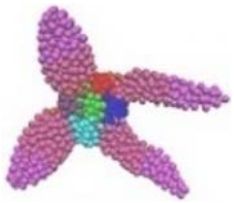


7th MEW at ECAL 2017

Morphogenetic Engineering Workshop, at the European Conference on Artificial Life (ECAL) 2017

September 4, 2017
LyonTech Campus, INSA Lyon, France

Program - Overview - Organizers - Past Editions
References - Call for Abstracts - Topics of Interest - Registration

This workshop aims to promote and expand Morphogenetic Engineering, a field of research exploring the artificial design and implementation of autonomous systems capable of developing complex, heterogeneous morphologies. Particular emphasis is set on the programmability and computing abilities of self-organization, properties that are often underappreciated in complex systems science—while, conversely, the benefits of self-organization are often underappreciated in engineering methodologies.

Program

The workshop will take place on **Monday, September 4 morning** at INSA Lyon, in the Rotunda of the LyonTech Campus:

- 9:05-9:10
  Welcome and introduction
  René Doursat

Part I: Artificial Plants & Biological Morphogenesis

- 9:10-9:40
  Towards an artificial polytrophic ecosystem
  Kevin Dubois, S. Cussat-Blanc & Y. Duthen
  University of Toulouse, France

- 9:40-10:10
  Vascular morphogenesis controller: Guiding morphology by competition for resource distribution
  Daniel Nicolas Hofstadler, P. Zahadat & T. Schmickl
  University of Graz, Austria

- 10:10-10:40
  A model and pipeline for interactive simulation of morphological biology
  Andreas Knote & S. Mammen
  University of Würzburg, Germany

- *10:40-11:05 - Coffee break*

Part II: Cellular Automata & Gene Regulatory Networks

- 11:05-11:35
  CA-NEAT: An evolved cellular automata morphogenetic system based on compositional pattern-producing network developmental mappings
  Stefano Nichele, M. B. Ose, S. Risi & G. Tufte
  HiOA Oslo, Norway / NTNU Trondheim, Norway / University of Copenhagen, Denmark

- 11:35-12:05
  Criticality of gene regulatory networks and robustness of morphogenesis against perturbations
  Hyobin Kim & H. Sayama
  Binghamton University, USA

- 12:05-12:35
  An autopoietic machine to achieve pure self-organization
  Rima Hiouani, S. Cussat-Blanc, N. Djedi & Y. Duthen
  University of Biskra, Algeria / University of Toulouse, France

- *12:35 - Lunch*

Overview

Traditional engineered products are generally made of a number of unique, heterogeneous components assembled in complicated but precise ways, and are intended to work deterministically following specifications given by their designers. By contrast, self-organization in natural complex systems (physical, biological, ecological, social) often emerges from the repetition of agents obeying identical rules under stochastic dynamics. These systems produce relatively regular patterns (spots, stripes, waves, trails, clusters, hubs, etc.) that can be characterized by a small number of statistical variables. They are random and/or shaped by boundary conditions, but do not exhibit an intrinsic architecture like engineered products do.

Two salient exceptions, however, strikingly demonstrate the possibility of combining pure self-organization and elaborate architectures: biological development (the self-assembly of myriads of cells into the body plans and appendages of organisms) and insect constructions (the stigmergic collaboration of colonies of social insects toward large and complicated nests). These structures are composed of segments and parts arranged in very specific ways that resemble the products of human inventiveness. Yet, they entirely self-assemble in a decentralized fashion, under the control of genetic or behavioral rules stored in every agent.

How do these collectives (cells or insects) achieve such impressive morphogenetic tasks so reliably? Can we export their precise self-formation capabilities to engineered systems? What are principles and best practices for the design and engineering of such morphogenetic systems?

Organizers

- René Doursat, Manchester Metropolitan University, UK
- Hiroki Sayama, Binghamton University, NY, US

Past Editions

This workshop is the 7th Morphogenetic Engineering Workshop or Special Session (MEW) of its kind. It follows:

- 6th MEW (2016), 15th International Conference on Artificial Life (ALife XV), Cancun, Mexico, July 4, 2016
- 5th MEW (2015), 13th European Conference on Artificial Life (ECAL'15), York, UK, July 20, 2015
- 4th MEW (2014), 14th International Conference on Artificial Life (ALife XIV), New York, July 31, 2014
- 3rd MEW (2011), 11th European Conference on Artificial Life (ECAL'11), Paris, August 12, 2011
- 2nd MEW (2010), 7th International Conference on Swarm Intelligence (ANTS 2010), Brussels, Sept 10, 2010
- 1st MEW (2009), Complex Systems Institute, Paris (ISC-PIF), June 19, 2009

References

- Doursat, R., Sayama, H. & Michel, O. (2013) A review of morphogenetic engineering. *"Frontiers of Natural Computing" (FNC 2012) Special Issue.* M. Lones, A. Tyrrell, S. Stepney & L. Caves, eds. *Natural Computing* **12**(2): 517-535 [19 pages]. **PAPER**

- Doursat, R., Sayama, H. & Michel, O., eds. (2012) *Morphogenetic Engineering: Toward Programmable Complex Systems*. *"Understanding Complex Systems" Series*, Springer-Verlag, ISBN 978-3-642-33901-1 [452 pages]. **OVERVIEW**

Call for Abstracts (closed)

Authors are invited to submit an abstract (up to 2 pages, figures and references welcome) on their research or a review and discussion about aspects of Morphogenetic Engineering. It should be prepared following the ECAL 2017 paper format. Work may be original or already published (please specify). Accepted abstracts will be compiled into workshop proceedings and published online on the MEW website for free download.

Please send your PDF abstract by email to both organizers: r.doursat@mmu.ac.uk, sayama@binghamton.edu

Important Dates:

- ~~*Deadline for abstract submission:* ***July 4, 2017***~~
- ~~*Notification of acceptance:* July 14, 2017~~
- ~~*Camera-ready abstract due:* July 31, 2017~~
- *Date of workshop:* **September 4, 2017**

The workshop will last about 3.5 hours and the total number of speakers is limited to 6. Submissions will be reviewed based on their relevance to the workshop, clarity, and overall quality. Whether submitting or simply attending, please register via the online ECAL 2017 conference registration system.

Topics of Interest

- New principles of morphogenesis in artificial systems
- Bio-inspiration from plant vs. animal development
- Programmability of self-organizing morphogenetic systems
- Indirect, decentralized control of morphogenetic systems
- Sensitivity to environmental/boundary conditions vs. endogenous drive
- Evolvability, by variations and selection, of morphogenetic systems
- Links with evolutionary computation, artificial embryogeny, "evo-devo" approaches
- Swarm-based approaches to morphogenetic systems
- Design techniques for morphogenetic engineering
- Causalities between micro and macro properties of morphogenetic systems
- Physical implementations
- Applications to real-world problems (swarm robots, synthetic biology, complex networks, etc.)
- Philosophical questions about morphogenetic engineering

Registration

Registration should be made through the ECAL 2017 website.

Towards an Artificial Polytrophic Ecosystem

Kevin Dubois[1], Sylvain Cussat-Blanc[1] and Yves Duthen[1]

[1]University of Toulouse, IRIT - CNRS UMR 5505, 2 rue du Doyen Gabriel Marty, 31042 Toulouse, France
{kevin.dubois, sylvain.cussat-blanc, yves.duthen}@irit.fr

Artificial Ecosystems

Ecosystems are modeled in disciplines ranging from ecology to art whether to produce accurate prediction tools or simply aesthetically pleasing environments. The computer science literature contains a number of works focusing either on plants (e.g. Bornhofen (2008)) or animals (e.g. Miconi (2008)).

This work lays the basis for a "Polytrophic" ecosystem that would exhibit a simplified food chain. The rationale behind this goal is to study the large amount of interactions between plants and animals observed in the natural kingdom (pollination, zoochory, etc.).

L-Systems proved to be powerful tools for encoding plant morphologies, yet their application to mobile creatures was more difficult, e.g. Komosinski (2003). In addition, black-box models such as GRNs, while flexible enough, were put aside due to their relatively high computational cost as well as their inability to produce intelligible genomic data. The directed graphs described by Sims (1994) (hereafter called 'graphtals') have been successfully used to generate complex yet functional body plans for animated creatures. However, despite their potential to be applied to plants, they have, to the best of our knowledge, not been so far. Nevertheless their expressive prowess and structural simplicity were deemed enough to model both the animal and vegetal kingdoms while allowing for insights into the mechanisms of evolution. This paper shows how graphtals can be used to generate plants which are growing from a seed in a physically simulated 3D world.

Model

Environment

In this work, plants are growing in a 3D environment composed of a flat ground, a light source and a simplified water cycle. Sun is designed as an infinitely far directional light whose position is a function of both night/day and seasonal cycles. These constraints should induce more robust behavior in evolved individuals as they have to find strategies to cope with unproductive night-time and low-angle light (during "winter") which would prevent most leaves from direct exposure.

The water cycle was modeled in two steps: First, rain patterns were generated pseudo-randomly (but consistently across evaluations) both in terms of occurrence and intensity so as to appear unforeseeable. Second, rain falls on the ground but is only accessible to plants once it is absorbed, at a slow rate, by voxels below the surface whose saturation level is rather low (2L/m^3). These levels increase linearly until the deepest layer, which behaves as a groundwater table. Moreover a portion of water is removed at each tick from the top (resp. bottom) layer to simulate evaporation (resp. water displacement). This aims at inducing two classes of behaviors observed in natural plants: large near-ground root networks to capture precipitations and digging tendencies to exploit deep water reserves.

Plant growth model

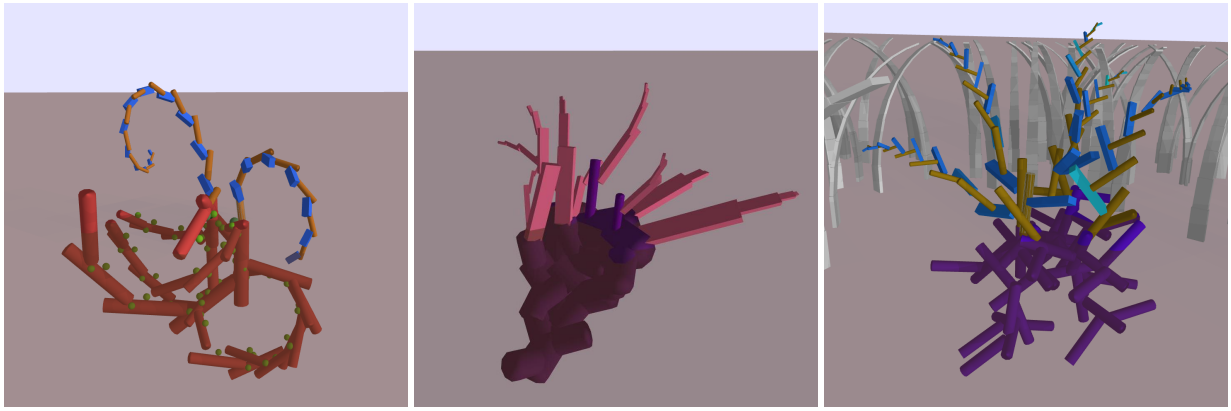
This work expands upon the original model by allowing each node to specify its shape (sphere, box, cylinder), skill (root, leaf), initial dimensions and anisotropic growth factor. Behavior is controlled by two tuples $A, S \in [0, 1]^E$ with E the number of elements (water and glucose in this experiment). A models an organ balance between production and consumption: a value of 0 (resp. 1) indicates a source (resp. sink). S enables quiescent behavior by imposing a threshold below which no growth or budding actions can be performed.

Evolving plants do not require the bilateral symmetry present in the original animat experiments by Sims, links in this model instead use an 'effect' to generate multiple child organs at once (e.g. Radial($\mathbf{V}, N$) creates $N - 1$ copies of the target organ uniformly rotated around a vector $\mathbf{V}$)

Metabolism

All individuals start from a seed, root and sprout. To maintain comparability between evolutions the seed is set to a spherical 2cm-radius organ saturated in both nutrients.

To survive, plants must draw water from the ground (using organs with the appropriate skill) and use a portion of it to generate a certain quantity of glucose in its leaves given by Eq. 1.



(a) Multiple sprouts (b) Grass-like (c) Upward growth

Figure 1: Various plant morphologies obtained by evolution[1]

$$k * \sum Surface_i * \mathbf{Light.Normal_i} \quad (1)$$

Resources distribution is centralized to prevent unnecessary complexity, each organ receiving a portion relative to its size and its genomic parameter A. Organs consume part of their reserves as a function of their skill (e.g. 150% for photosynthesis and 75% for the roots). A negative balance in either nutrient or disconnection from the parent triggers the organ's death which deletes the individual and all its children from the simulation. A seed behaves like an organ but its death does not affect its descendants.

Experiments

In a first experiment, individuals were evaluated in an empty environment with a sunset every 100 ticks and 300-day years. The sun started at its apex position ($3\pi/8$) and went as low as $\pi/8$ during winter. Rain patterns provided an average precipitation of 787mm per year, two thirds of which occurred during the first half of the year.

The fitness, computed as in Eq. 2, rewarded glucose production in such a way that individuals were incited to stay alive the maximal duration of 2 years (N=60,000 ticks) and develop multiple leaves (see Figures 1a and 1b).

$$Fitness = \frac{2}{N(N-1)} * \sum i * G_i \quad (2)$$

In the second experiment, 100 hand-made grass blades were placed around the seed to simulate the competition for light observed in nature and stimulate vertical growth. This induced a size increase of the evolved plants in order to rise above the grass blades (see Figure 1c).

Conclusion and Future Work

One the most crucial natural resources not included in the present work is the effect of heat on the plants. While its impact could be manifold, e.g. on the transpiration rate or the speed of chemical reactions, it could easily be coded by genomes through a bell curve with a 'preferred' temperature and a tolerance range.

From a broader perspective, as our end goal is the emergence of complex ecosystems, this work provided a proof-of-concept for the use of graphtals in plant modeling as well as a few promising initial individuals to seed such a world.

Indeed, populating large non-uniform environments would allow for competition and speciation processes to occur spontaneously. Further evolution of the topological and meteorological parameters through a classical genetic algorithm would allow for comparison between the complexity of the generated plants and that of their world.

Finally, including motorized connections and heterotroph capabilities in the genomes while providing central controller, such as an ANN, would see the emergence of animals and close the food chain.

Acknowledgements

This work was performed using HPC resources from CALMIP (Grant P16043).

References

Bornhofen, S. (2008). *Emergence de dynamiques evolutionnaires dans une approche multi-agents de plantes virtuelles*. PhD thesis.

Komosinski, M. (2003). The Framsticks system: versatile simulator of 3D agents and their evolution. *Kybernetes: The International Journal of Systems & Cybernetics*, (8):156–173.

Miconi, T. (2008). Evosphere: Evolutionary dynamics in a population of fighting virtual creatures. *2008 IEEE Congress on Evolutionary Computation, CEC 2008*, pages 3066–3073.

Sims, K. (1994). Evolving 3D Morphology and Behavior by Competition. *Artificial Life*, 1(4):353–372.

[1]Movies of these plants and more can be accessed at `https://vimeo.com/channels/1221252`

Vascular Morphogenesis Controller: Guiding Morphology by Competition for Resource Distribution

Daniel Nicolas Hofstadler[1], Payam Zahadat, Thomas Schmickl

University of Graz, Austria
[1]daniel.hofstadler@uni-graz.at

Biological morphogenesis is the manifestation of interactions between a genome, its products and the environment. While animals possess genetically defined body plans and cease to grow in adulthood, plants have evolved to grow indefinitely into potentially massive, enduring structures by means of a modular organization.

Approaches to developing morphologies of artificial structures (Doursat et al., 2013) include works inspired by biological processes such as embryogenesis (Wolpert, 1996; Cussat-Blanc and Pollack, 2014), as well as abstract generative encodings such as variants of L-systems (Lindenmayer, 1975; Hornby and Pollack, 2001; Sims, 1994).

We present a distributed algorithm, the Vascular Morphogenesis Controller (VMC, originally introduced in Zahadat et al. (2017b)), that draws its inspiration from the competitive dynamics of the plant vascular system, mediated by hormone signalling (Lucas et al., 2013).

A plant's architecture is the outcome of competition between individual branches, where better situated, more successful branches receive a greater share of common resources (Sachs, 2004; Leyser, 2011). The information needed to direct these resources to the most promising growth regions is relayed by the plant hormone auxin, which is primarily produced exactly there: in actively growing plant apices and unfolding leaves. It is transported rootward, and, crucially: where it flows more, more vascular tissue forms. Finally, a branch with more or larger vessels and better connectivity to the main stem will draw a greater share of the common nutrients available to the whole system. Depending on the scarcity of the environment (and genetic predispositions), the level of this inter-branch competition is either enhanced or relaxed (Sachs, 2006). These feedback mechanisms lead to a continuously globally adaptive morphology of the whole plant.

Algorithm: Vascular Morphogenesis Controller

We abstract these biological processes into a distributed controller for modular artificial growing structures.

The controller units of the modules are connected to their neighboring units forming a VMC-system. The relational structure of a VMC-system can be represented as an acyclic, directed graph, where each node corresponds to a controller unit and the edges between the nodes indicate the direction of common resource transportation (see Fig. 1).

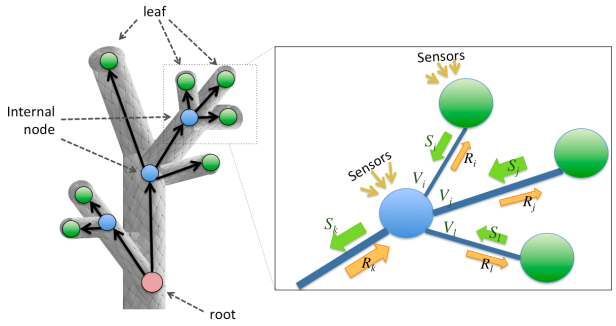


Figure 1: An example VMC system.

Each node has at least one *parent*-node, else it is a *root* of a VMC-system. If two branches fuse, a node has two parent-nodes. Nodes can in principle have an arbitrary number of *child*-nodes, but at least two need to be allowed to retain the ability to branch. Each node can have arbitrary sensors attached.

By analogy with auxin, our leaf-nodes of the graph produce "successin" (S), depending on sensor values and fixed parameters (from the *genome* of the VMC-system). The value of S is then sent on to the parent of the leaf, where it will again be modified and passed down towards the root. On the way, S modulates the weights of the edges—corresponding to vessel thickness, V— through which it travels. A limited, common resource R is distributed recursively from the root to all its children up to the leaves in proportion to the relative sizes of V among sibling-nodes. The amount of R in a leaf indicates its ability to grow.

At every leaf i, a quantity of successin S_i is produced as $S_i := \omega_{\text{const}} + \sum_{s \in \text{sensors}} \omega_s \cdot I_s$, where I_s is the input from sensor s. The ω_{const} and ω_s are constant and sensor-dependent production rates.

Successin flows towards the root. At a junc-

tion (internal node) i, the value of S is updated as $S_i := g(\rho_{\text{const}} + \sum_{s \in \text{sensors}} \rho_s \cdot I_s) \cdot \sum_{b \in \text{branches}} S_b$, where $g(x)$ is a sigmoid function. The ρ_{const} and ρ_s are constant and sensor-dependent transfer rates of successin.

For every edge connecting a node to its child i, V_i is adjusted at every time step based on the successin flowing through it. $V_i := \begin{cases} \min(S_i, (1-\gamma) \cdot V_i + \beta + \alpha \cdot (S_i - V_i)) & \text{if } S_i \geq V_i \\ \max(S_i, (1-\gamma) \cdot V_i) & \text{if } S_i < V_i \end{cases}$ where γ, β, and α, are respectively the decay, addition, and adjustment rates.

The limited common resource R initiates at the root node. The quantity R_i of a child i of node m is computed as: $R_i := R_m \cdot V_i / \sum_{b \in \text{children}} V_b$

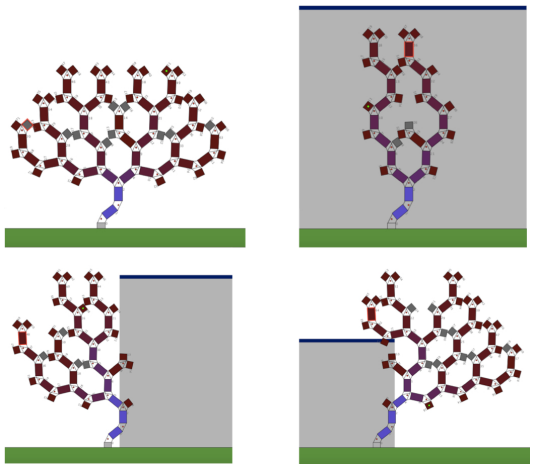


Figure 2: An identical parameter set allows different structures to grow in different light environments. The violet to black gradient indicates the amount of resource R at a module. [reprinted from Zahadat et al. (2017b)]

Implementations and Implications

Fig. 2 shows snapshots of a physics-based simulator of modular robots (detailed in Zahadat et al. (2017b)), where the same VMC-genome (parameter set) is grown in different environments. The simulated modules contain sensors for light and gravity which allow the structure to optimize its light-harvest while balancing against gravity. Clearly, the VMC-system adapts to its environment: It thrives in full light, grows out of the shade or, if completely shaded, invests into growing upwards (to increase the odds to escape shade and avoid obstacles, as it will grow along the obstacle's surface if the way up is blocked). The particular VMC shown in Fig. 2 was manually parametrized, but the genomes can just as well be evolved to exhibit desired properties and/or to thrive in adversary environment, depending on the types of sensors and objectives employed (Zahadat et al., 2017b). It has also been shown that the VMC algorithm can solve mazes much like slime molds (Nakagaki, 2001; Zahadat et al., 2017a).

The major power of VMC lies not in its capacity to mimic (the very much optimized) natural plant behaviour to grow ideal structures in the face of environmental constraints and hardships, but to extract its self-organizational core to apply it to a variety of problems not encountered by natural plants and doing so in a decentralized, scalable way.

Acknowledgment

This work was supported by EU-H2020 project 'flororobotica', no. 640959.

References

Cussat-Blanc, S. and Pollack, J. (2014). Cracking the Egg: Virtual Embryogenesis of Real Robots. *Artificial Life*, 20(3):361–383.

Doursat, R., Sayama, H., and Michel, O. (2013). A review of morphogenetic engineering. *Natural Computing*, 12(4):517–535.

Hornby, G. S. and Pollack, J. B. (2001). Body-Brain Co-evolution Using L-systems as a Generative Encoding. In *GECCO-2001*, pages 868–875, San Francisco, California, USA. Morgan Kaufmann.

Leyser, O. (2011). Auxin, self-organisation, and the colonial nature of plants. *Current Biology*, 21(9):R331–R337.

Lindenmayer, A. (1975). Developmental algorithms for multicellular organisms: A survey of L-systems. *Journal of Theoretical Biology*, 54(1):3–22.

Lucas, W. J., Groover, A., Lichtenberger, R., Furuta, K., Yadav, S.-R., Helariutta, Y., He, X.-Q., Fukuda, H., Kang, J., Brady, S. M., Patrick, J. W., Sperry, J., Yoshida, A., López-Millán, A.-F., Grusak, M. A., and Kachroo, P. (2013). The Plant Vascular System: Evolution, Development and Functions. *Journal of Integrative Plant Biology*, 55(4):294–388.

Nakagaki, T. (2001). Smart behavior of true slime mold in a labyrinth. *Research in Microbiology*, 152(9):767–770.

Sachs, T. (2004). Self-organization of tree form: A model for complex social systems. *Journal of Theoretical Biology*, 230(2):197–202.

Sachs, T. (2006). *Communication in Plants: Neuronal Aspects of Plant Life*, chapter How Can Plants Choose the Most Promising Organs?, pages 53–63. Springer Berlin Heidelberg, Berlin, Heidelberg.

Sims, K. (1994). Evolving 3D morphology and behavior by competition. In Brooks, R. and Maes, P., editors, *Artificial Life IV*, pages 28–39. MIT Press.

Wolpert, L. (1996). One hundred years of positional information. *Trends in Genetics*, 12(9):359–364.

Zahadat, P., Hofstadler, D. N., and Schmickl, T. (2017a). Development of morphology based on resource distribution: Finding the shortest path in a maze by vascular morphogenesis controller. In *14th European Conference on Artificial Life (ECAL-2017)*, in press.

Zahadat, P., Hofstadler, D. N., and Schmickl, T. (2017b). Vascular morphogenesis controller: A generative model for developing morphology of artificial structures. In *GECCO '17*, in press.

A Model and Pipeline for Interactive Simulation of Morphological Biology

Andreas Knote and Sebastian von Mammen

Julius-Maximilians-Universität, Würzburg
{andreas.knote, sebastian.von.mammen}@uni-wuerzburg.de

Abstract

In this work, we present our current efforts towards a comprehensive, human-in-the-loop modelling framework for the study of complex morphogenetic systems. The state of our physical cell model providing localized surface-based interactions and built on top of a real-time capable particle-based physics engine is summarized. We further outline our long-term concept towards an integrated pipeline for automated model generation and refinement based on empirical data and human-in-the-loop simulations. With it, we strive to seamlessly integrate with a biologist's workflow, for example through appropriate import and annotation tools for empirically obtained data, and intuitive and accessible tools and languages for behaviour description. To integrate the different software components into a real-time interactive system, we use *UnrealEngine4*, a state-of-the-art game engine.

Introduction

We aim to provide an interactive, immersive, and real-time framework for the modelling and simulation of morphogenetic systems, see Figure 1. At its core, our concept envisions a cell-centred simulation approach, where biological cells are represented as autonomous spatial agents with explicit physical shape and local, surface-based interactions embedded in a fluid dynamic simulation for substance diffusion. This core model needs to be augmented with an accessible user interface for modelling of cellular behaviour. By including the "human in the loop", modelling, retracing and exploring complex system behaviours is facilitated (Narayanan et al., 2011). Also, the study of and interaction with of complex morphologies benefit from spatial visualisation and freedom of exploration made possible by means of immersive virtual reality interfaces.

In order to closely align the resulting model with biologically valid empirical data and also in order to inform the biologists' work, our targeted framework needs to go beyond offering an extensible cell model and interactive simulation mechanics. To make use of the vast amount of empirical data generated by biologists, import and processing pipelines must be provided that seamlessly tie into the biologists' established toolchains. The user must be able to quickly and comprehensively define and test models, and to optimize their parameters. In addition, the integration of automated model-finding routines that mine the biological data are highly desirable.

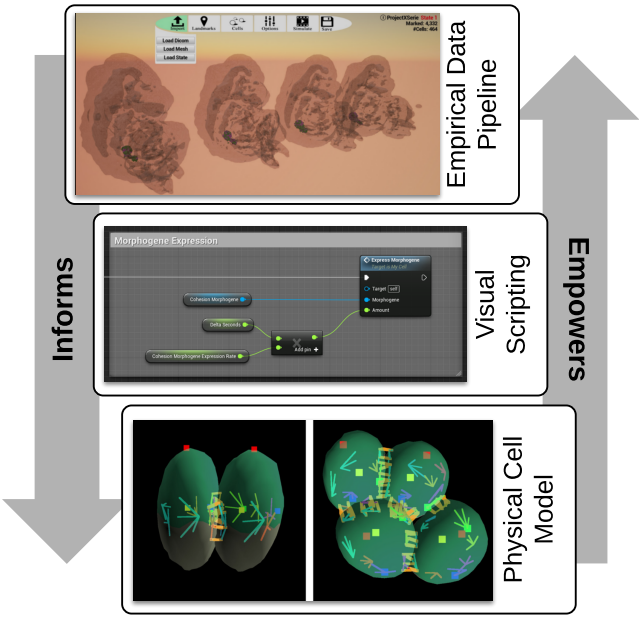


Figure 1: The basic components of our proposed concept. An interactive, particle-based physical cell model (bottom) can be programmed using accessible tools such as visual scripting languages (middle) and integrated directly with empirically obtained data (top). For the latter, a comprehensive import and annotation pipeline is provided. Based on this foundation, algorithms to generate or optimise models based on empirical data and simulation performance allow for automated model refinement.

In this extended abstract, we support our vision with outlines of system components that we have already implemented. In particular, we briefly present two implementations that should be merged in the near future: One that helps to utilise biological data and another one that focusses on the refinement of a real-time capable virtual cell model.

Related Work

Merks et al. (2005) point to the importance of cell-centred models and the similarities between current models of biological cells and the concept of autonomous agents. Recently, the importance of physical interactions in the simulation of complex behaviour of cellular systems has been stressed (Drasdo et al., 2007; Hamant et al., 2008; Uyttewaal et al., 2010). One approach is to model spherical, elastic bodies in a system of constraints (e.g. the Johnson-Kendall-Roberts model (Chu et al., 2005)). CellSys (Hoehme et al., 2010) and CompuCell3D (Swat et al., 2012) offer examples for an integrated design and visualisation approach. Several physical cell models have been realised and evaluated successfully (Delile et al., 2017; Hoehme et al., 2010; Disset et al., 2015; Swat et al., 2012), however without real-time interaction capabilities.

With regards to our long-term vision of integrated developmental frameworks with automated model building, recent progress has been made. For example, Faure et al. (2016) realized a pipeline for the reconstruction and visual analysis of cell lineages from developmental time series of embryonic cells in the form of image data.

Methodology

To create a rich real-time interactive experience, we draw from the available technology of state-of-the-art game engines. These systems provide efficient, high-quality visualisations, facilities for the design of accessible user interfaces, compatibility with current virtual reality interfaces, and a modular, extensible software design. Also, accessible visual scripting environments are often provided. We currently use UnrealEngine4 (EPIC Inc., 2017). We exploit the capabilities of current hardware through massive parallelization, offloading work to the GPU.

To create an interactive, cell-centred and physical simulation model, fast, efficient, and dynamic soft body simulation is required. Our current cell model is built on top of FleX, a real-time physics simulation that can provide plausible results at interactive speeds (Bender et al., 2013). Individual cells are modelled by a set of particles combined with internal constraints, allowing the simulation of deformable exteriors and localized interactions, such as adhesion. Fluid dynamics and diffusion simulation can be used to retrace the emergence of morphogen gradients, a fundamental mechanism in the appearance of distinct morphological features. The features of the model can be presented to the user at arbitrary degrees of complexity, e.g. through visual scripting.

First results towards an integrated developmental biology pipeline that integrates empirical data and automated parameter optimization have been made (Däschinger et al., 2017b). The system allows to parse volumetric data from CT scans and annotate it, defining time series data of the developmental stages of certain regions of the tissue. Such regions can then be populated with (various types of) cells, and their parametrization will be continuously optimized by the means of an genetic algorithm. This process is an example of Guided Self-Organisation (Däschinger et al., 2017a).

Future Work

The presented cell model and the steps towards a pipeline for automated parameter refinement and model building are at early stages. The cell model requires a quantitative analysis with respect to the accuracy of the model. Consequently, it is desirable to define clear implementation and usage constraints on NVidias FleX physics solver that guarantee for consistent and sufficiently accurate simulation results. The current fluid dynamics and diffusion model is overly simplistic and, though highly parallelized, still lacks in accuracy and scalability. Integrating different models for cellular behaviour on top of the physical model, such as Gene Regulatory Networks, should be investigated. The pipeline was currently limited both in the kind of data used as an input as well as the algorithms implemented for the parameter refinement. Also, the task of integrating the two projects remains.

References

Bender, J. et al. (2013). Position-Based Methods For The Simulation Of Solid Objects In Computer Graphics. In *Eurographics*.

Chu, Y.-S. et al. (2005). Johnson-Kendall-Roberts theory applied to living cells. *Physical review letters*.

Däschinger, M. et al. (2017a). An Evolutionary Approach to Behavioural Morphometrics. In *GECCO Proceedings*.

Däschinger, M. et al. (2017b). A Human-in-the-Loop Environment for Developmental Biology. In *ECAL Proceedings*.

Delile, J. et al. (2017). A cell-based computational model of early embryogenesis coupling mechanical behaviour and gene regulation. *Nature Communications*.

Disset, J. et al. (2015). Mecacell. In *ECAL Proceedings*.

Drasdo, D. et al. (2007). On the role of physics in the growth and pattern formation of multi-cellular systems: What can we learn from individual-cell based models? *Journal of Statistical Physics*.

EPIC Inc. (2017). UnrealEngine 4. `https://www.unrealengine.com`. Last retrieved 4.7.2017.

Faure, E. et al. (2016). A workflow to processsss 3D+time microscopy images of developing organisms and reconstruct their cell lineage. *Nature Communications*.

Hamant, O. et al. (2008). Developmental patterning by mechanical signals in Arabidopsis. *Science*.

Hoehme, S. et al. (2010). A cell-based simulation software for multi-cellular systems. *Bioinformatics*.

Merks, R. M. H. et al. (2005). A cell-centered approach to developmental biology. *Physica A*.

Narayanan, S. et al. (2011). Interactive Simulations: History, Features, and Trends. In *Human-in-the-Loop Simulations*.

Swat, M. H. et al. (2012). Multi-Scale Modeling of Tissues Using CompuCell3D. In *Computational Methods In Cell Biology*.

Uyttewaal, M. et al. (2010). Integrating physical stress, growth, and development. *Current opinion in plant biology*.

CA-NEAT: An Evolved Cellular Automata Morphogenetic System Based On Compositional Pattern-Producing Network Developmental Mappings

Stefano Nichele[1], Mathias Berild Ose[2], Sebastian Risi[3] and Gunnar Tufte[2]

[1]Oslo and Akershus University College of Applied Sciences, Oslo, Norway
[2]Norwegian University of Science and Technology, Trondheim, Norway
[3]IT University of Copenhagen, Copenhagen, Denmark
stefano.nichele@hioa.no

Abstract

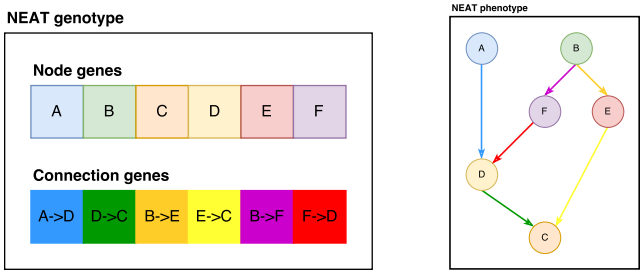
Complex self-architecturing systems are difficult to program, i.e. by top-down engineering. Kowaliw and Banzhaf (Kowaliw and Banzhaf, 2012) argue that the bottom-up methodology of artificial development is an appropriate means of approaching complex systems engineering. However, achieving some sort of self-architecturing properties, e.g. morphogenesis or self-replication, is not trivial. One way of "programming" such developmental systems is through artificial evolution, i.e. a combined evolutionary and developmental approach (EvoDevo). Searching for a solution for an artificial EvoDevo system that targets levels of complexity found in nature can be intractable. Therefore, an appropriate mapping that scales well and at the same time allows solutions to evolve incrementally, starting with a solution encoded into a small genome gradually complexified by adding new degrees of freedom, is desired.

In this work a cellular system is used as testbed for morphogenetic engineering. A traditional CA table-based encoding is replaced by a *Compositional Pattern Producing Network* (CPPN) mapping, a developmental encoding often used in systems without local interactions (Stanley, 2007). In our work a CPPN is used as developmental encoding based on local interactions, i.e. a true morphogenetic cellular system. The cellular automata CPPNs are evolved through a *NeuroEvolution of Augmenting Topologies* (NEAT) algorithm, a method that evolves increasingly complex networks (Stanley and Miikkulainen, 2002).

A NEAT genome consists of genes that encode nodes and connections between them. Figure 1 shows an example genotype-to-phenotype mapping. NEAT starts with an initial population of very simple networks, typically with just the input and output nodes and connections between them. Over generations, more nodes and vertices are added or disabled, activation functions are changed, and weights are adjusted. The process of gradually expanding the genome is called *complexification*, and intends to reflect how life on earth is believed to have started with simple organisms and gradually evolved into more complex creatures (Darnell and Doolittle, 1986; Pross, 2005).

The approach described in this work is termed CA-NEAT. All cells in the systems are uniform, i.e. they share the same genome network. Two benchmark problems are investigated: 2D morphogenesis and replication of structures of increasing complexity.

Figure 2 shows the results for the evolution of the "Tricolor" flag pattern morphogenesis in 100 independent runs. In 100 generations, 93 of the independent runs achieved a perfect solution. The initial populations contained 200 genomes which consisted of an input layer with one node



(a) Genotype (b) Phenotype

Figure 1: NEAT genotype and phenotype examples. The phenotype only shows the topology that the genotype encodes (weights and activation functions are omitted).

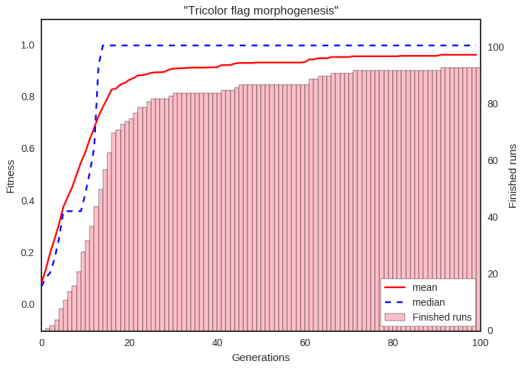


Figure 2: Tricolor flag pattern morphogenesis, first 100 generations.

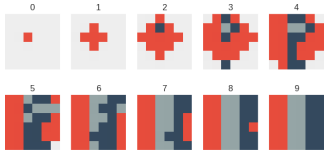


Figure 3: Example of morphogenesis.

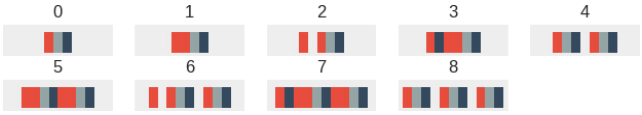


Figure 4: Example of replication.

per CA neighbor (von Neumann 5 neighbors) and one output layer with one node per possible cell state.

An example of evolved network for the "Tricolor" morphogenesis problem is shown in Figure 5. The two hidden nodes are not connected to output nodes and are thus "vestigial". Dashed lines represent disabled connections. An example of morphogenesis process is depicted in Figure 3 and an example of replication is represented in Figure 4. Morphologies and structures of increasing complexity have also been investigated (Nichele et al., 2017), but are not included in this abstract due to space constrains.

Results show that CA-NEAT is an appropriate means of approaching cellular systems engineering. We argue that CA-NEAT could provide a valuable mapping for morphogenetic systems, beyond cellular automata systems, where development through local interactions is desired. In natural processes of development such as embryogenesis, local interactions and developmental time are key requirements. Biological morphogenetic systems are the result of a continuous computation, i.e. development, where intermediate phenotypes emerge along the developmental path, and these intermediate phenotypes influence the decoding and regulation of the genotype for the next phenotypic stage.

References

Darnell, J. and Doolittle, W. (1986). Speculations on the early course of evolution. *Proceedings of the National Academy of Sciences*, 83(5):1271–1275.

Kowaliw, T. and Banzhaf, W. (2012). Mechanisms for complex systems engineering through artificial development. In *Morphogenetic Engineering*, pages 331–351. Springer.

Nichele, S., Ose, M., Risi, S., and Tufte, G. (IN PRESS, 2017). Ca-neat: Evolved computational pattern producing networks for cellular automata morphogenesis and replication. *IEEE Transactions on Cognitive and Developmental Systems*.

Pross, A. (2005). On the emergence of biological complexity: life as a kinetic state of matter. *Origins of Life and Evolution of Biospheres*, 35(2):151–166.

Stanley, K. O. (2007). Compositional pattern producing networks: A novel abstraction of development. *Genetic programming and evolvable machines*, 8(2):131–162.

Stanley, K. O. and Miikkulainen, R. (2002). Evolving neural networks through augmenting topologies. *Evolutionary computation*, 10(2):99–127.

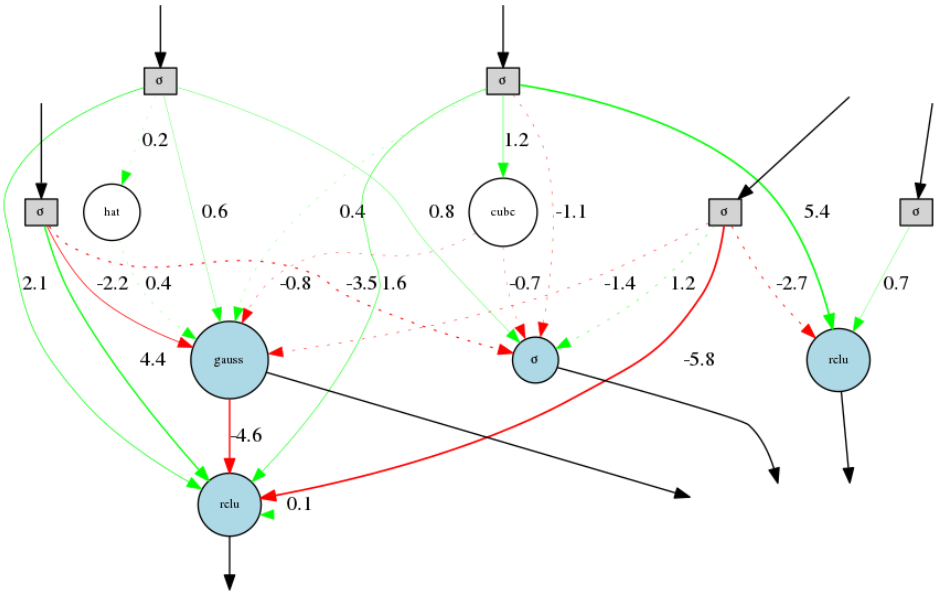


Figure 5: Network for "Tricolor" morphogenesis that reaches a point attractor equal to the target pattern. Dashed lines represent disabled connections. Green and red represent positive and negative values. The thickness represents the value intensity. Nodes can have different activation functions (sigmoid, gaussian, cube, hat, rectified linear unit, etc.) (Nichele et al., 2017).

Criticality of Gene Regulatory Networks and Robustness of Morphogenesis Against Perturbations

Hyobin Kim and Hiroki Sayama

Department of Systems Science and Industrial Engineering
Center for Collective Dynamics of Complex Systems
Binghamton University, State University of New York, Binghamton, NY, USA
hkim240@binghamton.edu

Abstract

We introduce perturbations to the gene regulatory networks (GRNs) of our model of morphogenetic systems and investigate if the role of "criticality" (dynamical behavior near phase transition between order and chaos) of GRNs facilitating the formation of nontrivial morphologies can be maintained. Our model starts with one seed cell and grows into a cell aggregate, in which all the cells have identical GRNs. In the present study, we perturbed the GRN of the seed cell by adding, deleting or switching one regulatory link. We focused on analyzing morphologies obtained from morphogenetic systems with evolvable GRNs that are robust against the perturbations because they are evolutionarily meaningful. We found that nontrivial spatial patterns were still generated most frequently when GRNs were put in a critical state by adding perturbations.

We have recently proposed morphogenetic systems using NK random Boolean networks (RBNs) as gene regulatory networks (GRNs) and spring-mass-damper kinetics for cellular movements. We revealed that the criticality of GRNs facilitated the formation of nontrivial morphologies (Kim et al., 2017), where the criticality of GRNs means dynamical behavior near phase transition between order and chaos. For perturbations flipping the states of one or more nodes in the GRN, if the Hamming distances of the original states and the perturbed states converge, the dynamics are ordered. On the contrary, if the Hamming distances diverge, the dynamics are chaotic. In our model, we did not consider perturbations (e.g., mutations) of GRNs in an evolutionary sense. Here we introduce perturbations to GRNs and investigate if the role of the criticality of GRNs can be maintained.

Our model starts with one seed cell and grows into a cell aggregate, in which all the cells have identical RBNs as GRNs (Fig. 1 top). The properties of GRNs change as the node in-degree K is varied; $K = 1$ leads to an ordered state, $K = 2$ to critical, and $K > 2$ to chaotic, on average (Kauffman, 1969). Based on empirical evidence that attractors of GRNs correspond to cell types/fates (Chang et al., 2008), we randomly assigned cell fates to attractors of GRNs. If there is only a single attractor, proliferation is assigned to the attractor. If there are two attractors, proliferation and differ-

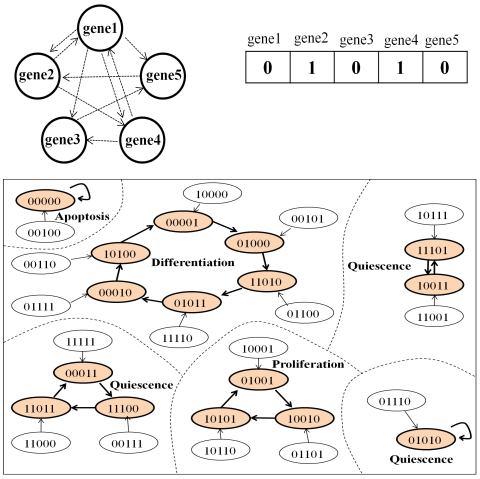


Figure 1: Schematic diagrams of a GRN and its state space. Top: A GRN (= RBN) with five nodes (genes) under $K = 2$ (16 nodes were used in actual simulations). Each node can be either ON (1) or OFF (0). Bottom: State space of the GRN with four randomly assigned cell fates. The state space consists of $2^5 = 32$ configurations and transitions among them. Highlighted are attractors, and the boundaries of their basins of attraction are shown by dashed lines.

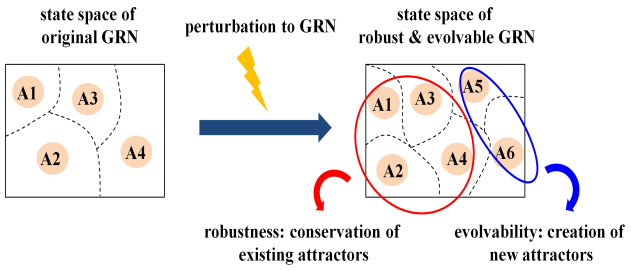


Figure 2: Schematic diagrams illustrating the concept of robust and evolvable GRN.

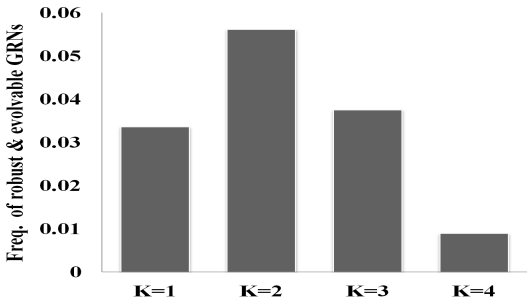


Figure 3: Probability of generating robust and evolvable GRNs per group ($K = 1, 2, 3, 4$).

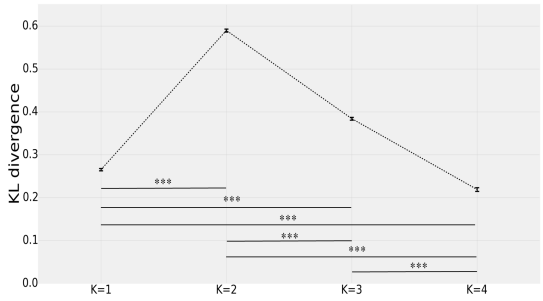


Figure 4: Comparison of the mean KL divergence between groups, where all the simulated patterns are obtained from morphogenetic systems with robust and evolable GRNs. (Kruskal-Wallis test: $p < 2.2^{-16}$, Nemenyi test (post-hoc): *** $p < 0.001$).

entiation are randomly assigned to the two attractors. Similarly, if there are three, proliferation, differentiation, and apoptosis are randomly assigned to those attractors. If there are four or more attractors, proliferation, differentiation, and apoptosis are randomly assigned to three attractors and quiescence is assigned to the rest of the attractors. (Fig. 1 bottom).

In the present study, the GRN of the seed cell is perturbed by adding, deleting, or switching one regulatory link. If GRNs conserve their existing attractors and create new attractors at the same time against the perturbations, the GRNs are considered robust and evolvable (Fig. 2) (Aldana et al., 2007). The robust and evolvable GRNs are evolutionarily meaningful because their robustness and evolvability are two essential properties of biological systems for evolution (Stelling et al., 2004). We performed 10,000 independent simulation runs for each value of K (from 1 to 4). We found that robust and evolvable GRNs were generated with the highest probability against the perturbations for K=2 (Fig. 3).

Focusing on morphologies acquired from morphogenetic systems having robust and evolvable GRNs, we measured the Kullback-Leibler (KL) divergence between pairwise particle distance distributions of a simulated pattern and a random pattern to detect nontrivial morphologies based on Sayama and Wong's approach (Sayama et al., 2011). Specifically, a pair of coordinates of cells were randomly sampled 10,000 times to generate an approximate pairwise particle distance distribution, first from the simulated pattern, then from a randomly distributed pattern made of the same number of cells within the same spatial dimensions.

To compare the means of the KL divergence for K=1, 2, 3, 4, we calculated the averages through 1,000 bootstrap iterations from the KL divergence values of robust and evolvable GRNs for each value of K. We found that the KL divergence was highest for K=2, which means that nontrivial morphologies were still generated most frequently after adding perturbations to GRNs (Fig. 4). Fig. 5 shows the examples of nontrivial morphologies for $K = 2$. This finding implies that the criticality of GRNs facilitates the formation of nontrivial morphologies in GRN-based morphogenetic systems, even in the presence of evolutionary perturbations.

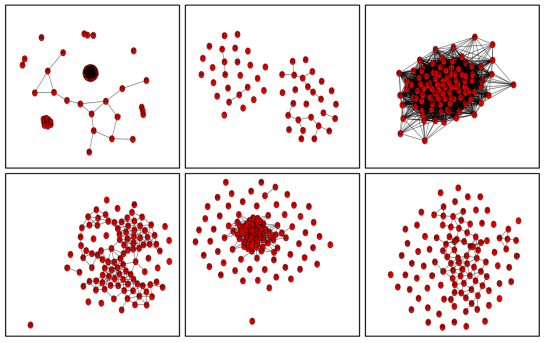


Figure 5: Examples of nontrivial morphologies for $K = 2$.

This work was supported by NSF grant No. 1319152 and by a travel support from the Department of Systems Science and Industrial Engineering at Binghamton University.

References

Aldana, M. et al. (2007). Robustness and evolvability in genetic regulatory networks. *J. Theor. Biol.*, 245(3):433–448.

Chang, H. H. et al. (2008). Transcriptome-wide noise controls lineage choice in mammalian progenitor cells. *Nature*, 453(7194):544–547.

Kauffman, S. A. (1969). Metabolic stability and epigenesis in randomly constructed genetic nets. *J. Theor. Biol.*, 22(3):437–467.

Kim, H. et al. (2017). Criticality of gene regulatory networks and the resulting morphogenesis. *In Proc. of the 14th ECAL, in press*.

Sayama, H. et al. (2011). Quantifying evolutionary dynamics of swarm chemistry. *ECAL*, pages 729–730.

Stelling, J. et al. (2004). Robustness of cellular functions. *Cell*, 118(6):675–685.

An Autopoietic Machine to Achieve Pure Self-Organization

Rima Hiouani[1], Sylvain Cussat-Blanc[2], NourEddine Djedi[1], Yves Duthen[2]

[1]Biskra University, LESIA Laboratory; BP 145 R.P.07000, Biskra, Algeria.
[2]University of Toulouse, IRIT – CNRS UMR 5505
rima.hiouani@gmail.com

Abstract

Many natural systems such as cells, chemical compounds, galaxies, organisms, and planets show self-organized construction. The theory of *autopoiesis* proposed to define the universal self-organization of living systems, where each natural system builds and regulates itself in an organizational "closure". Taking inspiration from these processes, Morphogenetic Engineering tries to reach the capacity and mechanisms of natural systems in self-creating and self-organization. In this work, we used concepts from the autopoeitic theory to create a machine able to display individual building and organization like an artificial embryogenesis process. In this paper, we discuss how our system is an autopoietic machine. Using this theory, our model shows that each entity (cell, tissue, organ) is an autopoietic machine, which creates and organizes itself as a cyclic network of production of components and exhibits self-organization.

Maturana and Varela believed that, although living systems are diverse, they still share a common organization which we implicitly call "living". They also claim that some biological processes such as reproduction and evolution are secondary to the establishment of this unitary organization. To the question "what is the necessary and sufficient organization for a given system to become a living unity?", they often argued that living organization is characterized by specifying the network of interactions of components to form the living system as a whole "unity". On this basis, they proposed the concept of "autopoiesis" to define the system that produces itself, which means self-production or self-creation. They affirmed that the autopoietic mechanisms of self-production are crucial in understanding both the diversity and the uniqueness of the living system. In short, autopoiesis is used to explain the basic characteristic of living systems, and can be viewed as a particular way of universal self-organization [2]. Maturana and Varela describe an autopoietic machine as "a machine organized (defined as a unity) as a network of processes of production (transformation and destruction) of components that produce the components which: (i) through their interactions and transformations continuously regenerate and realize the network of processes (relations) that produced them and (ii) constitute it (the machine) as a concrete unity in the space in which they (the components) exist by specifying the topological domain of its realization as such a network." [3].

Even though the theory of autopoietic systems was originally proposed in biology, this did not prevent to apply it in different fields such as sociology and the nature of creativity [4].

In this work, we use an interpretation of the autopoietic theory in one of its most complex processes studied in artificial life, that is "artificial embryogenesis", which combines self-organization and complex architecture. Because of the complexity of its natural equivalent, "multicellular development", biologists realized that multiple elements such as mechanical forces between cells, coupled with morphogen diffusion and gene regulation affect this process without fully understanding how these work together. Simulating these complex processes is a long journey which scientists only started. However, we can take inspiration from these mechanisms in order to produce system with equivalent capabilities and organization to build better and more reliable systems.

We choose to use the theory of autopoietic machines in the organization of our system, because they define the organization of a living system. However, this theory was successfully applied to a different level of organization in our system (MLAS) (for more details see [5]).

Our MLAS has several levels of organization: cell level, tissue level, and organ level. Fig.1a presents these different levels. At the beginning, the system is composed of a single morphogen in organ level which concentration is given by the "organ state" (Fig. 1a-1). In addition to this morphogen, the system has one inactive stem cell with irregular artificial GRN and chromosome of functions (Fig. 1a-2).

With this global function of the system (organ state) and the stem cell, the MLAS network organizes and creates itself to reach the second chromosome of the system (chromosome of fitness levels Fig. 1a-3).

This fitness chromosome provides a threshold for each level of organization to reach by the corresponding individual (organs, tissues or cells). Each individual in the system is an autopoietic machine in its process of production and regulation. They create and regulate themselves in an organizational closure by a network of component production. These components can interact together and even catalyse themselves (directly or indirectly). This cyclic production network shows the capacity of individuals to organize and create themselves without any external driver from the environment.

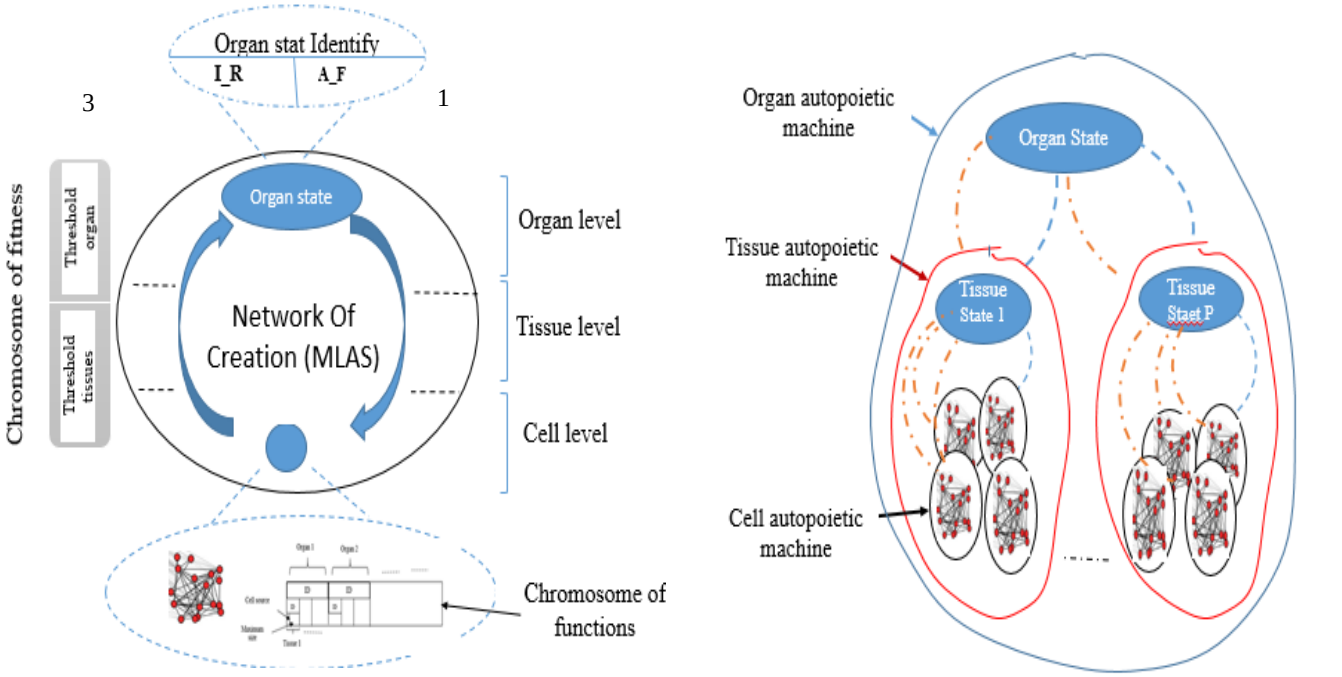


Figure 1: (a) The MLAS and its initial components. (b) The different autopoietic machines in the system and their components.

As presented in (Fig. 1b), the higher level of the system, the "organ autopoietic machine", begins with the first node "Organ state". The components of this individual, the tissues, are on a sub level. Tissues are themselves other autopoietic machines, with a production network and components to create themselves. Components in the tissues are cells, which constitute another autopoietic machine. The production network in cells is an artificial gene regulatory network (GRN), and its components are the actions executed by the GRN, Which regenerate and regulate itself, too. The cell autopoietic machine is self-created, meaning that cells can create and regulate their own pathway of actions and history.

The interactions between the production network and the components in the autopoietic machine lead the individuals to create and regulate themselves in an organizational "closure", which achieves to self-organization throughout the system.

Conclusion

Following Morphogenetic Engineering [1], we try to export from natural systems their abilities to self-create and self-organize. The autopoietic machine is one of the most important theories explaining how natural systems can create and organize themselves. Our ASML model is at the intersection between these two fields, where each individual is an autopoietic machine showing capacities for self-creation and organization.

References

[1] Doursat, R., Sayama, H. & Michel, O. (2013) A review of morphogenetic engineering. Natural Computing 12(2): 517-535.

[2] Fuchs, Christian. and Hofkirchner, Wolfgang. (2009). Autopoiesis and critical social systems theory. 111-129. Bingley, U.K Emerald

[3] Maturana, H. R., & Varela, F. J. (1991). Autopoiesis and cognition: The realization of the living (Vol. 42). Springer Science & Business Media.4.

[4] Iba, T. (2010). An autopoietic systems theory for creativity. Procedia-social and behavioral Sciences, 2(4), 6610-6625.

[5] Hiouani, R.,Cussat-Blanc , S., Djedi, N., Duthen,Y., " A Multi-Level Autopoietic System to Develop an artificial Organism." Late Breaking (ECAL 2017) accepted