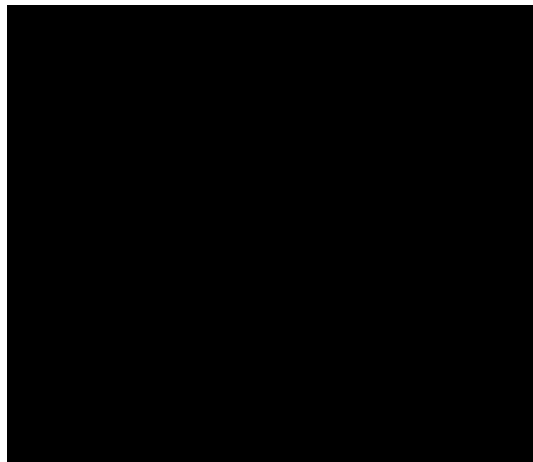


Example: Diffusion Limited Aggregation (DLA)

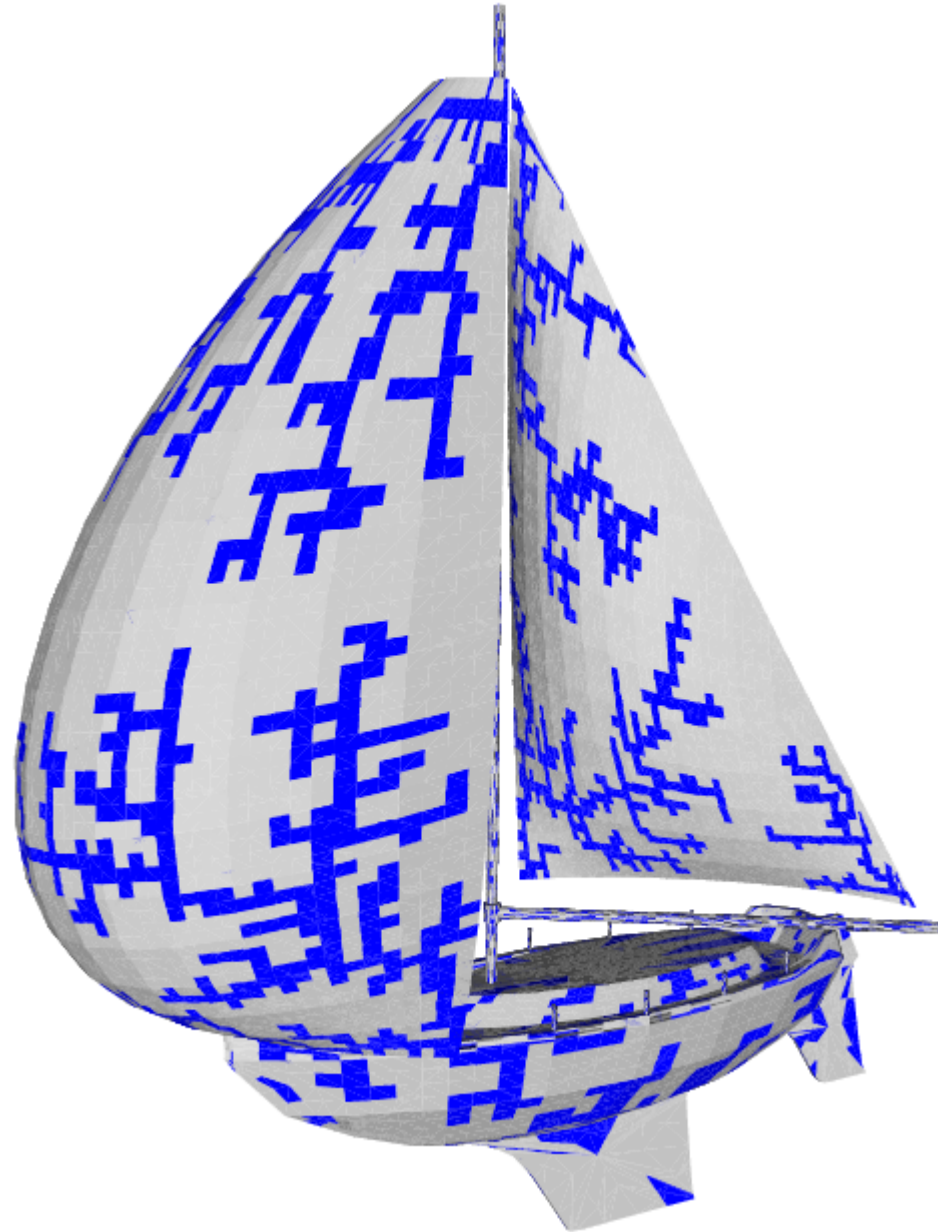
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    `mobile , <undef> => <undef>, `mobile  
}
```

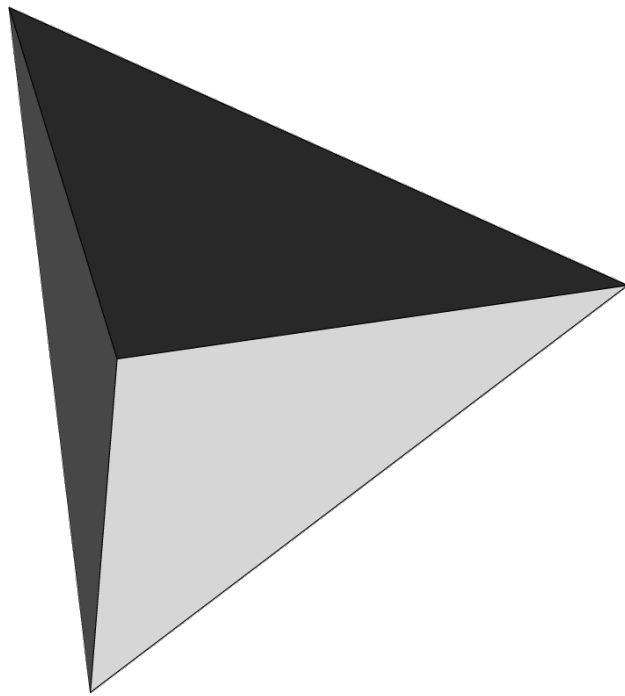
this transformation is an abstract process that can be applied to any kind of space



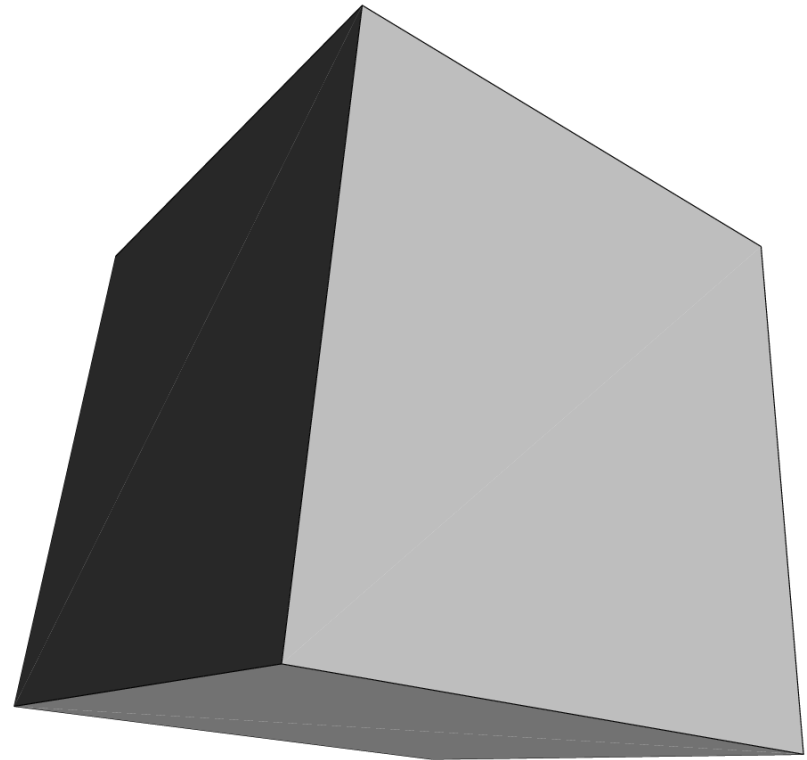
Polytypisme



Fractal construction by carving



Sierpinsky sponge (4 steps)



Menger sponge (2 steps)



The Growth of a Meristem

[PNAS 103(5), 1627-1632, 2006]

Pierre Barbier de Reuille

Mikaël Lucas

Jan Traas

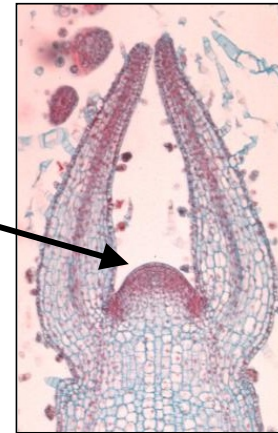
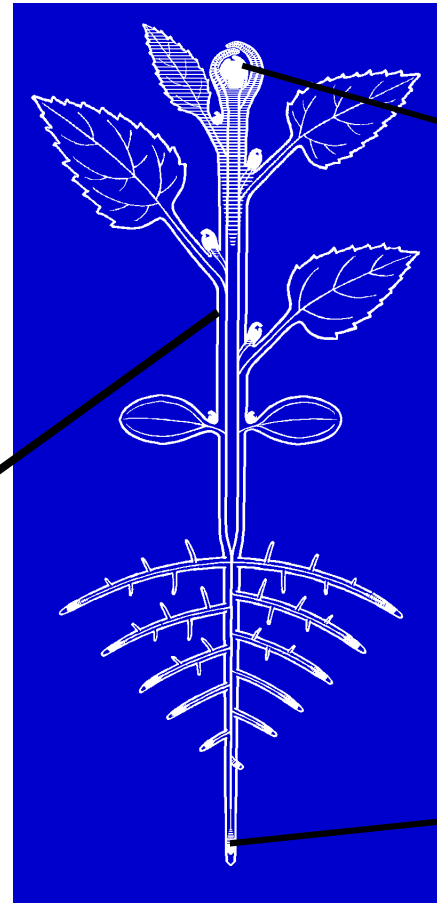
Christophe Godin

CIRAD/INRA/INRIA

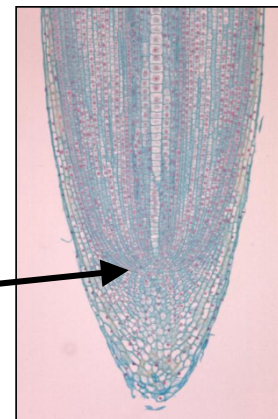


Organs
positioning
at the shoot
apex

Cambium

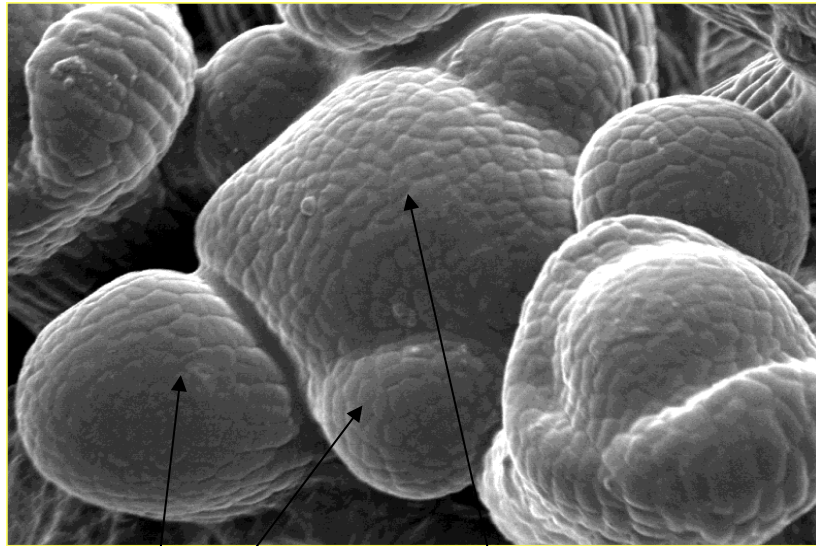


Shoot
apical
meristem



Root apical
meristem

A shoot apical meristem



Primordia

Central zone

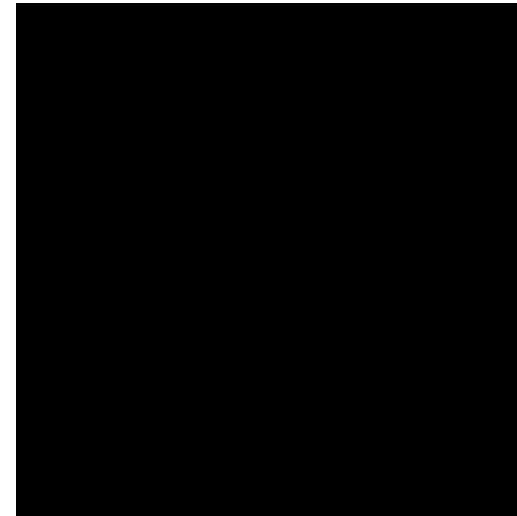
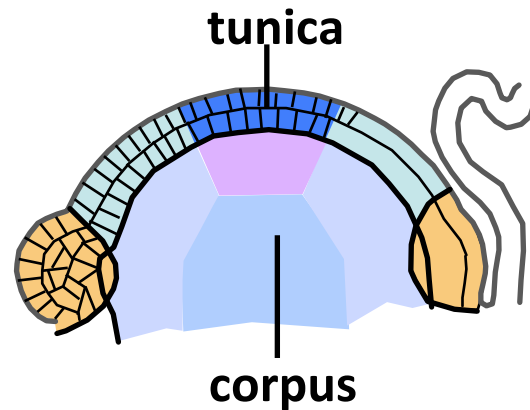


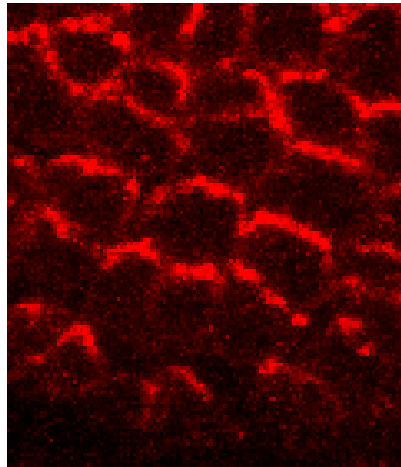
Image sequence showing cell division patterns via membrane-bound PIN1, in Shoot Apical Meristem (SAM), nearby floral meristems, and the boundaries between them (M. Heisler).

<http://computableplant.ics.uci.edu/> (E. Mjølness)

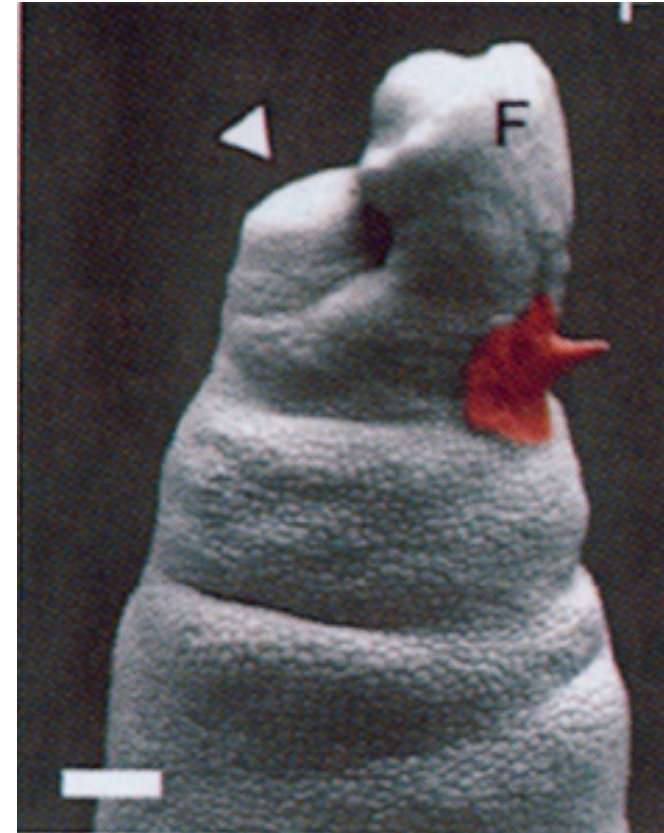


Active transport of auxine

wild
type

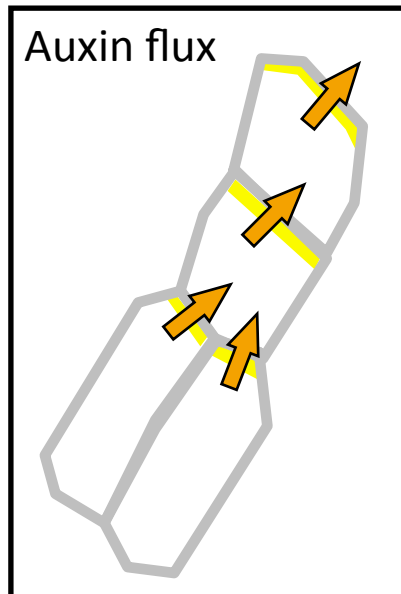


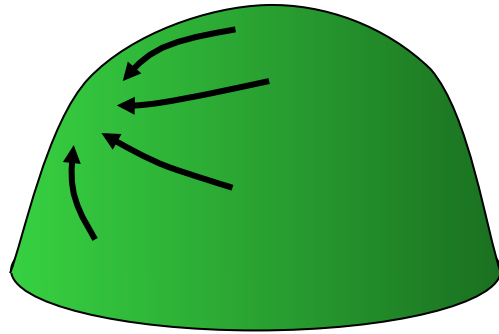
Immunolabelling of
PIN-FORMED1 protein



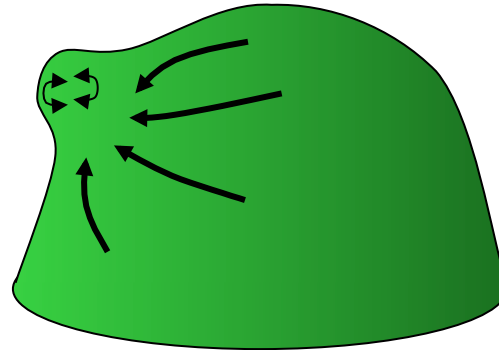
high concentration of
auxine induces organ initiation

pin-1
mutant

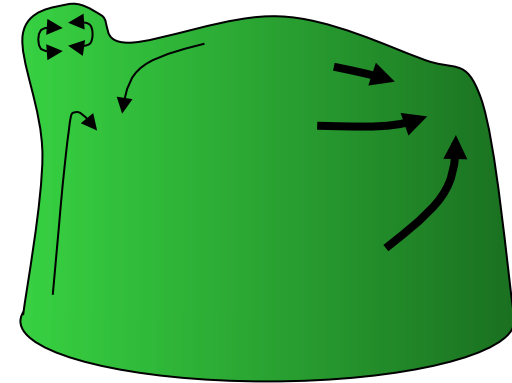




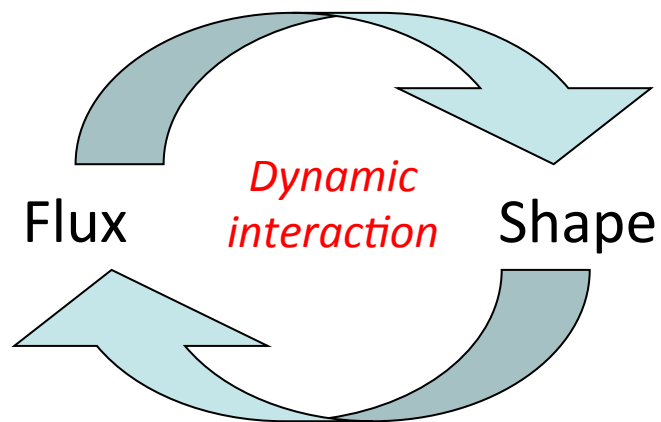
flux...



changes form...



which changes flux...



Model

- *Cell internal state and processes*

capacity of division, spring relaxed length,
primordium/center,

concentration of auxin (inhibitor), saturation, auxin
degradation / evacuation, promotion to primordium,
“pump magnetism”

- *Movement* (due to cell growth)

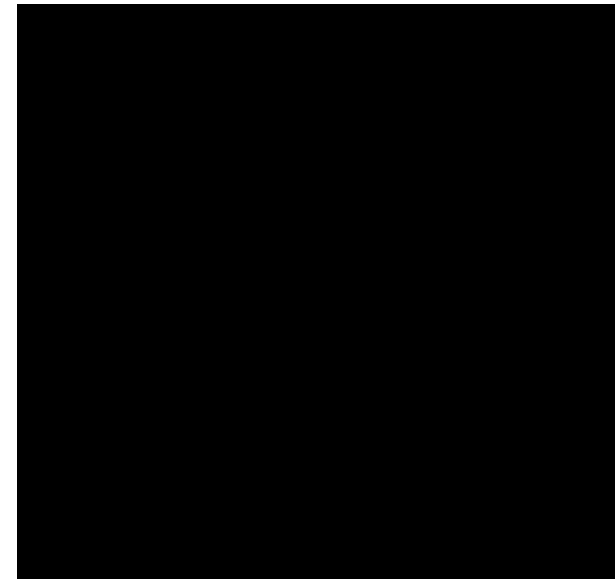
- *Growth*: increase of spring relaxed length

- *Division*: when size > threshold

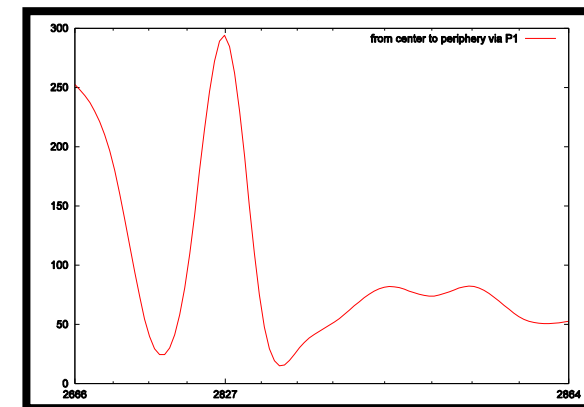
- *Cell interaction*

Passive diffusion of auxin, active pumping of auxin

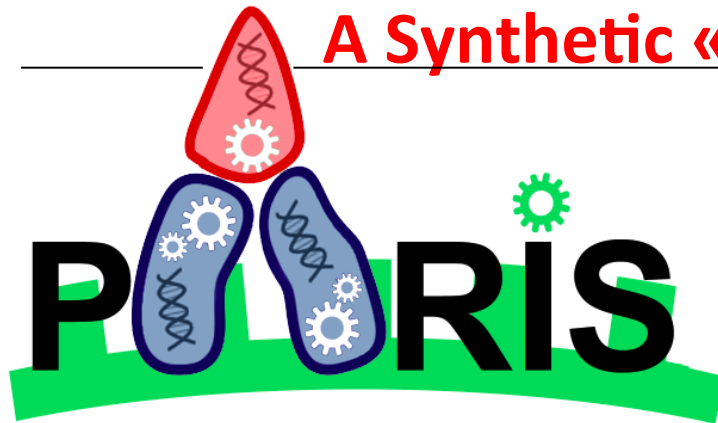
```
trans Auxin = {  
  x, y / pump(x, y)  
  → {x.auxin -= δ}, {y.auxin += δ}  
}
```



P. Barbier de Reuille



Auxin level



A Synthetic « Multicellular Bacterium »

Synthetic Biology is

- A) the design and construction of new biological parts, devices, and systems, and
- B) the re-design of existing, natural biological systems for useful purposes.

(Español)

Synthetic Biology Logo

- Home
- About
- Conferences
- Labs
- Courses
- Resources
- FAQ

Community news

- IET Synthetic Biology first issue includes iGEM 2006
- Synthetic Biology 3.0 Zurich proceedings. Download [here](#).
- BioBricks Foundation first [membership drive](#).
- [Synthetic Biology: Caught between Property Rights, the Public Domain, and the Commons](#)
- US HSPD-18. Guidance on openness and international transparency in biodefense work still needed.

Resources

- [Press articles](#)
- [Publications: citelike, connotes, PubMed](#)

Registry of Standard Biological Parts

Massachusetts Institute of Technology

Parts Catalog Click on the icons below to see parts by category. [more...](#)

Regulatory Reporter Inverter RNA Protein Generator Tag Parts List Deleted Cell Strain

RBS CDS Terminator Composite PROJECTS Cell-Cell Signalling Measurement Primer Other Plasmid T 7

Web Site Update

Registry web site changes in support of iGEM 2005 are under way.

- The new account manager is in place with better support for groups, group leaders, and editing.
- Part categories are becoming more detailed, see the signalling category for an example.
- The new part viewer and editor is on the way soon.
- New Rolling Assembly tool under development.

Educational Programs

The Registry supports design classes where students make simple systems from standard, interchangeable biological parts and operate them in living cells.

Thirteen schools are participating in the 2005 Intercollegiate Genetically Engineered Machine competition (iGEM 2005). The schools are: Berkeley, Caltech, Cambridge, Davidson, ETH Zurich, Harvard, MIT, Oklahoma, Penn State, Princeton, Toronto, UCSF, and UT Austin.

Employment

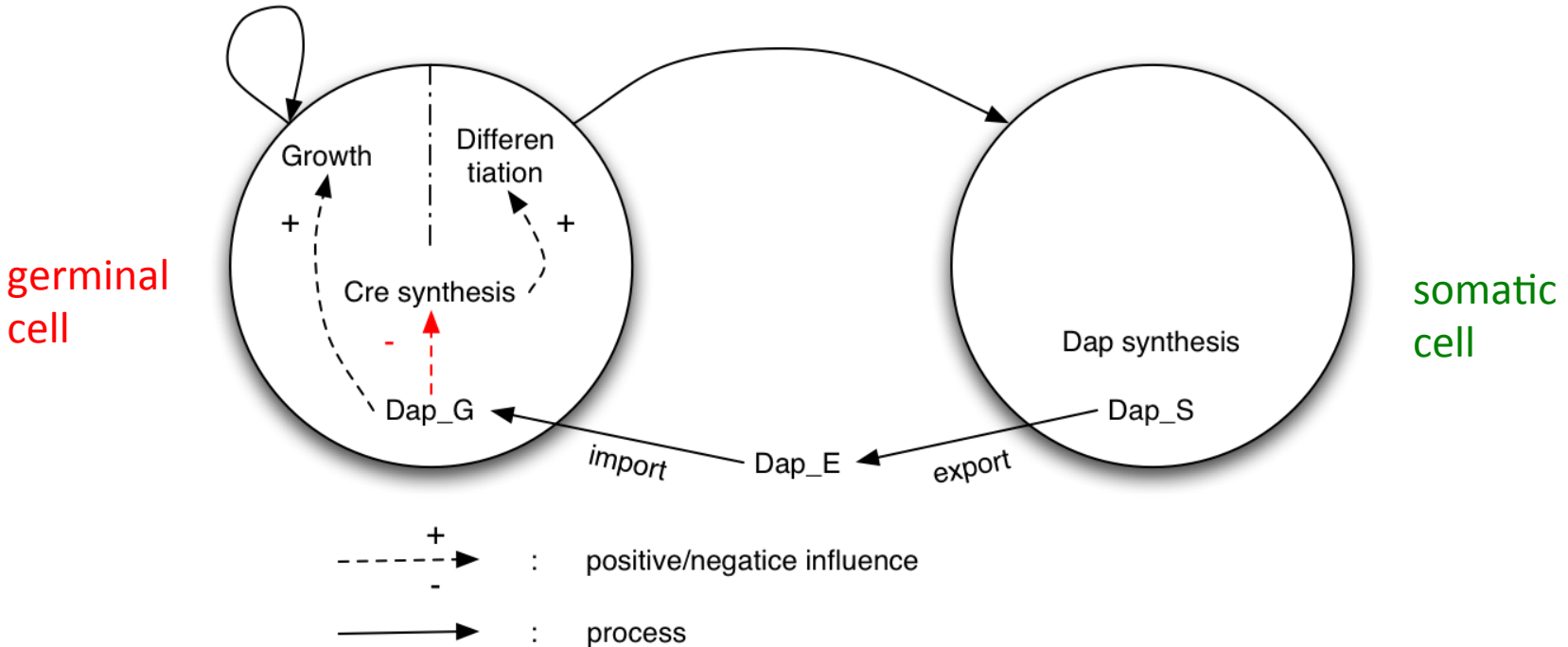
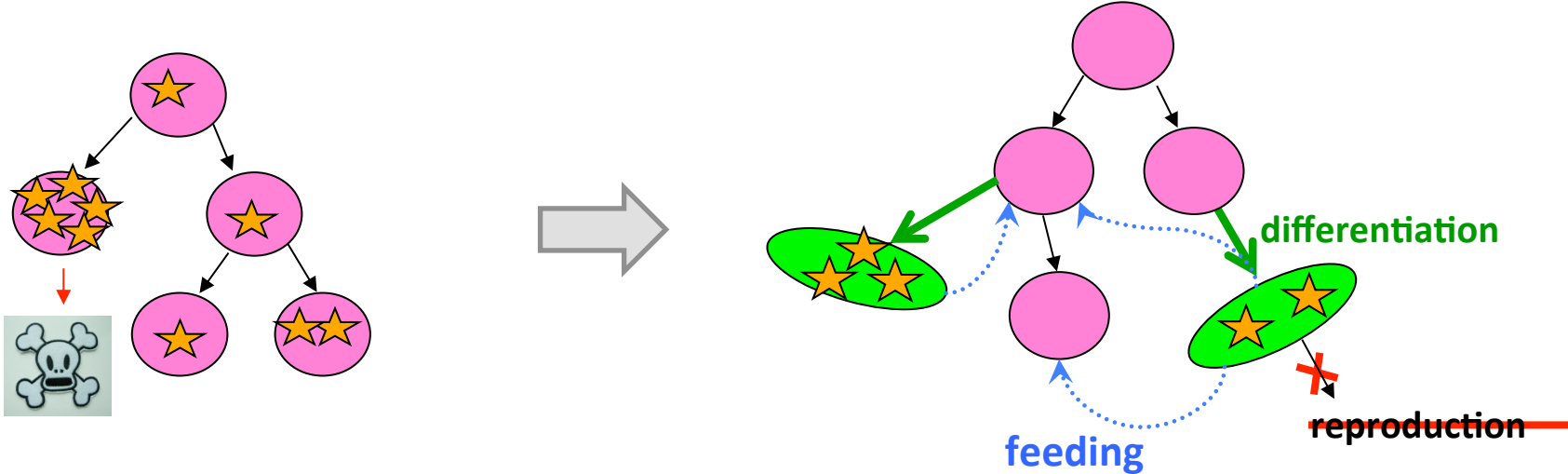
The Registry is looking for full-time Technical Assistants and Web Programmers. Please contact Staffing Services at MIT for details: [Technical Assistant](#), [Web Programmer](#).

Production at rosaling - 4.4.05

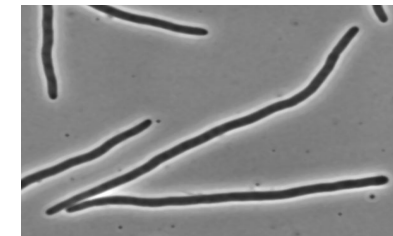
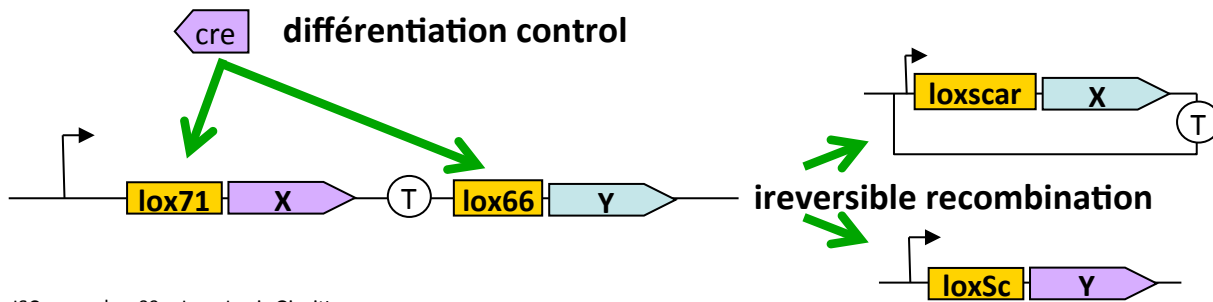
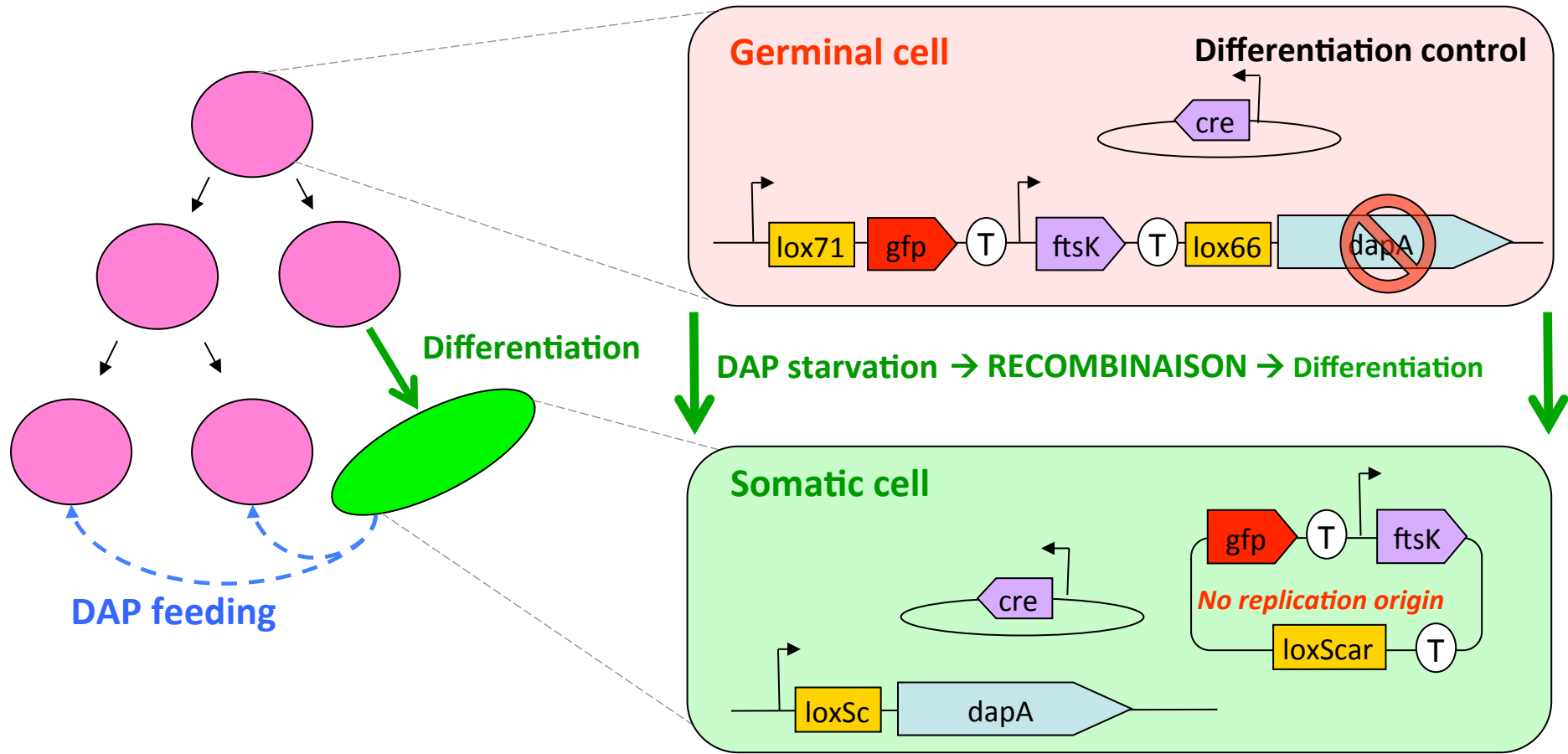


David Bikard, Thomas Landrain, David Puyraimond, Eimad Shotar, Gilles Vieira, Aurélien Rizk, David Guegan, Nicolas Chiaruttini, Thomas Clozel, Thomas Landrain

The Paris iGEM project: a « multicellular bacteria » to decouple growth and transgene expression



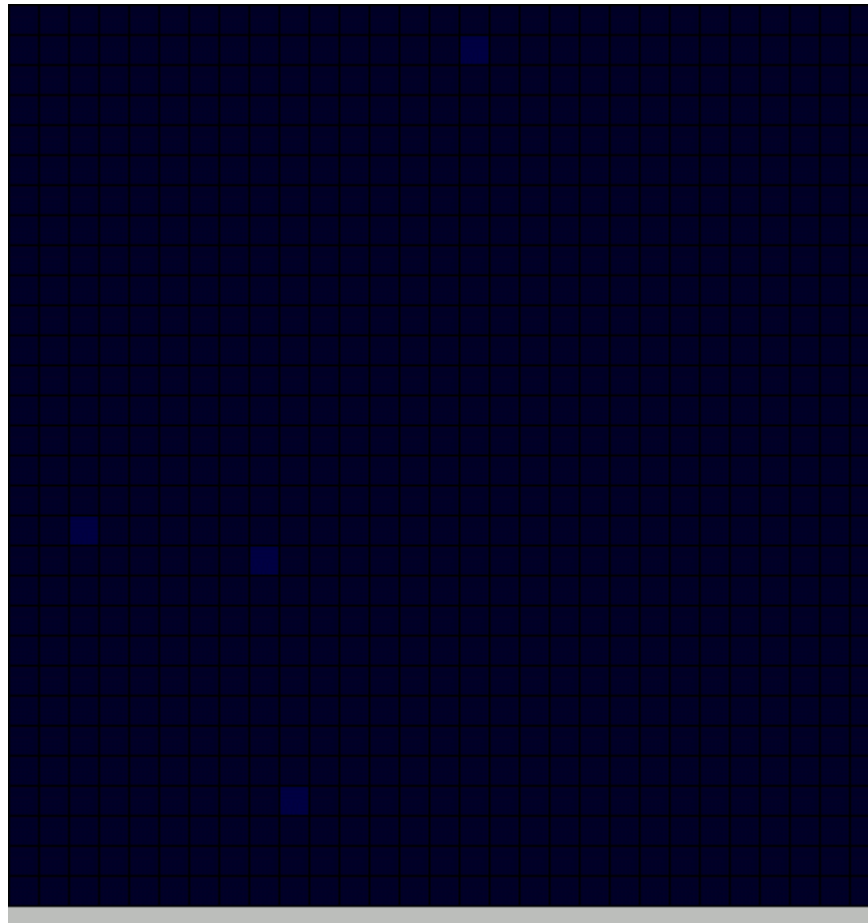
Implementation using BioBricks



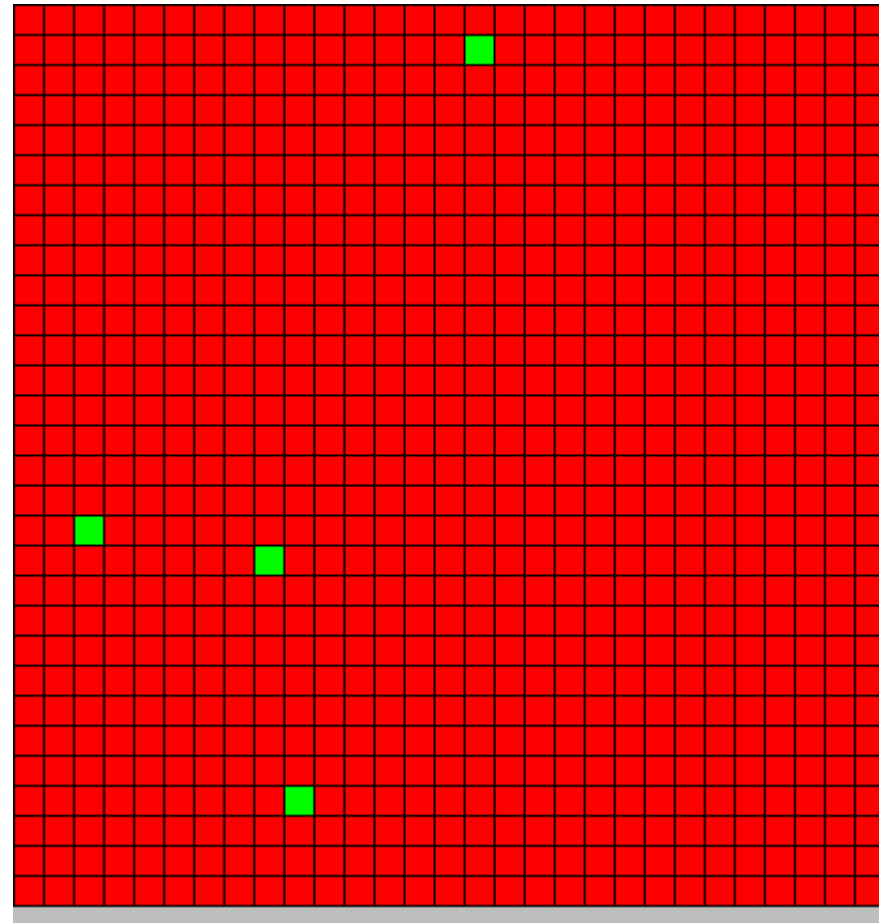
ftsK
needed for
cellular
division

Proof of Concept: Simulation to answer 4 questions

- **How does differentiation induces feeding?** (proof of concept)
cellular automaton (in MGS)



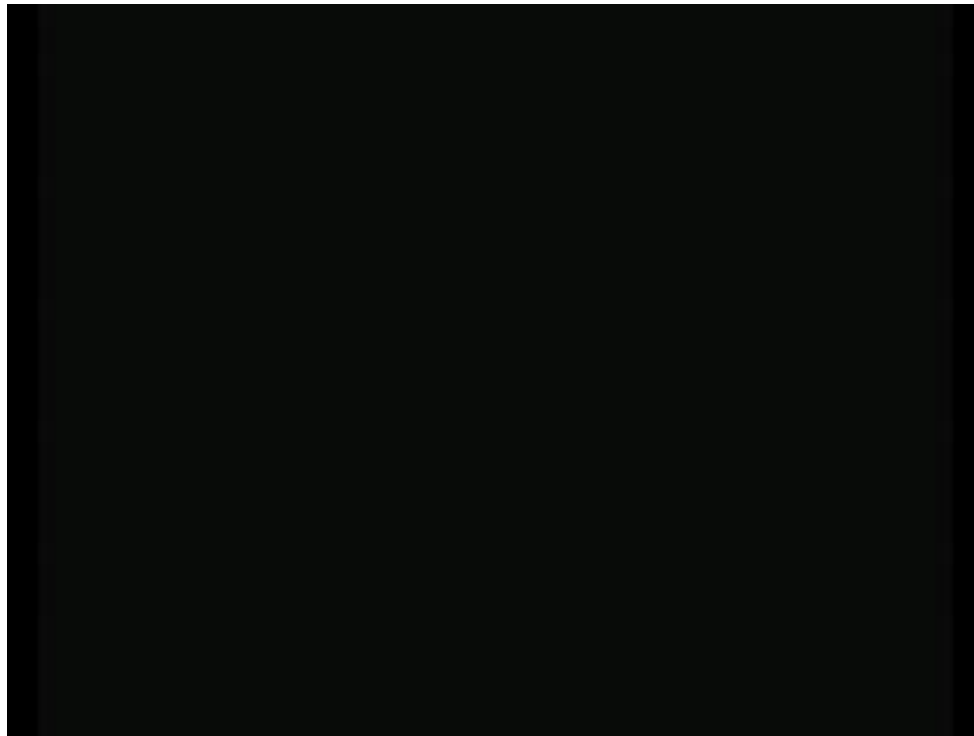
diffusion of DAP



somatic and germ cell

Proof of Concept: Simulation to answer 4 questions

- How does differentiation induces feeding? (proof of concept)
cellular automaton (in MGS)
- How do spatial organization and distribution evolve?
agents based system (in MGS)

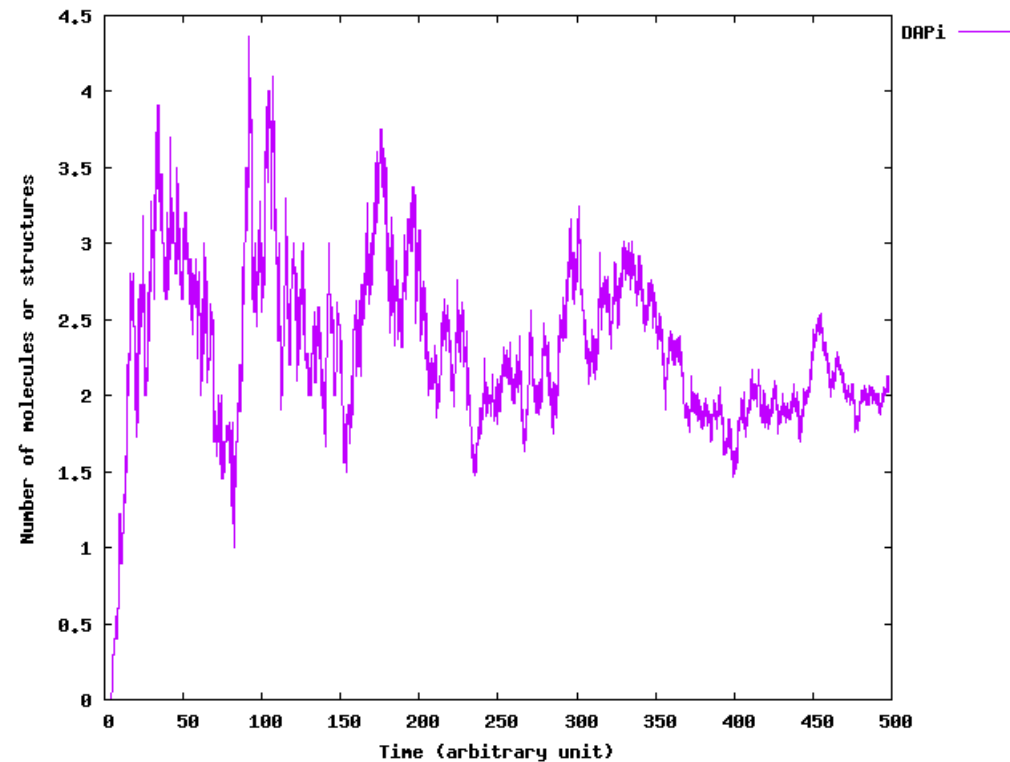
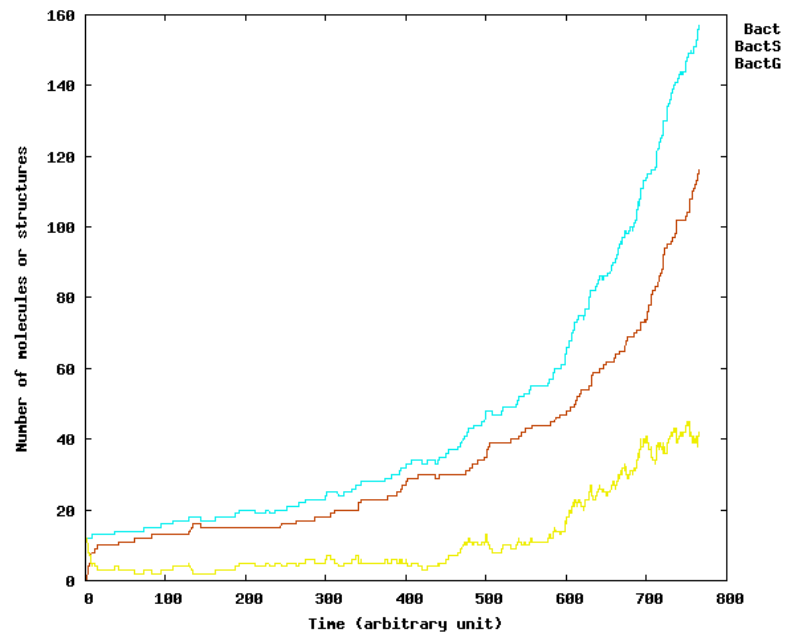


Proof of Concept: Simulation to answer 4 questions

- How does differentiation induces feeding? (proof of concept)
cellular automaton (in MGS)
- How do spatial organization and distribution evolve?
agents based system (in MGS)
- **How robust and tunable is the model?**
ODE kinetics (matlab)

Proof of Concept: Simulation to answer 4 questions

- How does differentiation induces feeding? (proof of concept)
cellular automaton (in MGS)
- How do spatial organization and distribution evolve?
agents based system (in MGS)
- How robust and tunable is the model?
ODE kinetics
- **How sensitive is the system to noise?**
Gillespie based simulation (in MGS)



MGS drawbacks and successes

Success

- Polytypisme is good
- Patterns/rules are expressive and usually concise
- Clean semantics

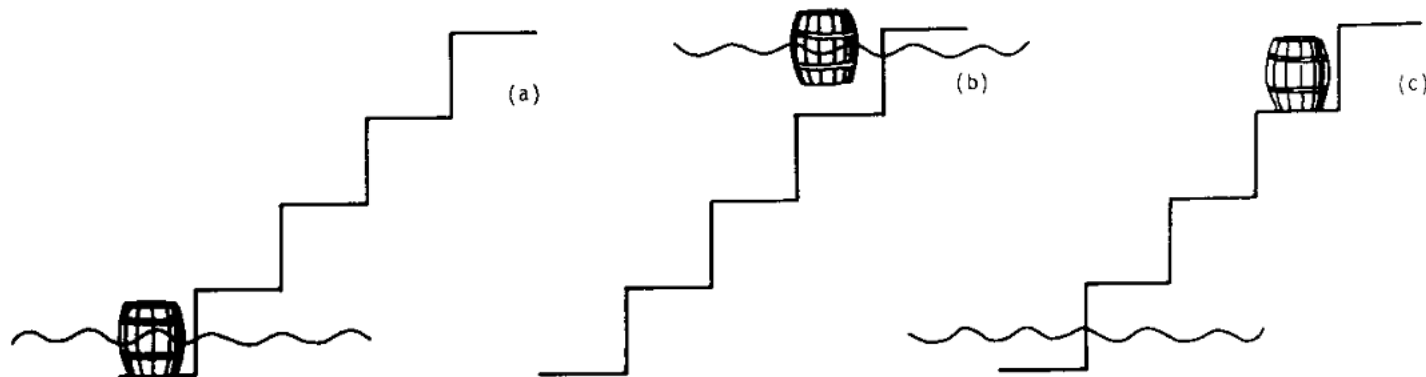
Shortcomings

- Rules may be heavy (e.g. 100 variables for the fractal sponge)
graphical drawing of rules
look for better notations (e.g. path pattern)
- Efficiency
well...
- Implicit methods (solvers) are hairy
use explicit ones

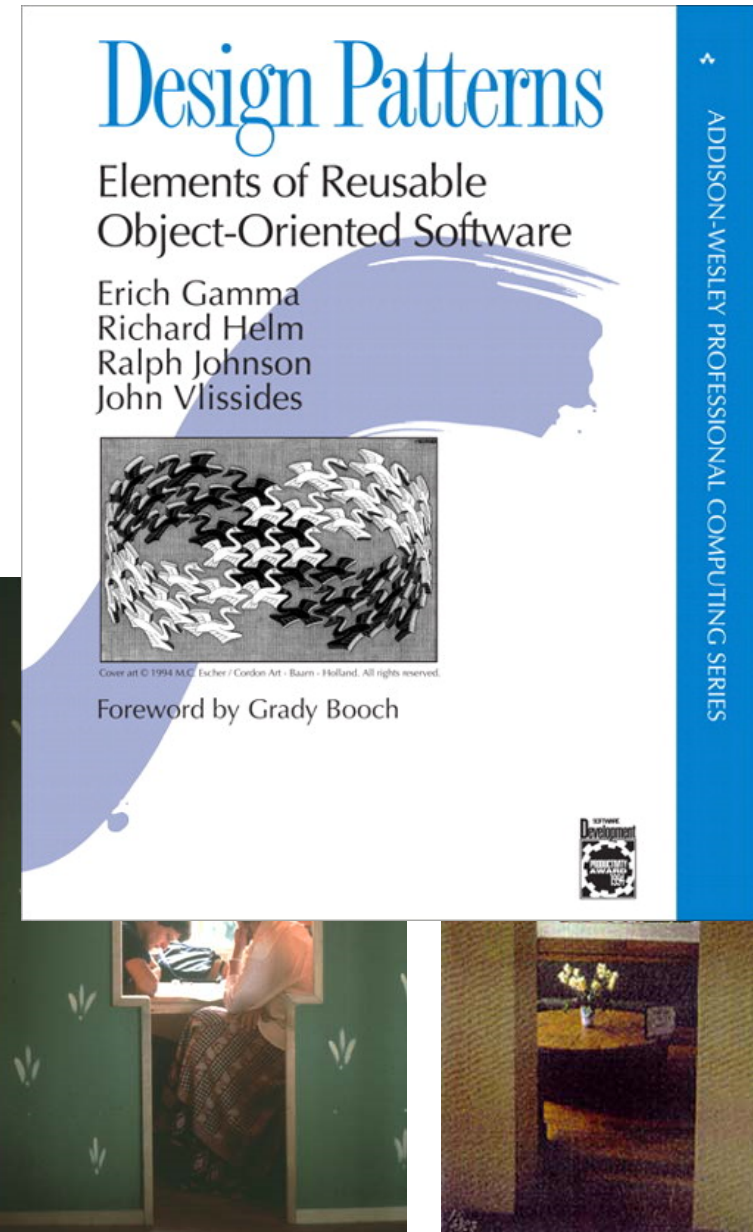
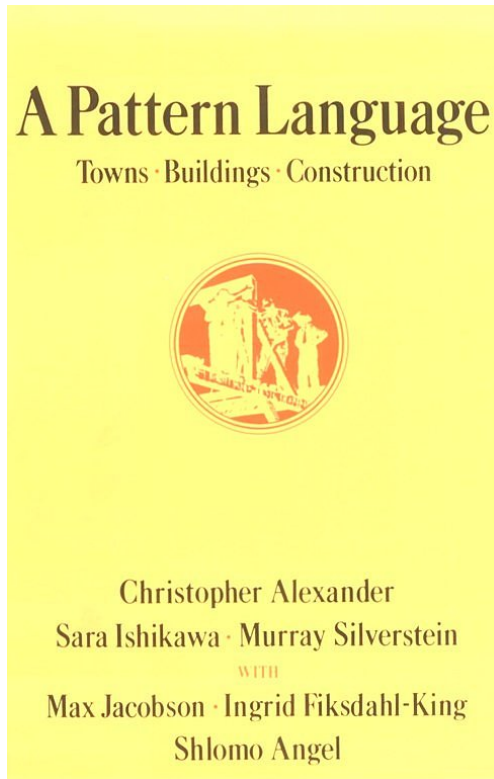
The need of design pattern

Multiple examples during the workshop

- Cassette, module, function, device, mechanism, gradient, amplification, diffusion, transport, diffusion-reaction, polarization...
→ abstracting biological processes
- Universal Mechanisms of Animal Development
(basic machinery of development is conserved amongst species, homologous proteins, etc.)
- “Biochemical specification” vs. “causal explication”



Design patterns



An analogy

« sort »

« **Function** »

« limb construction »



bubble-sort

algorithms

- establish positional information PI
- differentiate cell wrt. PI
- ...



iterate over elements

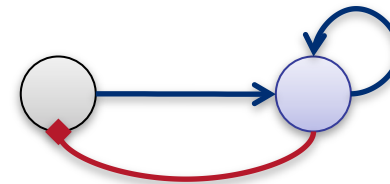
design patterns

space-dependant activation of genes



```
for (i = 0; i < n; i++)
```

implementation



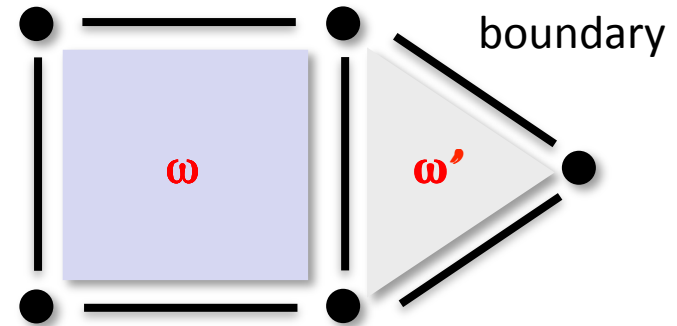
...

Purposes:

- Pedagogical
- Heuristic :
 - auto-stabilizing systems
 - resources consumptions (memory, time, energy)
 - ...
- Technical: compose and reuse models: towards an algebraic (relational) approach to biological processes

Example: (some special) Transformations as Cochains

- The Boundary Operator ∂
 - Starting point of the elaboration of a discrete diff. calculus
 - Transport of data *from cells to their faces*



- Cochains notation
The boundary operator is a cochain

$$\partial = \sum_{\sigma \in \mathcal{K}} \partial_{\sigma} \cdot \sigma \quad \text{with} \quad \forall \sigma \in \mathcal{K}, \partial_{\sigma}(g) = \sum_{\tau < \sigma} o_{\sigma\tau}(g) \cdot \tau$$

- MGS notation

$$\text{trans Boundary} = \{ \text{x} \Rightarrow \text{CofacesFold}(\text{fun } y \text{ acc} \rightarrow o_{\sim y \sim x}(y) +_G \text{acc}, 0_G, \hat{x}) \}$$

Transformation as Cochains

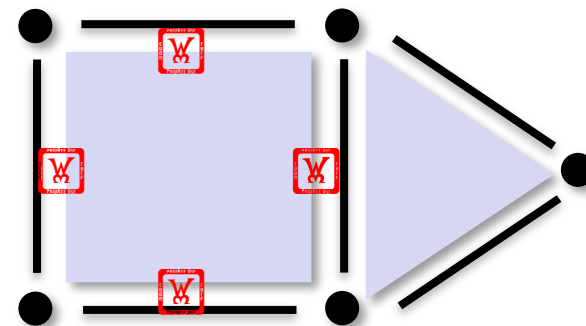
- Derivative Operator \mathbf{d}
 - Defined w.r.t. the discrete Stokes' Theorem

$$[\mathbf{d}T, c] = [T, \partial c]$$

- Cochains Notation
 - One can show that the derivative verifies

$$\mathbf{d} = \sum_{\tau \in \mathcal{K}} \mathbf{d}_{\tau} \cdot \tau \quad \text{with} \quad \forall \tau \in \mathcal{K}, \mathbf{d}_{\tau}(f) = \sum_{\tau < \sigma} (f \circ o_{\sigma\tau}) \cdot \sigma$$

- MGS Notation
 - We directly use the Stokes' Theorem



let Derivative $T = \text{fun } c \rightarrow T \text{ (Boundary } c)$

Transformation as Cochains

- Illustrative example : the Laplacian Operator Δ

- The Laplacian in terms of \mathbb{W} and \mathbf{d} [Desbrun *et al.*, 2006]

$$\Delta = \delta \mathbf{d} + \mathbf{d} \delta \quad \text{where } \delta = (-1)^{n(k-1)+1} \star \mathbf{d} \star$$

- MGS notation

Big assumption: the Hodge star \mathbb{W} is replaced by the co-derivative \mathbf{d}^{co}
(= uniform geometry)

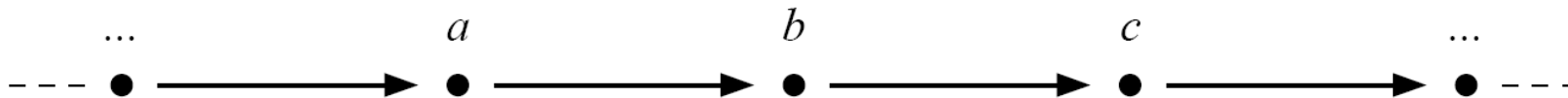
```
let Laplacian T =
  let Sg T' c' =
    T'(trans { x => -1**((dim c')*((dim ^x)-1)+1)*x }(c'))
  in
  fun c -> Derivative(Sg(Derivativeco(T)))(c)
    + Sg(Derivativeco(Derivative(T)))(c)
```

Transformation as Cochains

- Illustrative example : the Laplacian Operator 

– Corresponding Data Transport (case of dimension 1)

- Dimension 1: $\Delta = d^{co}d$
- Stokes' Theorem: $\text{équivalence with } \partial \circ \partial^{co}$

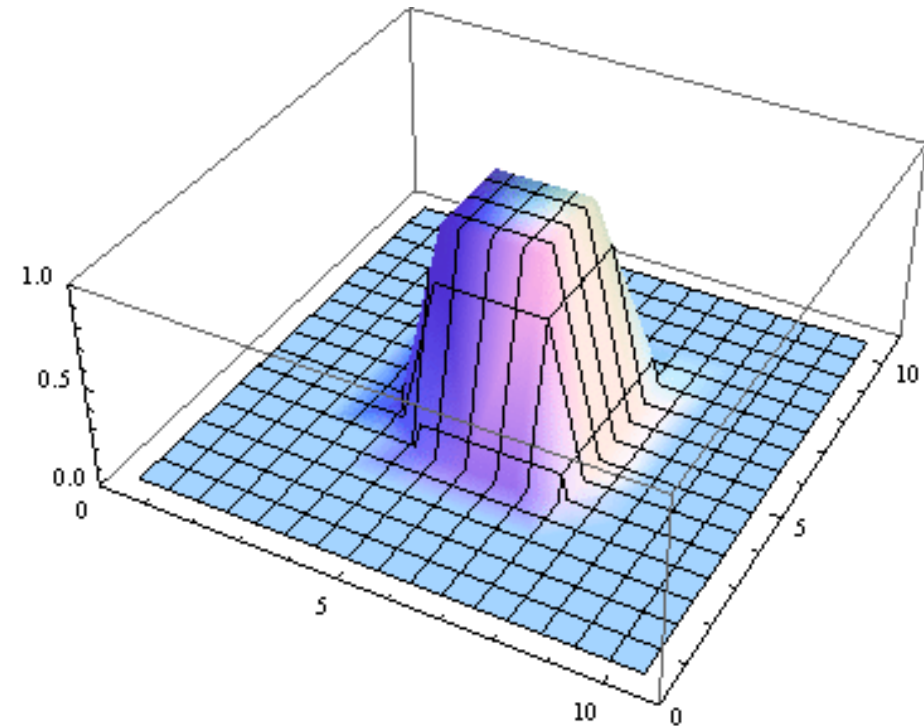
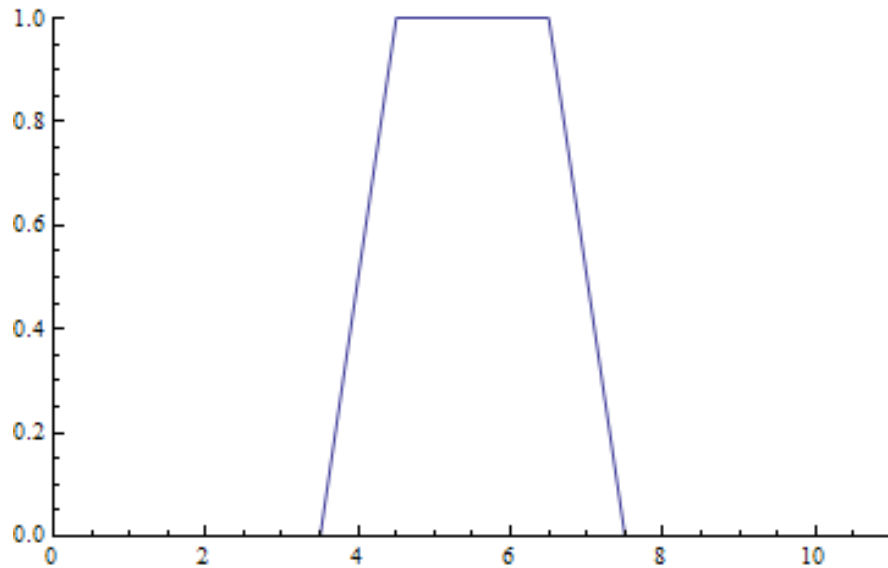


Transformation as Cochains

- Illustrative example : the Laplacian Operator Δ
 - Simulation of diffusion

$$\frac{\partial u}{\partial t} = D\Delta u$$

```
fun diffusion[D,orient] (u) =  
  u + D*Laplacian[orient=orient] (Id) (u) ;;
```



Thanks

ibisc



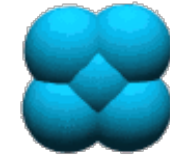
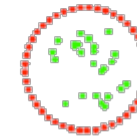
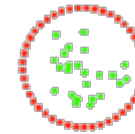
<http://mgs.spatial-computing.org>

- Antoine Spicher
- Olivier Michel
- PhD and other students

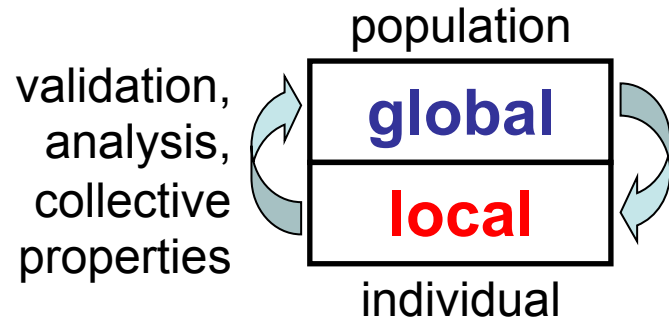
J. Cohen, P. Barbier de Reuille,
E. Delsinne, V. Larue, F. Letierce, B. Calvez,
F. Thonerieux, D. Boussié *and the others...*

- Collaborations

- A. Lesne (IHES, stochastic simulation)
- P. Prusinkiewicz (Calgary, declarative modeling)
- P. Barbier de Reuille (meristeme model)
- C. Godin (CIRAD, biological modeling)
- H. Berry (LRI, stochastic simulation)
- G. Malcolm (Liverpool, rewriting)
- J.-P. Banâtre (IRISA, programming)
- F. Delaplace (IBISC, synthetic biology)
- P. Dittrich (Jena, chemical organization)
- E. Goubault (CEA, topological formalization)
- F. Gruau (U. PXI, language and hardware)
- P. Liehnard (Poitiers, CAD, Gmap and quasi-manifold)

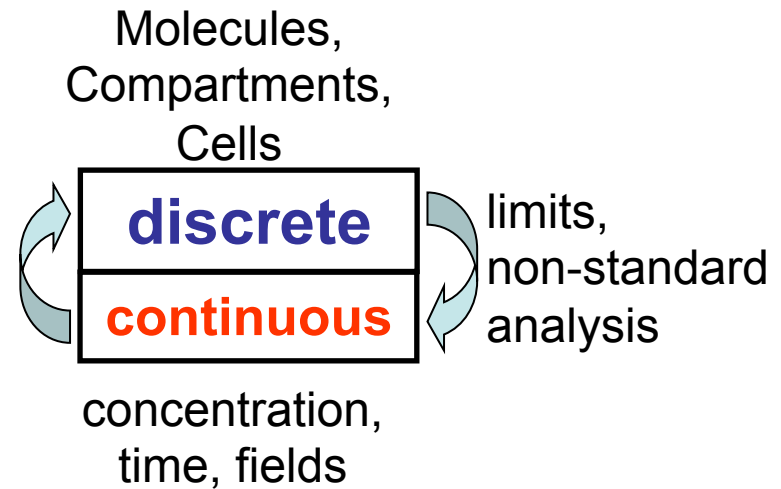


Three challenges and some tools



compilation,
engineered emergence

approximation,
numerical resolution,
partitioning



DNA
cellular
machinery

(...) An invagination of a germ layer may be explained on a basis of a pressure difference between the two surfaces (or sides) or by cell movements, and so forth. This can be considered as an 'explanation' until we ask about the origin of pressure differences, or the mechanisms involved in cell movement, etc. However, questions of this kind become trivial when a larger process, rather than its individual components becomes the main problem. Suppose for a moment that each element in the succession A, a, C... can be explained separately, e.g. A as a swelling, a as a chemical reaction, etc. Interesting as they may be, these explanations are of subordinate importance when related to the main question: Why indeed is a regular (emphasis added) succession of these obviously quite different processes taking place at all? Most biological problems are of this kind and all of embryogenesis is just such a single problem. Here we require a peculiar or, maybe, original explanatory principle... A process may become accessible to explanation only insofar as one can succeed in substituting [understanding of] a purely phenomenological multiplicity and diversity of events [for understanding] of a less diverse and less arbitrarily created picture correctly reflecting reality. The main aim of such a construction would be as follows. The entire process should be accessible for analysis into a finite, not very large number of stages, each stage being represented as a monotonic function of some definite initial conditions and a single variable such as time, or distance, etc. If this cannot be realized, we consider a given set of events as scientifically inaccessible. On the other hand, even a partial success of such an enterprise is an obvious step forward."

(Gurwitsch, 1944)

cited by Belousov in "Life of Alexander G. Gurwitsch and his relevant contribution to the theory of morphogenetic fields", *Int. J. Dev. Biol.* 41, 771-779 (1997)