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THE ROLE OF EMERGENCE THAT IS OPERATING WITHIN MASSIVELY-PARALLEL COMPUTING ENVIRONMENTS IN UNDERSTANDING BIOLOGICAL SYSTEMS FUNCTIONING

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ABSTRACT

This contribution serves as a brief primer in understanding emergence in not only biological systems. The latest progress that has been reached in the understanding of the operation of massively-parallel computing environments is revealing the critical importance of the decoding of multi-scale emergent systems that are operating within biological systems in all of their functional scales. Recently studied artificial emergent systems demonstrated unexpected insights into the capabilities of biological systems in their ability to recreate themselves and their adaptation to ever-changing environments. Simultaneously, it is a well-known fact that biological systems are capable of keeping their functionality and adapting to ever-changing conditions while their computing substrate is being *continuously repaired and even replaced. These observations are converging towards research, which will be partially reviewed in this contribution, that is decoding the very mathematical principles of error-resilient computations existing within massively-parallel computing environments. As already said, the prominent example is provided by all living systems. In this context, ecosystems could be understood within this framework as goal-oriented systems operating above the ever-changing substrate made of all species living within them.*

Keywords: *Emergence, emergent information processing, massively-parallel computation, cellular automaton, self-organization, error-resilience.*

1. Introduction

The current research of biological systems that is utilizing computational and theoretical tools based on massively-parallel methods is becoming quite broad and deep. Hence, it is desirable to have a brief primer that will help newcomers navigate this entire research area easily and effectively. This contribution aimed at spreading the knowledge about the latest developments in computational descriptions of complex systems, emergence, and self-organization, and it focuses on biological applications that are, as well, important in the understanding of ecosystems' functioning.

Computational and purely theoretical research on massively-parallel computations turned out to be very useful in our understanding of not only physics but also chemistry, bio-chemistry, and biology at all of their levels. The review [1] contains complete introductory information that is accompanied by many useful citations and links. The correct understanding of the design principles of massive-parallel computations, which is beyond the scope of this contribution, is critical to a deep understanding of the following text and can be found in [2, 3, 1, 4].

The contemporary computational research in complex systems (CS)— that is facilitated by utilization of massively-parallel computational systems such as cellular automata [2] and agent-based modeling [3]—where emergence [4], self-organization, self-repair, self-replication, and other phenomena are simulated and studied, is undergoing a surprisingly fast development; see [1, 5, 6, 7] and references there.

One of the frontiers of CS research is focusing on the study of massively-parallel systems that are represented by cellular automata (CA). Very crudely said (details and links in [2, 1]) a cellular automaton is a lattice of elements (in our case squares) that is completely covering the given region (a rectangular area). Each element, called a cell, has defined a list of neighbors called a neighborhood that is identical for all cells. The state of a given cell is updated according to a micro-evolution rule that operates above the cell's neighborhood (all animations presented in this text are made in this way; see more [5]).

2. Biologically Observed Massively-Parallel Systems

Surprisingly, when one looks at biological systems as on massively-parallel computing (MPC) systems, suddenly, it becomes obvious that many, if not all, phenomena observed within them can be traced, to a certain extent, back to MPCs. Examples are always the best; see the following list. A motivating MPC simulation is present in Figure 2.

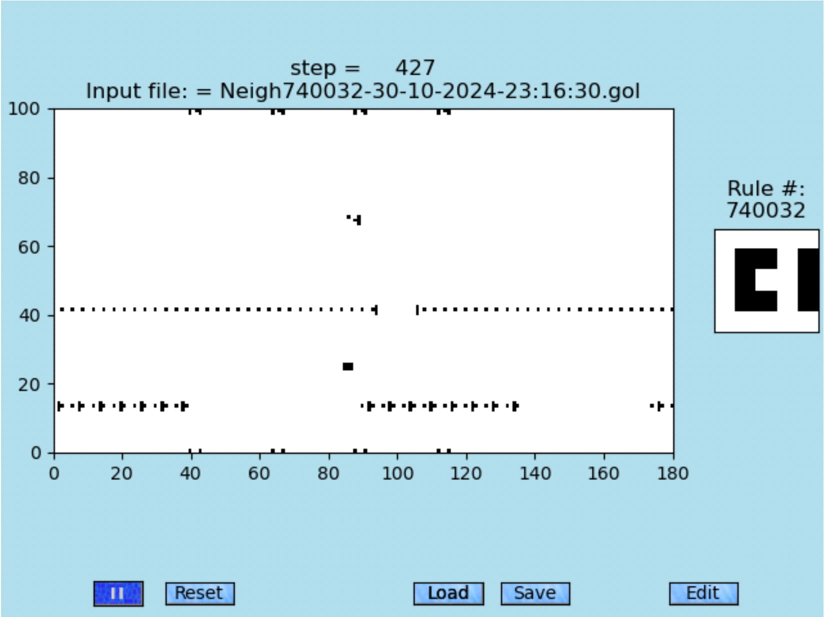


Figure 1. *An emergent solution to a synchronization problem (in 3 different stages: Y-axis of 0, 14, 42) that is arising completely from a majority of random initial conditions; see details in [8, 5] (applications in the text).*

Amoeba − > Fruiting Body: Amoebas of species Dictyostelium discoideum [9] are living their lives as single cells. Only, when food becomes scarce, they gather and create multicellular body with a fruiting body from which spores are spread. In such a case, it is possible to speak about the proto-morphology of fruiting bodies: the whole is built from cells using a rudimentary signaling network.

Cells − > Morphology: Morphological growth models are undergoing substantial progress in recent years [10, 11, 12]. The role of electric potential of cellular membranes in morphological growth, disease, or even cancer treatment [13] is being intensively researched.

Caterpillar − > Butterfly: A surprisingly complex process is observed in the transition between different developmental stages in insects, e.g., moths [14]. The previous developmental stage of completely disassembling itself and creating the next one. Yet, it is observed that some information can be retained through several stages even into adulthood.

Insect − > Swarms: Wasps, bees, fireflies, ants, and termites are representing the prominent examples of swarm behavior [15, 16], which create an emergent system from and through interactions of 'dumb' single insect entities. Similar processes operate in bird flocks (simulated by boids), fish schools, and animal herds. This system is expressing behavior(s) not encoded in single entities: it emerges from their mutual interactions.

Rhizome − > mushrooms: Rhizome is creating a fairly exended and mutually interwoven network of fibers that, when the time is right, creates fruiting bodies in the form of mushrooms [17]. In such a way, the rhizome is creating unseen highways of forests that are hidden to the sight of uninformed observers.

Trees + Rhizome − > Forest: Research in forestry is gradually uncovering intricate cooperation among trees in forests via rhizome. Nutrients, minerals, and even water are delivered among trees of the same species and even of different ones in such ways [18].

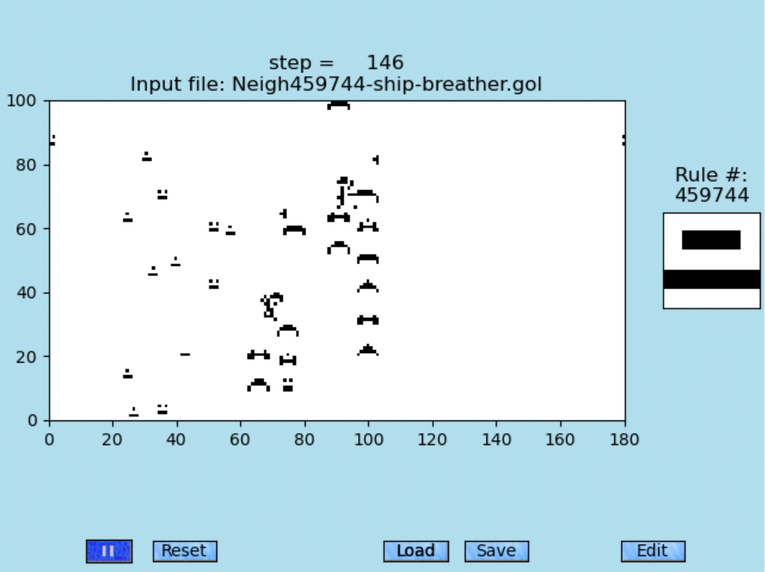


Figure 2. *Two-level emergent system, called a 'ship breeding ships,' [1] that is spontaneously arising from any initial condition. It can be easily 'implemented' in a biological system; see the animation link in [1, 5].*

3. Similarities Between Biological and Emergent Information Processing Systems

A striking similarity between emergents observed within physical, chemical, biochemical, and biological systems and those originating in simulated emergent information processing [1, 6, 7] is opening new horizons in research. The best way to explain this similarity lies in the use of pictures and even better animations [5].

Figure 2 is displaying a spontaneously arising two-level emergent system from any random condition [1, 5]. This emergent system is encoded only by the specific, applied neighborhood and totalistic micro-evolution rule. Figure 3 depicts emergents that might be hiding within fuzzy environments [1, 19, 5] without us even noticing them. Finally, Figure 4 displays emergent structures that are error-resilient, details in [1, 5] (animations [5] are important).

4. Prospective Directions in Theoretical Biological Research with Focuss on Ecosystems

The above-provided simplified description of emergent information processing, including the cited literature, leads us to an obvious observation. Emergent information processing—starting with the level of chemistry, continuing all the way up to the level of bodies, and ending with the level of ecosystems—has a surprisingly high expressivity in the description of biological systems.

Hence, it was decided to disseminate the basic concepts of this novel and promising computational approach among biologists and ecologists in the form of this easy-to-follow text with a rich citation apparatus and links to animations [5] that are critical in understanding those concepts by non-specialists. The author of this contribution is prepared to help everyone who is seriously interested in this subject of research to dive quickly into it. Additionally, there is an accessible open-source Python GoL-N24 program [7] that allows everyone to run their own simulations.

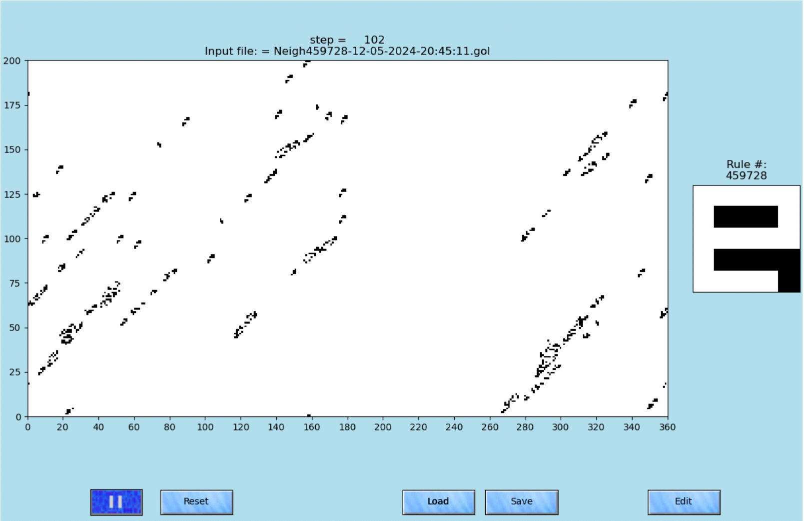
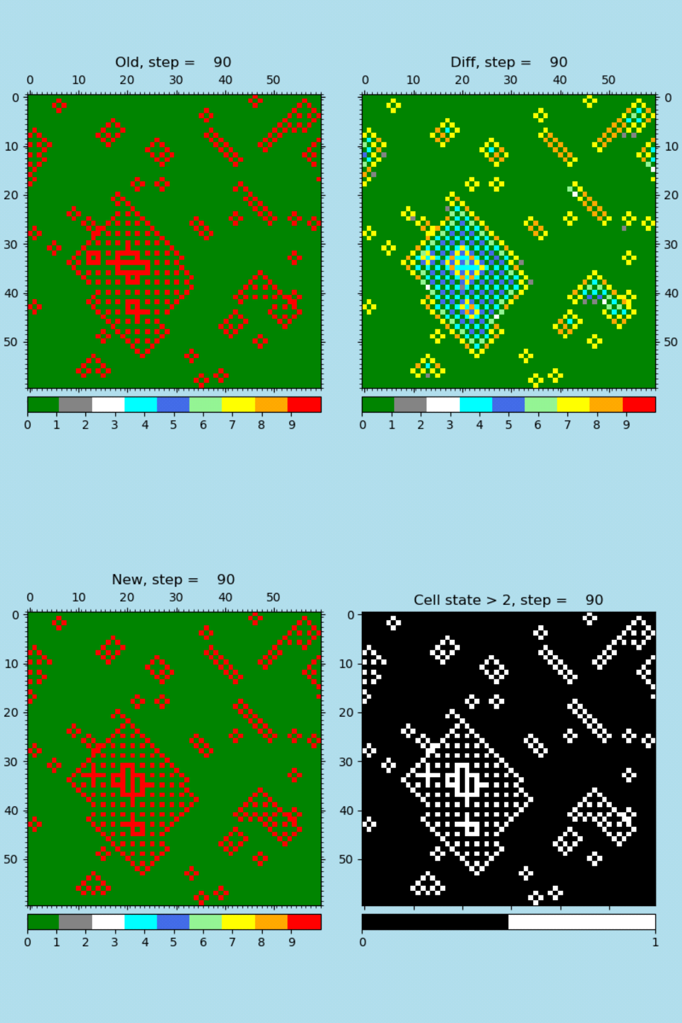


Figure 3. *Fuzzy emergents that are almost impossible to discern from random backgrounds [1, 19]; see the animation link in [1, 19, 5].*

It is a well-known fact that biological systems are capable of keeping their functionality and adapting to ever-changing conditions while their computing substrate is being continuously repaired and even replaced. Such capability was computationally demonstrated; see Figure 4.

Emergent information processing has a promising potential to describe living systems as ever-changing massively-parallel computational systems where each systemic part is solving its own ’things’ to keep itself alive, and the global behavior of the system emerges from and throughout interactions among its systemic parts.



Prospective models of living systems and ecosystems based on emergent information processing within massively-parallel computational systems could give us a tool that will eventually enable ecologists to build spatially realistic models of ecosystems and that will be possible to quantitatively compare with real ecosystems.

Figure 4. *Error-resilient emergent structures [1, 6] rising up from randomness; see the animations [1, 5].*

Conclusions

The text serves simultaneously as an invitation and starting package to carry on ones's own research on emergent information processing applied to biological systems. This is enabled by a unique combination of computational results with known biological systems in the way that enables an easy and quick dive into the roots
of this methodology.

The best way to explain emergent information processing is by the presentation of animations and snapshots of real simulations that are worth thousands of words. Animations are cited in the video-database and cited within publications dealing with emergent information processing. Everyone interested in emergence is welcome to pursue his or her own explorations of emergence within biology.

Supplementary materials

Open-source, Python program GoL-N24 [7] (the current version 1.4) and regularly updated Video-Database of observed emergents [5] with links to animations and publications.

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Abbreviations

CS - complex system
MPC - massively-parallel computations
SO - self-organization
EM - emergence
EIP - emergent information processing
CA - cellular automaton
GoL - 'Game of Life' cellular automaton
ABM - agent-based modeling

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