

A Framework for Complex Adaptive Systems

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ABSTRACT

In this paper, we provide a general purpose simulation framework for complex adaptive systems. Our framework will deal with a number of important criteria including self-organization, emergence, and others. We then show that the framework can capture the common underlying structure of complex adaptive systems through demonstrating its application in specific biological domains.

KEY WORDS

Complex Adaptive System (CAS), Multi-Agent System (MAS), Emergence, Self-Organization, Adaptivity

1. Introduction

A Complex Adaptive System (CAS) [1] is what the name suggests: a system consisting of large numbers of interacting adaptive compartments. These systems are dynamical (changes over the time) and nonlinear, in the sense that the behavior of a complex system cannot be obtained through simply summing up its parts (individuals). CASs are prevalent throughout the sciences and engineering, and determining a framework for depiction and simulation is a particularly important research endeavor. In this paper, we will present such a framework and its application specific to biological domains.

To begin, there are two important properties of CASs (beyond *adaptivity*) that must be considered in any framework. These are: *emergence*, and *self-organization*. Clearly, a system can perform a completely different job than that of a single individual. For example, in autocrine signaling in cell systems [2], a group of aggregated cells can generate a much higher concentration of a hormone than a single standing cell, and then induce a different reaction that needs high concentration thresholds. Emergence is used to indicate this kind of behavior.

Moreover, CAS is also labeled with self-organization, or a rising order of statistical complexity [3] without external supervision. Generally speaking, self-organization includes self-rising spatial/temporal/functional orders of a system behavior. As an example, consider the developmental process of an embryo, in which an agglomeration of cells evolves into an elaborating body structure at a well-controlled time course.

We note that the emergence property in CAS requires a very different approach than that of *reductionism*, which models the system as a whole, or models a single element. For example, reductionists may treat a multicellular organism as a continuous elastic solid or visco-elastic fluid, or just

model a single cell and make replicas in order to model multicellular properties. On the other hand, *emergentism* holds the belief that systematic behavior cannot be simply scaled from individual behavior. Naturally, emergentism induces a higher requirement on computational needs. One way in which to mitigate this may be to take a layered viewpoint of a complex system, decomposing it into multiple levels [4]. An obvious example is multi-scale biological research. Consider the area of ecology which focuses on the distributions and interactions of living organisms in their environments. Histology and anatomy operates on tissue and organ levels, cell biology studies cell cycles, organelles and other physiological properties of a cell, molecular biology, genetics and biochemistry care for the interactions and functions of macromolecules, such as DNA, proteins and other polymers inside a cell. In such a layered arrangement, lower level systems provide building blocks for upper level systems, and simplified models are used to capture the properties of lower level systems. The problem is in how we model the behaviors of lower level systems in a meaningful and efficient way. To solve this problem, we need to understand the significant system behaviors and their relationship with individual behaviors to simplify the individual model at an appropriate level.

As discussed above, self-organization is another important property of a CAS. The robustness of self-organization comes from adaptivity [5], which is described as “a change in the environment may influence the same system to generate a different task, without any change in the behavioural characteristics of its constituents” [6]. This type of adaptivity can help the system against fluctuations in environment so that self-organization can evolve stably. Furthermore, the rising order of a system indicates the rising *historical memory*, which is defined as the rising statistical complexity [3]. Thus, self-organization can be viewed as a process of increasing memory. We consider that this induces another type of adaptivity, which contains *memorial function* and can transfer transient events to long term effects. All in all, the self-organization phenomena are results of adaptivity.

Adaptivity should be captured by the individual model. It is not appropriate to model the adaptivity directly at the system level due to the decentralized control characteristic of a CAS. Consequently, we can derive the minimum set to build up the individual model: a module for short term adaptivity,

which helps maintain homeostasis, and a module for long term adaptivity, which remember transient events and generate effects in the future.

Clearly, designing a general framework imbued with these complicated characteristics is non-trivial. In this paper, we propose an agent-based modeling framework for CAS simulation. We will analyze and demonstrate how to address the issues discussed above. The remainder of the paper is organized as follows. Section 2 provides an overview on current work on CAS modeling and multi-agent systems. Section 3 presents our agent-based modeling framework. Section 4 provides an application in biology, illustrating how these complex adaptive systems fit into our framework. Conclusion and remarks are given in Section 5.

2. Background and Related work

In this section, we provide a brief overview of existing approaches, as well as, background material needed for the presentation of our framework.

2.1 Models employing Reductionism

Encouraged by the fact that many complex phenomena can be reduced into basic physical dynamics and chemical kinetics, reductionists tried to model complex adaptive systems using Partial Differential Equations (PDEs) for such basic physics and chemical reactions. For example, in modeling a multicellular organism, they treat it as a as a continuous elastic solid or visco-elastic fluid [7, 8]. Those models are efficient in calculating the continuous parameters of physical and chemical dynamics, but simply ignored the adaptivity of cells and local interactions. Another type of reductionist approaches only capture actions at an individual level, and try to derive the collective behaviors via simply scaling the individual behaviors. For example, some researchers provided a detailed single cell model [9] and work on the assumption that systematic properties can be obtained through making replicas.

2.2 Models employing Emergentism

Emergentism requires modeling individuals and their interaction. As such, an interaction model and an individual model would be needed in simulation. In this section, we will give brief historic overviews on cellular automata and multi-agent systems, which focus on interaction model and/or individual models.

2.2.1 Cellular Automata

As we mentioned above, a CAS is first a dynamical system, and it is critical to model the dynamical properties of interactions to perform a realistic simulation. That is, the interaction model needs to incorporate the parameters describing when and how strong the interactions are. Cellular Automata [10], has been widely used in this field. It is a discrete model on both time-scale and space-scale. It is defined on a lattice, in which each site has a finite number of states. It evolves with discrete time steps, in which each site will be updated once every step. The interactions happen between neighboring sites and are defined by the local rules. CA models are efficient to model large quantities of interactions with their dynamical properties at very low cost. However, it is not strong enough to model the complex interaction patterns, especially for heterogeneous interactions. For example, cells interact through chemical signals in a multicellular organism. Chemical signals can pass through channels that exist between contacting cells or diffuse in surrounding environment of cells. The two types of interactions happen in different distance scales, which pose difficulty in setting the lattice size of a Cellular Automata. Too big a lattice size would fail to model the contact-dependent chemical exchanges. Too small a lattice size would require the neighborhood to cover too many lattice sites, destroying the efficiency of implementation of CA model.

We note that the CA model has served as the basis of many simulations for complex adaptive systems. Most of them avoid the limitation of CA model through modeling homogeneous interaction patterns. However, we need a more flexible interaction paradigm for a more realistic simulation.

2.2.2 Agent-Based Model

The individual model in CAS simulation can be and is referred as agent-based model. The name of agent has various meanings in different areas. We limit this meaning to the computing area to a software component. It is distinguished from other software components from its autonomy [11], which implies an agent has control on its own behavior.

Conceptually, agent-based models were brought into complex system research by John Conway, who constructed the well-known Game of Life [12]. Conway used very simple rules to describe his agents, which only have two states: live and dead. Agents change their own states according to the

states of their neighboring agents and there is a direct mapping from the inputs (senses) of agents and outputs (actions) of agents. This type of agent is called a “reflex agent” and is efficient in the sense that large number of agents can be created and operated with limited computational resource, and has been used for many CAS simulations [13, 14]. Reflex agent is an efficient individual model, but is oversimplified. It fails to capture the adaptivity, which is critical to self-organization process.

More complex agent-based models have been developed with the term “rational agent” [15]. A typical model is a Belief-Desire-Intention (BDI) agent model [16]. Rational agent models emphasize the rationality of agent. It has an internal “world model”, which represents its perception on the whole system, and uses predefined goals or utility to coordinate the agents’ behaviors. Rational agent is useful in many areas, such as simulation for cognitive behaviors, data mining and autonomous e-commerce software. However, it is not efficient to employ rational agents in CAS simulation if we consider the number of individuals inside a CAS. It may also be cumbersome to map the conceptions such as the “desire” and “intention” to an individual such as a cell.

Therefore, we need an agent-based model that is both efficient and meaningful. We need to simplify the individual model at an appropriate level so that we can obtain a general basis for realistic CAS simulations.

3. Our Multi-Agent System Framework

Through analyzing the core properties of CAS and their relationships, we have come to the conclusion that a CAS model should include two sub-models: individual model and interaction model. The individual model should capture adaptivity, while the interaction model should provide mechanisms to parameterize the dynamical properties of interactions in a flexible way. These conditions make up the minimum set for a CAS simulation, so our MAS framework is based on them.

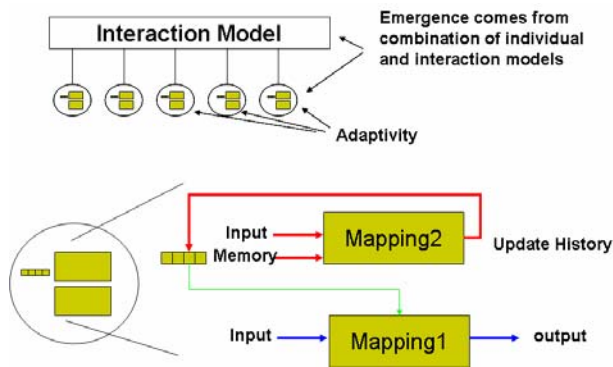


Figure 1: MAS Framework for CAS Simulation

3.1 Individual Model

As we discussed above, the individual model is used to simplify the lower level system into the building blocks of the upper level system. It is important to ignore irrelevant details and capture the key issues, in particular two types of adaptivity. Short term adaptivity is defined as the ability to maintain the homeostasis (dynamic equilibrium in an open system, critical to the system function, especially for biology), and long term adaptivity is defined as the ability to learn from experience. ‘Short’ and ‘long’ implies the system can be divided into a variable part and a persistent part, as shown in Figure 1 as mapping 1 and mapping 2, respectively.

Short term adaptivity is achieved through a negative feedback loop. Many physical processes, especially biological processes are maintained through negative feedback. For example, a cell can maintain its energy level through changing the level of enzyme and then the metabolism speed. In this process the difference between current energy level and normal level is linked back to the process of energy generation via adjusting enzyme activation. Short term adaptivity helps to reduce much of the detail in modeling individual behavior since we can simplify the continuous states into several discrete ones. The sub-module for short term adaptivity is showed in Figure 1 as mapping 1. The input and output are directly linked to the outside world.

Long term adaptivity is distinguished from short term adaptivity not only by the time scale, but also by the memorial function. An individual who has long term adaptivity can remember historic events and generate effects for the future. Thus, a memory module is associated with long term adaptivity while short term adaptivity is “memoryless”. The sub-module for long term adaptivity is showed in Figure 1 as mapping 2. The input is from a memory module

and the outside world (or through the short-term adaptivity module). The output is directed to the memory module for updates. The memory module is connected to the short term module to determine its functionality.

The memory module gives hints for self-organization, which can be viewed as a rising order process. Order can be thought of as the statistical complexity, which is treated as memory by Shalizi [3]. Thus, from this, one should see the pattern formation at system level, while the memory accumulation is in individuals.

3.2 Interaction Model

For the interaction model, we have discussed the CA paradigm, which is efficient but not sufficiently capable. In our framework, we propose an enhanced Asynchronous Message Passing (AMP) paradigm. We believe it provides enough flexibility for different CAS simulations and can be implemented efficiently. The problem is in how to add dynamical properties (time/strength) to message passing. In this section, we describe the message format and routing strategy to address this problem.

3.2.1 Message Format

To incorporate dynamical properties of interactions, one possibility we present is to add three parameters to a regular message: T (sending time), P (original power) and S (source coordinate). These parameters are filled by the sender when the message object is sent out. The strength of received message can be calculated by the receiver at the message arrival event. The calculation is not difficult as we know the original power and distance between sender and receiver. Thus, only the routing problem is left: who will be the receiver and when the message should arrive.

3.2.2 Routing Strategy

In the original AMP, message routing is determined only by communication pattern. In the new paradigm, message routing is determined by both dynamic properties (time/strength) and communication pattern.

There are two basic communication patterns in AMP: Point-2-Point (P2P) and Publish/Subscribe (Pub/Sub). Both patterns employ message brokers (message queues) as mediators to store/forward message. The work process is as follows. A sender pushes a message to a broker and continues running without waiting. The broker calculates the

destination agent and pushes the message to it (or to a remote message broker if the destination agent is located in a remote machine). The destination agent receives the message passively in the sense of being invoked by the message arrival event. To implement the new paradigm, what we need change is how broker calculate the destination and when it pushes out the message.

In P2P pattern, the destination agent is identical. In Pub/Sub pattern, destination should be calculated according to the strength of message and a threshold to determine if the message should be dropped. We need another parameter in the interaction model to define the threshold and a function to describe how messages propagate.

To deliver the message at the correct simulation time, we can consider employing a time-priority queue inside (both P2P and Pub/Sub) message brokers as a possibility. Compared with a regular queue, the time-priority queue does not follow a FIFO strategy but dequeues items with the smallest time stamp. The time here refers to the delivering time, which is derived from the sending time and how long the message propagation takes.

3.3 Summary

A new multi-agent system framework was proposed in this section, including an individual model and an interaction model. The agent template should incorporate the individual model and interfaces (the communication primitives for P2P and Pub/Sub communication patterns) to the interaction model. The multi-agent platform should provide a message service, which we have provided possible methods above. Physical modelers should provide specified definitions for mapping 1, mapping 2 and configuration for memorial modules. In addition, they should also provide the propagation function and set thresholds for message passing for the interaction model.

4. Application

In this section, we will demonstrate feasibility of our framework with an application in biology. We will work as a physical modeler, showing the process to fit the biological application into our framework. We note that we have discussed components of modeling in [17][18].

4.1 Simulating Developmental Process of Multicellular Organism

Development process of multicellular organisms, especially embryo development is one of most fascinating phenomena in nature, well formulated in structure/function with strict timeline. Scientists believe the secret is coded in DNA sequences. However, DNA sequences only directly determine the function of a cell. How the system behavior (multicellular development) relates to the individual behavior (cell functions) is still a question far from being solved. In this section, we will see how to utilize our framework to build up a simulation for the development process of multicellular organisms.

The rest of this section is organized in following way: we will analyze the cells' behavior to define their adaptivity and interaction. We then will set up the individual (cell agent) model and the interaction (cell interaction) model based on our framework.

4.2 Several Facts about Cell Behavior

A cell's function can be divided into a persistent part and a variable part. According to Central Dogma in biology [19], "information cannot be transferred from protein to either protein or nucleic acid". Genes can be transcript and then translated into proteins but not the vice versa. Proteins make up the "cell machine" and play all kinds of roles in cell functions, such as enzymes for metabolisms, receptors and mediators for signal transduction. These functions can happen in seconds or milliseconds. On the other hand, genes provide the blueprint for the "cell machine". The transcription and translation determine how genes are expressed. It takes hours or days to change the genes' expression, or the concentrations of proteins because of their long lifetimes. Thus the current function of a cell is a direct result of present proteins while the potential of a cell comes from its genes. We then treat the "cell machine" as the variable part or short term adaptivity module and genes with its expression as the persistent part or long term adaptivity module.

The cell machine (consisting of proteins) does show strong short term adaptivity. For example, a cell can adjust its sensitivity to external signal through deactivation its membrane receptors. This process is coordinated by negative feedback loops [2]. The signal sensitivity adjustment endows cell's ability to detect the signal gradient besides the concentration level. Many important physiological properties (such as chemotaxis) depend on this capability.

As we discussed above, memorial function is critical to long term adaptivity. In fact, memories are provided by positive feedback loops existing in gene expression [2]. In most cases, the change in gene expression is invoked by the external signals, received and mediated by the current proteins. The signal transduction only takes seconds or milliseconds, but the effect will take off in hours or days and can last life long. The different configurations of cells' memories make them behave differently although they share the same DNA copy. Actually, an epidermal cell has the exact same DNA as a nerve cell. Their gene expressions are so different because they experience different events (interactions with other cells and extra-cellular environment) and memorize them in their developmental processes.

Cells interact with each other through chemical or electrical signals, which can be divided into four categories: Contact-dependent, Autocrine/Paracrine, Synaptic and Endocrine.

4.3 Cell Agent Model and Cell Interaction Model

From our discussion above, we can easily fit cell behaviors into an individual model, which we call the cell agent model, shown in Figure 2.

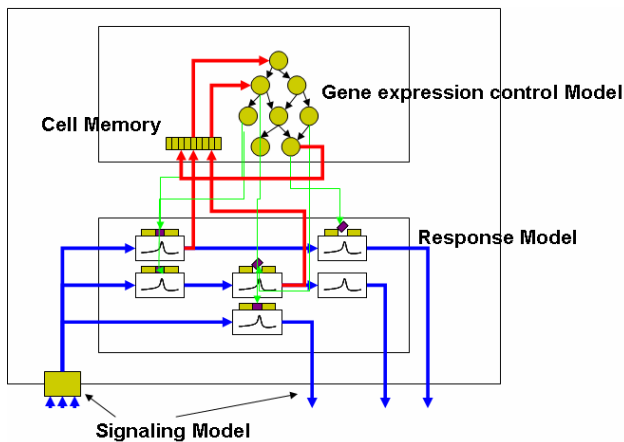


Figure 2: Cell Agent Model

The cell agent model contains four sub-models: Response Model (RM), Gene Expression Control Model (GECM), Singling Model (SM) and Cell Memory (CM). They can be mapped directly to the individual model as following:

- CM ≡ History log
- RM ≡ mapping1
- GECM ≡ mapping2

The cell interaction model is used to capture contact-dependent signaling and autocrine/paracrine signaling processes. They can be easily mapped to the P2P and Pub/Sub communication patterns, which are provided in the message services in our multi-agent platform.

5. Conclusion

In this paper, we provided a MAS based framework for CAS simulation. This framework deals with the important characteristics of CAS through modeling the short term and long term adaptivity of individuals and the dynamics of interactions. It is critical to provide a simplified model for CAS simulations without losing realism. We believe our model abstracts CAS at an appropriate level. We verified our model through demonstrating its use in an application in development biology. We believe the framework is general and can be used to model problems in different domains. In the future, we plan to explore how to set up the formal metrics to measure and quantify the properties of CAS. Thus we can analyze and evaluate experimental results in our framework.

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