Embryomorphic Engineering:
How to Design Hyper-Distributed Architectures Capable of Autonomous Segmentation, Rescaling and Shaping

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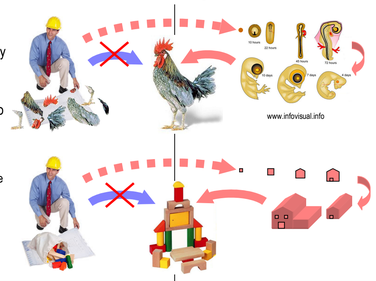
ABSTRACT

Exploding growth in computational systems forces us to gradually replace rigid design and control with decentralization and autonomy. Information technologies will progress by, instead, "meta-designing" mechanisms of system self-assembly, self-regulation and evolution. Nature offers a great variety of efficient complex systems, in which numerous small elements form large-scale, adaptive patterns. The new engineering challenge is to recreate this self-organization and let it freely generate innovative designs. This work presents an original model of artificial system growth inspired by embryogenesis. A virtual organism is a lattice of cells that proliferate, migrate and self-pattern into differentiated domains. Each cell's fate is guided by an internal gene regulatory network. ***Embryomorphic engineering*** emphasizes hyperdistributed architectures and their development as a prerequisite of evolutionary design.

1. DESIGNING COMPLEXITY

Rethinking the dogma of engineering

- instead of a centralized, heteronomous act of creation, take a "step back" and set generic conditions under which systems can be autonomous, i.e., self-assemble, self-regulate and evolve
- artificial systems ***are built*** exogenously, while biological organisms ***grow*** endogenously
- can we shift the paradigm, with inspiration from biology, and "***meta-design***" systems to grow and evolve?
- natural complex adaptive systems, biological or social, could become a new and powerful source of inspiration for future IT in its transition toward autonomy
- "emergent engineering" will be less about direct design and more about ***developmental*** and ***evolutionary*** meta-design
- it will also stress the importance of constituting fundamental laws of development and ***developmental variations*** before these variations can even be selected upon in the evolutionary stage
- it is conjectured that fine-grain, hyperdistributed systems will be uniquely able to provide the required "solution-rich" space for successful evolution by selection → See 7.



systems design	systems "meta-design"
heteronomous order	autonomous order
centralized control	decentralized control
manual, extensional design	automated, intentional design
engineer as a micromanager	engineer as a lawmaker
rigidly placed components	allowing fuzzy self-placement
tightly optimized systems	hyperdistributed & redundant systems
sensitive to part failures	insensitive to part failures
need to control	prepare to adapt and self-regulate
need to redesign	prepare to learn and evolve

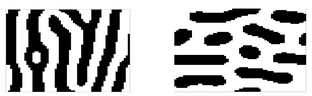
2. GENE-GUIDED FORMS

Free vs. guided morphogenesis

- organism development is only marginally the result of ***free-forming*** random instabilities (e.g., animal coat pigmentation); for the most part, the precisely arranged body plan of animals, made of modules and articulated segments, arises from a genetically ***guided*** morphogenesis process
- it is the latter kind that could serve as a new paradigm of reliable, information-driven systems growth

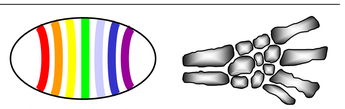
free forms

- ✓ reaction-diffusion, activator-inhibitor (Turing)
- ✓ randomly amplified fluctuations
- ✓ unpredictable: 4, 5 or 6 spots/stripes?
- ✓ statistically homogeneous; one scale



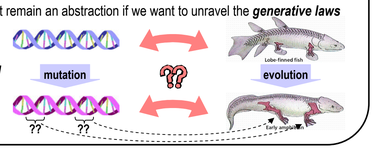
guided forms

- ✓ most aspects of organism development
- ✓ deterministic genetic control
- ✓ reproducible: exactly 4 limbs, 5 digits
- ✓ heterogeneous; rich in information



Development: the missing link of the Modern Synthesis

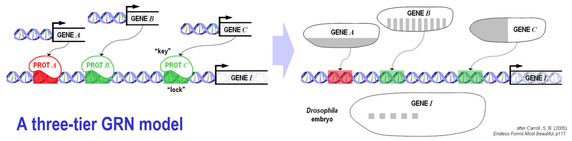
- biology's "Modern Synthesis" demonstrated the existence of a fundamental correlation between genotype and phenotype, yet the molecular and cellular ***mechanisms*** of development are still unclear
- the genotype-phenotype link cannot remain an abstraction if we want to unravel the ***generative laws*** of development and evolution
- understanding variation by comparing the actual ***developmental*** processes of different species is the primary concern of evolutionary development biology, or "evo-devo".



3. THE SELF-PAINTING CANVAS

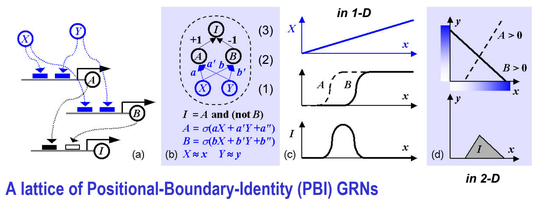
Genetic expression is controlled by genetic switches

- a genetic switch = a regulatory site ("lock") on the DNA upstream from a gene sequence + a protein ("key") that binds to this site, and ***promotes*** or ***represses*** the gene
- since switch proteins are themselves produced by genes, a cell can be modeled as a ***gene-gene regulatory network*** (GRN), in which proteins are considered hidden variables
- switches can combine to form complex regulatory functions, which create spatial domains by union and intersection, for example: $I = [(\text{not } A) \text{ and } B \text{ and } C] = (1 - A)BC$



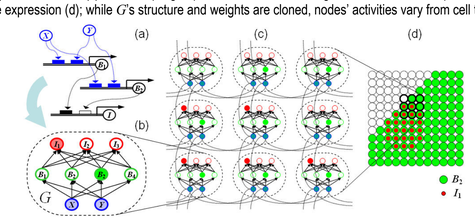
A three-tier GRN model

- (1) ***positional*** proteins X, Y, Z diffuse anisotropically to form concentration gradients; (2) these trigger the expression of ***boundary*** genes $A, B, ...$, under different thresholds of lock-key sensitivity, (3) which in turn promote or repress ***identity*** genes $I, J, ...$, creating different territories of gene expression



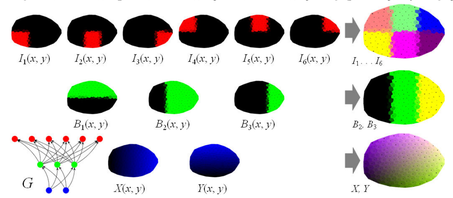
A lattice of Positional-Boundary-Identity (PBI) GRNs

- a network of networks: the GRN (a) is modeled by a PBI network G (b), which is repeated inside every cell of a lattice (c); local coupling of positional nodes creates gradients that create a pattern of gene expression (d); while G's structure and weights are cloned, nodes' activities vary from cell to cell



The hidden geography of the embryo

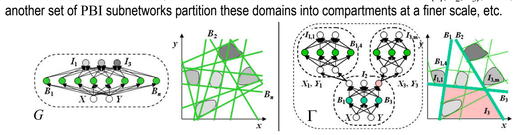
- a checkered self-patterning (top right) can be created by a simple 2P-3B-6I gene regulatory network G in a 200-cell oval-shaped embryo; each embryo view is selectively "dyed" for the expression map of one of the 11 genes, or a partial combination of these genes; with $X = x/x_{\max}$, $Y = y/y_{\max}$, weights are such that: $B_1 = \sigma(Y - 1/2)$, $B_2 = \sigma(X - 1/3)$, $B_3 = \sigma(X - 2/3)$; $I_5 = B_1B_2(1 - B_3)$, $I_6 = B_1B_3$, etc.



4. THE MODULAR CANVAS

Multiscale refinement using a hierarchical GRN (H-PBI)

- instead of a single PBI network G containing one flat tier of B nodes, we use a pyramid ***hierarchy*** of PBI modules Γ, in which the activation of an I node controls the onset of a new P layer (local gradients)
- in an H-PBI such as Γ: first, the base PBI subnetwork creates broad domains (I_1, I_2, I_3); then, another set of PBI subnetworks partition these domains into compartments at a finer scale, etc.



Multiscale refinement by iterative growth

- morphological details are added in a fractal fashion, by inclusion of small motifs into bigger ones, while, simultaneously, the embryo grows as cells continue to divide and proliferate
- ***multiscale patterning*** consists of: (1) the partitioning of identity domains into smaller identity domains, and (2) the continuing expansion of identity domains

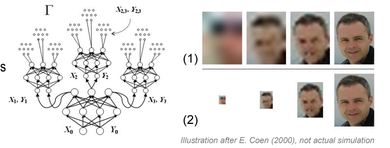
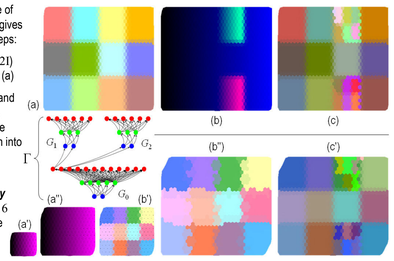


Illustration after E. Coen (2000), not actual simulation

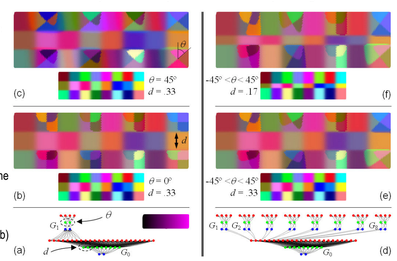
Static vs. growing multiscale canvas

- on this 32x32 hexagonal lattice of cells, an H-PBI gene network Γ gives rise to a "fractal" pattern in two steps:
- first, the base subnet G_0 (5B-12I) creates 12 rectangular segments (a)
- then, 2 secondary subnets G_1 and G_2 (3B-6I) triggered by I_1 and I_2 create local gradients in 2 of those segments (b), and subdivide them into 6 smaller domains (c)
- an equivalent pattern is also obtained by a cell mass ***uniformly expanding*** from 8x8 (a') to 16x16 (a"-b') to 32x32 cells (b"-c'), while patterns continue to form and gradients to diffuse, as in (a-c)



The inherent modularity of hierarchical GRNs

- organisms contain "homologous" parts in their body plan (arthropods' segments, vertebrates' teeth and vertebrae, etc.); homology also exists between different species (tetrapods' limbs); highly similar DNA sequences reveal that it is the evolutionary result of ***duplication*** followed by ***divergence***
- in artificial embryogenesis, genetic subnetworks can also be reused as units of local computation
- for example, several identity genes $I_1 \ldots I_6$ of a base network G_0 can be connected either to a ***unique*** subnetwork G_1 (a) or ***multiple copies*** of the same subnetwork: G_1, G_2, etc. (d)
- in the first case (left column), the local pattern generated by G_1 is always identical in all primary domains $I_1 \ldots I_6$, whether as original '+' shaped subdivisions (b) or mutated '×' subdivisions (c)

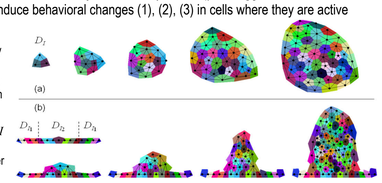


- in the second case (right column), local patterns can be initially identical (as in (b-c)), but then may evolve independently at each location and produce variants (different θ angles in (e)); additional mutations in base network G_0 can also change the whole body map (thinner center row d and thicker borders in (f)) without affecting the individual motifs G_1, G_2, ...

5. THE DEFORMABLE CANVAS

Cell adhesion, division and migration

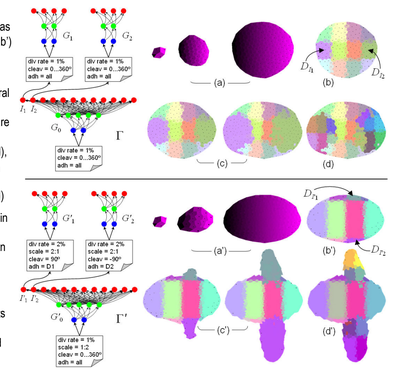
- the previous canvas was only growing uniformly; the model is now augmented with elements of cellular ***biomechanics*** and ***morphodynamics*** that can confer a nontrivial ***shape*** to the system
- cells' coordinates vary according to three mechanistic principles: (1) ***elastic*** cell rearrangement under differential adhesion, (2) inhomogeneous cell ***division***, and (3) tropic cell ***migration***
- these principles are linked to the self-patterning process through a ***functional dependency between cell identities and mechanical cell behaviors***: just as identity nodes I_k can trigger subordinate PBI modules, the same I_k can also induce behavioral changes (1), (2), (3) in cells where they are active
- a simple mesh model illustrates (1) differential cell adhesion and elasticity in a growing cell mass; no GRN is used here; cells have arbitrary colors; lattice edges and polygons result from a Delaunay-Voronoi tessellation
- (a) isotropic "blob" of identical type-I cells dividing at 1% rate, in which nearby daughter cells rearrange under elastic forces



- (b) anisotropic "limb" growth: from the initial 2-type cell sheet, only the center domain I_2 and its offspring divide (upward stretch due to $2x:y$ anisotropic rescaling). The 8 lateral cells have a different identity I_1 and no adhesion to the I_2 lineage

Inhomogeneous cell division

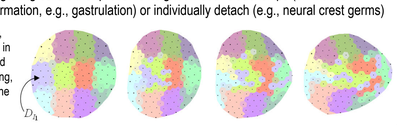
- cells divide according to a ***nonuniform*** probability that essentially depends on their ***genetic identity***, i.e., the domain of high I-node expression to which they belong
- example of "organogenesis" by nonuniform cell proliferation; first, as in Part 4, a checkered embryo (b, b') emerges from an H-PBI gene regulatory network Γ
- here (top), new cellular behavioral rules are added: cells with high levels of identity genes I_1 and I_2 are prompted to further divide at rate 1% (c) (while others have stopped), before expressing subpatterns G_1 and G_2 in their newly formed anterior and posterior territories (d)
- in Γ' (bottom), different weights in base module G'_0 make a thicker central row and place I'_1 and I'_2 on the dorsal and ventral sides
- moreover, different values of cleavage angles, anisotropic rescaling and adhesion coefficients provoke I'_1 and I'_2 cells to grow "limbs", that are also subpatterned by G'_1 and G'_2.



- thus, differential proliferation rates based on genetic identities produce bulges and deformations in the embryo shape, as some compartments expand faster than others (a-d), resembling organogenesis; using anisotropic cleavage planes and rescaling transformations $x:y \to ax:by$, this model can also generate directional offshoot akin to limb development (a'-d').

Tropic cell migration

- a specificity of animal development, largely absent from plant development, is cell ***migration***: cells burrow their way through the extracellular matrix to colonize remote locations of the developing embryo
- depending on adhesion, migrating cells either preserve neighborhood relationships (en masse "flocking" creating sheet deformation, e.g., gastrulation) or individually detach (e.g., neural crest germs)
- using a GRN similar to Γ above, the behavioral parameters of cells in domain I_1 (center left) are replaced with a migration rule: before dividing, they must push their way across the embryo toward increasing X concentration (here, to the right)



7. PLANNING THE AUTONOMY

Growth, function, evolution

- when meta-designing an embryomorphic artificial system, three main questions face an engineer: (1) how does the system ***grow***? (2) how does the system ***function***? (3) how does the system ***evolve***? the goal of the phases (1) and (2) is to define developmental and computing mechanisms; the goal of phase (3) is to define the rules of evolution of these mechanisms by variation and selection of their parameters

(1) growth: development results from a combination of elementary mechanisms, as described above: elements change their internal state, communicate, travel in clusters or individually, divide or die; starting from a single element, a complex and organized architecture develops by the repeated application of a set of these principles, identically programmed (i.e., prepared to react) inside each element; task (1) consists of combining these principles and designing their dynamics and parameters

(2) function: task (2) is about defining the nature of the elements and the type of computation that they carry out, including their input/output interface with the environment; are elements hardware components on a board, taking part in digital-analog electric or optical activity patterns? are they pieces of software logic that execute symbolic instructions? are they physical parts in a robot used in sensing, planning and acting? or even small robots that coordinate in swarm formations for collective performance? etc.

(3) evolution of both growth and function includes how the system varies (randomly) and how it is selected (nonrandomly); here, the constraints driving the fitness criteria and the artificial selection process can be of three types, in decreasing intensity: (a) selecting for a specific system ***architecture***, (b) selecting for a specific system ***function***, and (c) selecting the "***unexpected***"

(a) impose tight requirements to obtain particular shapes from the development process by reverse engineering: what genotype will reliably reproduce a given phenotype? one solution, if available, is the deterministic compilation of the genotype; another is to define a smooth transitional-shape fitness landscape base on some "distance" function to the desired architecture

(b) abstract further from morphological details and concentrate on selecting for the functionality of the system, otherwise leaving it complete freedom of architecture; the same gradual optimization strategy as in (a) can be employed, except that the distance would measure closeness of performance to predefined tasks to accomplish, not structure; candidate systems are ranked according to their partial success in fulfilling these tasks, then the best ones allowed to reproduce and mutate, etc.

(c) give up on specific selection requirements altogether: the ultimate reconciliation between autonomy and planning relies on *(i)* fine-grain variation-by-mutation mechanisms opening a large number of search paths and *(ii)* loose selection criteria allowing a large number of fitness maxima; complex systems inherently fulfill *(i)* by combinatorial tinkering on highly redundant parts; meta-designers could then fulfill *(ii)* by accepting to be surprised and harvest "interesting" systems from a free-range menagerie

6. THE EXCITABLE CANVAS?

- after the self-assembly stage, what type of ***computation*** could the embryomorphic system carry out? for ex., it is speculated here that the organism could become the substrate of ***excitable media*** dynamics
- after creating slow and quasi-static developmental patterns, local cell groups could engage in synchrony and form fast and transient dynamical patterns depending on their identity domain
- computation in the "excitable canvas" would consist of emerging patches of various regimes of collective spatio-temporal order: moving and shimmering spots, stripes, target & spiral waves, etc.
- such spatiotemporal patterns hold a great potential for representational and computing properties.